SciPy Reference Guide

Release 0.16.0

Written by the SciPy community

July 24, 2015

Release 0.16.0
Date July 24, 2015

SciPy (pronounced “Sigh Pie”) is open-source software for mathematics, science, and engineering.

CHAPTER

ONE

SCIPY TUTORIAL

1.1 Introduction

Contents

SciPy is a collection of mathematical algorithms and convenience functions built on the Numpy extension of Python. It adds significant power to the interactive Python session by providing the user with high-level commands and classes for manipulating and visualizing data. With SciPy an interactive Python session becomes a data-processing and system-prototyping environment rivaling sytems such as MATLAB, IDL, Octave, R-Lab, and SciLab.

The additional benefit of basing SciPy on Python is that this also makes a powerful programming language available for use in developing sophisticated programs and specialized applications. Scientific applications using SciPy benefit from the development of additional modules in numerous niche's of the software landscape by developers across the world. Everything from parallel programming to web and data-base subroutines and classes have been made available to the Python programmer. All of this power is available in addition to the mathematical libraries in SciPy.

This tutorial will acquaint the first-time user of SciPy with some of its most important features. It assumes that the user has already installed the SciPy package. Some general Python facility is also assumed, such as could be acquired by working through the Python distribution's Tutorial. For further introductory help the user is directed to the Numpy documentation.

For brevity and convenience, we will often assume that the main packages (numpy, scipy, and matplotlib) have been imported as:

```
>>> import numpy as np
>>> import matplotlib as mpl
>>> import matplotlib.pyplot as plt
```

These are the import conventions that our community has adopted after discussion on public mailing lists. You will see these conventions used throughout NumPy and SciPy source code and documentation. While we obviously don't require you to follow these conventions in your own code, it is highly recommended.

1.1.1 SciPy Organization

SciPy is organized into subpackages covering different scientific computing domains. These are summarized in the following table:

Subpackage	Description
`cluster`	Clustering algorithms
`constants`	Physical and mathematical constants
`fftpack`	Fast Fourier Transform routines
`integrate`	Integration and ordinary differential equation solvers
`interpolate`	Interpolation and smoothing splines
`io`	Input and Output
`linalg`	Linear algebra
`ndimage`	N-dimensional image processing
`odr`	Orthogonal distance regression
`optimize`	Optimization and root-finding routines
`signal`	Signal processing
`sparse`	Sparse matrices and associated routines
`spatial`	Spatial data structures and algorithms
`special`	Special functions
`stats`	Statistical distributions and functions
`weave`	C/C++ integration

Scipy sub-packages need to be imported separately, for example:

```
>>> from scipy import linalg, optimize
```

Because of their ubiquitousness, some of the functions in these subpackages are also made available in the `scipy` namespace to ease their use in interactive sessions and programs. In addition, many basic array functions from `numpy` are also available at the top-level of the `scipy` package. Before looking at the sub-packages individually, we will first look at some of these common functions.

1.1.2 Finding Documentation

SciPy and NumPy have documentation versions in both HTML and PDF format available at http://docs.scipy.org/, that cover nearly all available functionality. However, this documentation is still work-in-progress and some parts may be incomplete or sparse. As we are a volunteer organization and depend on the community for growth, your participation - everything from providing feedback to improving the documentation and code - is welcome and actively encouraged.

Python's documentation strings are used in SciPy for on-line documentation. There are two methods for reading them and getting help. One is Python's command `help` in the `pydoc` module. Entering this command with no arguments (i.e. `>>> help`) launches an interactive help session that allows searching through the keywords and modules available to all of Python. Secondly, running the command *help(obj)* with an object as the argument displays that object's calling signature, and documentation string.

The pydoc method of `help` is sophisticated but uses a pager to display the text. Sometimes this can interfere with the terminal you are running the interactive session within. A numpy/scipy-specific help system is also available under the command `numpy.info`. The signature and documentation string for the object passed to the `help` command are printed to standard output (or to a writeable object passed as the third argument). The second keyword argument of `numpy.info` defines the maximum width of the line for printing. If a module is passed as the argument to help than a list of the functions and classes defined in that module is printed. For example:

```
>>> np.info(optimize.fmin)
 fmin(func, x0, args=(), xtol=0.0001, ftol=0.0001, maxiter=None, maxfun=None,
      full_output=0, disp=1, retall=0, callback=None)

Minimize a function using the downhill simplex algorithm.

Parameters
----------
func : callable func(x,*args)
```

```
    The objective function to be minimized.
x0 : ndarray
    Initial guess.
args : tuple
    Extra arguments passed to func, i.e. ``f(x,*args)``.
callback : callable
    Called after each iteration, as callback(xk), where xk is the
    current parameter vector.

Returns
-------
xopt : ndarray
    Parameter that minimizes function.
fopt : float
    Value of function at minimum: ``fopt = func(xopt)``.
iter : int
    Number of iterations performed.
funcalls : int
    Number of function calls made.
warnflag : int
    1 : Maximum number of function evaluations made.
    2 : Maximum number of iterations reached.
allvecs : list
    Solution at each iteration.

Other parameters
----------------
xtol : float
    Relative error in xopt acceptable for convergence.
ftol : number
    Relative error in func(xopt) acceptable for convergence.
maxiter : int
    Maximum number of iterations to perform.
maxfun : number
    Maximum number of function evaluations to make.
full_output : bool
    Set to True if fopt and warnflag outputs are desired.
disp : bool
    Set to True to print convergence messages.
retall : bool
    Set to True to return list of solutions at each iteration.

Notes
-----
Uses a Nelder-Mead simplex algorithm to find the minimum of function of
one or more variables.
```

Another useful command is `source`. When given a function written in Python as an argument, it prints out a listing of the source code for that function. This can be helpful in learning about an algorithm or understanding exactly what a function is doing with its arguments. Also don't forget about the Python command `dir` which can be used to look at the namespace of a module or package.

1.2 Basic functions

Contents

1.2.1 Interaction with Numpy

Scipy builds on Numpy, and for all basic array handling needs you can use Numpy functions:

```
>>> import numpy as np
>>> np.some_function()
```

Rather than giving a detailed description of each of these functions (which is available in the Numpy Reference Guide or by using the `help`, `info` and `source` commands), this tutorial will discuss some of the more useful commands which require a little introduction to use to their full potential.

To use functions from some of the Scipy modules, you can do:

```
>>> from scipy import some_module
>>> some_module.some_function()
```

The top level of `scipy` also contains functions from `numpy` and `numpy.lib.scimath`. However, it is better to use them directly from the `numpy` module instead.

Index Tricks

There are some class instances that make special use of the slicing functionality to provide efficient means for array construction. This part will discuss the operation of `np.mgrid` , `np.ogrid` , `np.r_` , and `np.c_` for quickly constructing arrays.

For example, rather than writing something like the following

```
>>> concatenate(([3],[0]*5,arange(-1,1.002,2/9.0)))
```

with the `r_` command one can enter this as

```
>>> r_[3,[0]*5,-1:1:10j]
```

which can ease typing and make for more readable code. Notice how objects are concatenated, and the slicing syntax is (ab)used to construct ranges. The other term that deserves a little explanation is the use of the complex number 10j as the step size in the slicing syntax. This non-standard use allows the number to be interpreted as the number of points to produce in the range rather than as a step size (note we would have used the long integer notation, 10L, but this notation may go away in Python as the integers become unified). This non-standard usage may be unsightly to some, but it gives the user the ability to quickly construct complicated vectors in a very readable fashion. When the number of points is specified in this way, the end- point is inclusive.

The "r" stands for row concatenation because if the objects between commas are 2 dimensional arrays, they are stacked by rows (and thus must have commensurate columns). There is an equivalent command `c_` that stacks 2d arrays by columns but works identically to `r_` for 1d arrays.

Another very useful class instance which makes use of extended slicing notation is the function `mgrid`. In the simplest case, this function can be used to construct 1d ranges as a convenient substitute for arange. It also allows the use of complex-numbers in the step-size to indicate the number of points to place between the (inclusive) end-points. The real purpose of this function however is to produce N, N-d arrays which provide coordinate arrays for an N-dimensional volume. The easiest way to understand this is with an example of its usage:

```
>>> mgrid[0:5,0:5]
array([[[0, 0, 0, 0, 0],
        [1, 1, 1, 1, 1],
        [2, 2, 2, 2, 2],
        [3, 3, 3, 3, 3],
        [4, 4, 4, 4, 4]],
       [[0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4]]])
>>> mgrid[0:5:4j,0:5:4j]
array([[[ 0.    ,  0.    ,  0.    ,  0.    ],
        [ 1.6667,  1.6667,  1.6667,  1.6667],
        [ 3.3333,  3.3333,  3.3333,  3.3333],
        [ 5.    ,  5.    ,  5.    ,  5.    ]],
       [[ 0.    ,  1.6667,  3.3333,  5.    ],
        [ 0.    ,  1.6667,  3.3333,  5.    ],
        [ 0.    ,  1.6667,  3.3333,  5.    ],
        [ 0.    ,  1.6667,  3.3333,  5.    ]]])
```

Having meshed arrays like this is sometimes very useful. However, it is not always needed just to evaluate some N-dimensional function over a grid due to the array-broadcasting rules of Numpy and SciPy. If this is the only purpose for generating a meshgrid, you should instead use the function `ogrid` which generates an "open" grid using `newaxis` judiciously to create N, N-d arrays where only one dimension in each array has length greater than 1. This will save memory and create the same result if the only purpose for the meshgrid is to generate sample points for evaluation of an N-d function.

Shape manipulation

In this category of functions are routines for squeezing out length- one dimensions from N-dimensional arrays, ensuring that an array is at least 1-, 2-, or 3-dimensional, and stacking (concatenating) arrays by rows, columns, and "pages "(in the third dimension). Routines for splitting arrays (roughly the opposite of stacking arrays) are also available.

Polynomials

There are two (interchangeable) ways to deal with 1-d polynomials in SciPy. The first is to use the `poly1d` class from Numpy. This class accepts coefficients or polynomial roots to initialize a polynomial. The polynomial object can then be manipulated in algebraic expressions, integrated, differentiated, and evaluated. It even prints like a polynomial:

```
>>> p = poly1d([3,4,5])
>>> print p
   2
3 x + 4 x + 5
>>> print p*p
   4      3      2
9 x + 24 x + 46 x + 40 x + 25
>>> print p.integ(k=6)
 3     2
x + 2 x + 5 x + 6
```

```
>>> print p.deriv()
6 x + 4
>>> p([4,5])
array([ 69, 100])
```

The other way to handle polynomials is as an array of coefficients with the first element of the array giving the coefficient of the highest power. There are explicit functions to add, subtract, multiply, divide, integrate, differentiate, and evaluate polynomials represented as sequences of coefficients.

Vectorizing functions (vectorize)

One of the features that NumPy provides is a class `vectorize` to convert an ordinary Python function which accepts scalars and returns scalars into a "vectorized-function" with the same broadcasting rules as other Numpy functions (*i.e.* the Universal functions, or ufuncs). For example, suppose you have a Python function named `addsubtract` defined as:

```
>>> def addsubtract(a,b):
...    if a > b:
...        return a - b
...    else:
...        return a + b
```

which defines a function of two scalar variables and returns a scalar result. The class vectorize can be used to "vectorize "this function so that

```
>>> vec_addsubtract = vectorize(addsubtract)
```

returns a function which takes array arguments and returns an array result:

```
>>> vec_addsubtract([0,3,6,9],[1,3,5,7])
array([1, 6, 1, 2])
```

This particular function could have been written in vector form without the use of `vectorize` . But, what if the function you have written is the result of some optimization or integration routine. Such functions can likely only be vectorized using `vectorize.`

Type handling

Note the difference between `np.iscomplex`/`np.isreal` and `np.iscomplexobj`/`np.isrealobj`. The former command is array based and returns byte arrays of ones and zeros providing the result of the element-wise test. The latter command is object based and returns a scalar describing the result of the test on the entire object.

Often it is required to get just the real and/or imaginary part of a complex number. While complex numbers and arrays have attributes that return those values, if one is not sure whether or not the object will be complex-valued, it is better to use the functional forms `np.real` and `np.imag` . These functions succeed for anything that can be turned into a Numpy array. Consider also the function `np.real_if_close` which transforms a complex-valued number with tiny imaginary part into a real number.

Occasionally the need to check whether or not a number is a scalar (Python (long)int, Python float, Python complex, or rank-0 array) occurs in coding. This functionality is provided in the convenient function `np.isscalar` which returns a 1 or a 0.

Finally, ensuring that objects are a certain Numpy type occurs often enough that it has been given a convenient interface in SciPy through the use of the `np.cast` dictionary. The dictionary is keyed by the type it is desired to cast to and the dictionary stores functions to perform the casting. Thus, `np.cast['f'](d)` returns an array of `np.float32` from *d*. This function is also useful as an easy way to get a scalar of a certain type:

```
>>> np.cast['f'](np.pi)
array(3.1415927410125732, dtype=float32)
```

Other useful functions

There are also several other useful functions which should be mentioned. For doing phase processing, the functions `angle`, and `unwrap` are useful. Also, the `linspace` and `logspace` functions return equally spaced samples in a linear or log scale. Finally, it's useful to be aware of the indexing capabilities of Numpy. Mention should be made of the function `select` which extends the functionality of `where` to include multiple conditions and multiple choices. The calling convention is `select(condlist,choicelist,default=0)`. `select` is a vectorized form of the multiple if-statement. It allows rapid construction of a function which returns an array of results based on a list of conditions. Each element of the return array is taken from the array in a `choicelist` corresponding to the first condition in `condlist` that is true. For example

```
>>> x = r_[-2:3]
>>> x
array([-2, -1,  0,  1,  2])
>>> np.select([x > 3, x >= 0],[0,x+2])
array([0, 0, 2, 3, 4])
```

Some additional useful functions can also be found in the module `scipy.misc`. For example the `factorial` and `comb` functions compute $n!$ and $n!/k!(n-k)!$ using either exact integer arithmetic (thanks to Python's Long integer object), or by using floating-point precision and the gamma function. Another function returns a common image used in image processing: `lena`.

Finally, two functions are provided that are useful for approximating derivatives of functions using discrete-differences. The function `central_diff_weights` returns weighting coefficients for an equally-spaced N-point approximation to the derivative of order o. These weights must be multiplied by the function corresponding to these points and the results added to obtain the derivative approximation. This function is intended for use when only samples of the function are avaiable. When the function is an object that can be handed to a routine and evaluated, the function `derivative` can be used to automatically evaluate the object at the correct points to obtain an N-point approximation to the o-th derivative at a given point.

1.3 Special functions (`scipy.special`)

The main feature of the `scipy.special` package is the definition of numerous special functions of mathematical physics. Available functions include airy, elliptic, bessel, gamma, beta, hypergeometric, parabolic cylinder, mathieu, spheroidal wave, struve, and kelvin. There are also some low-level stats functions that are not intended for general use as an easier interface to these functions is provided by the `stats` module. Most of these functions can take array arguments and return array results following the same broadcasting rules as other math functions in Numerical Python. Many of these functions also accept complex numbers as input. For a complete list of the available functions with a one-line description type `>>> help(special)`. Each function also has its own documentation accessible using help. If you don't see a function you need, consider writing it and contributing it to the library. You can write the function in either C, Fortran, or Python. Look in the source code of the library for examples of each of these kinds of functions.

1.3.1 Bessel functions of real order(`jn`, `jn_zeros`)

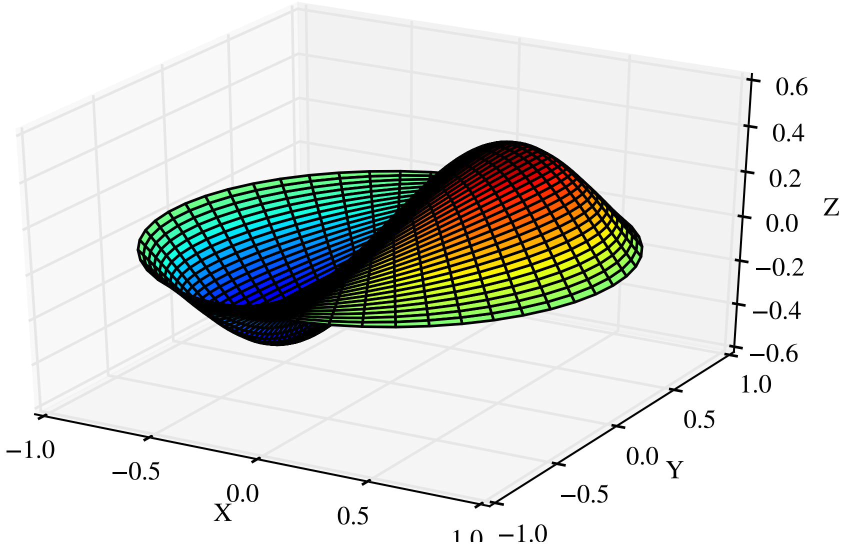
Bessel functions are a family of solutions to Bessel's differential equation with real or complex order alpha:

$$x^2\frac{d^2y}{dx^2}+x\frac{dy}{dx}+(x^2-\alpha^2)y=0$$

Among other uses, these functions arise in wave propagation problems such as the vibrational modes of a thin drum head. Here is an example of a circular drum head anchored at the edge:

```
>>> from scipy import special
>>> def drumhead_height(n, k, distance, angle, t):
...    kth_zero = special.jn_zeros(n, k)[-1]
...    return np.cos(t) * np.cos(n*angle) * special.jn(n, distance*kth_zero)
>>> theta = np.r_[0:2*np.pi:50j]
>>> radius = np.r_[0:1:50j]
>>> x = np.array([r * np.cos(theta) for r in radius])
>>> y = np.array([r * np.sin(theta) for r in radius])
>>> z = np.array([drumhead_height(1, 1, r, theta, 0.5) for r in radius])
```

```
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.mplot3d import Axes3D
>>> from matplotlib import cm
>>> fig = plt.figure()
>>> ax = Axes3D(fig)
>>> ax.plot_surface(x, y, z, rstride=1, cstride=1, cmap=cm.jet)
>>> ax.set_xlabel('X')
>>> ax.set_ylabel('Y')
>>> ax.set_zlabel('Z')
>>> plt.show()
```



1.4 Integration (`scipy.integrate`)

The `scipy.integrate` sub-package provides several integration techniques including an ordinary differential equation integrator. An overview of the module is provided by the help command:

```
>>> help(integrate)
 Methods for Integrating Functions given function object.

   quad          -- General purpose integration.
   dblquad       -- General purpose double integration.
   tplquad       -- General purpose triple integration.
   fixed_quad    -- Integrate func(x) using Gaussian quadrature of order n.
```

```
   quadrature    -- Integrate with given tolerance using Gaussian quadrature.
   romberg       -- Integrate func using Romberg integration.

 Methods for Integrating Functions given fixed samples.

   trapz         -- Use trapezoidal rule to compute integral from samples.
   cumtrapz      -- Use trapezoidal rule to cumulatively compute integral.
   simps         -- Use Simpson's rule to compute integral from samples.
   romb          -- Use Romberg Integration to compute integral from
                    (2**k + 1) evenly-spaced samples.

   See the special module's orthogonal polynomials (special) for Gaussian
      quadrature roots and weights for other weighting factors and regions.

 Interface to numerical integrators of ODE systems.

   odeint        -- General integration of ordinary differential equations.
   ode           -- Integrate ODE using VODE and ZVODE routines.
```

1.4.1 General integration (`quad`)

The function `quad` is provided to integrate a function of one variable between two points. The points can be $\pm\infty$ ($\pm$ `inf`) to indicate infinite limits. For example, suppose you wish to integrate a bessel function `jv(2.5,x)` along the interval $[0, 4.5]$.

$$I = \int_0^{4.5} J_{2.5}(x)\, dx.$$

This could be computed using `quad`:

```
>>> result = integrate.quad(lambda x: special.jv(2.5,x), 0, 4.5)
>>> print result
(1.1178179380783249, 7.8663172481899801e-09)

>>> I = sqrt(2/pi)*(18.0/27*sqrt(2)*cos(4.5)-4.0/27*sqrt(2)*sin(4.5)+
    sqrt(2*pi)*special.fresnel(3/sqrt(pi))[0])
>>> print I
1.117817938088701

>>> print abs(result[0]-I)
1.03761443881e-11
```

The first argument to quad is a "callable" Python object (*i.e* a function, method, or class instance). Notice the use of a lambda- function in this case as the argument. The next two arguments are the limits of integration. The return value is a tuple, with the first element holding the estimated value of the integral and the second element holding an upper bound on the error. Notice, that in this case, the true value of this integral is

$$I = \sqrt{\frac{2}{\pi}}\left(\frac{18}{27}\sqrt{2}\cos(4.5) - \frac{4}{27}\sqrt{2}\sin(4.5) + \sqrt{2\pi}\,\mathrm{Si}\left(\frac{3}{\sqrt{\pi}}\right)\right),$$

where

$$\mathrm{Si}(x) = \int_0^x \sin\left(\frac{\pi}{2}t^2\right) dt.$$

is the Fresnel sine integral. Note that the numerically-computed integral is within 1.04×10^{-11} of the exact result — well below the reported error bound.

If the function to integrate takes additional parameters, the can be provided in the *args* argument. Suppose that the following integral shall be calculated:

$$I(a,b) = \int_0^1 ax^2 + b\,dx.$$

This integral can be evaluated by using the following code:

```
>>> from scipy.integrate import quad
>>> def integrand(x, a, b):
...     return a * x + b
>>> a = 2
>>> b = 1
>>> I = quad(integrand, 0, 1, args=(a,b))
>>> I = (2.0, 2.220446049250313e-14)
```

Infinite inputs are also allowed in `quad` by using ± `inf` as one of the arguments. For example, suppose that a numerical value for the exponential integral:

$$E_n(x) = \int_1^\infty \frac{e^{-xt}}{t^n}\,dt.$$

is desired (and the fact that this integral can be computed as `special.expn(n,x)` is forgotten). The functionality of the function `special.expn` can be replicated by defining a new function `vec_expint` based on the routine `quad`:

```
>>> from scipy.integrate import quad
>>> def integrand(t, n, x):
...     return exp(-x*t) / t**n

>>> def expint(n, x):
...     return quad(integrand, 1, Inf, args=(n, x))[0]

>>> vec_expint = vectorize(expint)

>>> vec_expint(3,arange(1.0,4.0,0.5))
array([ 0.1097,  0.0567,  0.0301,  0.0163,  0.0089,  0.0049])
>>> special.expn(3,arange(1.0,4.0,0.5))
array([ 0.1097,  0.0567,  0.0301,  0.0163,  0.0089,  0.0049])
```

The function which is integrated can even use the quad argument (though the error bound may underestimate the error due to possible numerical error in the integrand from the use of `quad`). The integral in this case is

$$I_n = \int_0^\infty \int_1^\infty \frac{e^{-xt}}{t^n}\,dt\,dx = \frac{1}{n}.$$

```
>>> result = quad(lambda x: expint(3, x), 0, inf)
>>> print result
(0.33333333324560266, 2.8548934485373678e-09)

>>> I3 = 1.0/3.0
>>> print I3
0.333333333333

>>> print I3 - result[0]
8.77306560731e-11
```

This last example shows that multiple integration can be handled using repeated calls to `quad`.

1.4.2 General multiple integration (`dblquad`, `tplquad`, `nquad`)

The mechanics for double and triple integration have been wrapped up into the functions `dblquad` and `tplquad`. These functions take the function to integrate and four, or six arguments, respecively. The limits of all inner integrals need to be defined as functions.

An example of using double integration to compute several values of I_n is shown below:

```
>>> from scipy.integrate import quad, dblquad
>>> def I(n):
...     return dblquad(lambda t, x: exp(-x*t)/t**n, 0, Inf, lambda x: 1, lambda x: Inf)

>>> print I(4)
(0.25000000000435768, 1.0518245707751597e-09)
>>> print I(3)
(0.33333333325010883, 2.8604069919261191e-09)
>>> print I(2)
(0.49999999999857514, 1.8855523253868967e-09)
```

As example for non-constant limits consider the integral

$$I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}.$$

This integral can be evaluated using the expression below (Note the use of the non-constant lambda functions for the upper limit of the inner integral):

```
>>> from scipy.integrate import dblquad
>>> area = dblquad(lambda x, y: x*y, 0, 0.5, lambda x: 0, lambda x: 1-2*x)
>>> area
(0.010416666666666668, 1.1564823173178715e-16)
```

For n-fold integration, scipy provides the function `nquad`. The integration bounds are an iterable object: either a list of constant bounds, or a list of functions for the non-constant integration bounds. The order of integration (and therefore the bounds) is from the innermost integral to the outermost one.

The integral from above

$$I_n = \int_0^{\infty} \int_1^{\infty} \frac{e^{-xt}}{t^n} \, dt \, dx = \frac{1}{n}$$

can be calculated as

```
>>> from scipy import integrate
>>> N = 5
>>> def f(t, x):
>>>    return np.exp(-x*t) / t**N
>>> integrate.nquad(f, [[1, np.inf],[0, np.inf]])
(0.20000000000002294, 1.2239614263187945e-08)
```

Note that the order of arguments for f must match the order of the integration bounds; i.e. the inner integral with respect to t is on the interval $[1, \infty]$ and the outer integral with respect to x is on the interval $[0, \infty]$.

Non-constant integration bounds can be treated in a similar manner; the example from above

$$I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}.$$

can be evaluated by means of

```
>>> from scipy import integrate
>>> def f(x, y):
>>>     return x*y
>>> def bounds_y():
>>>     return [0, 0.5]
>>> def bounds_x(y):
>>>     return [0, 1-2*y]
>>> integrate.nquad(f, [bounds_x, bounds_y])
(0.010416666666666668, 4.101620128472366e-16)
```

which is the same result as before.

1.4.3 Gaussian quadrature

A few functions are also provided in order to perform simple Gaussian quadrature over a fixed interval. The first is `fixed_quad` which performs fixed-order Gaussian quadrature. The second function is `quadrature` which performs Gaussian quadrature of multiple orders until the difference in the integral estimate is beneath some tolerance supplied by the user. These functions both use the module `special.orthogonal` which can calculate the roots and quadrature weights of a large variety of orthogonal polynomials (the polynomials themselves are available as special functions returning instances of the polynomial class — e.g. `special.legendre`).

1.4.4 Romberg Integration

Romberg's method [WPR] is another method for numerically evaluating an integral. See the help function for `romberg` for further details.

1.4.5 Integrating using Samples

If the samples are equally-spaced and the number of samples available is $2^k + 1$ for some integer k, then Romberg `romb` integration can be used to obtain high-precision estimates of the integral using the available samples. Romberg integration uses the trapezoid rule at step-sizes related by a power of two and then performs Richardson extrapolation on these estimates to approximate the integral with a higher-degree of accuracy.

In case of arbitrary spaced samples, the two functions trapz (defined in numpy [NPT]) and `simps` are available. They are using Newton-Coates formulas of order 1 and 2 respectively to perform integration. The trapezoidal rule approximates the function as a straight line between adjacent points, while Simpson's rule approximates the function between three adjacent points as a parabola.

For an odd number of samples that are equally spaced Simpson's rule is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

```
>>> from scipy.integrate import simps
>>> import numpy as np
>>> def f(x):
...    return x**2
>>> def f2(x):
...    return x**3
>>> x = np.array([1,3,4])
>>> y1 = f1(x)
>>> I1 = integrate.simps(y1, x)
>>> print(I1)
21.0
```

This corresponds exactly to

$$\int_1^4 x^2 \, dx = 21,$$

whereas integrating the second function

```
>>> y2 = f2(x)
>>> I2 = integrate.simps(y2, x)
>>> print(I2)
61.5
```

does not correspond to

$$\int_1^4 x^3 \, dx = 63.75$$

because the order of the polynomial in f2 is larger than two.

1.4.6 Faster integration using Ctypes

A user desiring reduced integration times may pass a C function pointer through `ctypes` to `quad`, `dblquad`, `tplquad` or `nquad` and it will be integrated and return a result in Python. The performance increase here arises from two factors. The primary improvement is faster function evaluation, which is provided by compilation. This can also be achieved using a library like Cython or F2Py that compiles Python. Additionally we have a speedup provided by the removal of function calls between C and Python in `quad` - this cannot be achieved through Cython or F2Py. This method will provide a speed increase of ~2x for trivial functions such as sine but can produce a much more noticeable increase (10x+) for more complex functions. This feature then, is geared towards a user with numerically intensive integrations willing to write a little C to reduce computation time significantly.

`ctypes` integration can be done in a few simple steps:

1.) Write an integrand function in C with the function signature `double f(int n, double args[n])`, where `args` is an array containing the arguments of the function f.

```
//testlib.c
double f(int n, double args[n]){
    return args[0] - args[1] * args[2]; //corresponds to x0 - x1 * x2
}
```

2.) Now compile this file to a shared/dynamic library (a quick search will help with this as it is OS-dependent). The user must link any math libraries, etc. used. On linux this looks like:

```
$ gcc -shared -o testlib.so -fPIC testlib.c
```

The output library will be referred to as `testlib.so`, but it may have a different file extension. A library has now been created that can be loaded into Python with `ctypes`.

3.) Load shared library into Python using `ctypes` and set `restypes` and `argtypes` - this allows Scipy to interpret the function correctly:

```
>>> import ctypes
>>> from scipy import integrate
>>> lib = ctypes.CDLL('/**/testlib.so') # Use absolute path to testlib
>>> func = lib.f # Assign specific function to name func (for simplicity)
>>> func.restype = ctypes.c_double
>>> func.argtypes = (ctypes.c_int, ctypes.c_double)
```

Note that the `argtypes` will always be `(ctypes.c_int, ctypes.c_double)` regardless of the number of parameters, and `restype` will always be `ctypes.c_double`.

4.) Now integrate the library function as normally, here using `nquad`:

```
>>> integrate.nquad(func, [[0,10],[-10,0],[-1,1]])
(1000.0, 1.1102230246251565e-11)
```

And the Python tuple is returned as expected in a reduced amount of time. All optional parameters can be used with this method including specifying singularities, infinite bounds, etc.

1.4.7 Ordinary differential equations (`odeint`)

Integrating a set of ordinary differential equations (ODEs) given initial conditions is another useful example. The function `odeint` is available in SciPy for integrating a first-order vector differential equation:

$$\frac{d\mathbf{y}}{dt}=\mathbf{f}\left(\mathbf{y},t\right),$$

given initial conditions $\mathbf{y}\left(0\right)=y_{0}$, where $\mathbf{y}$ is a length N vector and $\mathbf{f}$ is a mapping from $\mathcal{R}^{N}$ to $\mathcal{R}^{N}$. A higher-order ordinary differential equation can always be reduced to a differential equation of this type by introducing intermediate derivatives into the $\mathbf{y}$ vector.

For example suppose it is desired to find the solution to the following second-order differential equation:

$$\frac{d^{2}w}{dz^{2}}-zw(z)=0$$

with initial conditions $w\left(0\right)=\frac{1}{\sqrt[3]{3^{2}}\Gamma\left(\frac{2}{3}\right)}$ and $\left.\frac{dw}{dz}\right|_{z=0}=-\frac{1}{\sqrt[3]{3}\Gamma\left(\frac{1}{3}\right)}.$ It is known that the solution to this differential equation with these boundary conditions is the Airy function

$$w=\textrm{Ai}\left(z\right),$$

which gives a means to check the integrator using `special.airy`.

First, convert this ODE into standard form by setting $\mathbf{y}=\left[\frac{dw}{dz},w\right]$ and $t=z$. Thus, the differential equation becomes

$$\frac{d\mathbf{y}}{dt}=\left[\begin{array}{c} ty_{1}\\ y_{0}\end{array}\right]=\left[\begin{array}{cc} 0 & t\\ 1 & 0\end{array}\right]\left[\begin{array}{c} y_{0}\\ y_{1}\end{array}\right]=\left[\begin{array}{cc} 0 & t\\ 1 & 0\end{array}\right]\mathbf{y}.$$

In other words,

$$\mathbf{f}\left(\mathbf{y},t\right)=\mathbf{A}\left(t\right)\mathbf{y}.$$

As an interesting reminder, if $\mathbf{A}\left(t\right)$ commutes with $\int_{0}^{t}\mathbf{A}\left(\tau\right)\, d\tau$ under matrix multiplication, then this linear differential equation has an exact solution using the matrix exponential:

$$\mathbf{y}\left(t\right)=\exp\left(\int_{0}^{t}\mathbf{A}\left(\tau\right)d\tau\right)\mathbf{y}\left(0\right),$$

However, in this case, $\mathbf{A}\left(t\right)$ and its integral do not commute.

There are many optional inputs and outputs available when using odeint which can help tune the solver. These additional inputs and outputs are not needed much of the time, however, and the three required input arguments and the output solution suffice. The required inputs are the function defining the derivative, *fprime*, the initial conditions vector, *y0*, and the time points to obtain a solution, *t*, (with the initial value point as the first element of this sequence). The output to `odeint` is a matrix where each row contains the solution vector at each requested time point (thus, the initial conditions are given in the first output row).

The following example illustrates the use of odeint including the usage of the *Dfun* option which allows the user to specify a gradient (with respect to $\mathbf{y}$) of the function, $\mathbf{f}\left(\mathbf{y},t\right)$.

```
>>> from scipy.integrate import odeint
>>> from scipy.special import gamma, airy
>>> y1_0 = 1.0 / 3**(2.0/3.0) / gamma(2.0/3.0)
>>> y0_0 = -1.0 / 3**(1.0/3.0) / gamma(1.0/3.0)
>>> y0 = [y0_0, y1_0]
>>> def func(y, t):
...     return [t*y[1],y[0]]

>>> def gradient(y, t):
...     return [[0,t], [1,0]]

>>> x = arange(0, 4.0, 0.01)
>>> t = x
>>> ychk = airy(x)[0]
>>> y = odeint(func, y0, t)
>>> y2 = odeint(func, y0, t, Dfun=gradient)

>>> print ychk[:36:6]
[ 0.355028  0.339511  0.324068  0.308763  0.293658  0.278806]

>>> print y[:36:6,1]
[ 0.355028  0.339511  0.324067  0.308763  0.293658  0.278806]

>>> print y2[:36:6,1]
[ 0.355028  0.339511  0.324067  0.308763  0.293658  0.278806]
```

References

1.5 Optimization (`scipy.optimize`)

The `scipy.optimize` package provides several commonly used optimization algorithms. A detailed listing is available: `scipy.optimize` (can also be found by `help(scipy.optimize)`).

The module contains:

1. Unconstrained and constrained minimization of multivariate scalar functions (`minimize`) using a variety of algorithms (e.g. BFGS, Nelder-Mead simplex, Newton Conjugate Gradient, COBYLA or SLSQP)
2. Global (brute-force) optimization routines (e.g. `basinhopping`, `differential_evolution`)
3. Least-squares minimization (`leastsq`) and curve fitting (`curve_fit`) algorithms
4. Scalar univariate functions minimizers (`minimize_scalar`) and root finders (`newton`)
5. Multivariate equation system solvers (`root`) using a variety of algorithms (e.g. hybrid Powell, Levenberg-Marquardt or large-scale methods such as Newton-Krylov).

Below, several examples demonstrate their basic usage.

1.5.1 Unconstrained minimization of multivariate scalar functions (`minimize`)

The `minimize` function provides a common interface to unconstrained and constrained minimization algorithms for multivariate scalar functions in `scipy.optimize`. To demonstrate the minimization function consider the problem of minimizing the Rosenbrock function of N variables: f($\mathbf{x}$) $= \sum_{i=1}^{N-1} 100\left(x_i - x_{i-1}^2\right)^2 + \left(1 - x_{i-1}\right)^2 .Theminimumvalueofthisfunctionis0whichisachievedwhenx_i = 1.$

Note that the Rosenbrock function and its derivatives are included in `scipy.optimize`. The implementations shown in the following sections provide examples of how to define an objective function as well as its jacobian and hessian functions.

Nelder-Mead Simplex algorithm (`method='Nelder-Mead'`)

In the example below, the `minimize` routine is used with the *Nelder-Mead* simplex algorithm (selected through the `method` parameter):

```
>>> import numpy as np
>>> from scipy.optimize import minimize

>>> def rosen(x):
...     """The Rosenbrock function"""
...     return sum(100.0*(x[1:]-x[:-1]**2.0)**2.0 + (1-x[:-1])**2.0)

>>> x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
>>> res = minimize(rosen, x0, method='nelder-mead',
...                options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 339
         Function evaluations: 571

>>> print(res.x)
[ 1.  1.  1.  1.  1.]
```

The simplex algorithm is probably the simplest way to minimize a fairly well-behaved function. It requires only function evaluations and is a good choice for simple minimization problems. However, because it does not use any gradient evaluations, it may take longer to find the minimum.

Another optimization algorithm that needs only function calls to find the minimum is *Powell*'s method available by setting `method='powell'` in `minimize`.

Broyden-Fletcher-Goldfarb-Shanno algorithm (`method='BFGS'`)

In order to converge more quickly to the solution, this routine uses the gradient of the objective function. If the gradient is not given by the user, then it is estimated using first-differences. The Broyden-Fletcher-Goldfarb-Shanno (BFGS) method typically requires fewer function calls than the simplex algorithm even when the gradient must be estimated.

To demonstrate this algorithm, the Rosenbrock function is again used. The gradient of the Rosenbrock function is the vector:

$$\begin{aligned}\frac{\partial f}{\partial x_j} &= \sum_{i=1}^{N} 200\left(x_i - x_{i-1}^2\right)\left(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}\right) - 2\left(1 - x_{i-1}\right)\delta_{i-1,j}. \\ &= 200\left(x_j - x_{j-1}^2\right) - 400x_j\left(x_{j+1} - x_j^2\right) - 2\left(1 - x_j\right).\end{aligned}$$

This expression is valid for the interior derivatives. Special cases are

$$\begin{aligned}\frac{\partial f}{\partial x_0} &= -400x_0\left(x_1 - x_0^2\right) - 2\left(1 - x_0\right), \\ \frac{\partial f}{\partial x_{N-1}} &= 200\left(x_{N-1} - x_{N-2}^2\right).\end{aligned}$$

A Python function which computes this gradient is constructed by the code-segment:

```
>>> def rosen_der(x):
...     xm = x[1:-1]
...     xm_m1 = x[:-2]
...     xm_p1 = x[2:]
...     der = np.zeros_like(x)
...     der[1:-1] = 200*(xm-xm_m1**2) - 400*(xm_p1 - xm**2)*xm - 2*(1-xm)
...     der[0] = -400*x[0]*(x[1]-x[0]**2) - 2*(1-x[0])
...     der[-1] = 200*(x[-1]-x[-2]**2)
...     return der
```

This gradient information is specified in the `minimize` function through the `jac` parameter as illustrated below.

```
>>> res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
...                options={'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 51
         Function evaluations: 63
         Gradient evaluations: 63
>>> print(res.x)
[ 1.  1.  1.  1.  1.]
```

Newton-Conjugate-Gradient algorithm (`method='Newton-CG'`)

The method which requires the fewest function calls and is therefore often the fastest method to minimize functions of many variables uses the Newton-Conjugate Gradient algorithm. This method is a modified Newton's method and uses a conjugate gradient algorithm to (approximately) invert the local Hessian. Newton's method is based on fitting the function locally to a quadratic form: $\mathrm{f}(\mathbf{x}) \approx f(\mathbf{x}_0) + \nabla f(\mathbf{x}_0) \cdot (\mathbf{x} - \mathbf{x}_0) + \frac{1}{2}(\mathbf{x} - \mathbf{x}_0)^T \mathbf{H}(\mathbf{x}_0)(\mathbf{x} - \mathbf{x}_0).where\mathbf{H}(\mathbf{x}_0)$ is a matrix of second-derivatives (the Hessian). If the Hessian is positive definite then the local minimum of this function can be found by setting the gradient of the quadratic form to zero, resulting in $\mathrm{x}_{\mathrm{opt}} = \mathbf{x}_0 - \mathbf{H}^{-1}\nabla f.TheinverseoftheHessianisevaluatedusingtheconjugate - gradientmethod.AnexampleofemployingthismethodtominimizingtheRosenbrockfunctionisgivenbelow.Totakefulladvanta$ $CGmethod,afunctionwhichcomputestheHessianmustbeprovided.TheHessianmatrixitselfdoesnotneedtobeconstructed,on$

Full Hessian example:

The Hessian of the Rosenbrock function is

$$\begin{aligned} H_{ij} = \frac{\partial^2 f}{\partial x_i \partial x_j} &= 200(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}) - 400x_i(\delta_{i+1,j} - 2x_i\delta_{i,j}) - 400\delta_{i,j}\left(x_{i+1} - x_i^2\right) + 2\delta_{i,j}, \\ &= \left(202 + 1200x_i^2 - 400x_{i+1}\right)\delta_{i,j} - 400x_i\delta_{i+1,j} - 400x_{i-1}\delta_{i-1,j}, \end{aligned}$$

if $i, j \in [1, N-2]$ with $i, j \in [0, N-1]$ defining the $N \times N$ matrix. Other non-zero entries of the matrix are

$$\begin{aligned} \frac{\partial^2 f}{\partial x_0^2} &= 1200x_0^2 - 400x_1 + 2, \\ \frac{\partial^2 f}{\partial x_0 \partial x_1} = \frac{\partial^2 f}{\partial x_1 \partial x_0} &= -400x_0, \\ \frac{\partial^2 f}{\partial x_{N-1} \partial x_{N-2}} = \frac{\partial^2 f}{\partial x_{N-2} \partial x_{N-1}} &= -400x_{N-2}, \\ \frac{\partial^2 f}{\partial x_{N-1}^2} &= 200. \end{aligned}$$

For example, the Hessian when $N = 5$ is H= $\left[\begin{array}{cccc} 1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 \\ -400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 \\ 0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400 \\ 0 & & -400x_2 & 202 + 1200 \\ 0 & 0 & 0 & -400 \end{array}\right.$

$CGmethodisshowninthefollowingexample:$

```
>>> def rosen_hess(x):
...     x = np.asarray(x)
...     H = np.diag(-400*x[:-1],1) - np.diag(400*x[:-1],-1)
...     diagonal = np.zeros_like(x)
...     diagonal[0] = 1200*x[0]**2-400*x[1]+2
...     diagonal[-1] = 200
...     diagonal[1:-1] = 202 + 1200*x[1:-1]**2 - 400*x[2:]
...     H = H + np.diag(diagonal)
...     return H

>>> res = minimize(rosen, x0, method='Newton-CG',
...                jac=rosen_der, hess=rosen_hess,
...                options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 19
         Function evaluations: 22
         Gradient evaluations: 19
         Hessian evaluations: 19
>>> print(res.x)
[ 1.  1.  1.  1.  1.]
```

Hessian product example:

For larger minimization problems, storing the entire Hessian matrix can consume considerable time and memory. The Newton-CG algorithm only needs the product of the Hessian times an arbitrary vector. As a result, the user can supply code to compute this product rather than the full Hessian by giving a `hess` function which take the minimization vector as the first argument and the arbitrary vector as the second argument (along with extra arguments passed to the function to be minimized). If possible, using Newton-CG with the Hessian product option is probably the fastest way to minimize the function.

In this case, the product of the Rosenbrock Hessian with an arbitrary vector is not difficult to compute. If $\mathbf{p}$ is the arbitrary vector, then $\mathbf{H}\left(\mathbf{x}\right)\mathbf{p}$ has elements: $\mathrm{H}(\mathbf{x})\,\mathbf{p} = \left[\begin{array}{c} \left(1200x_0^2 - 400x_1 + 2\right)p_0 - 400x_0p_1 \\ \vdots \\ -400x_{i-1}p_{i-1} + \left(202 + 1200x_i^2 - 400x_{i+1}\right)p_i - 400x_ip_{i+1} \\ \vdots \\ -400x_{N-2}p_{N-2} + 200p_{N-1} \end{array}\right] .CodewhichmakesuseofthisHessianproducttominimizetheR$

```
>>> def rosen_hess_p(x, p):
...     x = np.asarray(x)
...     Hp = np.zeros_like(x)
...     Hp[0] = (1200*x[0]**2 - 400*x[1] + 2)*p[0] - 400*x[0]*p[1]
...     Hp[1:-1] = -400*x[:-2]*p[:-2]+(202+1200*x[1:-1]**2-400*x[2:])*p[1:-1] \
...                -400*x[1:-1]*p[2:]
...     Hp[-1] = -400*x[-2]*p[-2] + 200*p[-1]
...     return Hp

>>> res = minimize(rosen, x0, method='Newton-CG',
...                jac=rosen_der, hessp=rosen_hess_p,
```

```
...                 options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 20
         Function evaluations: 23
         Gradient evaluations: 20
         Hessian evaluations: 44
>>> print(res.x)
[ 1.  1.  1.  1.  1.]
```

1.5.2 Constrained minimization of multivariate scalar functions (`minimize`)

The `minimize` function also provides an interface to several constrained minimization algorithm. As an example, the Sequential Least SQuares Programming optimization algorithm (SLSQP) will be considered here. This algorithm allows to deal with constrained minimization problems of the form:

$$
\begin{aligned}
&\min F(x) \\
&\text{subject to} \quad C_j(X) = 0, \quad j = 1, ..., \text{MEQ} \\
&\qquad\qquad\quad C_j(x) \geq 0, \quad j = \text{MEQ} + 1, ..., M \\
&\qquad\qquad XL \leq x \leq XU, \quad I = 1, ..., N.
\end{aligned}
$$

As an example, let us consider the problem of maximizing the function: `f(x, y) = 2 x y + 2 x - x`$^2 - 2y^2 subjecttoanequalityandaninequalityconstraintsdefinedas:to$ $x^3 - y = 0$ $y - 1 \geq 0$The objective function and its derivative are defined as follows.

```
>>> def func(x, sign=1.0):
...     """ Objective function """
...     return sign*(2*x[0]*x[1] + 2*x[0] - x[0]**2 - 2*x[1]**2)

>>> def func_deriv(x, sign=1.0):
...     """ Derivative of objective function """
...     dfdx0 = sign*(-2*x[0] + 2*x[1] + 2)
...     dfdx1 = sign*(2*x[0] - 4*x[1])
...     return np.array([ dfdx0, dfdx1 ])
```

Note that since `minimize` only minimizes functions, the `sign` parameter is introduced to multiply the objective function (and its derivative) by -1 in order to perform a maximization.

Then constraints are defined as a sequence of dictionaries, with keys `type`, `fun` and `jac`.

```
>>> cons = ({'type': 'eq',
...          'fun' : lambda x: np.array([x[0]**3 - x[1]]),
...          'jac' : lambda x: np.array([3.0*(x[0]**2.0), -1.0])},
...         {'type': 'ineq',
...          'fun' : lambda x: np.array([x[1] - 1]),
...          'jac' : lambda x: np.array([0.0, 1.0])})
```

Now an unconstrained optimization can be performed as:

```
>>> res = minimize(func, [-1.0,1.0], args=(-1.0,), jac=func_deriv,
...                 method='SLSQP', options={'disp': True})
Optimization terminated successfully.    (Exit mode 0)
            Current function value: -2.0
            Iterations: 4
            Function evaluations: 5
            Gradient evaluations: 4
```

```
>>> print(res.x)
[ 2.  1.]
```

and a constrained optimization as:

```
>>> res = minimize(func, [-1.0,1.0], args=(-1.0,), jac=func_deriv,
...                constraints=cons, method='SLSQP', options={'disp': True})
Optimization terminated successfully.    (Exit mode 0)
            Current function value: -1.00000018311
            Iterations: 9
            Function evaluations: 14
            Gradient evaluations: 9
>>> print(res.x)
[ 1.00000009  1.        ]
```

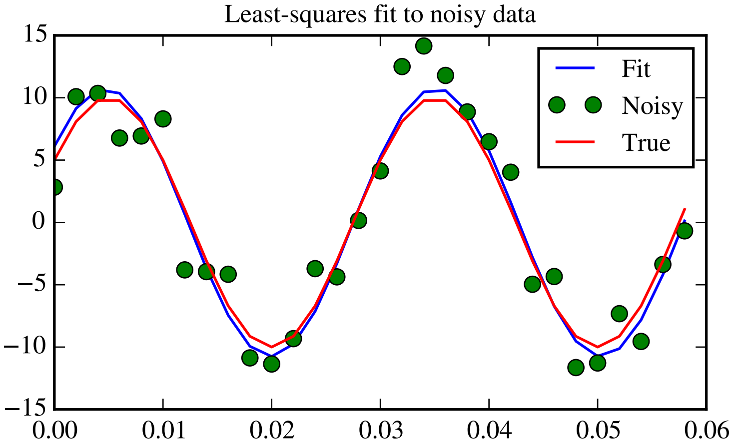
1.5.3 Least-square fitting (`leastsq`)

All of the previously-explained minimization procedures can be used to solve a least-squares problem provided the appropriate objective function is constructed. For example, suppose it is desired to fit a set of data $\{\mathbf{x}_i, \mathbf{y}_i\}$ to a known model, $\mathbf{y} = \mathbf{f}(\mathbf{x}, \mathbf{p})$ where $\mathbf{p}$ is a vector of parameters for the model that need to be found. A common method for determining which parameter vector gives the best fit to the data is to minimize the sum of squares of the residuals. The residual is usually defined for each observed data-point as $\mathrm{e}_i(\mathbf{p}, \mathbf{y}_i, \mathbf{x}_i) = \|\mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \mathbf{p})\| Anobjectivefunctiontopasstoanyofthepreviousminizationalgorithmstoobtainaleast - squaresfitis. J(\mathbf{p}) = \sum_{i=0}^{N-1} e_i^2(\mathbf{p}) .The$`leastsq`$algorithmperformsthissquaringandsummingoftheresidualsautomaticall$
and returns the value of $\mathbf{p}$ which minimizes $J(\mathbf{p}) = \mathbf{e}^T\mathbf{e}$ directly. The user is also encouraged to provide the Jacobian matrix of the function (with derivatives down the columns or across the rows). If the Jacobian is not provided, it is estimated.

An example should clarify the usage. Suppose it is believed some measured data follow a sinusoidal pattern $\mathrm{y}_i = A\sin(2\pi k x_i + \theta) wheretheparametersA, k$, and θ are unknown. The residual vector is $\mathrm{e}_i = |y_i - A\sin(2\pi k x_i + \theta)| .Bydefiningafunctiontocomputetheresidualsand(selectinganappropriatestartingposition), theleast$
$squaresfitroutinecanbeusedtofindthebest - fitparameters\hat{A},\ \hat{k},\ \hat{\theta}$. This is shown in the following example:

```
>>> from numpy import arange, sin, pi, random, array
>>> x = arange(0, 6e-2, 6e-2 / 30)
>>> A, k, theta = 10, 1.0 / 3e-2, pi / 6
>>> y_true = A * sin(2 * pi * k * x + theta)
>>> y_meas = y_true + 2*random.randn(len(x))

>>> def residuals(p, y, x):
...     A, k, theta = p
...     err = y - A * sin(2 * pi * k * x + theta)
...     return err

>>> def peval(x, p):
...     return p[0] * sin(2 * pi * p[1] * x + p[2])

>>> p0 = [8, 1 / 2.3e-2, pi / 3]
>>> print(array(p0))
[  8.      43.4783   1.0472]

>>> from scipy.optimize import leastsq
>>> plsq = leastsq(residuals, p0, args=(y_meas, x))
>>> print(plsq[0])
[ 10.9437  33.3605   0.5834]
```

```
>>> print(array([A, k, theta]))
[ 10.        33.3333    0.5236]

>>> import matplotlib.pyplot as plt
>>> plt.plot(x, peval(x, plsq[0]),x,y_meas,'o',x,y_true)
>>> plt.title('Least-squares fit to noisy data')
>>> plt.legend(['Fit', 'Noisy', 'True'])
>>> plt.show()
```



1.5.4 Univariate function minimizers (`minimize_scalar`)

Often only the minimum of an univariate function (i.e. a function that takes a scalar as input) is needed. In these circumstances, other optimization techniques have been developed that can work faster. These are accessible from the `minimize_scalar` function which proposes several algorithms.

Unconstrained minimization (`method='brent'`)

There are actually two methods that can be used to minimize an univariate function: `brent` and `golden`, but `golden` is included only for academic purposes and should rarely be used. These can be respectively selected through the *method* parameter in `minimize_scalar`. The `brent` method uses Brent's algorithm for locating a minimum. Optimally a bracket (the *bs* parameter) should be given which contains the minimum desired. A bracket is a triple (a, b, c) such that $f(a) > f(b) < f(c)$ and $a < b < c$. If this is not given, then alternatively two starting points can be chosen and a bracket will be found from these points using a simple marching algorithm. If these two starting points are not provided *0* and *1* will be used (this may not be the right choice for your function and result in an unexpected minimum being returned).

Here is an example:

```
>>> from scipy.optimize import minimize_scalar
>>> f = lambda x: (x - 2) * (x + 1)**2
>>> res = minimize_scalar(f, method='brent')
>>> print(res.x)
1.0
```

Bounded minimization (`method='bounded'`)

Very often, there are constraints that can be placed on the solution space before minimization occurs. The *bounded* method in `minimize_scalar` is an example of a constrained minimization procedure that provides a rudimentary interval constraint for scalar functions. The interval constraint allows the minimization to occur only between two fixed endpoints, specified using the mandatory *bs* parameter.

For example, to find the minimum of $J_1(x)$ near $x = 5$, `minimize_scalar` can be called using the interval $[4, 7]$ as a constraint. The result is $x_{\text{min}} = 5.3314$:

```
>>> from scipy.special import j1
>>> res = minimize_scalar(j1, bs=(4, 7), method='bounded')
>>> print(res.x)
5.33144184241
```

1.5.5 Custom minimizers

Sometimes, it may be useful to use a custom method as a (multivariate or univariate) minimizer, for example when using some library wrappers of `minimize` (e.g. `basinhopping`).

We can achieve that by, instead of passing a method name, we pass a callable (either a function or an object implementing a *__call__* method) as the *method* parameter.

Let us consider an (admittedly rather virtual) need to use a trivial custom multivariate minimization method that will just search the neighborhood in each dimension independently with a fixed step size:

```
>>> def custmin(fun, x0, args=(), maxfev=None, stepsize=0.1,
...         maxiter=100, callback=None, **options):
...     bestx = x0
...     besty = fun(x0)
...     funcalls = 1
...     niter = 0
...     improved = True
...     stop = False
...
...     while improved and not stop and niter < maxiter:
...         improved = False
...         niter += 1
...         for dim in range(np.size(x0)):
...             for s in [bestx[dim] - stepsize, bestx[dim] + stepsize]:
...                 testx = np.copy(bestx)
...                 testx[dim] = s
...                 testy = fun(testx, *args)
...                 funcalls += 1
...                 if testy < besty:
...                     besty = testy
...                     bestx = testx
...                     improved = True
...             if callback is not None:
...                 callback(bestx)
...             if maxfev is not None and funcalls >= maxfev:
...                 stop = True
...                 break
...
...     return OptimizeResult(fun=besty, x=bestx, nit=niter,
...                           nfev=funcalls, success=(niter > 1))
>>> x0 = [1.35, 0.9, 0.8, 1.1, 1.2]
>>> res = minimize(rosen, x0, method=custmin, options=dict(stepsize=0.05))
```

```
>>> res.x
[ 1.  1.  1.  1.  1.]
```

This will work just as well in case of univariate optimization:

```
>>> def custmin(fun, bracket, args=(), maxfev=None, stepsize=0.1,
...         maxiter=100, callback=None, **options):
...     bestx = (bracket[1] + bracket[0]) / 2.0
...     besty = fun(bestx)
...     funcalls = 1
...     niter = 0
...     improved = True
...     stop = False
...
...     while improved and not stop and niter < maxiter:
...         improved = False
...         niter += 1
...         for testx in [bestx - stepsize, bestx + stepsize]:
...             testy = fun(testx, *args)
...             funcalls += 1
...             if testy < besty:
...                 besty = testy
...                 bestx = testx
...                 improved = True
...         if callback is not None:
...             callback(bestx)
...         if maxfev is not None and funcalls >= maxfev:
...             stop = True
...             break
...
...     return OptimizeResult(fun=besty, x=bestx, nit=niter,
...                           nfev=funcalls, success=(niter > 1))
>>> res = minimize_scalar(f, bracket=(-3.5, 0), method=custmin,
...                       options=dict(stepsize = 0.05))
>>> res.x
-2.0
```

1.5.6 Root finding

Scalar functions

If one has a single-variable equation, there are four different root finding algorithms that can be tried. Each of these algorithms requires the endpoints of an interval in which a root is expected (because the function changes signs). In general `brentq` is the best choice, but the other methods may be useful in certain circumstances or for academic purposes.

Fixed-point solving

A problem closely related to finding the zeros of a function is the problem of finding a fixed-point of a function. A fixed point of a function is the point at which evaluation of the function returns the point: $g(x) = x$. Clearly the fixed point of g is the root of $f(x) = g(x) - x$. Equivalently, the root of f is the fixed_point of $g(x) = f(x) + x$. The routine `fixed_point` provides a simple iterative method using Aitkens sequence acceleration to estimate the fixed point of g given a starting point.

Sets of equations

Finding a root of a set of non-linear equations can be achieve using the `root` function. Several methods are available, amongst which `hybr` (the default) and `lm` which respectively use the hybrid method of Powell and the Levenberg-Marquardt method from MINPACK.

The following example considers the single-variable transcendental equation x+2cos $(x) = 0, arootofwhichcanbefoundasfollows:$

```
>>> import numpy as np
>>> from scipy.optimize import root
>>> def func(x):
...     return x + 2 * np.cos(x)
>>> sol = root(func, 0.3)
>>> sol.x
array([-1.02986653])
>>> sol.fun
array([ -6.66133815e-16])
```

Consider now a set of non-linear equations

$$\begin{aligned} x_0 \cos(x_1) &= 4, \\ x_0 x_1 - x_1 &= 5. \end{aligned}$$

We define the objective function so that it also returns the Jacobian and indicate this by setting the `jac` parameter to `True`. Also, the Levenberg-Marquardt solver is used here.

```
>>> def func2(x):
...     f = [x[0] * np.cos(x[1]) - 4,
...          x[1]*x[0] - x[1] - 5]
...     df = np.array([[np.cos(x[1]), -x[0] * np.sin(x[1])],
...                    [x[1], x[0] - 1]])
...     return f, df
>>> sol = root(func2, [1, 1], jac=True, method='lm')
>>> sol.x
array([ 6.50409711,  0.90841421])
```

Root finding for large problems

Methods `hybr` and `lm` in `root` cannot deal with a very large number of variables (*N*), as they need to calculate and invert a dense *N x N* Jacobian matrix on every Newton step. This becomes rather inefficient when *N* grows.

Consider for instance the following problem: we need to solve the following integrodifferential equation on the square $[0, 1] \times [0, 1]$:

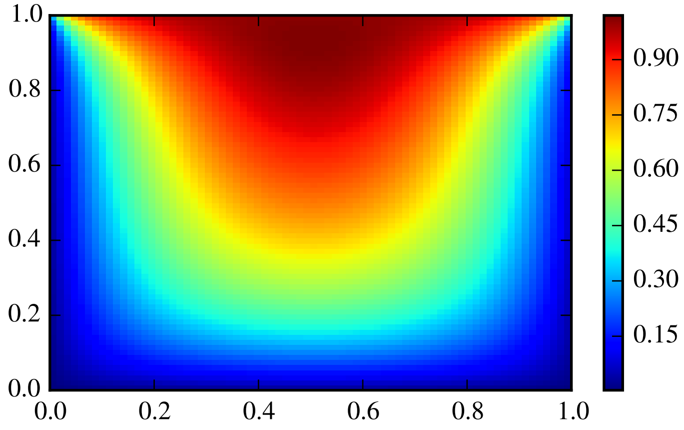
$$(\partial_x^2 + \partial_y^2) P + 5 \left(\int_0^1 \int_0^1 \cosh(P)\, dx\, dy \right)^2 = 0$$

with the boundary condition $P(x, 1) = 1$ on the upper edge and $P = 0$ elsewhere on the boundary of the square. This can be done by approximating the continuous function *P* by its values on a grid, $P_{n,m} \approx P(nh, mh)$, with a small grid spacing h. The derivatives and integrals can then be approximated; for instance $\partial_x^2 P(x, y) \approx (P(x + h, y) - 2P(x, y) + P(x - h, y))/h^2$. The problem is then equivalent to finding the root of some function `residual(P)`, where `P` is a vector of length $N_x N_y$.

Now, because $N_x N_y$ can be large, methods `hybr` or `lm` in `root` will take a long time to solve this problem. The solution can however be found using one of the large-scale solvers, for example `krylov`, `broyden2`, or `anderson`. These use what is known as the inexact Newton method, which instead of computing the Jacobian matrix exactly, forms an approximation for it.

The problem we have can now be solved as follows:

```
import numpy as np
from scipy.optimize import root
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def residual(P):
   d2x = zeros_like(P)
   d2y = zeros_like(P)

   d2x[1:-1] = (P[2:]    - 2*P[1:-1] + P[:-2]) / hx/hx
   d2x[0]    = (P[1]     - 2*P[0]    + P_left)/hx/hx
   d2x[-1]   = (P_right - 2*P[-1]    + P[-2])/hx/hx

   d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
   d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
   d2y[:,-1]   = (P_top   - 2*P[:,-1]   + P[:,-2])/hy/hy

   return d2x + d2y + 5*cosh(P).mean()**2

# solve
guess = zeros((nx, ny), float)
sol = root(residual, guess, method='krylov', options={'disp': True})
#sol = root(residual, guess, method='broyden2', options={'disp': True, 'max_rank': 50})
#sol = root(residual, guess, method='anderson', options={'disp': True, 'M': 10})
print('Residual: %g' % abs(residual(sol.x)).max())

# visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolor(x, y, sol.x)
plt.colorbar()
plt.show()
```



Still too slow? Preconditioning.

When looking for the zero of the functions $f_i(\mathbf{x}) = 0$, *i = 1, 2, ..., N*, the `krylov` solver spends most of its time inverting the Jacobian matrix,

$$J_{ij} = \frac{\partial f_i}{\partial x_j}.$$

If you have an approximation for the inverse matrix $M \approx J^{-1}$, you can use it for *preconditioning* the linear inversion problem. The idea is that instead of solving $J\mathbf{s} = \mathbf{y}$ one solves $MJ\mathbf{s} = M\mathbf{y}$: since matrix MJ is "closer" to the identity matrix than J is, the equation should be easier for the Krylov method to deal with.

The matrix M can be passed to `root` with method `krylov` as an option `options['jac_options']['inner_M']`. It can be a (sparse) matrix or a `scipy.sparse.linalg.LinearOperator` instance.

For the problem in the previous section, we note that the function to solve consists of two parts: the first one is application of the Laplace operator, $[\partial_x^2 + \partial_y^2]P$, and the second is the integral. We can actually easily compute the Jacobian corresponding to the Laplace operator part: we know that in one dimension

$$\partial_x^2 \approx \frac{1}{h_x^2} \begin{pmatrix} -2 & 1 & 0 & 0\cdots \\ 1 & -2 & 1 & 0\cdots \\ 0 & 1 & -2 & 1\cdots \\ \ldots \end{pmatrix} = h_x^{-2} L$$

so that the whole 2-D operator is represented by

$$J_1 = \partial_x^2 + \partial_y^2 \simeq h_x^{-2} L \otimes I + h_y^{-2} I \otimes L$$

The matrix J_2 of the Jacobian corresponding to the integral is more difficult to calculate, and since *all* of it entries are nonzero, it will be difficult to invert. J_1 on the other hand is a relatively simple matrix, and can be inverted by `scipy.sparse.linalg.splu` (or the inverse can be approximated by `scipy.sparse.linalg.spilu`). So we are content to take $M \approx J_1^{-1}$ and hope for the best.

In the example below, we use the preconditioner $M = J_1^{-1}$.

```
import numpy as np
from scipy.optimize import root
from scipy.sparse import spdiags, kron
from scipy.sparse.linalg import spilu, LinearOperator
from numpy import cosh, zeros_like, mgrid, zeros, eye

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def get_preconditioner():
    """Compute the preconditioner M"""
    diags_x = zeros((3, nx))
    diags_x[0,:] = 1/hx/hx
    diags_x[1,:] = -2/hx/hx
    diags_x[2,:] = 1/hx/hx
    Lx = spdiags(diags_x, [-1,0,1], nx, nx)

    diags_y = zeros((3, ny))
    diags_y[0,:] = 1/hy/hy
    diags_y[1,:] = -2/hy/hy
    diags_y[2,:] = 1/hy/hy
    Ly = spdiags(diags_y, [-1,0,1], ny, ny)

    J1 = kron(Lx, eye(ny)) + kron(eye(nx), Ly)

    # Now we have the matrix `J_1`. We need to find its inverse `M` --
    # however, since an approximate inverse is enough, we can use
    # the *incomplete LU* decomposition

    J1_ilu = spilu(J1)

    # This returns an object with a method .solve() that evaluates
    # the corresponding matrix-vector product. We need to wrap it into
    # a LinearOperator before it can be passed to the Krylov methods:

    M = LinearOperator(shape=(nx*ny, nx*ny), matvec=J1_ilu.solve)
    return M

def solve(preconditioning=True):
    """Compute the solution"""
    count = [0]

    def residual(P):
        count[0] += 1

        d2x = zeros_like(P)
        d2y = zeros_like(P)

        d2x[1:-1] = (P[2:]    - 2*P[1:-1] + P[:-2])/hx/hx
        d2x[0]    = (P[1]     - 2*P[0]    + P_left)/hx/hx
        d2x[-1]   = (P_right - 2*P[-1]    + P[-2])/hx/hx

        d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
        d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
```

```
        d2y[:,-1]    = (P_top    - 2*P[:,-1]    + P[:,-2])/hy/hy

        return d2x + d2y + 5*cosh(P).mean()**2

    # preconditioner
    if preconditioning:
        M = get_preconditioner()
    else:
        M = None

    # solve
    guess = zeros((nx, ny), float)

    sol = root(residual, guess, method='krylov',
               options={'disp': True,
                        'jac_options': {'inner_M': M}})
    print 'Residual', abs(residual(sol.x)).max()
    print 'Evaluations', count[0]

    return sol.x

def main():
    sol = solve(preconditioning=True)

    # visualize
    import matplotlib.pyplot as plt
    x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
    plt.clf()
    plt.pcolor(x, y, sol)
    plt.clim(0, 1)
    plt.colorbar()
    plt.show()

if __name__ == "__main__":
    main()
```

Resulting run, first without preconditioning:

```
0:  |F(x)| = 803.614; step 1; tol 0.000257947
1:  |F(x)| = 345.912; step 1; tol 0.166755
2:  |F(x)| = 139.159; step 1; tol 0.145657
3:  |F(x)| = 27.3682; step 1; tol 0.0348109
4:  |F(x)| = 1.03303; step 1; tol 0.00128227
5:  |F(x)| = 0.0406634; step 1; tol 0.00139451
6:  |F(x)| = 0.00344341; step 1; tol 0.00645373
7:  |F(x)| = 0.000153671; step 1; tol 0.00179246
8:  |F(x)| = 6.7424e-06; step 1; tol 0.00173256
Residual 3.57078908664e-07
Evaluations 317
```

and then with preconditioning:

```
0:  |F(x)| = 136.993; step 1; tol 7.49599e-06
1:  |F(x)| = 4.80983; step 1; tol 0.00110945
2:  |F(x)| = 0.195942; step 1; tol 0.00149362
3:  |F(x)| = 0.000563597; step 1; tol 7.44604e-06
4:  |F(x)| = 1.00698e-09; step 1; tol 2.87308e-12
Residual 9.29603061195e-11
Evaluations 77
```

Using a preconditioner reduced the number of evaluations of the `residual` function by a factor of *4*. For problems where the residual is expensive to compute, good preconditioning can be crucial — it can even decide whether the problem is solvable in practice or not.

Preconditioning is an art, science, and industry. Here, we were lucky in making a simple choice that worked reasonably well, but there is a lot more depth to this topic than is shown here.

References

Some further reading and related software:

1.6 Interpolation (`scipy.interpolate`)

Contents

There are several general interpolation facilities available in SciPy, for data in 1, 2, and higher dimensions:

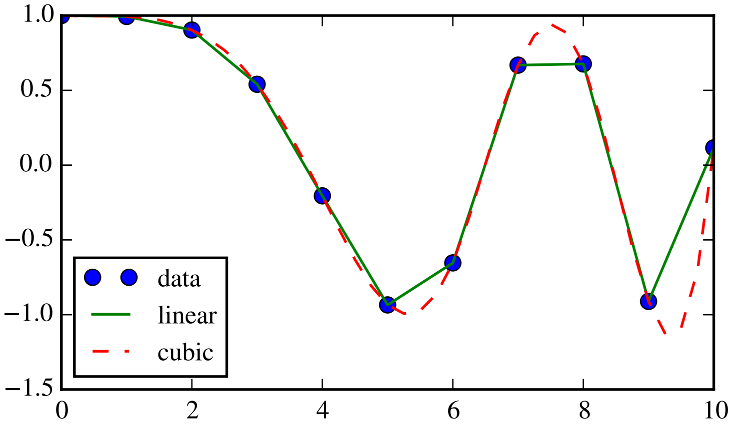
- A class representing an interpolant (`interp1d`) in 1-D, offering several interpolation methods.
- Convenience function `griddata` offering a simple interface to interpolation in N dimensions (N = 1, 2, 3, 4, ...). Object-oriented interface for the underlying routines is also available.
- Functions for 1- and 2-dimensional (smoothed) cubic-spline interpolation, based on the FORTRAN library FITPACK. There are both procedural and object-oriented interfaces for the FITPACK library.
- Interpolation using Radial Basis Functions.

1.6.1 1-D interpolation (`interp1d`)

The `interp1d` class in `scipy.interpolate` is a convenient method to create a function based on fixed data points which can be evaluated anywhere within the domain defined by the given data using linear interpolation. An instance of this class is created by passing the 1-d vectors comprising the data. The instance of this class defines a __call__ method and can therefore by treated like a function which interpolates between known data values to obtain unknown values (it also has a docstring for help). Behavior at the boundary can be specified at instantiation time. The following example demonstrates its use, for linear and cubic spline interpolation:

```
>>> from scipy.interpolate import interp1d

>>> x = np.linspace(0, 10, num=11, endpoint=True)
>>> y = np.cos(-x**2/9.0)
>>> f = interp1d(x, y)
>>> f2 = interp1d(x, y, kind='cubic')
```

```
>>> xnew = np.linspace(0, 10, num=41, endpoint=True)
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o', xnew, f(xnew), '-', xnew, f2(xnew), '--')
>>> plt.legend(['data', 'linear', 'cubic'], loc='best')
>>> plt.show()
```



1.6.2 Multivariate data interpolation (`griddata`)

Suppose you have multidimensional data, for instance for an underlying function *f(x, y)* you only know the values at points *(x[i], y[i])* that do not form a regular grid.

Suppose we want to interpolate the 2-D function

```
>>> def func(x, y):
>>>     return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```

on a grid in [0, 1]x[0, 1]

```
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

```
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```

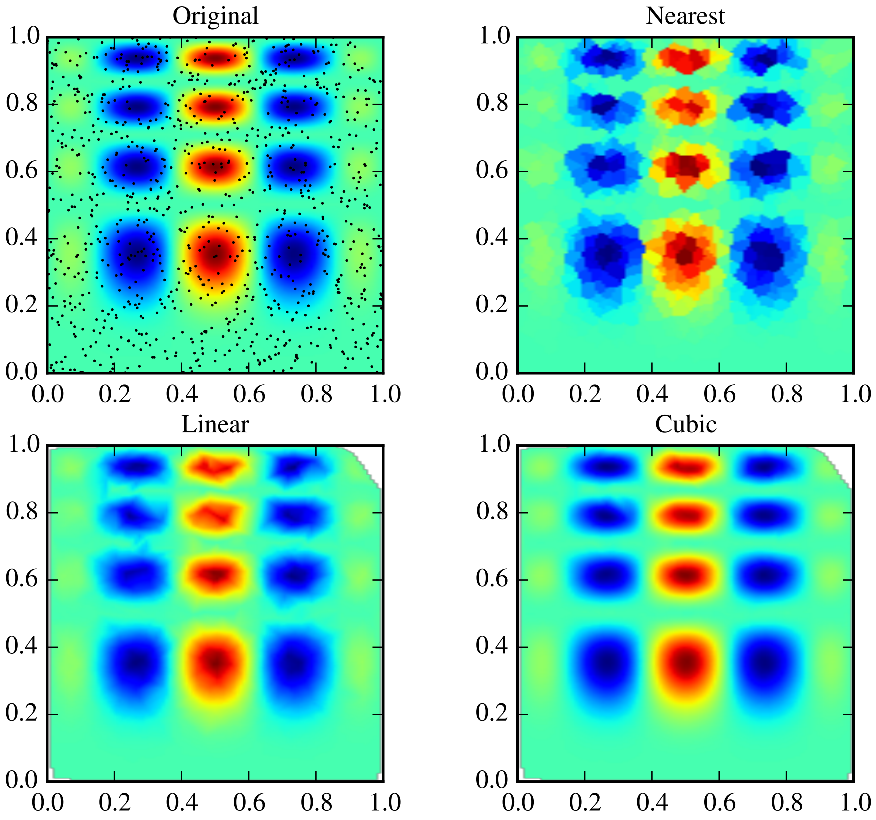
This can be done with `griddata` – below we try out all of the interpolation methods:

```
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(221)
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
```

```
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```



1.6.3 Spline interpolation

Spline interpolation in 1-d: Procedural (interpolate.splXXX)

Spline interpolation requires two essential steps: (1) a spline representation of the curve is computed, and (2) the spline is evaluated at the desired points. In order to find the spline representation, there are two different ways to represent a curve and obtain (smoothing) spline coefficients: directly and parametrically. The direct method finds the spline representation of a curve in a two- dimensional plane using the function `splrep`. The first two arguments are the only ones required, and these provide the x and y components of the curve. The normal output is a 3-tuple, (t, c, k) , containing the knot-points, t , the coefficients c and the order k of the spline. The default spline order is cubic, but this can be changed with the input keyword, *k.*

For curves in N -dimensional space the function `splprep` allows defining the curve parametrically. For this function only 1 input argument is required. This input is a list of N -arrays representing the curve in N -dimensional space. The length of each array is the number of curve points, and each array provides one component of the N -dimensional data point. The parameter variable is given with the keword argument, *u,* which defaults to an equally-spaced monotonic sequence between 0 and 1 . The default output consists of two objects: a 3-tuple, (t, c, k) , containing the spline representation and the parameter variable u.

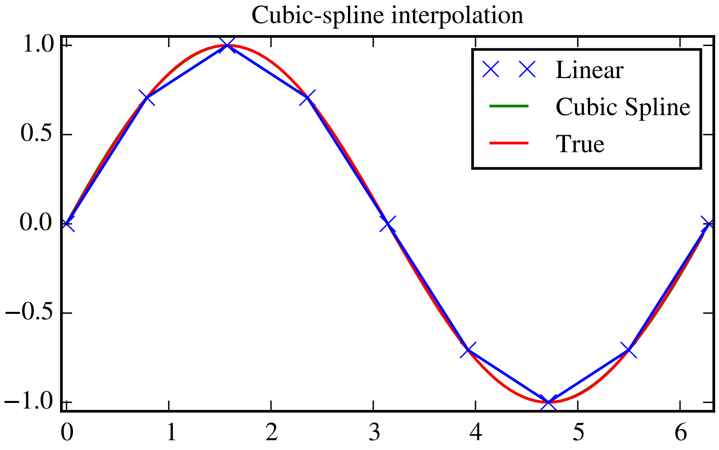
The keyword argument, s , is used to specify the amount of smoothing to perform during the spline fit. The default value of s is $s = m - \sqrt{2m}$ where m is the number of data-points being fit. Therefore, **if no smoothing is desired a value of s $= 0$ should be passed to the routines.**

Once the spline representation of the data has been determined, functions are available for evaluating the spline (`splev`) and its derivatives (`splev`, `spalde`) at any point and the integral of the spline between any two points (`splint`). In addition, for cubic splines ($k = 3$) with 8 or more knots, the roots of the spline can be estimated (`sproot`). These functions are demonstrated in the example that follows.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
```

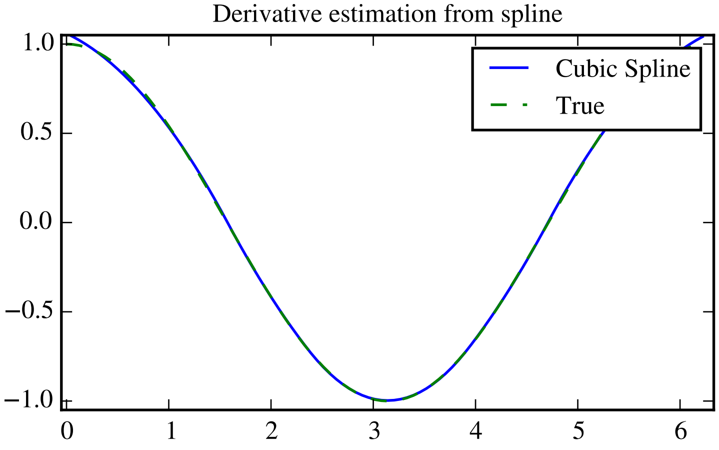
Cubic-spline

```
>>> x = np.arange(0, 2*np.pi+np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> tck = interpolate.splrep(x, y, s=0)
>>> xnew = np.arange(0,2*np.pi,np.pi/50)
>>> ynew = interpolate.splev(xnew, tck, der=0)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Cubic-spline interpolation')
>>> plt.show()
```



Derivative of spline

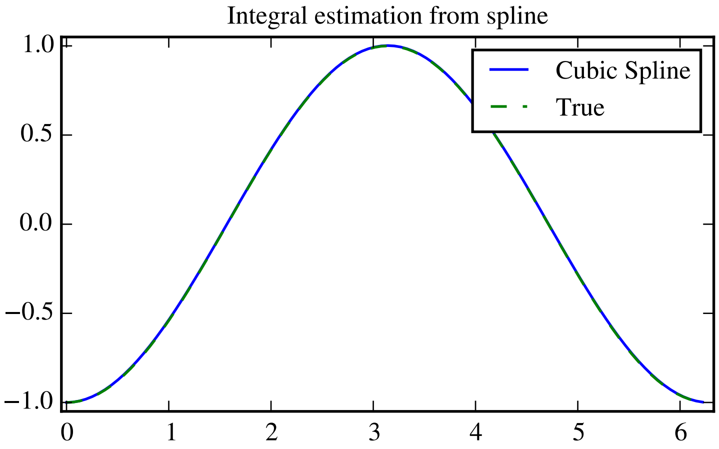
```
>>> yder = interpolate.splev(xnew, tck, der=1)
>>> plt.figure()
>>> plt.plot(xnew,yder,xnew,np.cos(xnew),'--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Derivative estimation from spline')
>>> plt.show()
```



Integral of spline

```
>>> def integ(x, tck, constant=-1):
>>>     x = np.atleast_1d(x)
>>>     out = np.zeros(x.shape, dtype=x.dtype)
>>>     for n in xrange(len(out)):
>>>         out[n] = interpolate.splint(0, x[n], tck)
>>>     out += constant
```

```
>>>     return out
>>>
>>> yint = integ(xnew, tck)
>>> plt.figure()
>>> plt.plot(xnew, yint, xnew, -np.cos(xnew), '--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Integral estimation from spline')
>>> plt.show()
```

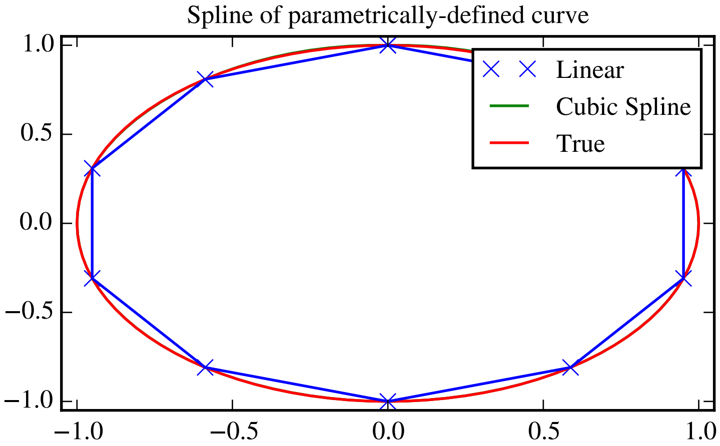


Roots of spline

```
>>> print(interpolate.sproot(tck))
[ 0.      3.1416]
```

Parametric spline

```
>>> t = np.arange(0, 1.1, .1)
>>> x = np.sin(2*np.pi*t)
>>> y = np.cos(2*np.pi*t)
>>> tck,u = interpolate.splprep([x,y], s=0)
>>> unew = np.arange(0, 1.01, 0.01)
>>> out = interpolate.splev(unew, tck)
>>> plt.figure()
>>> plt.plot(x, y, 'x', out[0], out[1], np.sin(2*np.pi*unew), np.cos(2*np.pi*unew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-1.05, 1.05, -1.05, 1.05])
>>> plt.title('Spline of parametrically-defined curve')
>>> plt.show()
```



Spline interpolation in 1-d: Object-oriented (`UnivariateSpline`)

The spline-fitting capabilities described above are also available via an objected-oriented interface. The one dimensional splines are objects of the `UnivariateSpline` class, and are created with the x and y components of the curve provided as arguments to the constructor. The class defines `__call__`, allowing the object to be called with the x-axis values at which the spline should be evaluated, returning the interpolated y-values. This is shown in the example below for the subclass `InterpolatedUnivariateSpline`. The `integral`, `derivatives`, and `roots` methods are also available on `UnivariateSpline` objects, allowing definite integrals, derivatives, and roots to be computed for the spline.

The UnivariateSpline class can also be used to smooth data by providing a non-zero value of the smoothing parameter `s`, with the same meaning as the `s` keyword of the `splrep` function described above. This results in a spline that has fewer knots than the number of data points, and hence is no longer strictly an interpolating spline, but rather a smoothing spline. If this is not desired, the `InterpolatedUnivariateSpline` class is available. It is a subclass of `UnivariateSpline` that always passes through all points (equivalent to forcing the smoothing parameter to 0). This class is demonstrated in the example below.

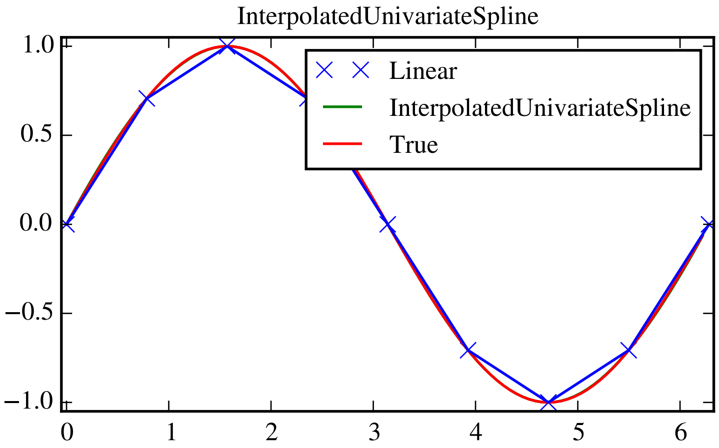
The `LSQUnivariateSpline` class is the other subclass of `UnivariateSpline`. It allows the user to specify the number and location of internal knots explicitly with the parameter *t*. This allows creation of customized splines with non-linear spacing, to interpolate in some domains and smooth in others, or change the character of the spline.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
```

InterpolatedUnivariateSpline

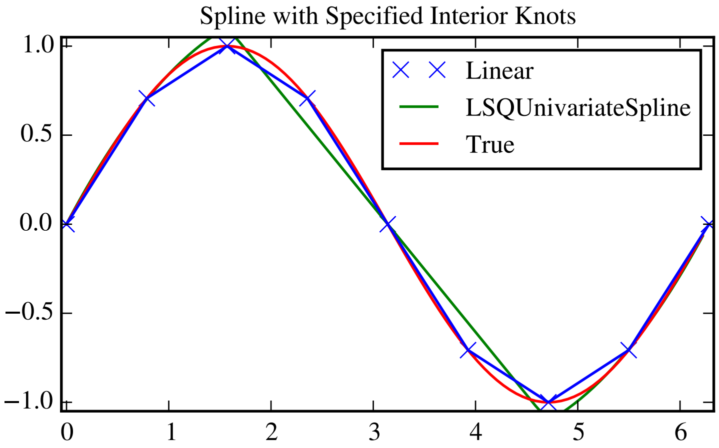
```
>>> x = np.arange(0, 2*np.pi+np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> s = interpolate.InterpolatedUnivariateSpline(x, y)
>>> xnew = np.arange(0, 2*np.pi, np.pi/50)
>>> ynew = s(xnew)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'InterpolatedUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
```

```
>>> plt.title('InterpolatedUnivariateSpline')
>>> plt.show()
```



LSQUnivarateSpline with non-uniform knots

```
>>> t = [np.pi/2-.1, np.pi/2+.1, 3*np.pi/2-.1, 3*np.pi/2+.1]
>>> s = interpolate.LSQUnivariateSpline(x, y, t, k=2)
>>> ynew = s(xnew)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'LSQUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Spline with Specified Interior Knots')
>>> plt.show()
```



Two-dimensional spline representation: Procedural (`bisplrep`)

For (smooth) spline-fitting to a two dimensional surface, the function `bisplrep` is available. This function takes as required inputs the **1-D** arrays *x*, *y*, and *z* which represent points on the surface $z = f(x, y)$. The default output is a list $[tx, ty, c, kx, ky]$ whose entries represent respectively, the components of the knot positions, the coefficients of the spline, and the order of the spline in each coordinate. It is convenient to hold this list in a single object, *tck,* so that it can be passed easily to the function `bisplev`. The keyword, s , can be used to change the amount of smoothing performed on the data while determining the appropriate spline. The default value is $s = m - \sqrt{2m}$ where m is the number of data points in the *x, y,* and *z* vectors. As a result, if no smoothing is desired, then $s = 0$ should be passed to `bisplrep`.

To evaluate the two-dimensional spline and it's partial derivatives (up to the order of the spline), the function `bisplev` is required. This function takes as the first two arguments **two 1-D arrays** whose cross-product specifies the domain over which to evaluate the spline. The third argument is the *tck* list returned from `bisplrep`. If desired, the fourth and fifth arguments provide the orders of the partial derivative in the x and y direction respectively.

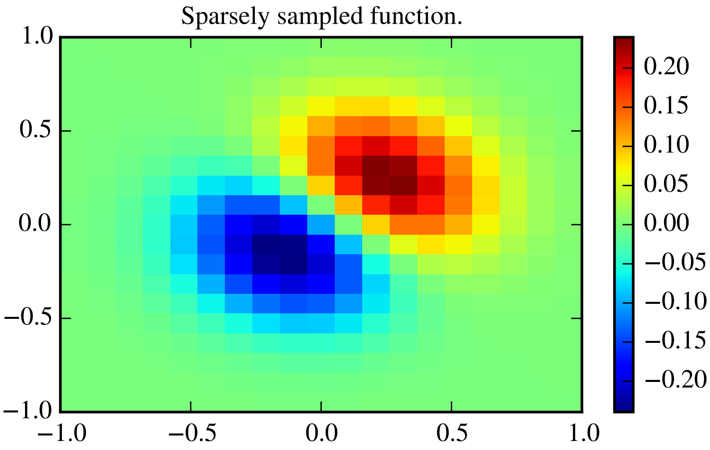
It is important to note that two dimensional interpolation should not be used to find the spline representation of images. The algorithm used is not amenable to large numbers of input points. The signal processing toolbox contains more appropriate algorithms for finding the spline representation of an image. The two dimensional interpolation commands are intended for use when interpolating a two dimensional function as shown in the example that follows. This example uses the `mgrid` command in NumPy which is useful for defining a "mesh-grid" in many dimensions. (See also the `ogrid` command if the full-mesh is not needed). The number of output arguments and the number of dimensions of each argument is determined by the number of indexing objects passed in `mgrid`.

```
>>> import numpy as np
>>> from scipy import interpolate
>>> import matplotlib.pyplot as plt
```

Define function over sparse 20x20 grid

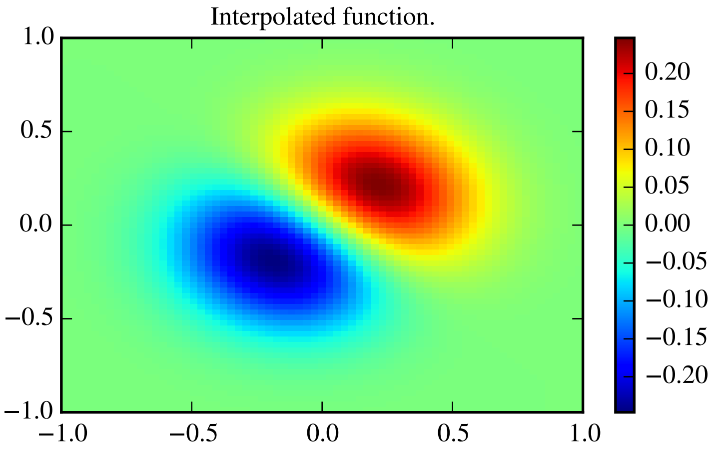
```
>>> x, y = np.mgrid[-1:1:20j, -1:1:20j]
>>> z = (x+y) * np.exp(-6.0*(x*x+y*y))
```

```
>>> plt.figure()
>>> plt.pcolor(x, y, z)
>>> plt.colorbar()
>>> plt.title("Sparsely sampled function.")
>>> plt.show()
```



Interpolate function over new 70x70 grid

```
>>> xnew, ynew = np.mgrid[-1:1:70j, -1:1:70j]
>>> tck = interpolate.bisplrep(x, y, z, s=0)
>>> znew = interpolate.bisplev(xnew[:,0], ynew[0,:], tck)

>>> plt.figure()
>>> plt.pcolor(xnew, ynew, znew)
>>> plt.colorbar()
>>> plt.title("Interpolated function.")
>>> plt.show()
```



Two-dimensional spline representation: Object-oriented (`BivariateSpline`)

The `BivariateSpline` class is the 2-dimensional analog of the `UnivariateSpline` class. It and its subclasses implement the FITPACK functions described above in an object oriented fashion, allowing objects to be instantiated that can be called to compute the spline value by passing in the two coordinates as the two arguments.

1.6.4 Using radial basis functions for smoothing/interpolation

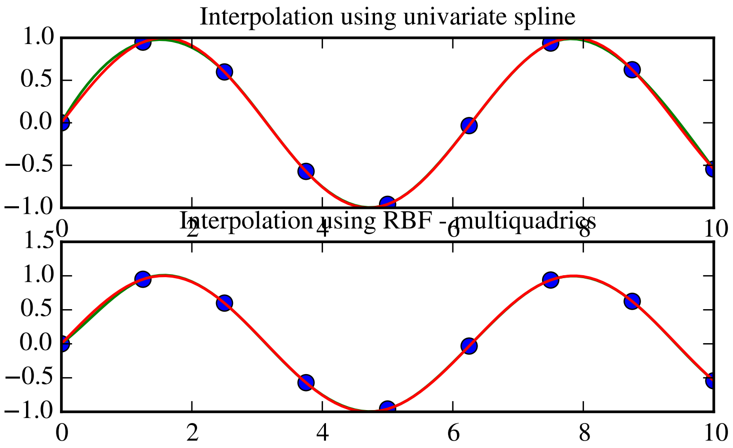
Radial basis functions can be used for smoothing/interpolating scattered data in n-dimensions, but should be used with caution for extrapolation outside of the observed data range.

1-d Example

This example compares the usage of the `Rbf` and `UnivariateSpline` classes from the scipy.interpolate module.

```
>>> import numpy as np
>>> from scipy.interpolate import Rbf, InterpolatedUnivariateSpline
>>> import matplotlib.pyplot as plt

>>> # setup data
>>> x = np.linspace(0, 10, 9)
>>> y = np.sin(x)
>>> xi = np.linspace(0, 10, 101)
```

```
>>> # use fitpack2 method
>>> ius = InterpolatedUnivariateSpline(x, y)
>>> yi = ius(xi)

>>> plt.subplot(2, 1, 1)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, yi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using univariate spline')

>>> # use RBF method
>>> rbf = Rbf(x, y)
>>> fi = rbf(xi)

>>> plt.subplot(2, 1, 2)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, fi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using RBF - multiquadrics')
>>> plt.show()
```

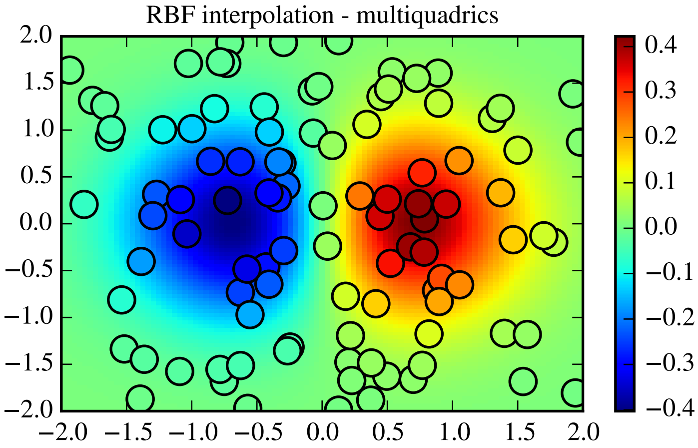


2-d Example

This example shows how to interpolate scattered 2d data.

```
>>> import numpy as np
>>> from scipy.interpolate import Rbf
>>> import matplotlib.pyplot as plt
>>> from matplotlib import cm

>>> # 2-d tests - setup scattered data
>>> x = np.random.rand(100)*4.0-2.0
>>> y = np.random.rand(100)*4.0-2.0
>>> z = x*np.exp(-x**2-y**2)
>>> ti = np.linspace(-2.0, 2.0, 100)
>>> XI, YI = np.meshgrid(ti, ti)
```

```
>>> # use RBF
>>> rbf = Rbf(x, y, z, epsilon=2)
>>> ZI = rbf(XI, YI)

>>> # plot the result
>>> n = plt.normalize(-2., 2.)
>>> plt.subplot(1, 1, 1)
>>> plt.pcolor(XI, YI, ZI, cmap=cm.jet)
>>> plt.scatter(x, y, 100, z, cmap=cm.jet)
>>> plt.title('RBF interpolation - multiquadrics')
>>> plt.xlim(-2, 2)
>>> plt.ylim(-2, 2)
>>> plt.colorbar()
```



1.7 Fourier Transforms (`scipy.fftpack`)

Contents

Fourier analysis is a method for expressing a function as a sum of periodic components, and for recovering the signal from those components. When both the function and its Fourier transform are replaced with discretized counterparts, it is called the discrete Fourier transform (DFT). The DFT has become a mainstay of numerical computing in part because of a very fast algorithm for computing it, called the Fast Fourier Transform (FFT), which was known to Gauss (1805) and was brought to light in its current form by Cooley and Tukey [CT65]. Press et al. [NR] provide an accessible introduction to Fourier analysis and its applications.

1.7.1 Fast Fourier transforms

One dimensional discrete Fourier transforms

The FFT *y[k]* of length N of the length-N sequence *x[n]* is defined as

$$y[k] = \sum_{n=0}^{N-1} e^{-2\pi j \frac{kn}{N}} x[n] \, ,$$

and the inverse transform is defined as follows

$$x[n] = \frac{1}{N} \sum_{n=0}^{N-1} e^{2\pi j \frac{kn}{N}} y[k] \, .$$

These transforms can be calculated by means of `fft` and `ifft`, respectively as shown in the following example.

```
>>> from scipy.fftpack import fft, ifft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> y = fft(x)
>>> y
[ 4.50000000+0.j          2.08155948-1.65109876j -1.83155948+1.60822041j
 -1.83155948-1.60822041j  2.08155948+1.65109876j]
>>> yinv = ifft(y)
>>> yinv
[ 1.0+0.j  2.0+0.j  1.0+0.j -1.0+0.j  1.5+0.j]
```

From the definition of the FFT it can be seen that

$$y[0] = \sum_{n=0}^{N-1} x[n]\,.$$

In the example

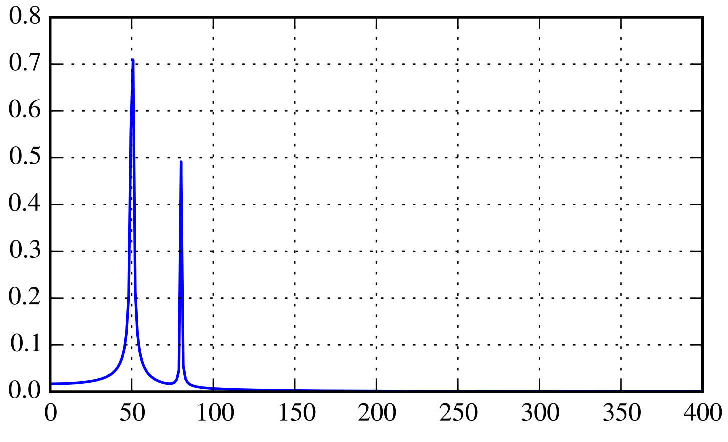
```
>>> np.sum(x)
4.5
```

which corresponds to $y[0]$. For N even, the elements $y[1]...y[N/2-1]$ contain the positive-frequency terms, and the elements $y[N/2]...y[N-1]$ contain the negative-frequency terms, in order of decreasingly negative frequency. For N odd, the elements $y[1]...y[(N-1)/2]$ contain the positive- frequency terms, and the elements $y[(N+1)/2]...y[N-1]$ contain the negative- frequency terms, in order of decreasingly negative frequency.

In case the sequence x is real-valued, the values of $y[n]$ for positive frequencies is the conjugate of the values $y[n]$ for negative frequencies (because the spectrum is symmetric). Typically, only the FFT corresponding to positive frequencies is plotted.

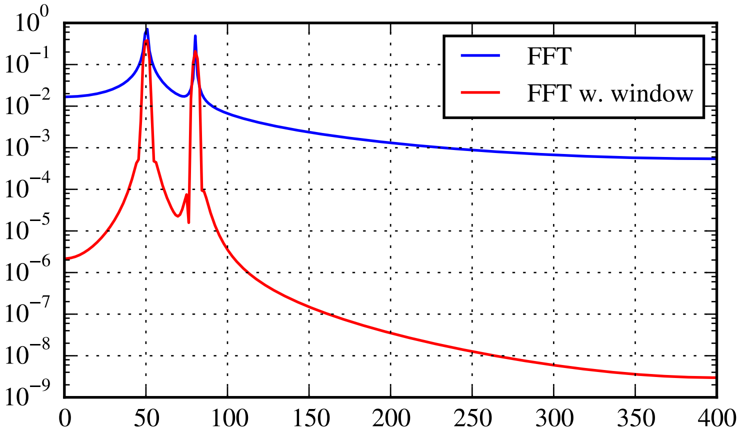
The example plots the FFT of the sum of two sines.

```
>>> from scipy.fftpack import fft
>>> # Number of samplepoints
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> xf = np.linspace(0.0, 1.0/(2.0*T), N/2)
>>> import matplotlib.pyplot as plt
>>> plt.plot(xf, 2.0/N * np.abs(yf[0:N/2]))
>>> plt.grid()
>>> plt.show()
```



The FFT input signal is inherently truncated. This truncation can be modelled as multiplication of an inifinte signal with a rectangular window function. In the spectral domain this multiplication becomes convolution of the signal spectrum with the window function spectrum, being of form $sin(x)/x$. This convolution is the cause of an effect called spectral leakage (see [WPW]). Windowing the signal with a dedicated window function helps mitigate spectral leakage. The example below uses a Blackman window from scipy.signal and shows the effect of windowing (the zero component of the FFT has been truncated illustrative purposes).

```
>>> from scipy.fftpack import fft
>>> # Number of samplepoints
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> from scipy.signal import blackman
>>> w = blackman(N)
>>> ywf = fft(y*w)
>>> xf = np.linspace(0.0, 1.0/(2.0*T), N/2)
>>> import matplotlib.pyplot as plt
>>> plt.semilogy(xf[1:N/2], 2.0/N * np.abs(yf[1:N/2]), '-b')
>>> plt.semilogy(xf[1:N/2], 2.0/N * np.abs(ywf[1:N/2]), '-r')
>>> plt.legend(['FFT', 'FFT w. window'])
>>> plt.grid()
>>> plt.show()
```



In case the sequence x is complex-valued, the spectrum is no longer symmetric. To simplify working wit the FFT functions, scipy provides the following two helper functions.

The function `fftfreq` returns the FFT sample frequency points.

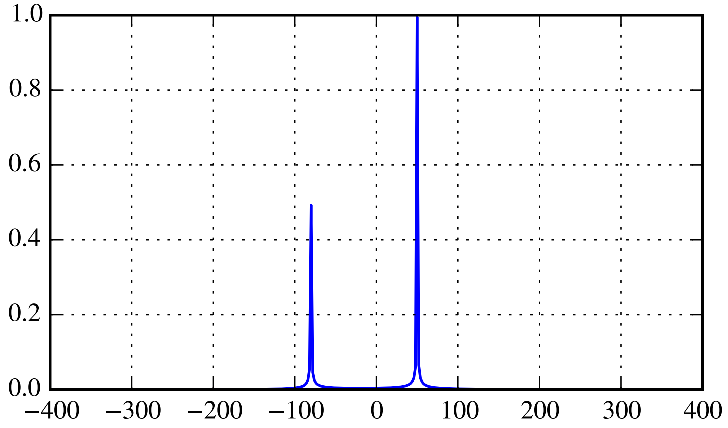
```
>>> from scipy.fftpack import fftfreq
>>> freq = fftfreq(np.arange(8), 0.125)
[ 0.  1.  2.  3. -4. -3. -2. -1.]
```

In a similar spirit, the function `fftshift` allows swapping the lower and upper halves of a vector, so that it becomes suitable for display.

```
>>> from scipy.fftpack import fftfreq
>>> x = np.arange(8)
>>> sf.fftshift(x)
[4 5 6 7 0 1 2 3]
```

The example below plots the FFT of two complex exponentials; note the asymmetric spectrum.

```
>>> from scipy.fftpack import fft, fftfreq, fftshift
>>> # number of signal points
>>> N = 400
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.exp(50.0 * 1.j * 2.0*np.pi*x) + 0.5*np.exp(-80.0 * 1.j * 2.0*np.pi*x)
>>> yf = fft(y)
>>> xf = fftfreq(N, T)
>>> xf = fftshift(xf)
>>> yplot = fftshift(yf)
>>> import matplotlib.pyplot as plt
>>> plt.plot(xf, 1.0/N * np.abs(yplot))
>>> plt.grid()
>>> plt.show()
```



The function `rfft` calculates the FFT of a real sequence and outputs the FFT coefficients $y[n]$ with separate real and imaginary parts. In case of N being even: $[y[0], Re(y[1]), Im(y[1]), ..., Re(y[N/2])]$; in case N being odd $[y[0], Re(y[1]), Im(y[1]), ..., Re(y[N/2]), Im(y[N/2])]$.

The corresponding function `irfft` calculates the IFFT of the FFT coefficients with this special ordering.

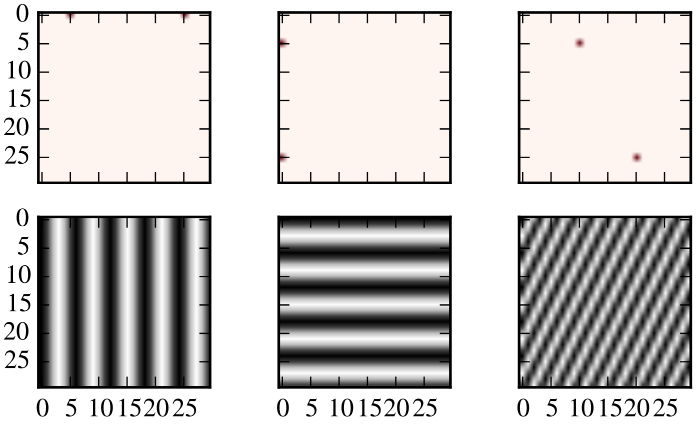
```
>>> from scipy.fftpack import fft, rfft, irfft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5, 1.0])
>>> fft(x)
[ 5.50+0.j          2.25-0.4330127j  -2.75-1.29903811j  1.50+0.j
 -2.75+1.29903811j  2.25+0.4330127j ]
>>> yr = rfft(x)
[ 5.5         2.25        -0.4330127  -2.75        -1.29903811  1.5        ]
>>> irfft(yr)
[ 1.   2.   1.  -1.   1.5  1. ]
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> fft(x)
[ 4.50000000+0.j          2.08155948-1.65109876j -1.83155948+1.60822041j
 -1.83155948-1.60822041j  2.08155948+1.65109876j]
>>> yr = rfft(x)
[ 4.5         2.08155948 -1.65109876 -1.83155948  1.60822041]
```

Two and n-dimensional discrete Fourier transforms

The functions `fft2` and `ifft2` provide 2-dimensional FFT, and IFFT, respectively. Similar, `fftn` and `ifftn` provide n-dimensional FFT, and IFFT, respectively.

The example below demonstrates a 2-dimensional IFFT and plots the resulting (2-dimensional) time-domain signals.

```
>>> from scipy.fftpack import ifftn
>>> import matplotlib.pyplot as plt
>>> import matplotlib.cm as cm
>>> N = 30
>>> f, ((ax1, ax2, ax3), (ax4, ax5, ax6)) = plt.subplots(2, 3, sharex='col', sharey='row')
>>> xf = np.zeros((N,N))
>>> xf[0, 5] = 1
>>> xf[0, N-5] = 1
>>> Z = ifftn(xf)
>>> ax1.imshow(xf, cmap=cm.Reds)
>>> ax4.imshow(np.real(Z), cmap=cm.binary)
>>> xf = np.zeros((N, N))
>>> xf[5, 0] = 1
>>> xf[N-5, 0] = 1
>>> Z = ifftn(xf)
>>> ax2.imshow(xf, cmap=cm.Reds)
>>> ax5.imshow(np.real(Z), cmap=cm.binary)
>>> xf = np.zeros((N, N))
>>> xf[5, 10] = 1
>>> xf[N-5, N-10] = 1
>>> Z = ifftn(xf)
>>> ax3.imshow(xf, cmap=cm.Reds)
>>> ax6.imshow(np.real(Z), cmap=cm.binary)
>>> plt.show()
```



FFT convolution

`scipy.fftpack.convolve` performs a convolution of two one-dimensional arrays in frequency domain.

1.7.2 Discrete Cosine Transforms

Scipy provides a DCT with the function `dct` and a corresponding IDCT with the function `idct`. There are 8 types of the DCT [WPC], [Mak]; however, only the first 3 types are implemented in scipy. "The" DCT generally refers to DCT type 2, and "the" Inverse DCT generally refers to DCT type 3. In addition, the DCT coefficients can be normalized differently (for most types, scipy provides `None` and `ortho`). Two parameters of the dct/idct function calls allow setting the DCT type and coefficient normalization.

For a single dimension array x, dct(x, norm='ortho') is equal to MATLAB dct(x).

Type I DCT

Scipy uses the following definition of the unnormalized DCT-I (`norm='None'`):

$$y[k] = x_0 + (-1)^k x_{N-1} + 2\sum_{n=1}^{N-2} x[n]\cos\left(\frac{\pi nk}{N-1}\right), \qquad 0 \le k < N.$$

Only `None` is supported as normalization mode for DCT-I. Note also that the DCT-I is only supported for input size > 1

Type II DCT

Scipy uses the following definition of the unnormalized DCT-II (`norm='None'`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n]\cos\left(\frac{\pi(2n+1)k}{2N}\right) \qquad 0 \le k < N.$$

In case of the normalized DCT (`norm='ortho'`), the DCT coefficients $y[k]$ are multiplied by a scaling factor f:

$$f = \begin{cases} \sqrt{1/(4N)}, & \text{if } k = 0 \\ \sqrt{1/(2N)}, & \text{otherwise} \end{cases}.$$

In this case, the DCT "base functions" $\phi_k[n] = 2f\cos\left(\frac{\pi(2n+1)k}{2N}\right)$ become orthonormal:

$$\sum_{n=0}^{N-1} \phi_k[n]\phi_l[n] = \delta_{lk}$$

Type III DCT

Scipy uses the following definition of the unnormalized DCT-III (`norm='None'`):

$$y[k] = x_0 + 2\sum_{n=1}^{N-1} x[n]\cos\left(\frac{\pi n(2k+1)}{2N}\right) \qquad 0 \le k < N,$$

or, for `norm='ortho'`:

$$y[k] = \frac{x_0}{\sqrt{N}} + \frac{2}{\sqrt{N}}\sum_{n=1}^{N-1} x[n]\cos\left(\frac{\pi n(2k+1)}{2N}\right) \qquad 0 \le k < N.$$

DCT and IDCT

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor *2N*. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT- II. The function `idct` performs the mappings between the DCT and IDCT types.

The example below shows the relation between DCT and IDCT for different types and normalizations.

```
>>> from scipy.fftpack import dct, idct
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> dct(dct(x, type=2, norm='ortho'), type=3, norm='ortho')
[1.0, 2.0, 1.0, -1.0, 1.5]
>>>  # scaling factor 2*N = 10
>>> idct(dct(x, type=2), type=2)
[ 10.  20.  10. -10.  15.]
>>>  # no scaling factor
>>> idct(dct(x, type=2, norm='ortho'), type=2, norm='ortho')
[ 1.   2.   1.  -1.   1.5]
>>>  # scaling factor 2*N = 10
>>> idct(dct(x, type=3), type=3)
[ 10.  20.  10. -10.  15.]
>>>  # no scaling factor
>>> idct(dct(x, type=3, norm='ortho'), type=3, norm='ortho')
[ 1.   2.   1.  -1.   1.5]
>>>  # scaling factor 2*(N-1) = 8
>>> idct(dct(x, type=1), type=1)
[  8.  16.   8.  -8.  12.]
```

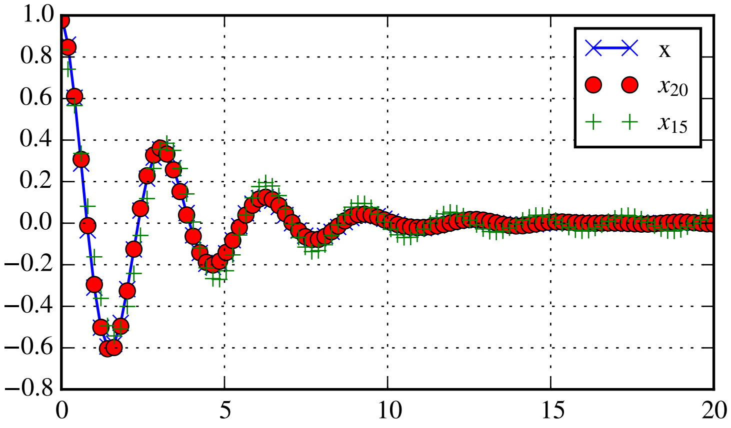
Example

The DCT exhibits the "energy compaction property", meaning that for many signals only the first few DCT coefficients have significant magnitude. Zeroing out the other coefficients leads to a small reconstruction error, a fact which is exploited in lossy signal compression (e.g. JPEG compression).

The example below shows a signal x and two reconstructions (x_{20} and x_{15})from the signal's DCT coefficients. The signal x_{20} is reconstructed from the first 20 DCT coefficients, x_{15} is reconstructed from the first 15 DCT coefficients. It can be seen that the relative error of using 20 coefficients is still very small (~0.1%), but provides a five-fold compression rate.

```
>>> from scipy.fftpack import dct, idct
>>> import matplotlib.pyplot as plt
>>> N = 100
>>> t = np.linspace(0,20,N)
>>> x = np.exp(-t/3)*np.cos(2*t)
>>> y = dct(x, norm='ortho')
>>> window = np.zeros(N)
>>> window[:20] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.0010901402257
>>> plt.plot(t, x, '-bx')
>>> plt.plot(t, yr, 'ro')
>>> window = np.zeros(N)
>>> window[:15] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.0718818065008
>>> plt.plot(t, yr, 'g+')
```

```
>>> plt.legend(['x', '$x_{20}$', '$x_{15}$'])
>>> plt.grid()
>>> plt.show()
```



1.7.3 Discrete Sine Transforms

Scipy provides a DST [Mak] with the function `dst` and a corresponding IDST with the function `idst`.

There are theoretically 8 types of the DST for different combinations of even/odd boundary conditions and boundary off sets [WPS], only the first 3 types are implemented in scipy.

Type I DST

DST-I assumes the input is odd around n=-1 and n=N. Scipy uses the following definition of the unnormalized DST-I (`norm='None'`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n]\sin\left(\frac{\pi(n+1)(k+1)}{N+1}\right), \qquad 0 \le k < N.$$

Only `None` is supported as normalization mode for DST-I. Note also that the DST-I is only supported for input size > 1. The (unnormalized) DST-I is its own inverse, up to a factor *2(N+1)*.

Type II DST

DST-II assumes the input is odd around n=-1/2 and even around n=N. Scipy uses the following definition of the unnormalized DST-II (`norm='None'`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n]\sin\left(\frac{\pi(n+1/2)(k+1)}{N}\right), \qquad 0 \le k < N.$$

Type III DST

DST-III assumes the input is odd around n=-1 and even around n=N-1. Scipy uses the following definition of the unnormalized DST-III (`norm='None'`):

$$y[k] = (-1)^k x[N-1] + 2\sum_{n=0}^{N-2} x[n]\sin\left(\frac{\pi(n+1)(k+1/2)}{N}\right), \qquad 0 \le k < N.$$

DST and IDST

The example below shows the relation between DST and IDST for different types and normalizations.

```
>>> from scipy.fftpack import dst, idst
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>>  # scaling factor 2*N = 10
>>> idst(dst(x, type=2), type=2)
[ 10.  20.  10. -10.  15.]
>>>  # no scaling factor
>>> idst(dst(x, type=2, norm='ortho'), type=2, norm='ortho')
[ 1.   2.   1.  -1.   1.5]
>>>  # scaling factor 2*N = 10
>>> idst(dst(x, type=3), type=3)
[ 10.  20.  10. -10.  15.]
>>>  # no scaling factor
>>> idst(dst(x, type=3, norm='ortho'), type=3, norm='ortho')
[ 1.   2.   1.  -1.   1.5]
>>>  # scaling factor 2*(N+1) = 8
>>> idst(dst(x, type=1), type=1)
[  8.  16.   8.  -8.  12.]
```

1.7.4 Cache Destruction

To accelerate repeat transforms on arrays of the same shape and dtype, scipy.fftpack keeps a cache of the prime factorization of length of the array and pre-computed trigonometric functions. These caches can be destroyed by calling the appropriate function in `scipy.fftpack._fftpack`. dst(type=1) and idst(type=1) share a cache (`*dst1_cache`). As do dst(type=2), dst(type=3), idst(type=3), and idst(type=3) (`*dst2_cache`).

1.7.5 References

1.8 Signal Processing (`scipy.signal`)

The signal processing toolbox currently contains some filtering functions, a limited set of filter design tools, and a few B-spline interpolation algorithms for one- and two-dimensional data. While the B-spline algorithms could technically be placed under the interpolation category, they are included here because they only work with equally-spaced data and make heavy use of filter-theory and transfer-function formalism to provide a fast B-spline transform. To understand this section you will need to understand that a signal in SciPy is an array of real or complex numbers.

1.8.1 B-splines

A B-spline is an approximation of a continuous function over a finite- domain in terms of B-spline coefficients and knot points. If the knot- points are equally spaced with spacing Δx , then the B-spline approximation to a 1-dimensional function is the finite-basis expansion.

$$y\left(x\right)\approx\sum_{j}c_{j}\beta^{o}\left(\frac{x}{\Delta x}-j\right).$$

In two dimensions with knot-spacing Δx and Δy , the function representation is

$$z\left(x,y\right)\approx\sum_{j}\sum_{k}c_{jk}\beta^{o}\left(\frac{x}{\Delta x}-j\right)\beta^{o}\left(\frac{y}{\Delta y}-k\right).$$

In these expressions, $\beta^{o}\left(\cdot\right)$ is the space-limited B-spline basis function of order, o . The requirement of equally-spaced knot-points and equally-spaced data points, allows the development of fast (inverse-filtering) algorithms for determining the coefficients, c_{j} , from sample-values, y_{n} . Unlike the general spline interpolation algorithms, these algorithms can quickly find the spline coefficients for large images.

The advantage of representing a set of samples via B-spline basis functions is that continuous-domain operators (derivatives, re- sampling, integral, etc.) which assume that the data samples are drawn from an underlying continuous function can be computed with relative ease from the spline coefficients. For example, the second-derivative of a spline is

$$y^{\prime\prime}\left(x\right)=\frac{1}{\Delta x^{2}}\sum_{j}c_{j}\beta^{o\prime\prime}\left(\frac{x}{\Delta x}-j\right).$$

Using the property of B-splines that

$$\frac{d^{2}\beta^{o}\left(w\right)}{dw^{2}}=\beta^{o-2}\left(w+1\right)-2\beta^{o-2}\left(w\right)+\beta^{o-2}\left(w-1\right)$$

it can be seen that

$$y^{\prime\prime}\left(x\right)=\frac{1}{\Delta x^{2}}\sum_{j}c_{j}\left[\beta^{o-2}\left(\frac{x}{\Delta x}-j+1\right)-2\beta^{o-2}\left(\frac{x}{\Delta x}-j\right)+\beta^{o-2}\left(\frac{x}{\Delta x}-j-1\right)\right].$$

If $o=3$, then at the sample points,

$$\begin{aligned}\Delta x^{2}\left.y^{\prime}\left(x\right)\right|_{x=n\Delta x} &= \sum_{j}c_{j}\delta_{n-j+1}-2c_{j}\delta_{n-j}+c_{j}\delta_{n-j-1},\\ &= c_{n+1}-2c_{n}+c_{n-1}.\end{aligned}$$

Thus, the second-derivative signal can be easily calculated from the spline fit. if desired, smoothing splines can be found to make the second-derivative less sensitive to random-errors.

The savvy reader will have already noticed that the data samples are related to the knot coefficients via a convolution operator, so that simple convolution with the sampled B-spline function recovers the original data from the spline coefficients. The output of convolutions can change depending on how boundaries are handled (this becomes increasingly more important as the number of dimensions in the data- set increases). The algorithms relating to B-splines in the signal- processing sub package assume mirror-symmetric boundary conditions. Thus, spline coefficients are computed based on that assumption, and data-samples can be recovered exactly from the spline coefficients by assuming them to be mirror-symmetric also.

Currently the package provides functions for determining second- and third- order cubic spline coefficients from equally spaced samples in one- and two- dimensions (`qspline1d`, `qspline2d`, `cspline1d`, `cspline2d`). The package also supplies a function (`bspline`) for evaluating the bspline basis function, $\beta^{o}\left(x\right)$ for arbitrary order and x. For large o , the B-spline basis function can be approximated well by a zero-mean Gaussian function with standard-deviation equal to $\sigma_{o}=\left(o+1\right)/12$:

$$\beta^{o}\left(x\right)\approx\frac{1}{\sqrt{2\pi\sigma_{o}^{2}}}\exp\left(-\frac{x^{2}}{2\sigma_{o}}\right).$$

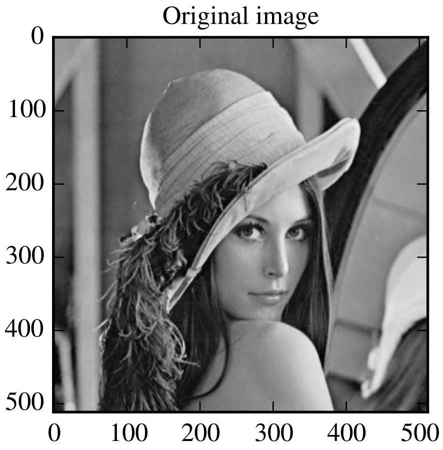
A function to compute this Gaussian for arbitrary x and o is also available (`gauss_spline`). The following code and Figure uses spline-filtering to compute an edge-image (the second-derivative of a smoothed spline) of Lena's face which is an array returned by the command `misc.lena`. The command `sepfir2d` was used to apply a separable two-dimensional FIR filter with mirror- symmetric boundary conditions to the spline coefficients. This function is ideally suited for reconstructing samples from spline coefficients and is faster than `convolve2d` which convolves arbitrary two-dimensional filters and allows for choosing mirror-symmetric boundary conditions.

```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.lena().astype(np.float32)
>>> derfilt = np.array([1.0, -2, 1.0], dtype=np.float32)
>>> ck = signal.cspline2d(image, 8.0)
>>> deriv = (signal.sepfir2d(ck, derfilt, [1]) +
...          signal.sepfir2d(ck, [1], derfilt))
```

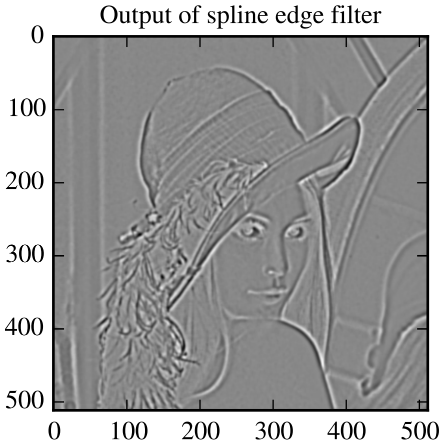
Alternatively we could have done:

```
laplacian = np.array([[0,1,0], [1,-4,1], [0,1,0]], dtype=np.float32)
deriv2 = signal.convolve2d(ck,laplacian,mode='same',boundary='symm')
```

```
>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```



```
>>> plt.figure()
>>> plt.imshow(deriv)
>>> plt.gray()
>>> plt.title('Output of spline edge filter')
>>> plt.show()
```



1.8.2 Filtering

Filtering is a generic name for any system that modifies an input signal in some way. In SciPy a signal can be thought of as a Numpy array. There are different kinds of filters for different kinds of operations. There are two broad kinds of filtering operations: linear and non-linear. Linear filters can always be reduced to multiplication of the flattened Numpy array by an appropriate matrix resulting in another flattened Numpy array. Of course, this is not usually the best way to compute the filter as the matrices and vectors involved may be huge. For example filtering a 512×512 image with this method would require multiplication of a $512^2 \times 512^2$ matrix with a 512^2 vector. Just trying to store the $512^2 \times 512^2$ matrix using a standard Numpy array would require $68,719,476,736$ elements. At 4 bytes per element this would require $256\mathrm{GB}$ of memory. In most applications most of the elements of this matrix are zero and a different method for computing the output of the filter is employed.

Convolution/Correlation

Many linear filters also have the property of shift-invariance. This means that the filtering operation is the same at different locations in the signal and it implies that the filtering matrix can be constructed from knowledge of one row (or column) of the matrix alone. In this case, the matrix multiplication can be accomplished using Fourier transforms.

Let $x[n]$ define a one-dimensional signal indexed by the integer n. Full convolution of two one-dimensional signals can be expressed as

$$y[n] = \sum_{k=-\infty}^{\infty} x[k]\, h[n-k]\,.$$

This equation can only be implemented directly if we limit the sequences to finite support sequences that can be stored in a computer, choose $n = 0$ to be the starting point of both sequences, let $K+1$ be that value for which $y[n] = 0$ for all $n > K+1$ and $M+1$ be that value for which $x[n] = 0$ for all $n > M+1$, then the discrete convolution expression is

$$y[n] = \sum_{k=\max(n-M,0)}^{\min(n,K)} x[k]\, h[n-k]\,.$$

For convenience assume $K \geq M$. Then, more explicitly the output of this operation is

$$\begin{aligned}
y[0] &= x[0]\,h[0] \\
y[1] &= x[0]\,h[1] + x[1]\,h[0] \\
y[2] &= x[0]\,h[2] + x[1]\,h[1] + x[2]\,h[0] \\
\vdots \quad &\vdots \quad \vdots \\
y[M] &= x[0]\,h[M] + x[1]\,h[M-1] + \cdots + x[M]\,h[0] \\
y[M+1] &= x[1]\,h[M] + x[2]\,h[M-1] + \cdots + x[M+1]\,h[0] \\
\vdots \quad &\vdots \quad \vdots \\
y[K] &= x[K-M]\,h[M] + \cdots + x[K]\,h[0] \\
y[K+1] &= x[K+1-M]\,h[M] + \cdots + x[K]\,h[1] \\
\vdots \quad &\vdots \quad \vdots \\
y[K+M-1] &= x[K-1]\,h[M] + x[K]\,h[M-1] \\
y[K+M] &= x[K]\,h[M]\,.
\end{aligned}$$

Thus, the full discrete convolution of two finite sequences of lengths $K+1$ and $M+1$ respectively results in a finite sequence of length $K+M+1=(K+1)+(M+1)-1.$

One dimensional convolution is implemented in SciPy with the function `convolve`. This function takes as inputs the signals x, h , and an optional flag and returns the signal y. The optional flag allows for specification of which part of the output signal to return. The default value of 'full' returns the entire signal. If the flag has a value of 'same' then only the middle K values are returned starting at $y\left[\left\lfloor \frac{M-1}{2}\right\rfloor\right]$ so that the output has the same length as the first input. If the flag has a value of 'valid' then only the middle $K-M+1=(K+1)-(M+1)+1$ output values are returned where z depends on all of the values of the smallest input from $h[0]$ to $h[M]$. In other words only the values $y[M]$ to $y[K]$ inclusive are returned.

The code below shows a simple example for convolution of 2 sequences

```
>>> x = np.array([1.0, 2.0, 3.0])
>>> h = np.array([0.0, 1.0, 0.0, 0.0, 0.0])
>>> signal.convolve(x, h)
[ 0.  1.  2.  3.  0.  0.  0.]
>>> signal.convolve(x, h, 'same')
[ 2.  3.  0.]
```

This same function `convolve` can actually take N -dimensional arrays as inputs and will return the N -dimensional convolution of the two arrays as is shown in the code example below. The same input flags are available for that case as well.

```
>>> x = np.array([[1., 1., 0., 0.],[1., 1., 0., 0.],[0., 0., 0., 0.],[0., 0., 0., 0.]])
>>> h = np.array([[1., 0., 0., 0.],[0., 0., 0., 0.],[0., 0., 1., 0.],[0., 0., 0., 0.]])
>>> signal.convolve(x, h)
[[ 1.  1.  0.  0.  0.  0.  0.]
 [ 1.  1.  0.  0.  0.  0.  0.]
 [ 0.  0.  1.  1.  0.  0.  0.]
 [ 0.  0.  1.  1.  0.  0.  0.]
 [ 0.  0.  0.  0.  0.  0.  0.]
 [ 0.  0.  0.  0.  0.  0.  0.]
 [ 0.  0.  0.  0.  0.  0.  0.]]
```

Correlation is very similar to convolution except for the minus sign becomes a plus sign. Thus

$$w[n] = \sum_{k=-\infty}^{\infty} y[k]\,x[n+k]$$

is the (cross) correlation of the signals y and x. For finite-length signals with $y[n]=0$ outside of the range $[0,K]$ and $x[n]=0$ outside of the range $[0,M]$, the summation can simplify to

$$w[n]=\sum_{k=\max(0,-n)}^{\min(K,M-n)} y[k]\,x[n+k]\,.$$

Assuming again that $K\geq M$ this is

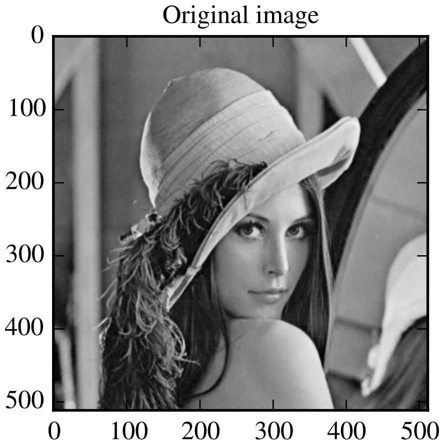
$$\begin{array}{rcl} w[-K] & = & y[K]\,x[0] \\ w[-K+1] & = & y[K-1]\,x[0]+y[K]\,x[1] \\ \vdots & \vdots & \vdots \\ w[M-K] & = & y[K-M]\,x[0]+y[K-M+1]\,x[1]+\cdots+y[K]\,x[M] \\ w[M-K+1] & = & y[K-M-1]\,x[0]+\cdots+y[K-1]\,x[M] \\ \vdots & \vdots & \vdots \\ w[-1] & = & y[1]\,x[0]+y[2]\,x[1]+\cdots+y[M+1]\,x[M] \\ w[0] & = & y[0]\,x[0]+y[1]\,x[1]+\cdots+y[M]\,x[M] \\ w[1] & = & y[0]\,x[1]+y[1]\,x[2]+\cdots+y[M-1]\,x[M] \\ w[2] & = & y[0]\,x[2]+y[1]\,x[3]+\cdots+y[M-2]\,x[M] \\ \vdots & \vdots & \vdots \\ w[M-1] & = & y[0]\,x[M-1]+y[1]\,x[M] \\ w[M] & = & y[0]\,x[M]\,. \end{array}$$

The SciPy function `correlate` implements this operation. Equivalent flags are available for this operation to return the full $K+M+1$ length sequence ('full') or a sequence with the same size as the largest sequence starting at $w\left[-K+\left\lfloor\frac{M-1}{2}\right\rfloor\right]$ ('same') or a sequence where the values depend on all the values of the smallest sequence ('valid'). This final option returns the $K-M+1$ values $w[M-K]$ to $w[0]$ inclusive.

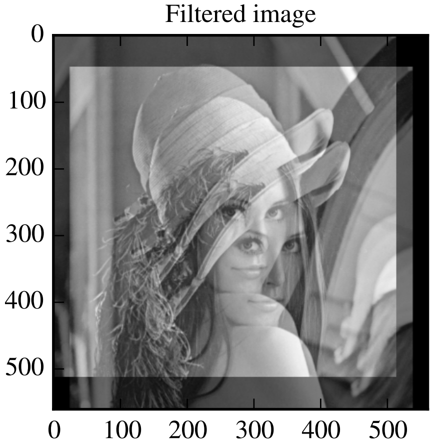
The function `correlate` can also take arbitrary N -dimensional arrays as input and return the N -dimensional convolution of the two arrays on output.

When $N=2$, `correlate` and/or `convolve` can be used to construct arbitrary image filters to perform actions such as blurring, enhancing, and edge-detection for an image.

```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.lena()
>>> w = np.zeros((50, 50))
>>> w[0][0] = 1.0
>>> w[49][25] = 1.0
>>> image_new = signal.fftconvolve(image, w)

>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```



```
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```



Using `convolve` in the above example would take quite long to run. Calculating the convolution in the time domain as above is mainly used for filtering when one of the signals is much smaller than the other ($K \gg M$), otherwise linear filtering is more efficiently calculated in the frequency domain provided by the function `fftconvolve`.

If the filter function $w[n,m]$ can be factored according to

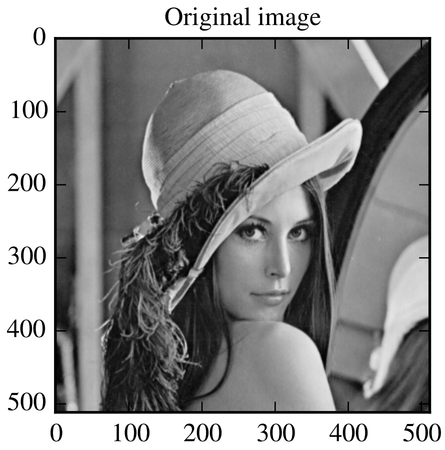
$$h[n,m] = h_1[n] h_2[m],$$

convolution can be calculated by means of the function `sepfir2d`. As an example we consider a Gaussian filter `gaussian`

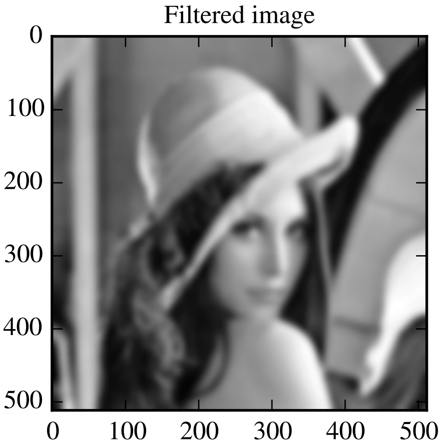
$$h[n,m] \propto e^{-x^2-y^2} = e^{-x^2} e^{-y^2}$$

which is often used for blurring.

```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.lena()
>>> w = signal.gaussian(50, 5.0)
>>> image_new = signal.sepfir2d(image, w, w)

>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```



```
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```



Difference-equation filtering

A general class of linear one-dimensional filters (that includes convolution filters) are filters described by the difference equation

$$\sum_{k=0}^{N} a_k y[n-k] = \sum_{k=0}^{M} b_k x[n-k]$$

where $x[n]$ is the input sequence and $y[n]$ is the output sequence. If we assume initial rest so that $y[n] = 0$ for $n < 0$, then this kind of filter can be implemented using convolution. However, the convolution filter sequence $h[n]$ could be infinite if $a_k \neq 0$ for $k \geq 1$. In addition, this general class of linear filter allows initial conditions to be placed on $y[n]$ for $n < 0$ resulting in a filter that cannot be expressed using convolution.

The difference equation filter can be thought of as finding $y[n]$ recursively in terms of it's previous values

$$a_0 y[n] = -a_1 y[n-1] - \cdots - a_N y[n-N] + \cdots + b_0 x[n] + \cdots + b_M x[n-M].$$

Often $a_0 = 1$ is chosen for normalization. The implementation in SciPy of this general difference equation filter is a little more complicated then would be implied by the previous equation. It is implemented so that only one signal needs to be delayed. The actual implementation equations are (assuming $a_0 = 1$).

$$\begin{array}{rcl} y[n] & = & b_0 x[n] + z_0[n-1] \\ z_0[n] & = & b_1 x[n] + z_1[n-1] - a_1 y[n] \\ z_1[n] & = & b_2 x[n] + z_2[n-1] - a_2 y[n] \\ \vdots & \vdots & \vdots \\ z_{K-2}[n] & = & b_{K-1} x[n] + z_{K-1}[n-1] - a_{K-1} y[n] \\ z_{K-1}[n] & = & b_K x[n] - a_K y[n], \end{array}$$

where $K = \max(N, M)$. Note that $b_K = 0$ if $K > M$ and $a_K = 0$ if $K > N$. In this way, the output at time n depends only on the input at time n and the value of z_0 at the previous time. This can always be calculated as long as the K values $z_0[n-1] \ldots z_{K-1}[n-1]$ are computed and stored at each time step.

The difference-equation filter is called using the command `lfilter` in SciPy. This command takes as inputs the vector b, the vector, a, a signal x and returns the vector y (the same length as x) computed using the equation given above. If x is N -dimensional, then the filter is computed along the axis provided. If, desired, initial conditions providing the values of $z_0[-1]$ to $z_{K-1}[-1]$ can be provided or else it will be assumed that they are all zero. If initial conditions are provided, then the final conditions on the intermediate variables are also returned. These could be used, for example, to restart the calculation in the same state.

Sometimes it is more convenient to express the initial conditions in terms of the signals $x[n]$ and $y[n]$. In other words, perhaps you have the values of $x[-M]$ to $x[-1]$ and the values of $y[-N]$ to $y[-1]$ and would like to determine what values of $z_m[-1]$ should be delivered as initial conditions to the difference-equation filter. It is not difficult to show that for $0 \leq m < K$,

$$z_m[n] = \sum_{p=0}^{K-m-1} \left(b_{m+p+1} x[n-p] - a_{m+p+1} y[n-p]\right).$$

Using this formula we can find the initial condition vector $z_0[-1]$ to $z_{K-1}[-1]$ given initial conditions on y (and x). The command `lfiltic` performs this function.

As an example consider the following system:

$$y[n] = \frac{1}{2}x[n] + \frac{1}{4}x[n-1] + \frac{1}{3}y[n-1]$$

The code calculates the signal $y[n]$ for a given signal $x[n]$; first for initial condidiitions $y[-1] = 0$ (default case), then for $y[-1] = 2$ by means of `lfiltic`.

```
>>> import numpy as np
>>> from scipy import signal

>>> x = np.array([1., 0., 0., 0.])
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.lfilter(b, a, x)
[ 0.5         0.41666667  0.13888889  0.0462963 ]
>>> zi = signal.lfiltic(b, a, y=[2.])
>>> signal.lfilter(b, a, x, zi=zi)
[ 1.16666667,  0.63888889,  0.21296296,  0.07098765]
```

Note that the output signal $y[n]$ has the same length as the length as the input signal $x[n]$.

Analysis of Linear Systems

Linear system described a linear difference equation can be fully described by the coefficient vectors a and b as was done above; an alternative representation is to provide a factor k, N_z zeros z_k and N_p poles p_k, respectively, to describe the system by means of its transfer function $H(z)$ according to

$$H(z) = k\frac{(z-z_1)(z-z_2)...(z-z_{N_z})}{(z-p_1)(z-p_2)...(z-p_{N_p})}$$

This alternative representation can be obtain wit hthe scipy function `tf2zpk`; the inverse is provided by `zpk2tf`.

For the example from above we have

```
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.tf2zpk(b, a)
[-0.5] [ 0.33333333] 0.5
```

i.e. the system has a zero at $z = -1/2$ and a pole at $z = 1/3$.

The scipy function `freqz` allows calculation of the frequency response of a system described by the coeffcients a_k and b_k. See the help of the `freqz` function of a comprehensive example.

Filter Design

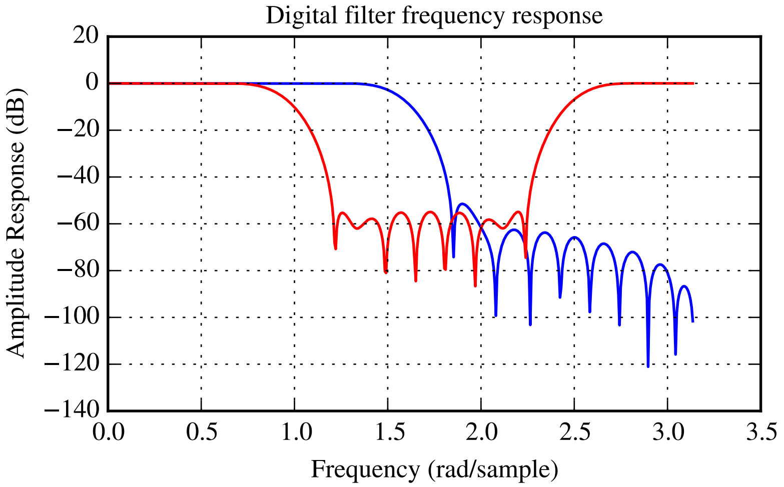
Time-discrete filters can be classified into finite response (FIR) filters and infinite response (IIR) filters. FIR filters provide a linear phase response, whereas IIR filters do not exhibit this behaviour. Scipy provides functions for designing both types of filters.

FIR Filter

The function `firwin` designs filters according to the window method. Depending on the provided arguments, the function returns different filter types (e.g. low-pass, band-pass...).

The example below designs a low-pass and a band-stop filter, respectively.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b1 = signal.firwin(40, 0.5)
>>> b2 = signal.firwin(41, [0.3, 0.8])
>>> w1, h1 = signal.freqz(b1)
>>> w2, h2 = signal.freqz(b2)

>>> plt.title('Digital filter frequency response')
>>> plt.plot(w1, 20*np.log10(np.abs(h1)), 'b')
>>> plt.plot(w2, 20*np.log10(np.abs(h2)), 'r')
>>> plt.ylabel('Amplitude Response (dB)')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```

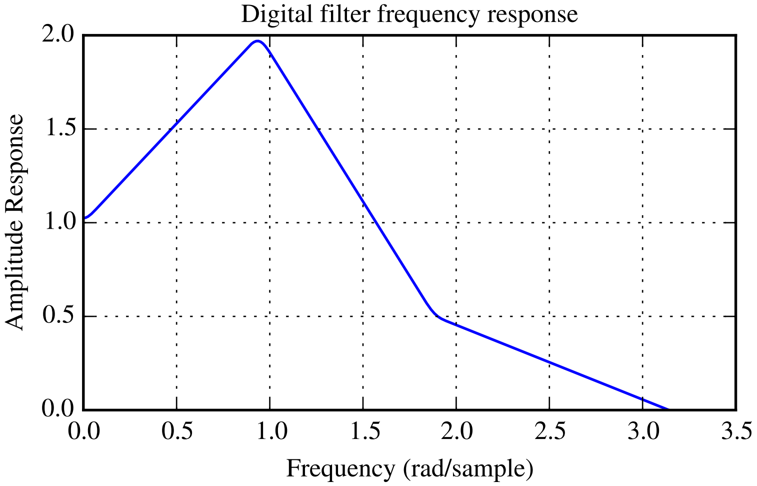


Note that `firwin` uses per default a normalized frequency defined such that the value 1 corresponds to the Nyquist frequency, whereas the function `freqz` is defined such that the value π corresponds to the Nyquist frequency.

The function `firwin2` allows design of almost arbitrary frequency responses by specifying an array of corner frequencies and corresponding gains, respectively.

The example below designs a filter with such an arbitrary amplitude response.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b = signal.firwin2(150, [0.0, 0.3, 0.6, 1.0], [1.0, 2.0, 0.5, 0.0])
>>> w, h = signal.freqz(b)

>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, np.abs(h))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```



Note the linear scaling of the y-axis and the different definition of the Nyquist frequency in `firwin2` and `freqz` (as explained above).

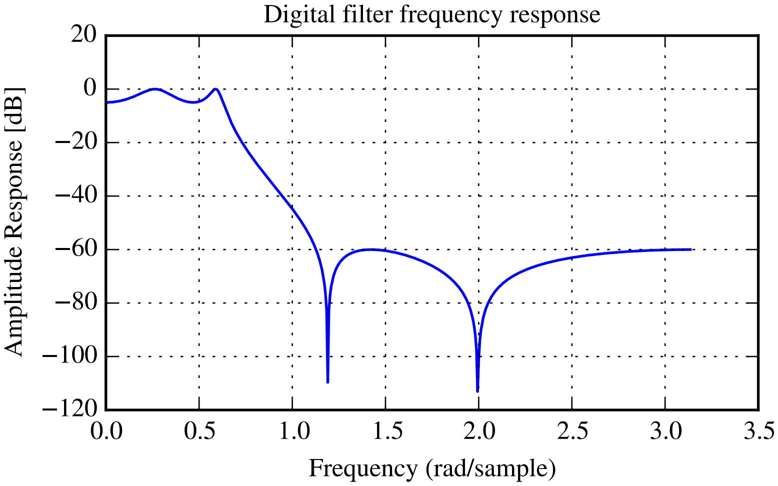
IIR Filter

Scipy provides two functions to directly design IIR `iirdesign` and `iirfilter` where the filter type (e.g. elliptic) is passed as an argument and several more filter design functions for specific filter types; e.g. `ellip`.

The example below designs an elliptic low-pass filter with defined passband and stopband ripple, respectively. Note the much lower filter order (order 4) compared with the FIR filters from the examples above in order to reach the same stop-band attenuation of $\approx$ 60 dB.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.iirfilter(4, Wn=0.2, rp=5, rs=60, btype='lowpass', ftype='ellip')
>>> w, h = signal.freqz(b, a)

>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, 20*np.log10(np.abs(h)))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response [dB]')
```

```
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```



Other filters

The signal processing package provides many more filters as well.

Median Filter

A median filter is commonly applied when noise is markedly non-Gaussian or when it is desired to preserve edges. The median filter works by sorting all of the array pixel values in a rectangular region surrounding the point of interest. The sample median of this list of neighborhood pixel values is used as the value for the output array. The sample median is the middle array value in a sorted list of neighborhood values. If there are an even number of elements in the neighborhood, then the average of the middle two values is used as the median. A general purpose median filter that works on N-dimensional arrays is `medfilt` . A specialized version that works only for two-dimensional arrays is available as `medfilt2d` .

Order Filter

A median filter is a specific example of a more general class of filters called order filters. To compute the output at a particular pixel, all order filters use the array values in a region surrounding that pixel. These array values are sorted and then one of them is selected as the output value. For the median filter, the sample median of the list of array values is used as the output. A general order filter allows the user to select which of the sorted values will be used as the output. So, for example one could choose to pick the maximum in the list or the minimum. The order filter takes an additional argument besides the input array and the region mask that specifies which of the elements in the sorted list of neighbor array values should be used as the output. The command to perform an order filter is `order_filter`.

Wiener filter

The Wiener filter is a simple deblurring filter for denoising images. This is not the Wiener filter commonly described in image reconstruction problems but instead it is a simple, local-mean filter. Let x be the input signal, then the output is

$$y = \begin{cases} \frac{\sigma^2}{\sigma_x^2} m_x + \left(1 - \frac{\sigma^2}{\sigma_x^2}\right) x & \sigma_x^2 \geq \sigma^2, \\ m_x & \sigma_x^2 < \sigma^2, \end{cases}$$

where m_x is the local estimate of the mean and σ_x^2 is the local estimate of the variance. The window for these estimates is an optional input parameter (default is 3×3). The parameter σ^2 is a threshold noise parameter. If σ is not given then it is estimated as the average of the local variances.

Hilbert filter

The Hilbert transform constructs the complex-valued analytic signal from a real signal. For example if $x = \cos \omega n$ then $y = \operatorname{hilbert}(x)$ would return (except near the edges) $y = \exp(j\omega n)$. In the frequency domain, the hilbert transform performs

$$Y = X \cdot H$$

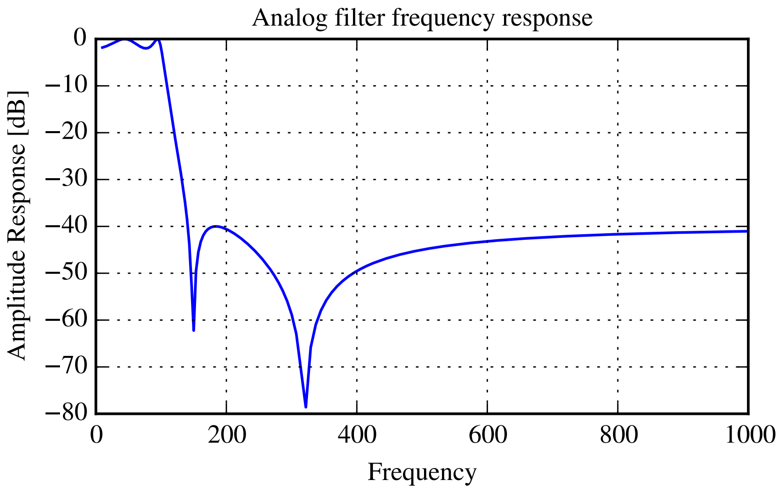
where H is 2 for positive frequencies, 0 for negative frequencies and 1 for zero-frequencies.

Analog Filter Design

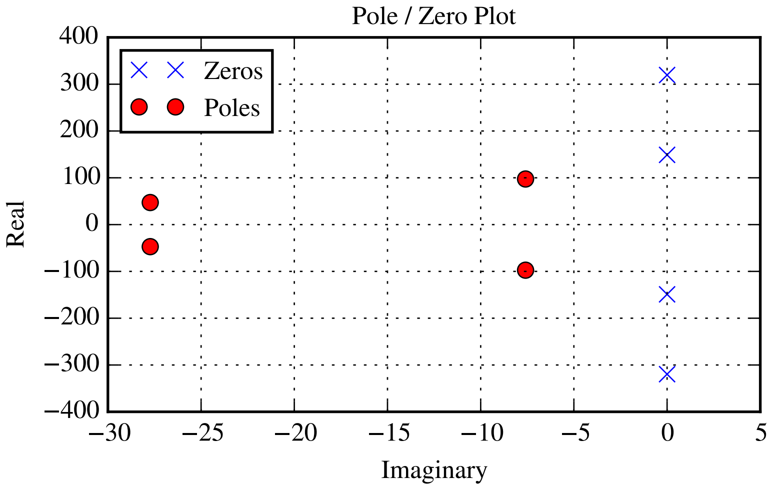
The functions `iirdesign`, `iirfilter`, and the filter design functions for specific filter types (e.g. `ellip`) all have a flag *analog* which allows design of analog filters as well.

The example below designs an analog (IIR) filter, obtains via `tf2zpk` the poles and zeros and plots them in the complex s-plane. The zeros at $\omega \approx 150$ and $\omega \approx 300$ can be clearly seen in the amplitude response.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.iirdesign(wp=100, ws=200, gpass=2.0, gstop=40., analog=True)
>>> w, h = signal.freqs(b, a)

>>> plt.title('Analog filter frequency response')
>>> plt.plot(w, 20*np.log10(np.abs(h)))
>>> plt.ylabel('Amplitude Response [dB]')
>>> plt.xlabel('Frequency')
>>> plt.grid()
>>> plt.show()
```



```
>>> z, p, k = signal.tf2zpk(b, a)

>>> plt.plot(np.real(z), np.imag(z), 'xb')
>>> plt.plot(np.real(p), np.imag(p), 'or')
>>> plt.legend(['Zeros', 'Poles'], loc=2)

>>> plt.title('Pole / Zero Plot')
>>> plt.ylabel('Real')
>>> plt.xlabel('Imaginary')
>>> plt.grid()
>>> plt.show()
```



1.8.3 Spectral Analysis

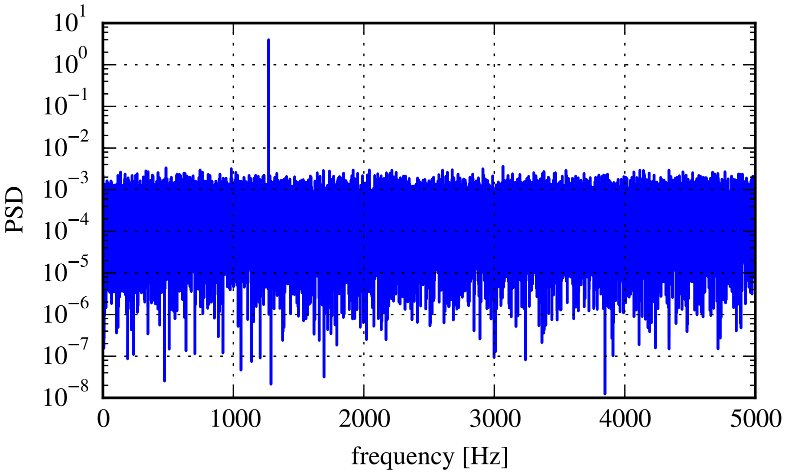
Periodogram Measurements

The scipy function `periodogram` provides a method to estimate the spectral density using the periodogram method.

The example below calculates the periodogram of a sine signal in white Gaussian noise.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1270.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)

>>> f, Pper_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
```

```
>>> plt.semilogy(f, Pper_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```

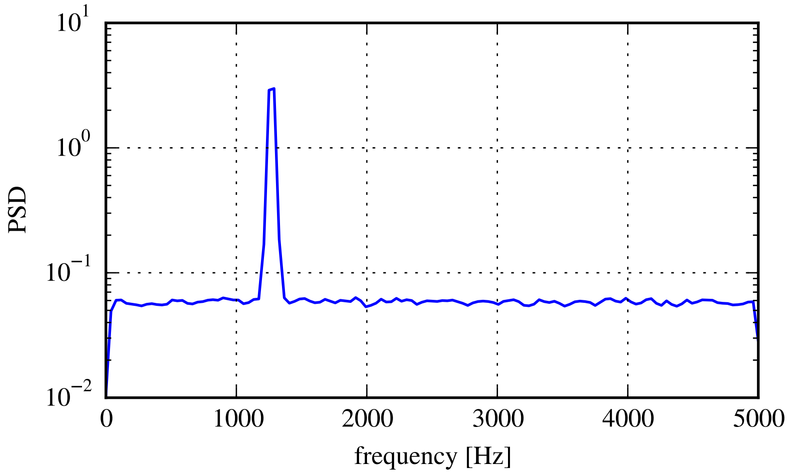


Spectral Analysis using Welch's Method

An improved method, especially with respect to noise immunity, is Welch's method which is implemented by the scipy function `welch`.

The example below estimates the spectrum using Welch's method and uses the same parameters as the example above. Note the much smoother noise floor of the spectogram.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1270.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)

>>> f, Pwelch_spec = signal.welch(x, fs, scaling='spectrum')

>>> plt.semilogy(f, Pwelch_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```



Lomb-Scargle Periodograms (`lombscargle`)

Least-squares spectral analysis (LSSA) is a method of estimating a frequency spectrum, based on a least squares fit of sinusoids to data samples, similar to Fourier analysis. Fourier analysis, the most used spectral method in science, generally boosts long-periodic noise in long gapped records; LSSA mitigates such problems.

The Lomb-Scargle method performs spectral analysis on unevenly sampled data and is known to be a powerful way to find, and test the significance of, weak periodic signals.

For a time series comprising N_t measurements $X_j \equiv X(t_j)$ sampled at times t_j where $(j = 1, \ldots, N_t)$, assumed to have been scaled and shifted such that its mean is zero and its variance is unity, the normalized Lomb-Scargle periodogram at frequency f is

$$P_n(f)\frac{1}{2}\left\{\frac{\left[\sum_j^{N_t} X_j \cos\omega(t_j-\tau)\right]^2}{\sum_j^{N_t}\cos^2\omega(t_j-\tau)}+\frac{\left[\sum_j^{N_t} X_j \sin\omega(t_j-\tau)\right]^2}{\sum_j^{N_t}\sin^2\omega(t_j-\tau)}\right\}.$$

Here, $\omega \equiv 2\pi f$ is the angular frequency. The frequency dependent time offset τ is given by

$$\tan 2\omega\tau = \frac{\sum_j^{N_t}\sin 2\omega t_j}{\sum_j^{N_t}\cos 2\omega t_j}.$$

The `lombscargle` function calculates the periodogram using a slightly modified algorithm due to Townsend [1] which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The equation is refactored as:

$$P_n(f) = \frac{1}{2}\left[\frac{(c_\tau XC + s_\tau XS)^2}{c_\tau^2 CC + 2c_\tau s_\tau CS + s_\tau^2 SS} + \frac{(c_\tau XS - s_\tau XC)^2}{c_\tau^2 SS - 2c_\tau s_\tau CS + s_\tau^2 CC}\right]$$

and

$$\tan 2\omega\tau = \frac{2CS}{CC - SS}.$$

---

[1] R.H.D. Townsend, "Fast calculation of the Lomb-Scargle periodogram using graphics processing units.", The Astrophysical Journal Supplement Series, vol 191, pp. 247-253, 2010

Here,

$$c_\tau = \cos \omega\tau, \qquad s_\tau = \sin \omega\tau$$

while the sums are

$$XC = \sum_j^{N_t} X_j \cos \omega t_j$$

$$XS = \sum_j^{N_t} X_j \sin \omega t_j$$

$$CC = \sum_j^{N_t} \cos^2 \omega t_j$$

$$SS = \sum_j^{N_t} \sin^2 \omega t_j$$

$$CS = \sum_j^{N_t} \cos \omega t_j \sin \omega t_j.$$

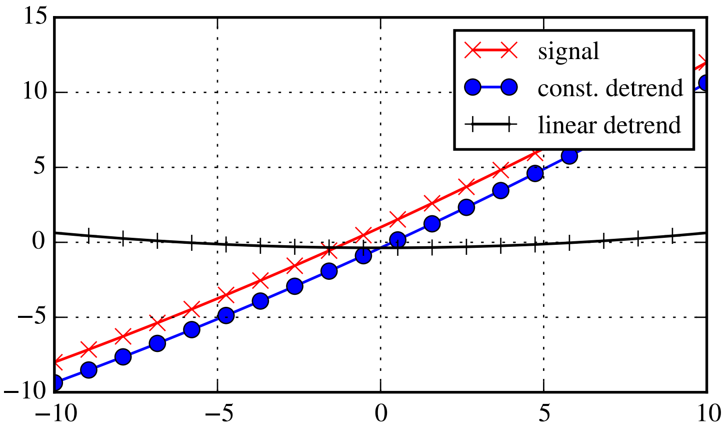
This requires $N_f(2N_t+3)$ trigonometric function evaluations giving a factor of ~ 2 speed increase over the straightforward implementation.

1.8.4 Detrend

Scipy provides the function `detrend` to remove a constant or linear trend in a data series in order to see effect of higher order.

The example below removes the constant and linear trend of a 2-nd order polynomial time series and plots the remaining signal components.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> t = np.linspace(-10, 10, 20)
>>> y = 1 + t + 0.01*t**2
>>> yconst = signal.detrend(y, type='constant')
>>> ylin = signal.detrend(y, type='linear')

>>> plt.plot(t, y, '-rx')
>>> plt.plot(t, yconst, '-bo')
>>> plt.plot(t, ylin, '-k+')
>>> plt.grid()
>>> plt.legend(['signal', 'const. detrend', 'linear detrend'])
>>> plt.show()
```



References

Some further reading and related software:

1.9 Linear Algebra (`scipy.linalg`)

When SciPy is built using the optimized ATLAS LAPACK and BLAS libraries, it has very fast linear algebra capabilities. If you dig deep enough, all of the raw lapack and blas libraries are available for your use for even more speed. In this section, some easier-to-use interfaces to these routines are described.

All of these linear algebra routines expect an object that can be converted into a 2-dimensional array. The output of these routines is also a two-dimensional array.

`scipy.linalg` contains all the functions in `numpy.linalg`. plus some other more advanced ones not contained in `numpy.linalg`

Another advantage of using `scipy.linalg` over `numpy.linalg` is that it is always compiled with BLAS/LAPACK support, while for numpy this is optional. Therefore, the scipy version might be faster depending on how numpy was installed.

Therefore, unless you don't want to add `scipy` as a dependency to your `numpy` program, use `scipy.linalg` instead of `numpy.linalg`

1.9.1 numpy.matrix vs 2D numpy.ndarray

The classes that represent matrices, and basic operations such as matrix multiplications and transpose are a part of `numpy`. For convenience, we summarize the differences between `numpy.matrix` and `numpy.ndarray` here.

`numpy.matrix` is matrix class that has a more convenient interface than `numpy.ndarray` for matrix operations. This class supports for example MATLAB-like creation syntax via the, has matrix multiplication as default for the `*` operator, and contains `I` and `T` members that serve as shortcuts for inverse and transpose:

```
>>> import numpy as np
>>> A = np.mat('[1 2;3 4]')
>>> A
matrix([[1, 2],
```

```
        [3, 4]])
>>> A.I
matrix([[-2. ,  1. ],
        [ 1.5, -0.5]])
>>> b = np.mat('[5 6]')
>>> b
matrix([[5, 6]])
>>> b.T
matrix([[5],
        [6]])
>>> A*b.T
matrix([[17],
        [39]])
```

Despite its convenience, the use of the `numpy.matrix` class is discouraged, since it adds nothing that cannot be accomplished with 2D `numpy.ndarray` objects, and may lead to a confusion of which class is being used. For example, the above code can be rewritten as:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
      [3, 4]])
>>> linalg.inv(A)
array([[-2. ,  1. ],
      [ 1.5, -0.5]])
>>> b = np.array([[5,6]]) #2D array
>>> b
array([[5, 6]])
>>> b.T
array([[5],
      [6]])
>>> A*b #not matrix multiplication!
array([[ 5, 12],
      [15, 24]])
>>> A.dot(b.T) #matrix multiplication
array([[17],
      [39]])
>>> b = np.array([5,6]) #1D array
>>> b
array([5, 6])
>>> b.T  #not matrix transpose!
array([5, 6])
>>> A.dot(b)  #does not matter for multiplication
array([17, 39])
```

`scipy.linalg` operations can be applied equally to `numpy.matrix` or to 2D `numpy.ndarray` objects.

1.9.2 Basic routines

Finding Inverse

The inverse of a matrix $\mathbf{A}$ is the matrix $\mathbf{B}$ such that $\mathbf{AB} = \mathbf{I}$ where $\mathbf{I}$ is the identity matrix consisting of ones down the main diagonal. Usually $\mathbf{B}$ is denoted $\mathbf{B} = \mathbf{A}^{-1}$. In SciPy, the matrix inverse of the Numpy array, A, is obtained using `linalg.inv (A)` , or using `A.I` if `A` is a Matrix. For example, let

$$\mathbf{A}=\left[\begin{array}{ccc} 1 & 3 & 5\\ 2 & 5 & 1\\ 2 & 3 & 8\end{array}\right]$$

then

$$\mathbf{A^{-1}}=\frac{1}{25}\left[\begin{array}{ccc} -37 & 9 & 22\\ 14 & 2 & -9\\ 4 & -3 & 1\end{array}\right]=\left[\begin{array}{ccc} -1.48 & 0.36 & 0.88\\ 0.56 & 0.08 & -0.36\\ 0.16 & -0.12 & 0.04\end{array}\right].$$

The following example demonstrates this computation in SciPy

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
array([[1, 2],
      [3, 4]])
>>> linalg.inv(A)
array([[-2. ,  1. ],
      [ 1.5, -0.5]])
>>> A.dot(linalg.inv(A)) #double check
array([[  1.00000000e+00,   0.00000000e+00],
      [  4.44089210e-16,   1.00000000e+00]])
```

Solving linear system

Solving linear systems of equations is straightforward using the scipy command `linalg.solve`. This command expects an input matrix and a right-hand-side vector. The solution vector is then computed. An option for entering a symmetrix matrix is offered which can speed up the processing when applicable. As an example, suppose it is desired to solve the following simultaneous equations:

$$\begin{aligned} x+3y+5z &= 10\\ 2x+5y+z &= 8\\ 2x+3y+8z &= 3\end{aligned}$$

We could find the solution vector using a matrix inverse:

$$\left[\begin{array}{c} x\\ y\\ z\end{array}\right]=\left[\begin{array}{ccc} 1 & 3 & 5\\ 2 & 5 & 1\\ 2 & 3 & 8\end{array}\right]^{-1}\left[\begin{array}{c} 10\\ 8\\ 3\end{array}\right]=\frac{1}{25}\left[\begin{array}{c} -232\\ 129\\ 19\end{array}\right]=\left[\begin{array}{c} -9.28\\ 5.16\\ 0.76\end{array}\right].$$

However, it is better to use the linalg.solve command which can be faster and more numerically stable. In this case it however gives the same answer as shown in the following example:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
      [3, 4]])
>>> b = np.array([[5],[6]])
>>> b
array([[5],
      [6]])
>>> linalg.inv(A).dot(b) #slow
```

```
array([[-4. ],
      [ 4.5]]
>>> A.dot(linalg.inv(A).dot(b))-b #check
array([[  8.88178420e-16],
      [  2.66453526e-15]])
>>> np.linalg.solve(A,b) #fast
array([[-4. ],
      [ 4.5]])
>>> A.dot(np.linalg.solve(A,b))-b #check
array([[ 0.],
      [ 0.]])
```

Finding Determinant

The determinant of a square matrix $\mathbf{A}$ is often denoted $|\mathbf{A}|$ and is a quantity often used in linear algebra. Suppose a_{ij} are the elements of the matrix $\mathbf{A}$ and let $M_{ij} = |\mathbf{A}_{ij}|$ be the determinant of the matrix left by removing the i^{th} row and j^{th} column from $\mathbf{A}$. Then for any row i,

$$|\mathbf{A}| = \sum_j (-1)^{i+j} a_{ij} M_{ij}.$$

This is a recursive way to define the determinant where the base case is defined by accepting that the determinant of a 1×1 matrix is the only matrix element. In SciPy the determinant can be calculated with `linalg.det` . For example, the determinant of

$$\mathbf{A} = \left[\begin{array}{ccc} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{array}\right]$$

is

$$\begin{aligned} |\mathbf{A}| &= 1\left|\begin{array}{cc} 5 & 1 \\ 3 & 8 \end{array}\right| - 3\left|\begin{array}{cc} 2 & 1 \\ 2 & 8 \end{array}\right| + 5\left|\begin{array}{cc} 2 & 5 \\ 2 & 3 \end{array}\right| \\ &= 1\left(5\cdot 8 - 3\cdot 1\right) - 3\left(2\cdot 8 - 2\cdot 1\right) + 5\left(2\cdot 3 - 2\cdot 5\right) = -25. \end{aligned}$$

In SciPy this is computed as shown in this example:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
      [3, 4]])
>>> linalg.det(A)
-2.0
```

Computing norms

Matrix and vector norms can also be computed with SciPy. A wide range of norm definitions are available using different parameters to the order argument of `linalg.norm` . This function takes a rank-1 (vectors) or a rank-2 (matrices) array and an optional order argument (default is 2). Based on these inputs a vector or matrix norm of the requested order is computed.

For vector x , the order parameter can be any real number including `inf` or `-inf`. The computed norm is

$$\|\mathbf{x}\| = \begin{cases} \max |x_i| & \text{ord} = \text{inf} \\ \min |x_i| & \text{ord} = -\text{inf} \\ \left(\sum_i |x_i|^{\text{ord}}\right)^{1/\text{ord}} & |\text{ord}| < \infty. \end{cases}$$

For matrix $\mathbf{A}$ the only valid values for norm are $\pm 2, \pm 1, \pm$ inf, and 'fro' (or 'f') Thus,

$$\|\mathbf{A}\| = \begin{cases} \max_i \sum_j |a_{ij}| & \text{ord} = \text{inf} \\ \min_i \sum_j |a_{ij}| & \text{ord} = -\text{inf} \\ \max_j \sum_i |a_{ij}| & \text{ord} = 1 \\ \min_j \sum_i |a_{ij}| & \text{ord} = -1 \\ \max \sigma_i & \text{ord} = 2 \\ \min \sigma_i & \text{ord} = -2 \\ \sqrt{\text{trace}\left(\mathbf{A}^H \mathbf{A}\right)} & \text{ord} = \text{'fro'} \end{cases}$$

where σ_i are the singular values of $\mathbf{A}$.

Examples:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A=np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.norm(A)
5.4772255750516612
>>> linalg.norm(A,'fro') # frobenius norm is the default
5.4772255750516612
>>> linalg.norm(A,1) # L1 norm (max column sum)
6
>>> linalg.norm(A,-1)
4
>>> linalg.norm(A,inf) # L inf norm (max row sum)
7
```

Solving linear least-squares problems and pseudo-inverses

Linear least-squares problems occur in many branches of applied mathematics. In this problem a set of linear scaling coefficients is sought that allow a model to fit data. In particular it is assumed that data y_i is related to data $\mathbf{x}_i$ through a set of coefficients c_j and model functions $f_j(\mathbf{x}_i)$ via the model

$$y_i = \sum_j c_j f_j(\mathbf{x}_i) + \epsilon_i$$

where ϵ_i represents uncertainty in the data. The strategy of least squares is to pick the coefficients c_j to minimize

$$J(\mathbf{c}) = \sum_i \left| y_i - \sum_j c_j f_j(x_i) \right|^2 .$$

Theoretically, a global minimum will occur when

$$\frac{\partial J}{\partial c_n^*} = 0 = \sum_i \left(y_i - \sum_j c_j f_j(x_i) \right) \left(-f_n^*(x_i)\right)$$

or

$$\begin{aligned}\sum_j c_j \sum_i f_j(x_i) f_n^*(x_i) &= \sum_i y_i f_n^*(x_i) \\ \mathbf{A}^H \mathbf{A} \mathbf{c} &= \mathbf{A}^H \mathbf{y}\end{aligned}$$

where

$$\{\mathbf{A}\}_{ij} = f_j(x_i).$$

When $\mathbf{A^H A}$ is invertible, then

$$\mathbf{c} = \left(\mathbf{A}^H \mathbf{A}\right)^{-1} \mathbf{A}^H \mathbf{y} = \mathbf{A}^\dagger \mathbf{y}$$

where $\mathbf{A}^\dagger$ is called the pseudo-inverse of $\mathbf{A}$. Notice that using this definition of $\mathbf{A}$ the model can be written

$$\mathbf{y} = \mathbf{A}\mathbf{c} + \boldsymbol{\epsilon}.$$

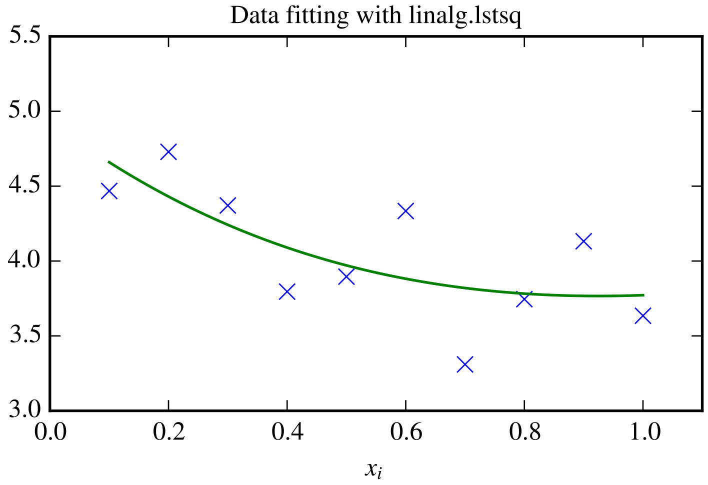
The command `linalg.lstsq` will solve the linear least squares problem for $\mathbf{c}$ given $\mathbf{A}$ and $\mathbf{y}$. In addition `linalg.pinv` or `linalg.pinv2` (uses a different method based on singular value decomposition) will find $\mathbf{A}^\dagger$ given $\mathbf{A}$.

The following example and figure demonstrate the use of `linalg.lstsq` and `linalg.pinv` for solving a data-fitting problem. The data shown below were generated using the model:

$$y_i = c_1 e^{-x_i} + c_2 x_i$$

where $x_i = 0.1i$ for $i = 1 \ldots 10$, $c_1 = 5$, and $c_2 = 4$. Noise is added to y_i and the coefficients c_1 and c_2 are estimated using linear least squares.

```
>>> import numpy as np
>>> from scipy import linalg
>>> import matplotlib.pyplot as plt

>>> c1, c2 = 5.0, 2.0
>>> i = np.r_[1:11]
>>> xi = 0.1*i
>>> yi = c1*np.exp(-xi) + c2*xi
>>> zi = yi + 0.05 * np.max(yi) * np.random.randn(len(yi))

>>> A = np.c_[np.exp(-xi)[:, np.newaxis], xi[:, np.newaxis]]
>>> c, resid, rank, sigma = linalg.lstsq(A, zi)

>>> xi2 = np.r_[0.1:1.0:100j]
>>> yi2 = c[0]*np.exp(-xi2) + c[1]*xi2

>>> plt.plot(xi,zi,'x',xi2,yi2)
>>> plt.axis([0,1.1,3.0,5.5])
>>> plt.xlabel('$x_i$')
>>> plt.title('Data fitting with linalg.lstsq')
>>> plt.show()
```



Generalized inverse

The generalized inverse is calculated using the command `linalg.pinv` or `linalg.pinv2`. These two commands differ in how they compute the generalized inverse. The first uses the linalg.lstsq algorithm while the second uses singular value decomposition. Let $\mathbf{A}$ be an $M \times N$ matrix, then if $M > N$ the generalized inverse is

$$\mathbf{A}^{\dagger} = \left(\mathbf{A}^{H}\mathbf{A}\right)^{-1}\mathbf{A}^{H}$$

while if $M < N$ matrix the generalized inverse is

$$\mathbf{A}^{\#} = \mathbf{A}^{H}\left(\mathbf{A}\mathbf{A}^{H}\right)^{-1}.$$

In both cases for $M = N$, then

$$\mathbf{A}^{\dagger} = \mathbf{A}^{\#} = \mathbf{A}^{-1}$$

as long as $\mathbf{A}$ is invertible.

1.9.3 Decompositions

In many applications it is useful to decompose a matrix using other representations. There are several decompositions supported by SciPy.

Eigenvalues and eigenvectors

The eigenvalue-eigenvector problem is one of the most commonly employed linear algebra operations. In one popular form, the eigenvalue-eigenvector problem is to find for some square matrix $\mathbf{A}$ scalars λ and corresponding vectors $\mathbf{v}$ such that

$$\mathbf{A}\mathbf{v} = \lambda\mathbf{v}.$$

For an $N \times N$ matrix, there are N (not necessarily distinct) eigenvalues — roots of the (characteristic) polynomial

$$\left|\mathbf{A} - \lambda\mathbf{I}\right| = 0.$$

The eigenvectors, $\mathbf{v}$, are also sometimes called right eigenvectors to distinguish them from another set of left eigenvectors that satisfy

$$\mathbf{v}_L^H\mathbf{A} = \lambda\mathbf{v}_L^H$$

or

$$\mathbf{A}^H\mathbf{v}_L = \lambda^*\mathbf{v}_L.$$

With it's default optional arguments, the command `linalg.eig` returns λ and $\mathbf{v}$. However, it can also return $\mathbf{v}_L$ and just λ by itself (`linalg.eigvals` returns just λ as well).

In addition, `linalg.eig` can also solve the more general eigenvalue problem

$$\begin{aligned} \mathbf{Av} &= \lambda\mathbf{Bv} \\ \mathbf{A}^H\mathbf{v}_L &= \lambda^*\mathbf{B}^H\mathbf{v}_L \end{aligned}$$

for square matrices $\mathbf{A}$ and $\mathbf{B}$. The standard eigenvalue problem is an example of the general eigenvalue problem for $\mathbf{B} = \mathbf{I}$. When a generalized eigenvalue problem can be solved, then it provides a decomposition of $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{BV\Lambda V}^{-1}$$

where $\mathbf{V}$ is the collection of eigenvectors into columns and $\mathbf{\Lambda}$ is a diagonal matrix of eigenvalues.

By definition, eigenvectors are only defined up to a constant scale factor. In SciPy, the scaling factor for the eigenvectors is chosen so that $\|\mathbf{v}\|^2 = \sum_i v_i^2 = 1$.

As an example, consider finding the eigenvalues and eigenvectors of the matrix

$$\mathbf{A} = \left[\begin{array}{ccc} 1 & 5 & 2 \\ 2 & 4 & 1 \\ 3 & 6 & 2 \end{array}\right].$$

The characteristic polynomial is

$$\begin{aligned} |\mathbf{A} - \lambda\mathbf{I}| &= (1-\lambda)\left[(4-\lambda)(2-\lambda)-6\right] - \\ & \quad 5\left[2(2-\lambda)-3\right] + 2\left[12-3(4-\lambda)\right] \\ &= -\lambda^3 + 7\lambda^2 + 8\lambda - 3. \end{aligned}$$

The roots of this polynomial are the eigenvalues of $\mathbf{A}$:

$$\begin{aligned} \lambda_1 &= 7.9579 \\ \lambda_2 &= -1.2577 \\ \lambda_3 &= 0.2997. \end{aligned}$$

The eigenvectors corresponding to each eigenvalue can be found using the original equation. The eigenvectors associated with these eigenvalues can then be found.

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> la,v = linalg.eig(A)
>>> l1,l2 = la
>>> print l1, l2  #eigenvalues
(-0.372281323269+0j) (5.37228132327+0j)
>>> print v[:,0]  #first eigenvector
[-0.82456484  0.56576746]
>>> print v[:,1]  #second eigenvector
```

```
[-0.41597356 -0.90937671]
>>> print np.sum(abs(v**2),axis=0) #eigenvectors are unitary
[ 1.  1. ]
>>> v1 = np.array(v[:,0]).T
>>> print linalg.norm(A.dot(v1)-l1*v1) #check the computation
3.23682852457e-16
```

Singular value decomposition

Singular Value Decomposition (SVD) can be thought of as an extension of the eigenvalue problem to matrices that are not square. Let $\mathbf{A}$ be an $M \times N$ matrix with M and N arbitrary. The matrices $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$ are square hermitian matrices [2] of size $N \times N$ and $M \times M$ respectively. It is known that the eigenvalues of square hermitian matrices are real and non-negative. In addition, there are at most $\min(M, N)$ identical non-zero eigenvalues of $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$. Define these positive eigenvalues as σ_i^2. The square-root of these are called singular values of $\mathbf{A}$. The eigenvectors of $\mathbf{A}^H\mathbf{A}$ are collected by columns into an $N \times N$ unitary [3] matrix $\mathbf{V}$ while the eigenvectors of $\mathbf{A}\mathbf{A}^H$ are collected by columns in the unitary matrix $\mathbf{U}$, the singular values are collected in an $M \times N$ zero matrix $\mathbf{\Sigma}$ with main diagonal entries set to the singular values. Then

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^H$$

is the singular-value decomposition of $\mathbf{A}$. Every matrix has a singular value decomposition. Sometimes, the singular values are called the spectrum of $\mathbf{A}$. The command `linalg.svd` will return $\mathbf{U}$, $\mathbf{V}^H$, and σ_i as an array of the singular values. To obtain the matrix $\mathbf{\Sigma}$ use `linalg.diagsvd`. The following example illustrates the use of `linalg.svd`.

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2,3],[4,5,6]])
>>> A
array([[1, 2, 3],
       [4, 5, 6]])
>>> M,N = A.shape
>>> U,s,Vh = linalg.svd(A)
>>> Sig = linalg.diagsvd(s,M,N)
>>> U, Vh = U, Vh
>>> U
array([[-0.3863177 , -0.92236578],
       [-0.92236578,  0.3863177 ]])
>>> Sig
array([[ 9.508032  ,  0.        ,  0.        ],
       [ 0.        ,  0.77286964,  0.        ]])
>>> Vh
array([[-0.42866713, -0.56630692, -0.7039467 ],
       [ 0.80596391,  0.11238241, -0.58119908],
       [ 0.40824829, -0.81649658,  0.40824829]])
>>> U.dot(Sig.dot(Vh)) #check computation
array([[ 1.,  2.,  3.],
       [ 4.,  5.,  6.]])
```

LU decomposition

The LU decomposition finds a representation for the $M \times N$ matrix $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{P}\,\mathbf{L}\,\mathbf{U}$$

---

[2] A hermitian matrix $\mathbf{D}$ satisfies $\mathbf{D}^H = \mathbf{D}$.

[3] A unitary matrix $\mathbf{D}$ satisfies $\mathbf{D}^H\mathbf{D} = \mathbf{I} = \mathbf{D}\mathbf{D}^H$ so that $\mathbf{D}^{-1} = \mathbf{D}^H$.

where $\mathbf{P}$ is an $M \times M$ permutation matrix (a permutation of the rows of the identity matrix), $\mathbf{L}$ is in $M \times K$ lower triangular or trapezoidal matrix ($K = \min(M, N)$) with unit-diagonal, and $\mathbf{U}$ is an upper triangular or trapezoidal matrix. The SciPy command for this decomposition is `linalg.lu` .

Such a decomposition is often useful for solving many simultaneous equations where the left-hand-side does not change but the right hand side does. For example, suppose we are going to solve

$$\mathbf{A}\mathbf{x}_i = \mathbf{b}_i$$

for many different $\mathbf{b}_i$. The LU decomposition allows this to be written as

$$\mathbf{P}\mathbf{L}\mathbf{U}\mathbf{x}_i = \mathbf{b}_i.$$

Because $\mathbf{L}$ is lower-triangular, the equation can be solved for $\mathbf{U}\mathbf{x}_i$ and finally $\mathbf{x}_i$ very rapidly using forward- and back-substitution. An initial time spent factoring $\mathbf{A}$ allows for very rapid solution of similar systems of equations in the future. If the intent for performing LU decomposition is for solving linear systems then the command `linalg.lu_factor` should be used followed by repeated applications of the command `linalg.lu_solve` to solve the system for each new right-hand-side.

Cholesky decomposition

Cholesky decomposition is a special case of LU decomposition applicable to Hermitian positive definite matrices. When $\mathbf{A} = \mathbf{A}^H$ and $\mathbf{x}^H\mathbf{A}\mathbf{x} \geq 0$ for all $\mathbf{x}$, then decompositions of $\mathbf{A}$ can be found so that

$$\begin{aligned}\mathbf{A} &= \mathbf{U}^H\mathbf{U} \\ \mathbf{A} &= \mathbf{L}\mathbf{L}^H\end{aligned}$$

where $\mathbf{L}$ is lower-triangular and $\mathbf{U}$ is upper triangular. Notice that $\mathbf{L} = \mathbf{U}^H$. The command `linalg.cholesky` computes the cholesky factorization. For using cholesky factorization to solve systems of equations there are also `linalg.cho_factor` and `linalg.cho_solve` routines that work similarly to their LU decomposition counterparts.

QR decomposition

The QR decomposition (sometimes called a polar decomposition) works for any $M \times N$ array and finds an $M \times M$ unitary matrix $\mathbf{Q}$ and an $M \times N$ upper-trapezoidal matrix $\mathbf{R}$ such that

$$\mathbf{A} = \mathbf{Q}\mathbf{R}.$$

Notice that if the SVD of $\mathbf{A}$ is known then the QR decomposition can be found

$$\mathbf{A} = \mathbf{U}\boldsymbol{\Sigma}\mathbf{V}^H = \mathbf{Q}\mathbf{R}$$

implies that $\mathbf{Q} = \mathbf{U}$ and $\mathbf{R} = \boldsymbol{\Sigma}\mathbf{V}^H$. Note, however, that in SciPy independent algorithms are used to find QR and SVD decompositions. The command for QR decomposition is `linalg.qr` .

Schur decomposition

For a square $N \times N$ matrix, $\mathbf{A}$, the Schur decomposition finds (not-necessarily unique) matrices $\mathbf{T}$ and $\mathbf{Z}$ such that

$$\mathbf{A} = \mathbf{Z}\mathbf{T}\mathbf{Z}^H$$

where $\mathbf{Z}$ is a unitary matrix and $\mathbf{T}$ is either upper-triangular or quasi-upper triangular depending on whether or not a real schur form or complex schur form is requested. For a real schur form both $\mathbf{T}$ and $\mathbf{Z}$ are real-valued when $\mathbf{A}$ is real-valued. When $\mathbf{A}$ is a real-valued matrix the real schur form is only quasi-upper triangular because 2×2 blocks extrude from the main diagonal corresponding to any complex- valued eigenvalues. The command `linalg.schur` finds the Schur decomposition while the command `linalg.rsf2csf` converts $\mathbf{T}$ and $\mathbf{Z}$ from a real Schur form to a complex Schur form. The Schur form is especially useful in calculating functions of matrices.

The following example illustrates the schur decomposition:

```
>>> from scipy import linalg
>>> A = mat('[1 3 2; 1 4 5; 2 3 6]')
>>> T,Z = linalg.schur(A)
>>> T1,Z1 = linalg.schur(A,'complex')
>>> T2,Z2 = linalg.rsf2csf(T,Z)
>>> print T
[[ 9.90012467  1.78947961 -0.65498528]
 [ 0.          0.54993766 -1.57754789]
 [ 0.          0.51260928  0.54993766]]
>>> print T2
[[ 9.90012467 +0.00000000e+00j -0.32436598 +1.55463542e+00j
  -0.88619748 +5.69027615e-01j]
 [ 0.00000000 +0.00000000e+00j  0.54993766 +8.99258408e-01j
   1.06493862 +1.37016050e-17j]
 [ 0.00000000 +0.00000000e+00j  0.00000000 +0.00000000e+00j
   0.54993766 -8.99258408e-01j]]
>>> print abs(T1-T2) # different
[[  1.24357637e-14   2.09205364e+00   6.56028192e-01]
 [  0.00000000e+00   4.00296604e-16   1.83223097e+00]
 [  0.00000000e+00   0.00000000e+00   4.57756680e-16]]
>>> print abs(Z1-Z2) # different
[[ 0.06833781  1.10591375  0.23662249]
 [ 0.11857169  0.5585604   0.29617525]
 [ 0.12624999  0.75656818  0.22975038]]
>>> T,Z,T1,Z1,T2,Z2 = map(mat,(T,Z,T1,Z1,T2,Z2))
>>> print abs(A-Z*T*Z.H) # same
[[  1.11022302e-16   4.44089210e-16   4.44089210e-16]
 [  4.44089210e-16   1.33226763e-15   8.88178420e-16]
 [  8.88178420e-16   4.44089210e-16   2.66453526e-15]]
>>> print abs(A-Z1*T1*Z1.H) # same
[[  1.00043248e-15   2.22301403e-15   5.55749485e-15]
 [  2.88899660e-15   8.44927041e-15   9.77322008e-15]
 [  3.11291538e-15   1.15463228e-14   1.15464861e-14]]
>>> print abs(A-Z2*T2*Z2.H) # same
[[  3.34058710e-16   8.88611201e-16   4.18773089e-18]
 [  1.48694940e-16   8.95109973e-16   8.92966151e-16]
 [  1.33228956e-15   1.33582317e-15   3.55373104e-15]]
```

Interpolative Decomposition

`scipy.linalg.interpolative` contains routines for computing the interpolative decomposition (ID) of a matrix. For a matrix $A \in C^{m \times n}$ of rank $k \leq \min\{m, n\}$ this is a factorization

$$A\Pi = \begin{bmatrix} A\Pi_1 & A\Pi_2 \end{bmatrix} = A\Pi_1 \begin{bmatrix} I & T \end{bmatrix},$$

where $\Pi = [\Pi_1, \Pi_2]$ is a permutation matrix with $\Pi_1 \in \{0, 1\}^{n \times k}$, i.e., $A\Pi_2 = A\Pi_1 T$. This can equivalently be written as $A = BP$, where $B = A\Pi_1$ and $P = [I, T]\Pi^{\mathsf{T}}$ are the *skeleton* and *interpolation matrices*, respectively.

See also:

`scipy.linalg.interpolative` — for more information.

1.9.4 Matrix Functions

Consider the function $f\left(x\right)$ with Taylor series expansion

$$f\left(x\right)=\sum_{k=0}^{\infty}\frac{f^{\left(k\right)}\left(0\right)}{k!}x^{k}.$$

A matrix function can be defined using this Taylor series for the square matrix $\mathbf{A}$ as

$$f\left(\mathbf{A}\right)=\sum_{k=0}^{\infty}\frac{f^{\left(k\right)}\left(0\right)}{k!}\mathbf{A}^{k}.$$

While, this serves as a useful representation of a matrix function, it is rarely the best way to calculate a matrix function.

Exponential and logarithm functions

The matrix exponential is one of the more common matrix functions. It can be defined for square matrices as

$$e^{\mathbf{A}}=\sum_{k=0}^{\infty}\frac{1}{k!}\mathbf{A}^{k}.$$

The command `linalg.expm3` uses this Taylor series definition to compute the matrix exponential. Due to poor convergence properties it is not often used.

Another method to compute the matrix exponential is to find an eigenvalue decomposition of $\mathbf{A}$:

$$\mathbf{A}=\mathbf{V}\boldsymbol{\Lambda}\mathbf{V}^{-1}$$

and note that

$$e^{\mathbf{A}}=\mathbf{V}e^{\boldsymbol{\Lambda}}\mathbf{V}^{-1}$$

where the matrix exponential of the diagonal matrix $\boldsymbol{\Lambda}$ is just the exponential of its elements. This method is implemented in `linalg.expm2` .

The preferred method for implementing the matrix exponential is to use scaling and a Padé approximation for e^{x} . This algorithm is implemented as `linalg.expm` .

The inverse of the matrix exponential is the matrix logarithm defined as the inverse of the matrix exponential.

$$\mathbf{A}\equiv\exp\left(\log\left(\mathbf{A}\right)\right).$$

The matrix logarithm can be obtained with `linalg.logm` .

Trigonometric functions

The trigonometric functions $\sin$, $\cos$, and $\tan$ are implemented for matrices in `linalg.sinm`, `linalg.cosm`, and `linalg.tanm` respectively. The matrix sin and cosine can be defined using Euler's identity as

$$\begin{aligned}\sin\left(\mathbf{A}\right) &= \frac{e^{j\mathbf{A}}-e^{-j\mathbf{A}}}{2j}\\ \cos\left(\mathbf{A}\right) &= \frac{e^{j\mathbf{A}}+e^{-j\mathbf{A}}}{2}.\end{aligned}$$

The tangent is

$$\tan\left(x\right)=\frac{\sin\left(x\right)}{\cos\left(x\right)}=\left[\cos\left(x\right)\right]^{-1}\sin\left(x\right)$$

and so the matrix tangent is defined as

$$\left[\cos\left(\mathbf{A}\right)\right]^{-1}\sin\left(\mathbf{A}\right).$$

Hyperbolic trigonometric functions

The hyperbolic trigonemetric functions $\sinh$, $\cosh$, and $\tanh$ can also be defined for matrices using the familiar definitions:

$$\begin{aligned}
\sinh\left(\mathbf{A}\right) & = & \frac{e^{\mathbf{A}}-e^{-\mathbf{A}}}{2}\\
\cosh\left(\mathbf{A}\right) & = & \frac{e^{\mathbf{A}}+e^{-\mathbf{A}}}{2}\\
\tanh\left(\mathbf{A}\right) & = & \left[\cosh\left(\mathbf{A}\right)\right]^{-1}\sinh\left(\mathbf{A}\right).
\end{aligned}$$

These matrix functions can be found using `linalg.sinhm`, `linalg.coshm` , and `linalg.tanhm`.

Arbitrary function

Finally, any arbitrary function that takes one complex number and returns a complex number can be called as a matrix function using the command `linalg.funm`. This command takes the matrix and an arbitrary Python function. It then implements an algorithm from Golub and Van Loan's book "Matrix Computations "to compute function applied to the matrix using a Schur decomposition. Note that *the function needs to accept complex numbers* as input in order to work with this algorithm. For example the following code computes the zeroth-order Bessel function applied to a matrix.

```
>>> from scipy import special, random, linalg
>>> A = random.rand(3,3)
>>> B = linalg.funm(A,lambda x: special.jv(0,x))
>>> print A
[[ 0.72578091  0.34105276  0.79570345]
 [ 0.65767207  0.73855618  0.541453  ]
 [ 0.78397086  0.68043507  0.4837898 ]]
>>> print B
[[ 0.72599893 -0.20545711 -0.22721101]
 [-0.27426769  0.77255139 -0.23422637]
 [-0.27612103 -0.21754832  0.7556849 ]]
>>> print linalg.eigvals(A)
[ 1.91262611+0.j  0.21846476+0.j -0.18296399+0.j]
>>> print special.jv(0, linalg.eigvals(A))
[ 0.27448286+0.j  0.98810383+0.j  0.99164854+0.j]
>>> print linalg.eigvals(B)
[ 0.27448286+0.j  0.98810383+0.j  0.99164854+0.j]
```

Note how, by virtue of how matrix analytic functions are defined, the Bessel function has acted on the matrix eigenvalues.

1.9.5 Special matrices

SciPy and NumPy provide several functions for creating special matrices that are frequently used in engineering and science.

Type	Function	Description
block diagonal	`scipy.linalg.block_diag`	Create a block diagonal matrix from the provided arrays.
circulant	`scipy.linalg.circulant`	Construct a circulant matrix.
companion	`scipy.linalg.companion`	Create a companion matrix.
Hadamard	`scipy.linalg.hadamard`	Construct a Hadamard matrix.
Hankel	`scipy.linalg.hankel`	Construct a Hankel matrix.
Hilbert	`scipy.linalg.hilbert`	Construct a Hilbert matrix.
Inverse Hilbert	`scipy.linalg.invhilbert`	Construct the inverse of a Hilbert matrix.
Leslie	`scipy.linalg.leslie`	Create a Leslie matrix.
Pascal	`scipy.linalg.pascal`	Create a Pascal matrix.
Toeplitz	`scipy.linalg.toeplitz`	Construct a Toeplitz matrix.
Van der Monde	`numpy.vander`	Generate a Van der Monde matrix.

For examples of the use of these functions, see their respective docstrings.

1.10 Sparse Eigenvalue Problems with ARPACK

1.10.1 Introduction

ARPACK is a Fortran package which provides routines for quickly finding a few eigenvalues/eigenvectors of large sparse matrices. In order to find these solutions, it requires only left-multiplication by the matrix in question. This operation is performed through a *reverse-communication* interface. The result of this structure is that ARPACK is able to find eigenvalues and eigenvectors of any linear function mapping a vector to a vector.

All of the functionality provided in ARPACK is contained within the two high-level interfaces `scipy.sparse.linalg.eigs` and `scipy.sparse.linalg.eigsh`. `eigs` provides interfaces to find the eigenvalues/vectors of real or complex nonsymmetric square matrices, while `eigsh` provides interfaces for real-symmetric or complex-hermitian matrices.

1.10.2 Basic Functionality

ARPACK can solve either standard eigenvalue problems of the form

$$A\mathbf{x} = \lambda\mathbf{x}$$

or general eigenvalue problems of the form

$$A\mathbf{x} = \lambda M\mathbf{x}$$

The power of ARPACK is that it can compute only a specified subset of eigenvalue/eigenvector pairs. This is accomplished through the keyword `which`. The following values of `which` are available:

- `which = 'LM'` : Eigenvalues with largest magnitude (`eigs`, `eigsh`), that is, largest eigenvalues in the euclidean norm of complex numbers.
- `which = 'SM'` : Eigenvalues with smallest magnitude (`eigs`, `eigsh`), that is, smallest eigenvalues in the euclidean norm of complex numbers.
- `which = 'LR'` : Eigenvalues with largest real part (`eigs`)
- `which = 'SR'` : Eigenvalues with smallest real part (`eigs`)
- `which = 'LI'` : Eigenvalues with largest imaginary part (`eigs`)
- `which = 'SI'` : Eigenvalues with smallest imaginary part (`eigs`)

- `which = 'LA'` : Eigenvalues with largest algebraic value (`eigsh`), that is, largest eigenvalues inclusive of any negative sign.
- `which = 'SA'` : Eigenvalues with smallest algebraic value (`eigsh`), that is, smallest eigenvalues inclusive of any negative sign.
- `which = 'BE'` : Eigenvalues from both ends of the spectrum (`eigsh`)

Note that ARPACK is generally better at finding extremal eigenvalues: that is, eigenvalues with large magnitudes. In particular, using `which = 'SM'` may lead to slow execution time and/or anomalous results. A better approach is to use *shift-invert mode*.

1.10.3 Shift-Invert Mode

Shift invert mode relies on the following observation. For the generalized eigenvalue problem

$$A\mathbf{x} = \lambda M\mathbf{x}$$

it can be shown that

$$(A - \sigma M)^{-1} M\mathbf{x} = \nu\mathbf{x}$$

where

$$\nu = \frac{1}{\lambda - \sigma}$$

1.10.4 Examples

Imagine you'd like to find the smallest and largest eigenvalues and the corresponding eigenvectors for a large matrix. ARPACK can handle many forms of input: dense matrices such as `numpy.ndarray` instances, sparse matrices such as `scipy.sparse.csr_matrix`, or a general linear operator derived from `scipy.sparse.linalg.LinearOperator`. For this example, for simplicity, we'll construct a symmetric, positive-definite matrix.

```
>>> import numpy as np
>>> from scipy.linalg import eigh
>>> from scipy.sparse.linalg import eigsh
>>> np.set_printoptions(suppress=True)
>>>
>>> np.random.seed(0)
>>> X = np.random.random((100,100)) - 0.5
>>> X = np.dot(X, X.T) #create a symmetric matrix
```

We now have a symmetric matrix `X` with which to test the routines. First compute a standard eigenvalue decomposition using `eigh`:

```
>>> evals_all, evecs_all = eigh(X)
```

As the dimension of `X` grows, this routine becomes very slow. Especially if only a few eigenvectors and eigenvalues are needed, `ARPACK` can be a better option. First let's compute the largest eigenvalues (`which = 'LM'`) of `X` and compare them to the known results:

```
>>> evals_large, evecs_large = eigsh(X, 3, which='LM')
>>> print evals_all[-3:]
[ 29.1446102   30.05821805  31.19467646]
>>> print evals_large
[ 29.1446102   30.05821805  31.19467646]
```

```
>>> print np.dot(evecs_large.T, evecs_all[:,-3:])
[[-1.  0.  0.]
 [ 0.  1.  0.]
 [-0.  0. -1.]]
```

The results are as expected. ARPACK recovers the desired eigenvalues, and they match the previously known results. Furthermore, the eigenvectors are orthogonal, as we'd expect. Now let's attempt to solve for the eigenvalues with smallest magnitude:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM')
scipy.sparse.linalg.eigen.arpack.arpack.ArpackNoConvergence:
ARPACK error -1: No convergence (1001 iterations, 0/3 eigenvectors converged)
```

Oops. We see that as mentioned above, `ARPACK` is not quite as adept at finding small eigenvalues. There are a few ways this problem can be addressed. We could increase the tolerance (`tol`) to lead to faster convergence:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', tol=1E-2)
>>> print evals_all[:3]
[ 0.0003783   0.00122714  0.00715878]
>>> print evals_small
[ 0.00037831  0.00122714  0.00715881]
>>> print np.dot(evecs_small.T, evecs_all[:,:3])
[[ 0.99999999  0.00000024 -0.00000049]
 [-0.00000023  0.99999999  0.00000056]
 [ 0.00000031 -0.00000037  0.99999852]]
```

This works, but we lose the precision in the results. Another option is to increase the maximum number of iterations (`maxiter`) from 1000 to 5000:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', maxiter=5000)
>>> print evals_all[:3]
[ 0.0003783   0.00122714  0.00715878]
>>> print evals_small
[ 0.0003783   0.00122714  0.00715878]
>>> print np.dot(evecs_small.T, evecs_all[:,:3])
[[ 1.  0.  0.]
 [-0.  1.  0.]
 [ 0.  0. -1.]]
```

We get the results we'd hoped for, but the computation time is much longer. Fortunately, `ARPACK` contains a mode that allows quick determination of non-external eigenvalues: *shift-invert mode*. As mentioned above, this mode involves transforming the eigenvalue problem to an equivalent problem with different eigenvalues. In this case, we hope to find eigenvalues near zero, so we'll choose `sigma = 0`. The transformed eigenvalues will then satisfy $\nu = 1/(\sigma - \lambda) = 1/\lambda$, so our small eigenvalues λ become large eigenvalues ν.

```
>>> evals_small, evecs_small = eigsh(X, 3, sigma=0, which='LM')
>>> print evals_all[:3]
[ 0.0003783   0.00122714  0.00715878]
>>> print evals_small
[ 0.0003783   0.00122714  0.00715878]
>>> print np.dot(evecs_small.T, evecs_all[:,:3])
[[ 1.  0.  0.]
 [ 0. -1. -0.]
 [-0. -0.  1.]]
```

We get the results we were hoping for, with much less computational time. Note that the transformation from $\nu \rightarrow \lambda$ takes place entirely in the background. The user need not worry about the details.

The shift-invert mode provides more than just a fast way to obtain a few small eigenvalues. Say you desire to find internal eigenvalues and eigenvectors, e.g. those nearest to $\lambda = 1$. Simply set `sigma = 1` and ARPACK takes care of the rest:

```
>>> evals_mid, evecs_mid = eigsh(X, 3, sigma=1, which='LM')
>>> i_sort = np.argsort(abs(1. / (1 - evals_all)))[-3:]
>>> print evals_all[i_sort]
[ 1.16577199  0.85081388  1.06642272]
>>> print evals_mid
[ 0.85081388  1.06642272  1.16577199]
>>> print np.dot(evecs_mid.T, evecs_all[:,i_sort])
[[-0.  1.  0.]
 [-0. -0.  1.]
 [ 1.  0.  0.]]
```

The eigenvalues come out in a different order, but they're all there. Note that the shift-invert mode requires the internal solution of a matrix inverse. This is taken care of automatically by `eigsh` and `eigs`, but the operation can also be specified by the user. See the docstring of `scipy.sparse.linalg.eigsh` and `scipy.sparse.linalg.eigs` for details.

1.10.5 References

1.11 Compressed Sparse Graph Routines (`scipy.sparse.csgraph`)

1.11.1 Example: Word Ladders

A Word Ladder is a word game invented by Lewis Carroll in which players find paths between words by switching one letter at a time. For example, one can link "ape" and "man" in the following way:

$$\text{ape} \to \text{apt} \to \text{ait} \to \text{bit} \to \text{big} \to \text{bag} \to \text{mag} \to \text{man}$$

Note that each step involves changing just one letter of the word. This is just one possible path from "ape" to "man", but is it the shortest possible path? If we desire to find the shortest word ladder path between two given words, the sparse graph submodule can help.

First we need a list of valid words. Many operating systems have such a list built-in. For example, on linux, a word list can often be found at one of the following locations:

```
/usr/share/dict
/var/lib/dict
```

Another easy source for words are the scrabble word lists available at various sites around the internet (search with your favorite search engine). We'll first create this list. The system word lists consist of a file with one word per line. The following should be modified to use the particular word list you have available:

```
>>> word_list = open('/usr/share/dict/words').readlines()
>>> word_list = map(str.strip, word_list)
```

We want to look at words of length 3, so let's select just those words of the correct length. We'll also eliminate words which start with upper-case (proper nouns) or contain non alpha-numeric characters like apostrophes and hyphens. Finally, we'll make sure everything is lower-case for comparison later:

```
>>> word_list = [word for word in word_list if len(word) == 3]
>>> word_list = [word for word in word_list if word[0].islower()]
>>> word_list = [word for word in word_list if word.isalpha()]
>>> word_list = map(str.lower, word_list)
>>> len(word_list)
586
```

Now we have a list of 586 valid three-letter words (the exact number may change depending on the particular list used). Each of these words will become a node in our graph, and we will create edges connecting the nodes associated with each pair of words which differs by only one letter.

There are efficient ways to do this, and inefficient ways to do this. To do this as efficiently as possible, we're going to use some sophisticated numpy array manipulation:

```
>>> import numpy as np
>>> word_list = np.asarray(word_list)
>>> word_list.dtype
dtype('|S3')
>>> word_list.sort()  # sort for quick searching later
```

We have an array where each entry is three bytes. We'd like to find all pairs where exactly one byte is different. We'll start by converting each word to a three-dimensional vector:

```
>>> word_bytes = np.ndarray((word_list.size, word_list.itemsize),
...                         dtype='int8',
...                         buffer=word_list.data)
>>> word_bytes.shape
(586, 3)
```

Now we'll use the Hamming distance between each point to determine which pairs of words are connected. The Hamming distance measures the fraction of entries between two vectors which differ: any two words with a hamming distance equal to $1/N$, where N is the number of letters, are connected in the word ladder:

```
>>> from scipy.spatial.distance import pdist, squareform
>>> from scipy.sparse import csr_matrix
>>> hamming_dist = pdist(word_bytes, metric='hamming')
>>> graph = csr_matrix(squareform(hamming_dist < 1.5 / word_list.itemsize))
```

When comparing the distances, we don't use an equality because this can be unstable for floating point values. The inequality produces the desired result as long as no two entries of the word list are identical. Now that our graph is set up, we'll use a shortest path search to find the path between any two words in the graph:

```
>>> i1 = word_list.searchsorted('ape')
>>> i2 = word_list.searchsorted('man')
>>> word_list[i1]
'ape'
>>> word_list[i2]
'man'
```

We need to check that these match, because if the words are not in the list that will not be the case. Now all we need is to find the shortest path between these two indices in the graph. We'll use dijkstra's algorithm, because it allows us to find the path for just one node:

```
>>> from scipy.sparse.csgraph import dijkstra
>>> distances, predecessors = dijkstra(graph, indices=i1,
...                                    return_predecessors=True)
>>> print distances[i2]
5.0
```

So we see that the shortest path between 'ape' and 'man' contains only five steps. We can use the predecessors returned by the algorithm to reconstruct this path:

```
>>> path = []
>>> i = i2
>>> while i != i1:
>>>     path.append(word_list[i])
>>>     i = predecessors[i]
```

```
>>> path.append(word_list[i1])
>>> print path[::-1]
['ape', 'apt', 'opt', 'oat', 'mat', 'man']
```

This is three fewer links than our initial example: the path from ape to man is only five steps.

Using other tools in the module, we can answer other questions. For example, are there three-letter words which are not linked in a word ladder? This is a question of connected components in the graph:

```
>>> from scipy.sparse.csgraph import connected_components
>>> N_components, component_list = connected_components(graph)
>>> print N_components
15
```

In this particular sample of three-letter words, there are 15 connected components: that is, 15 distinct sets of words with no paths between the sets. How many words are in each of these sets? We can learn this from the list of components:

```
>>> [np.sum(component_list == i) for i in range(15)]
[571, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1]
```

There is one large connected set, and 14 smaller ones. Let's look at the words in the smaller ones:

```
>>> [list(word_list[np.where(component_list == i)]) for i in range(1, 15)]
[['aha'],
 ['chi'],
 ['ebb'],
 ['ems', 'emu'],
 ['gnu'],
 ['ism'],
 ['khz'],
 ['nth'],
 ['ova'],
 ['qua'],
 ['ugh'],
 ['ups'],
 ['urn'],
 ['use']]
```

These are all the three-letter words which do not connect to others via a word ladder.

We might also be curious about which words are maximally separated. Which two words take the most links to connect? We can determine this by computing the matrix of all shortest paths. Note that by convention, the distance between two non-connected points is reported to be infinity, so we'll need to remove these before finding the maximum:

```
>>> distances, predecessors = dijkstra(graph, return_predecessors=True)
>>> np.max(distances[~np.isinf(distances)])
13.0
```

So there is at least one pair of words which takes 13 steps to get from one to the other! Let's determine which these are:

```
>>> i1, i2 = np.where(distances == 13)
>>> zip(word_list[i1], word_list[i2])
[('imp', 'ohm'),
 ('imp', 'ohs'),
 ('ohm', 'imp'),
 ('ohm', 'ump'),
 ('ohs', 'imp'),
 ('ohs', 'ump'),
```

```
 ('ump', 'ohm'),
 ('ump', 'ohs')]
```

We see that there are two pairs of words which are maximally separated from each other: ‘imp’ and ‘ump’ on one hand, and ‘ohm’ and ‘ohs’ on the other hand. We can find the connecting list in the same way as above:

```
>>> path = []
>>> i = i2[0]
>>> while i != i1[0]:
>>>     path.append(word_list[i])
>>>     i = predecessors[i1[0], i]
>>> path.append(word_list[i1[0]])
>>> print path[::-1]
['imp', 'amp', 'asp', 'ask', 'ark', 'are', 'aye', 'rye', 'roe', 'woe', 'woo', 'who', 'oho', 'ohm']
```

This gives us the path we desired to see.

Word ladders are just one potential application of scipy’s fast graph algorithms for sparse matrices. Graph theory makes appearances in many areas of mathematics, data analysis, and machine learning. The sparse graph tools are flexible enough to handle many of these situations.

1.12 Spatial data structures and algorithms (`scipy.spatial`)

`scipy.spatial` can compute triangulations, Voronoi diagrams, and convex hulls of a set of points, by leveraging the Qhull library.

Moreover, it contains `KDTree` implementations for nearest-neighbor point queries, and utilities for distance computations in various metrics.

1.12.1 Delaunay triangulations

The Delaunay triangulation is a subdivision of a set of points into a non-overlapping set of triangles, such that no point is inside the circumcircle of any triangle. In practice, such triangulations tend to avoid triangles with small angles.

Delaunay triangulation can be computed using `scipy.spatial` as follows:

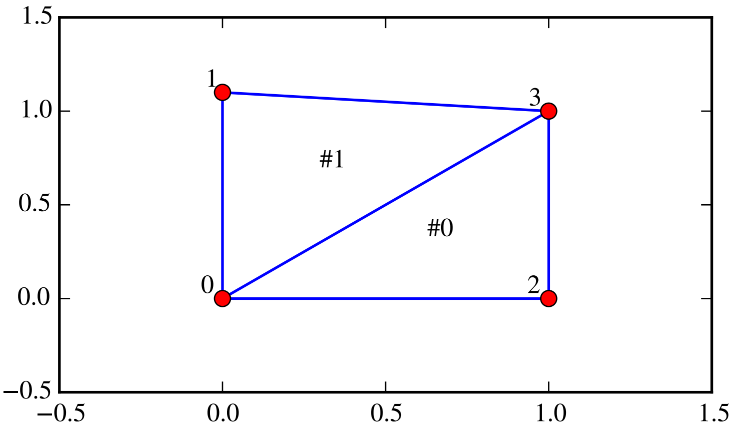
```
>>> from scipy.spatial import Delaunay
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> tri = Delaunay(points)
```

We can visualize it:

```
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices.copy())
>>> plt.plot(points[:,0], points[:,1], 'o')
```

And add some further decorations:

```
>>> for j, p in enumerate(points):
...     plt.text(p[0]-0.03, p[1]+0.03, j, ha='right') # label the points
>>> for j, s in enumerate(tri.simplices):
...     p = points[s].mean(axis=0)
...     plt.text(p[0], p[1], '#%d' % j, ha='center') # label triangles
>>> plt.xlim(-0.5, 1.5); plt.ylim(-0.5, 1.5)
>>> plt.show()
```



The structure of the triangulation is encoded in the following way: the `simplices` attribute contains the indices of the points in the `points` array that make up the triangle. For instance:

```
>>> i = 1
>>> tri.simplices[i,:]
array([3, 1, 0], dtype=int32)
>>> points[tri.simplices[i,:]]
array([[ 1. ,  1. ],
       [ 0. ,  1.1],
       [ 0. ,  0. ]])
```

Moreover, neighboring triangles can also be found out:

```
>>> tri.neighbors[i]
array([-1,  0, -1], dtype=int32)
```

What this tells us is that this triangle has triangle #0 as a neighbor, but no other neighbors. Moreover, it tells us that neighbor 0 is opposite the vertex 1 of the triangle:

```
>>> points[tri.simplices[i, 1]]
array([ 0. ,  1.1])
```

Indeed, from the figure we see that this is the case.

Qhull can also perform tesselations to simplices also for higher-dimensional point sets (for instance, subdivision into tetrahedra in 3-D).

Coplanar points

It is important to note that not *all* points necessarily appear as vertices of the triangulation, due to numerical precision issues in forming the triangulation. Consider the above with a duplicated point:

```
>>> points = np.array([[0, 0], [0, 1], [1, 0], [1, 1], [1, 1]])
>>> tri = Delaunay(points)
>>> np.unique(tri.simplices.ravel())
array([0, 1, 2, 3], dtype=int32)
```

Observe that point #4, which is a duplicate, does not occur as a vertex of the triangulation. That this happened is recorded:

```
>>> tri.coplanar
array([[4, 0, 3]], dtype=int32)
```

This means that point 4 resides near triangle 0 and vertex 3, but is not included in the triangulation.

Note that such degeneracies can occur not only because of duplicated points, but also for more complicated geometrical reasons, even in point sets that at first sight seem well-behaved.

However, Qhull has the "QJ" option, which instructs it to perturb the input data randomly until degeneracies are resolved:

```
>>> tri = Delaunay(points, qhull_options="QJ Pp")
>>> points[tri.simplices]
array([[[1, 1],
        [1, 0],
        [0, 0]],
       [[1, 1],
        [1, 1],
        [1, 0]],
       [[0, 1],
        [1, 1],
        [0, 0]],
       [[0, 1],
        [1, 1],
        [1, 1]]])
```

Two new triangles appeared. However, we see that they are degenerate and have zero area.

1.12.2 Convex hulls

Convex hull is the smallest convex object containing all points in a given point set.

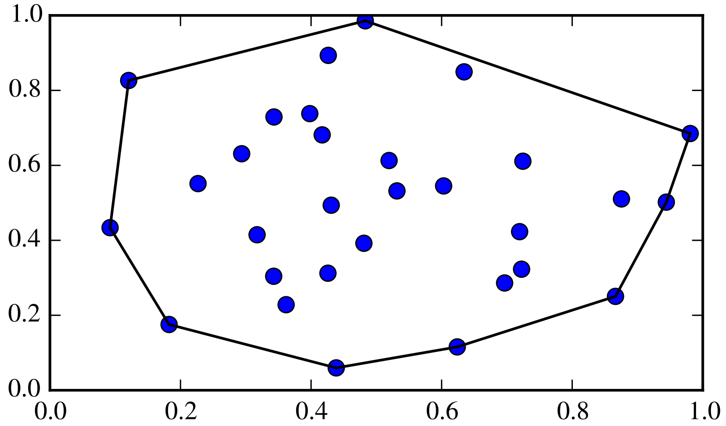
These can be computed via the Qhull wrappers in `scipy.spatial` as follows:

```
>>> from scipy.spatial import ConvexHull
>>> points = np.random.rand(30, 2)   # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

The convex hull is represented as a set of N-1 dimensional simplices, which in 2-D means line segments. The storage scheme is exactly the same as for the simplices in the Delaunay triangulation discussed above.

We can illustrate the above result:

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
>>>     plt.plot(points[simplex,0], points[simplex,1], 'k-')
>>> plt.show()
```



The same can be achieved with `scipy.spatial.convex_hull_plot_2d`.

1.12.3 Voronoi diagrams

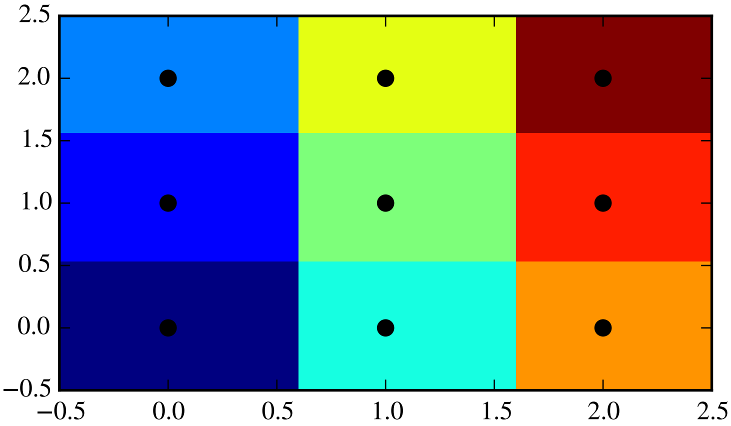
A Voronoi diagram is a subdivision of the space into the nearest neighborhoods of a given set of points.

There are two ways to approach this object using `scipy.spatial`. First, one can use the `KDTree` to answer the question "which of the points is closest to this one", and define the regions that way:

```
>>> from scipy.spatial import KDTree
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
...                    [2, 0], [2, 1], [2, 2]])
>>> tree = KDTree(points)
>>> tree.query([0.1, 0.1])
(0.14142135623730953, 0)
```

So the point `(0.1, 0.1)` belongs to region `0`. In color:

```
>>> x = np.linspace(-0.5, 2.5, 31)
>>> y = np.linspace(-0.5, 2.5, 33)
>>> xx, yy = np.meshgrid(x, y)
>>> xy = np.c_[xx.ravel(), yy.ravel()]
>>> import matplotlib.pyplot as plt
>>> plt.pcolor(x, y, tree.query(xy)[1].reshape(33, 31))
>>> plt.plot(points[:,0], points[:,1], 'ko')
>>> plt.show()
```



This does not, however, give the Voronoi diagram as a geometrical object.

The representation in terms of lines and points can be again obtained via the Qhull wrappers in `scipy.spatial`:

```
>>> from scipy.spatial import Voronoi
>>> vor = Voronoi(points)
>>> vor.vertices
array([[ 0.5,  0.5],
       [ 1.5,  0.5],
       [ 0.5,  1.5],
       [ 1.5,  1.5]])
```

The Voronoi vertices denote the set of points forming the polygonal edges of the Voronoi regions. In this case, there are 9 different regions:

```
>>> vor.regions
[[-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [3, 1, 0, 2], [2, -1, 0], [3, -1, 1]]
```

Negative value `-1` again indicates a point at infinity. Indeed, only one of the regions, `[3, 1, 0, 2]`, is bounded. Note here that due to similar numerical precision issues as in Delaunay triangulation above, there may be fewer Voronoi regions than input points.

The ridges (lines in 2-D) separating the regions are described as a similar collection of simplices as the convex hull pieces:

```
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1, 3], [-1, 2], [0, 2], [1,
```

These numbers indicate indices of the Voronoi vertices making up the line segments. `-1` is again a point at infinity — only four of the 12 lines is a bounded line segment while the others extend to infinity.

The Voronoi ridges are perpendicular to lines drawn between the input points. Which two points each ridge corresponds to is also recorded:

```
>>> vor.ridge_points
array([[0, 3],
       [0, 1],
       [6, 3],
       [6, 7],
       [3, 4],
```

```
       [5, 8],
       [5, 2],
       [5, 4],
       [8, 7],
       [2, 1],
       [4, 1],
       [4, 7]], dtype=int32)
```

This information, taken together, is enough to construct the full diagram.

We can plot it as follows. First the points and the Voronoi vertices:

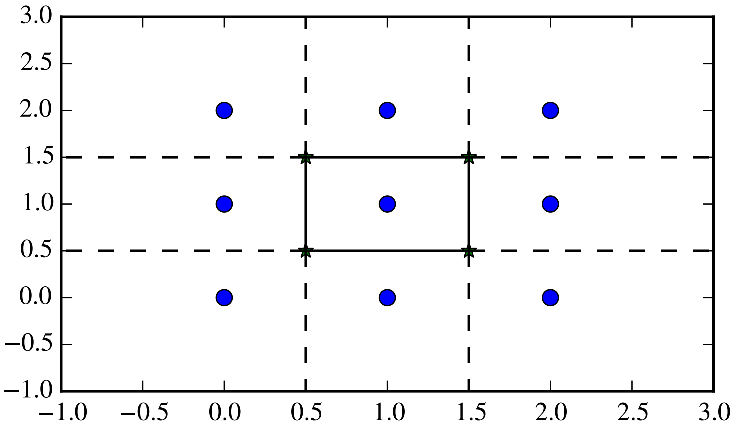
```
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> plt.plot(vor.vertices[:,0], vor.vertices[:,1], '*')
>>> plt.xlim(-1, 3); plt.ylim(-1, 3)
```

Plotting the finite line segments goes as for the convex hull, but now we have to guard for the infinite edges:

```
>>> for simplex in vor.ridge_vertices:
>>>     simplex = np.asarray(simplex)
>>>     if np.all(simplex >= 0):
>>>         plt.plot(vor.vertices[simplex,0], vor.vertices[simplex,1], 'k-')
```

The ridges extending to infinity require a bit more care:

```
>>> center = points.mean(axis=0)
>>> for pointidx, simplex in zip(vor.ridge_points, vor.ridge_vertices):
>>>     simplex = np.asarray(simplex)
>>>     if np.any(simplex < 0):
>>>         i = simplex[simplex >= 0][0] # finite end Voronoi vertex
>>>         t = points[pointidx[1]] - points[pointidx[0]] # tangent
>>>         t /= np.linalg.norm(t)
>>>         n = np.array([-t[1], t[0]]) # normal
>>>         midpoint = points[pointidx].mean(axis=0)
>>>         far_point = vor.vertices[i] + np.sign(np.dot(midpoint - center, n)) * n * 100
>>>         plt.plot([vor.vertices[i,0], far_point[0]],
...                  [vor.vertices[i,1], far_point[1]], 'k--')
>>> plt.show()
```



This plot can also be created using `scipy.spatial.voronoi_plot_2d`.

1.13 Statistics (`scipy.stats`)

1.13.1 Introduction

In this tutorial we discuss many, but certainly not all, features of `scipy.stats`. The intention here is to provide a user with a working knowledge of this package. We refer to the reference manual for further details.

Note: This documentation is work in progress.

1.13.2 Random Variables

There are two general distribution classes that have been implemented for encapsulating *continuous random variables* and *discrete random variables* . Over 80 continuous random variables (RVs) and 10 discrete random variables have been implemented using these classes. Besides this, new routines and distributions can easily added by the end user. (If you create one, please contribute it).

All of the statistics functions are located in the sub-package `scipy.stats` and a fairly complete listing of these functions can be obtained using `info(stats)`. The list of the random variables available can also be obtained from the docstring for the stats sub-package.

In the discussion below we mostly focus on continuous RVs. Nearly all applies to discrete variables also, but we point out some differences here: *Specific Points for Discrete Distributions*.

Getting Help

First of all, all distributions are accompanied with help functions. To obtain just some basic information we can call

```
>>> from scipy import stats
>>> from scipy.stats import norm
>>> print norm.__doc__
```

To find the support, i.e., upper and lower bound of the distribution, call:

```
>>> print 'bounds of distribution lower: %s, upper: %s' % (norm.a,norm.b)
bounds of distribution lower: -inf, upper: inf
```

We can list all methods and properties of the distribution with `dir(norm)`. As it turns out, some of the methods are private methods although they are not named as such (their name does not start with a leading underscore), for example `veccdf`, are only available for internal calculation (those methods will give warnings when one tries to use them, and will be removed at some point).

To obtain the *real* main methods, we list the methods of the frozen distribution. (We explain the meaning of a *frozen* distribution below).

```
>>> rv = norm()
>>> dir(rv)  # reformatted
    ['__class__', '__delattr__', '__dict__', '__doc__', '__getattribute__',
    '__hash__', '__init__', '__module__', '__new__', '__reduce__', '__reduce_ex__',
    '__repr__', '__setattr__', '__str__', '__weakref__', 'args', 'cdf', 'dist',
    'entropy', 'isf', 'kwds', 'moment', 'pdf', 'pmf', 'ppf', 'rvs', 'sf', 'stats']
```

Finally, we can obtain the list of available distribution through introspection:

```
>>> import warnings
>>> warnings.simplefilter('ignore', DeprecationWarning)
>>> dist_continu = [d for d in dir(stats) if
...                 isinstance(getattr(stats,d), stats.rv_continuous)]
>>> dist_discrete = [d for d in dir(stats) if
...                  isinstance(getattr(stats,d), stats.rv_discrete)]
>>> print 'number of continuous distributions:', len(dist_continu)
number of continuous distributions: 84
>>> print 'number of discrete distributions:   ', len(dist_discrete)
number of discrete distributions:   12
```

Common Methods

The main public methods for continuous RVs are:

- rvs: Random Variates
- pdf: Probability Density Function
- cdf: Cumulative Distribution Function
- sf: Survival Function (1-CDF)
- ppf: Percent Point Function (Inverse of CDF)
- isf: Inverse Survival Function (Inverse of SF)
- stats: Return mean, variance, (Fisher's) skew, or (Fisher's) kurtosis
- moment: non-central moments of the distribution

Let's take a normal RV as an example.

```
>>> norm.cdf(0)
0.5
```

To compute the `cdf` at a number of points, we can pass a list or a numpy array.

```
>>> norm.cdf([-1., 0, 1])
array([ 0.15865525,  0.5       ,  0.84134475])
>>> import numpy as np
>>> norm.cdf(np.array([-1., 0, 1]))
array([ 0.15865525,  0.5       ,  0.84134475])
```

Thus, the basic methods such as *pdf*, *cdf*, and so on are vectorized with `np.vectorize`.

Other generally useful methods are supported too:

```
>>> norm.mean(), norm.std(), norm.var()
(0.0, 1.0, 1.0)
>>> norm.stats(moments = "mv")
(array(0.0), array(1.0))
```

To find the median of a distribution we can use the percent point function `ppf`, which is the inverse of the `cdf`:

```
>>> norm.ppf(0.5)
0.0
```

To generate a sequence of random variates, use the `size` keyword argument:

```
>>> norm.rvs(size=5)
array([-0.35687759,  1.34347647, -0.11710531, -1.00725181, -0.51275702])
```

Don't think that `norm.rvs(5)` generates 5 variates:

```
>>> norm.rvs(5)
7.131624370075814
```

Here, `5` with no keyword is being interpreted as the first possible keyword argument, `loc`, which is the first of a pair of keyword arguments taken by all continuous distributions. This brings us to the topic of the next subsection.

Shifting and Scaling

All continuous distributions take `loc` and `scale` as keyword parameters to adjust the location and scale of the distribution, e.g. for the standard normal distribution the location is the mean and the scale is the standard deviation.

```
>>> norm.stats(loc = 3, scale = 4, moments = "mv")
(array(3.0), array(16.0))
```

In many cases the standardized distribution for a random variable `X` is obtained through the transformation `(X - loc) / scale`. The default values are `loc = 0` and `scale = 1`.

Smart use of `loc` and `scale` can help modify the standard distributions in many ways. To illustrate the scaling further, the `cdf` of an exponentially distributed RV with mean $1/\lambda$ is given by

$$F(x) = 1 - \exp(-\lambda x)$$

By applying the scaling rule above, it can be seen that by taking `scale = 1./lambda` we get the proper scale.

```
>>> from scipy.stats import expon
>>> expon.mean(scale=3.)
3.0
```

Note: Distributions that take shape parameters may require more than simple application of `loc` and/or `scale` to achieve the desired form. For example, the distribution of 2-D vector lengths given a constant vector of length R perturbed by independent N(0, σ^2) deviations in each component is rice(R/σ, scale= σ). The first argument is a shape parameter that needs to be scaled along with x.

The uniform distribution is also interesting:

```
>>> from scipy.stats import uniform
>>> uniform.cdf([0, 1, 2, 3, 4, 5], loc = 1, scale = 4)
array([ 0.  ,  0.  ,  0.25,  0.5 ,  0.75,  1.  ])
```

Finally, recall from the previous paragraph that we are left with the problem of the meaning of `norm.rvs(5)`. As it turns out, calling a distribution like this, the first argument, i.e., the 5, gets passed to set the `loc` parameter. Let's see:

```
>>> np.mean(norm.rvs(5, size=500))
4.983550784784704
```

Thus, to explain the output of the example of the last section: `norm.rvs(5)` generates a single normally distributed random variate with mean `loc=5`, because of the default `size=1`.

We recommend that you set `loc` and `scale` parameters explicitly, by passing the values as keywords rather than as arguments. Repetition can be minimized when calling more than one method of a given RV by using the technique of Freezing a Distribution, as explained below.

Shape Parameters

While a general continuous random variable can be shifted and scaled with the `loc` and `scale` parameters, some distributions require additional shape parameters. For instance, the gamma distribution, with density

$$\gamma(x, a) = \frac{\lambda(\lambda x)^{a-1}}{\Gamma(a)} e^{-\lambda x} ,$$

requires the shape parameter a. Observe that setting λ can be obtained by setting the `scale` keyword to $1/\lambda$.

Let's check the number and name of the shape parameters of the gamma distribution. (We know from the above that this should be 1.)

```
>>> from scipy.stats import gamma
>>> gamma.numargs
1
>>> gamma.shapes
'a'
```

Now we set the value of the shape variable to 1 to obtain the exponential distribution, so that we compare easily whether we get the results we expect.

```
>>>  gamma(1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Notice that we can also specify shape parameters as keywords:

```
>>> gamma(a=1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Freezing a Distribution

Passing the `loc` and `scale` keywords time and again can become quite bothersome. The concept of *freezing* a RV is used to solve such problems.

```
>>> rv = gamma(1, scale=2.)
```

By using `rv` we no longer have to include the scale or the shape parameters anymore. Thus, distributions can be used in one of two ways, either by passing all distribution parameters to each method call (such as we did earlier) or by freezing the parameters for the instance of the distribution. Let us check this:

```
>>> rv.mean(), rv.std()
(2.0, 2.0)
```

This is indeed what we should get.

Broadcasting

The basic methods `pdf` and so on satisfy the usual numpy broadcasting rules. For example, we can calculate the critical values for the upper tail of the t distribution for different probabilites and degrees of freedom.

```
>>> stats.t.isf([0.1, 0.05, 0.01], [[10], [11]])
array([[ 1.37218364,  1.81246112,  2.76376946],
       [ 1.36343032,  1.79588482,  2.71807918]])
```

Here, the first row are the critical values for 10 degrees of freedom and the second row for 11 degrees of freedom (d.o.f.). Thus, the broadcasting rules give the same result of calling `isf` twice:

```
>>> stats.t.isf([0.1, 0.05, 0.01], 10)
array([ 1.37218364,  1.81246112,  2.76376946])
>>> stats.t.isf([0.1, 0.05, 0.01], 11)
array([ 1.36343032,  1.79588482,  2.71807918])
```

If the array with probabilities, i.e, `[0.1, 0.05, 0.01]` and the array of degrees of freedom i.e., `[10, 11, 12]`, have the same array shape, then element wise matching is used. As an example, we can obtain the 10% tail for 10 d.o.f., the 5% tail for 11 d.o.f. and the 1% tail for 12 d.o.f. by calling

```
>>> stats.t.isf([0.1, 0.05, 0.01], [10, 11, 12])
array([ 1.37218364,  1.79588482,  2.68099799])
```

Specific Points for Discrete Distributions

Discrete distribution have mostly the same basic methods as the continuous distributions. However `pdf` is replaced the probability mass function `pmf`, no estimation methods, such as fit, are available, and `scale` is not a valid keyword parameter. The location parameter, keyword `loc` can still be used to shift the distribution.

The computation of the cdf requires some extra attention. In the case of continuous distribution the cumulative distribution function is in most standard cases strictly monotonic increasing in the bounds (a,b) and has therefore a unique inverse. The cdf of a discrete distribution, however, is a step function, hence the inverse cdf, i.e., the percent point function, requires a different definition:

```
ppf(q) = min{x : cdf(x) >= q, x integer}
```

For further info, see the docs here.

We can look at the hypergeometric distribution as an example

```
>>> from scipy.stats import hypergeom
>>> [M, n, N] = [20, 7, 12]
```

If we use the cdf at some integer points and then evaluate the ppf at those cdf values, we get the initial integers back, for example

```
>>> x = np.arange(4)*2
>>> x
array([0, 2, 4, 6])
>>> prb = hypergeom.cdf(x, M, n, N)
>>> prb
array([ 0.0001031991744066,  0.0521155830753351,  0.6083591331269301,
        0.9897832817337386])
>>> hypergeom.ppf(prb, M, n, N)
array([ 0.,  2.,  4.,  6.])
```

If we use values that are not at the kinks of the cdf step function, we get the next higher integer back:

```
>>> hypergeom.ppf(prb + 1e-8, M, n, N)
array([ 1.,  3.,  5.,  7.])
>>> hypergeom.ppf(prb - 1e-8, M, n, N)
array([ 0.,  2.,  4.,  6.])
```

Fitting Distributions

The main additional methods of the not frozen distribution are related to the estimation of distribution parameters:

- ***fit*: maximum likelihood estimation of distribution parameters, including location**
  and scale
- fit_loc_scale: estimation of location and scale when shape parameters are given
- nnlf: negative log likelihood function
- expect: Calculate the expectation of a function against the pdf or pmf

Performance Issues and Cautionary Remarks

The performance of the individual methods, in terms of speed, varies widely by distribution and method. The results of a method are obtained in one of two ways: either by explicit calculation, or by a generic algorithm that is independent of the specific distribution.

Explicit calculation, on the one hand, requires that the method is directly specified for the given distribution, either through analytic formulas or through special functions in `scipy.special` or `numpy.random` for `rvs`. These are usually relatively fast calculations.

The generic methods, on the other hand, are used if the distribution does not specify any explicit calculation. To define a distribution, only one of pdf or cdf is necessary; all other methods can be derived using numeric integration and root finding. However, these indirect methods can be *very* slow. As an example, `rgh = stats.gausshyper.rvs(0.5, 2, 2, 2, size=100)` creates random variables in a very indirect way and takes about 19 seconds for 100 random variables on my computer, while one million random variables from the standard normal or from the t distribution take just above one second.

Remaining Issues

The distributions in `scipy.stats` have recently been corrected and improved and gained a considerable test suite, however a few issues remain:

- the distributions have been tested over some range of parameters, however in some corner ranges, a few incorrect results may remain.
- the maximum likelihood estimation in *fit* does not work with default starting parameters for all distributions and the user needs to supply good starting parameters. Also, for some distribution using a maximum likelihood estimator might inherently not be the best choice.

1.13.3 Building Specific Distributions

The next examples shows how to build your own distributions. Further examples show the usage of the distributions and some statistical tests.

Making a Continuous Distribution, i.e., Subclassing `rv_continuous`

Making continuous distributions is fairly simple.

```
>>> from scipy import stats
>>> class deterministic_gen(stats.rv_continuous):
...     def _cdf(self, x):
...         return np.where(x < 0, 0., 1.)
...     def _stats(self):
...         return 0., 0., 0., 0.
```

```
>>> deterministic = deterministic_gen(name="deterministic")
>>> deterministic.cdf(np.arange(-3, 3, 0.5))
array([ 0.,   0.,   0.,   0.,   0.,   0.,   1.,   1.,   1.,   1.,   1.,   1.])
```

Interestingly, the `pdf` is now computed automatically:

```
>>> deterministic.pdf(np.arange(-3, 3, 0.5))
array([  0.00000000e+00,   0.00000000e+00,   0.00000000e+00,
         0.00000000e+00,   0.00000000e+00,   0.00000000e+00,
         5.83333333e+04,   4.16333634e-12,   4.16333634e-12,
         4.16333634e-12,   4.16333634e-12,   4.16333634e-12])
```

Be aware of the performance issues mentions in *Performance Issues and Cautionary Remarks*. The computation of unspecified common methods can become very slow, since only general methods are called which, by their very nature, cannot use any specific information about the distribution. Thus, as a cautionary example:

```
>>> from scipy.integrate import quad
>>> quad(deterministic.pdf, -1e-1, 1e-1)
(4.163336342344337e-13, 0.0)
```

But this is not correct: the integral over this pdf should be 1. Let's make the integration interval smaller:

```
>>> quad(deterministic.pdf, -1e-3, 1e-3)  # warning removed
(1.000076872229173, 0.0010625571718182458)
```

This looks better. However, the problem originated from the fact that the pdf is not specified in the class definition of the deterministic distribution.

Subclassing `rv_discrete`

In the following we use `stats.rv_discrete` to generate a discrete distribution that has the probabilities of the truncated normal for the intervals centered around the integers.

General Info

From the docstring of rv_discrete, i.e.,

```
>>> from scipy.stats import rv_discrete
>>> help(rv_discrete)
```

we learn that:

> "You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk, pk) which describes only those values of X (xk) that occur with nonzero probability (pk)."

Next to this, there are some further requirements for this approach to work:

- The keyword *name* is required.
- The support points of the distribution xk have to be integers.
- The number of significant digits (decimals) needs to be specified.

In fact, if the last two requirements are not satisfied an exception may be raised or the resulting numbers may be incorrect.

An Example

Let's do the work. First

```
>>> npoints = 20   # number of integer support points of the distribution minus 1
>>> npointsh = npoints / 2
>>> npointsf = float(npoints)
>>> nbound = 4   # bounds for the truncated normal
>>> normbound = (1+1/npointsf) * nbound   # actual bounds of truncated normal
>>> grid = np.arange(-npointsh, npointsh+2, 1)   # integer grid
>>> gridlimitsnorm = (grid-0.5) / npointsh * nbound   # bin limits for the truncnorm
>>> gridlimits = grid - 0.5   # used later in the analysis
>>> grid = grid[:-1]
>>> probs = np.diff(stats.truncnorm.cdf(gridlimitsnorm, -normbound, normbound))
>>> gridint = grid
```

And finally we can subclass `rv_discrete`:

```
>>> normdiscrete = stats.rv_discrete(values=(gridint,
...              np.round(probs, decimals=7)), name='normdiscrete')
```

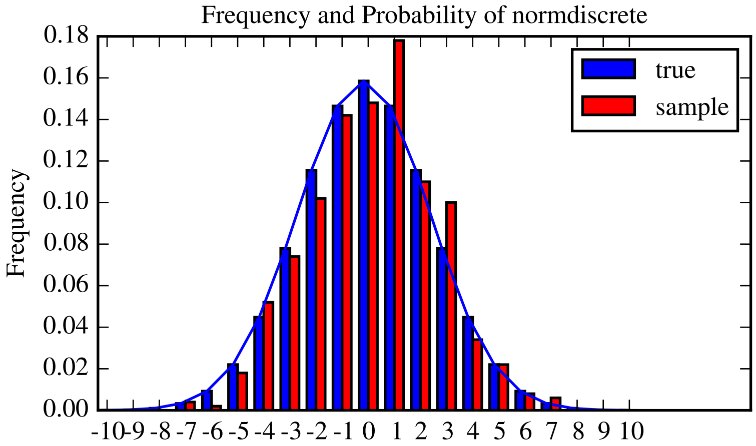
Now that we have defined the distribution, we have access to all common methods of discrete distributions.

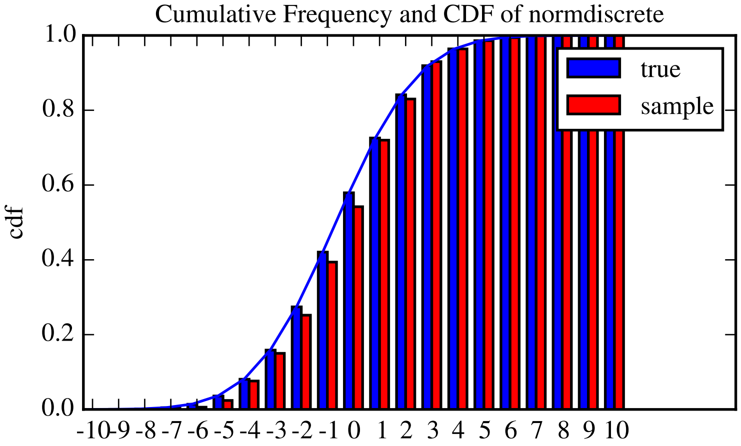
```
>>> print 'mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis = %6.4f'% \
...       normdiscrete.stats(moments =  'mvsk')
mean = -0.0000, variance = 6.3302, skew = 0.0000, kurtosis = -0.0076

>>> nd_std = np.sqrt(normdiscrete.stats(moments='v'))
```

Testing the Implementation

Let’s generate a random sample and compare observed frequencies with the probabilities.

```
>>> n_sample = 500
>>> np.random.seed(87655678)   # fix the seed for replicability
>>> rvs = normdiscrete.rvs(size=n_sample)
>>> rvsnd = rvs
>>> f, l = np.histogram(rvs, bins=gridlimits)
>>> sfreq = np.vstack([gridint, f, probs*n_sample]).T
>>> print sfreq
[[ -1.00000000e+01   0.00000000e+00   2.95019349e-02]
 [ -9.00000000e+00   0.00000000e+00   1.32294142e-01]
 [ -8.00000000e+00   0.00000000e+00   5.06497902e-01]
 [ -7.00000000e+00   2.00000000e+00   1.65568919e+00]
 [ -6.00000000e+00   1.00000000e+00   4.62125309e+00]
 [ -5.00000000e+00   9.00000000e+00   1.10137298e+01]
 [ -4.00000000e+00   2.60000000e+01   2.24137683e+01]
 [ -3.00000000e+00   3.70000000e+01   3.89503370e+01]
 [ -2.00000000e+00   5.10000000e+01   5.78004747e+01]
 [ -1.00000000e+00   7.10000000e+01   7.32455414e+01]
 [  0.00000000e+00   7.40000000e+01   7.92618251e+01]
 [  1.00000000e+00   8.90000000e+01   7.32455414e+01]
 [  2.00000000e+00   5.50000000e+01   5.78004747e+01]
 [  3.00000000e+00   5.00000000e+01   3.89503370e+01]
 [  4.00000000e+00   1.70000000e+01   2.24137683e+01]
 [  5.00000000e+00   1.10000000e+01   1.10137298e+01]
 [  6.00000000e+00   4.00000000e+00   4.62125309e+00]
 [  7.00000000e+00   3.00000000e+00   1.65568919e+00]
 [  8.00000000e+00   0.00000000e+00   5.06497902e-01]
 [  9.00000000e+00   0.00000000e+00   1.32294142e-01]
 [  1.00000000e+01   0.00000000e+00   2.95019349e-02]]
```





Next, we can test, whether our sample was generated by our normdiscrete distribution. This also verifies whether the random numbers are generated correctly.

The chisquare test requires that there are a minimum number of observations in each bin. We combine the tail bins into larger bins so that they contain enough observations.

```
>>> f2 = np.hstack([f[:5].sum(), f[5:-5], f[-5:].sum()])
>>> p2 = np.hstack([probs[:5].sum(), probs[5:-5], probs[-5:].sum()])
>>> ch2, pval = stats.chisquare(f2, p2*n_sample)

>>> print 'chisquare for normdiscrete: chi2 = %6.3f pvalue = %6.4f' % (ch2, pval)
chisquare for normdiscrete: chi2 = 12.466 pvalue = 0.4090
```

The pvalue in this case is high, so we can be quite confident that our random sample was actually generated by the distribution.

1.13.4 Analysing One Sample

First, we create some random variables. We set a seed so that in each run we get identical results to look at. As an example we take a sample from the Student t distribution:

```
>>> np.random.seed(282629734)
>>> x = stats.t.rvs(10, size=1000)
```

Here, we set the required shape parameter of the t distribution, which in statistics corresponds to the degrees of freedom, to 10. Using size=1000 means that our sample consists of 1000 independently drawn (pseudo) random numbers. Since we did not specify the keyword arguments *loc* and *scale*, those are set to their default values zero and one.

Descriptive Statistics

x is a numpy array, and we have direct access to all array methods, e.g.

```
>>> print x.max(), x.min()  # equivalent to np.max(x), np.min(x)
5.26327732981 -3.78975572422
>>> print x.mean(), x.var() # equivalent to np.mean(x), np.var(x)
0.0140610663985 1.28899386208
```

How do the some sample properties compare to their theoretical counterparts?

```
>>> m, v, s, k = stats.t.stats(10, moments='mvsk')
>>> n, (smin, smax), sm, sv, ss, sk = stats.describe(x)

>>> print 'distribution:',
distribution:
>>> sstr = 'mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis = %6.4f'
>>> print sstr %(m, v, s ,k)
mean = 0.0000, variance = 1.2500, skew = 0.0000, kurtosis = 1.0000
>>> print 'sample:      ',
sample:
>>> print sstr %(sm, sv, ss, sk)
mean = 0.0141, variance = 1.2903, skew = 0.2165, kurtosis = 1.0556
```

Note: stats.describe uses the unbiased estimator for the variance, while np.var is the biased estimator.

For our sample the sample statistics differ a by a small amount from their theoretical counterparts.

T-test and KS-test

We can use the t-test to test whether the mean of our sample differs in a statistcally significant way from the theoretical expectation.

```
>>> print 't-statistic = %6.3f pvalue = %6.4f' %  stats.ttest_1samp(x, m)
t-statistic =  0.391 pvalue = 0.6955
```

The pvalue is 0.7, this means that with an alpha error of, for example, 10%, we cannot reject the hypothesis that the sample mean is equal to zero, the expectation of the standard t-distribution.

As an exercise, we can calculate our ttest also directly without using the provided function, which should give us the same answer, and so it does:

```
>>> tt = (sm-m)/np.sqrt(sv/float(n))  # t-statistic for mean
>>> pval = stats.t.sf(np.abs(tt), n-1)*2  # two-sided pvalue = Prob(abs(t)>tt)
```

```
>>> print 't-statistic = %6.3f pvalue = %6.4f' % (tt, pval)
t-statistic =  0.391 pvalue = 0.6955
```

The Kolmogorov-Smirnov test can be used to test the hypothesis that the sample comes from the standard t-distribution

```
>>> print 'KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x, 't', (10,))
KS-statistic D =  0.016 pvalue = 0.9606
```

Again the p-value is high enough that we cannot reject the hypothesis that the random sample really is distributed according to the t-distribution. In real applications, we don't know what the underlying distribution is. If we perform the Kolmogorov-Smirnov test of our sample against the standard normal distribution, then we also cannot reject the hypothesis that our sample was generated by the normal distribution given that in this example the p-value is almost 40%.

```
>>> print 'KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x,'norm')
KS-statistic D =  0.028 pvalue = 0.3949
```

However, the standard normal distribution has a variance of 1, while our sample has a variance of 1.29. If we standardize our sample and test it against the normal distribution, then the p-value is again large enough that we cannot reject the hypothesis that the sample came form the normal distribution.

```
>>> d, pval = stats.kstest((x-x.mean())/x.std(), 'norm')
>>> print 'KS-statistic D = %6.3f pvalue = %6.4f' % (d, pval)
KS-statistic D =  0.032 pvalue = 0.2402
```

Note: The Kolmogorov-Smirnov test assumes that we test against a distribution with given parameters, since in the last case we estimated mean and variance, this assumption is violated, and the distribution of the test statistic on which the p-value is based, is not correct.

Tails of the distribution

Finally, we can check the upper tail of the distribution. We can use the percent point function ppf, which is the inverse of the cdf function, to obtain the critical values, or, more directly, we can use the inverse of the survival function

```
>>> crit01, crit05, crit10 = stats.t.ppf([1-0.01, 1-0.05, 1-0.10], 10)
>>> print 'critical values from ppf at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f'% (crit01, crit05, crit10
critical values from ppf at 1%, 5% and 10%   2.7638   1.8125   1.3722
>>> print 'critical values from isf at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f'% tuple(stats.t.isf([0.01
critical values from isf at 1%, 5% and 10%   2.7638   1.8125   1.3722

>>> freq01 = np.sum(x>crit01) / float(n) * 100
>>> freq05 = np.sum(x>crit05) / float(n) * 100
>>> freq10 = np.sum(x>crit10) / float(n) * 100
>>> print 'sample %%-frequency at 1%%, 5%% and 10%% tail %8.4f %8.4f %8.4f'% (freq01, freq05, freq10
sample %-frequency at 1%, 5% and 10% tail   1.4000   5.8000  10.5000
```

In all three cases, our sample has more weight in the top tail than the underlying distribution. We can briefly check a larger sample to see if we get a closer match. In this case the empirical frequency is quite close to the theoretical probability, but if we repeat this several times the fluctuations are still pretty large.

```
>>> freq05l = np.sum(stats.t.rvs(10, size=10000) > crit05) / 10000.0 * 100
>>> print 'larger sample %%-frequency at 5%% tail %8.4f'% freq05l
larger sample %-frequency at 5% tail   4.8000
```

We can also compare it with the tail of the normal distribution, which has less weight in the tails:

```
>>> print 'tail prob. of normal at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f'% \
...       tuple(stats.norm.sf([crit01, crit05, crit10])*100)
tail prob. of normal at 1%, 5% and 10%   0.2857   3.4957   8.5003
```

The chisquare test can be used to test, whether for a finite number of bins, the observed frequencies differ significantly from the probabilites of the hypothesized distribution.

```
>>> quantiles = [0.0, 0.01, 0.05, 0.1, 1-0.10, 1-0.05, 1-0.01, 1.0]
>>> crit = stats.t.ppf(quantiles, 10)
>>> print crit
[       -Inf -2.76376946 -1.81246112 -1.37218364  1.37218364  1.81246112
  2.76376946         Inf]
>>> n_sample = x.size
>>> freqcount = np.histogram(x, bins=crit)[0]
>>> tprob = np.diff(quantiles)
>>> nprob = np.diff(stats.norm.cdf(crit))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print 'chisquare for t:      chi2 = %6.3f pvalue = %6.4f' % (tch, tpval)
chisquare for t:      chi2 =  2.300 pvalue = 0.8901
>>> print 'chisquare for normal: chi2 = %6.3f pvalue = %6.4f' % (nch, npval)
chisquare for normal: chi2 = 64.605 pvalue = 0.0000
```

We see that the standard normal distribution is clearly rejected while the standard t-distribution cannot be rejected. Since the variance of our sample differs from both standard distribution, we can again redo the test taking the estimate for scale and location into account.

The fit method of the distributions can be used to estimate the parameters of the distribution, and the test is repeated using probabilites of the estimated distribution.

```
>>> tdof, tloc, tscale = stats.t.fit(x)
>>> nloc, nscale = stats.norm.fit(x)
>>> tprob = np.diff(stats.t.cdf(crit, tdof, loc=tloc, scale=tscale))
>>> nprob = np.diff(stats.norm.cdf(crit, loc=nloc, scale=nscale))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print 'chisquare for t:      chi2 = %6.3f pvalue = %6.4f' % (tch, tpval)
chisquare for t:      chi2 =  1.577 pvalue = 0.9542
>>> print 'chisquare for normal: chi2 = %6.3f pvalue = %6.4f' % (nch, npval)
chisquare for normal: chi2 = 11.084 pvalue = 0.0858
```

Taking account of the estimated parameters, we can still reject the hypothesis that our sample came from a normal distribution (at the 5% level), but again, with a p-value of 0.95, we cannot reject the t distribution.

Special tests for normal distributions

Since the normal distribution is the most common distribution in statistics, there are several additional functions available to test whether a sample could have been drawn from a normal distribution

First we can test if skew and kurtosis of our sample differ significantly from those of a normal distribution:

```
>>> print 'normal skewtest teststat = %6.3f pvalue = %6.4f' % stats.skewtest(x)
normal skewtest teststat =  2.785 pvalue = 0.0054
>>> print 'normal kurtosistest teststat = %6.3f pvalue = %6.4f' % stats.kurtosistest(x)
normal kurtosistest teststat =  4.757 pvalue = 0.0000
```

These two tests are combined in the normality test

```
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % stats.normaltest(x)
normaltest teststat = 30.379 pvalue = 0.0000
```

In all three tests the p-values are very low and we can reject the hypothesis that the our sample has skew and kurtosis of the normal distribution.

Since skew and kurtosis of our sample are based on central moments, we get exactly the same results if we test the standardized sample:

```
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % \
...                       stats.normaltest((x-x.mean())/x.std())
normaltest teststat = 30.379 pvalue = 0.0000
```

Because normality is rejected so strongly, we can check whether the normaltest gives reasonable results for other cases:

```
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % stats.normaltest(stats.t.rvs(10, size=100))
normaltest teststat =  4.698 pvalue = 0.0955
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % stats.normaltest(stats.norm.rvs(size=1000))
normaltest teststat =  0.613 pvalue = 0.7361
```

When testing for normality of a small sample of t-distributed observations and a large sample of normal distributed observation, then in neither case can we reject the null hypothesis that the sample comes from a normal distribution. In the first case this is because the test is not powerful enough to distinguish a t and a normally distributed random variable in a small sample.

1.13.5 Comparing two samples

In the following, we are given two samples, which can come either from the same or from different distribution, and we want to test whether these samples have the same statistical properties.

Comparing means

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> rvs2 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs2)
(-0.54890361750888583, 0.5831943748663857)
```

Test with sample with different means:

```
>>> rvs3 = stats.norm.rvs(loc=8, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-4.5334142901750321, 6.507128186505895e-006)
```

Kolmogorov-Smirnov test for two samples ks_2samp

For the example where both samples are drawn from the same distribution, we cannot reject the null hypothesis since the pvalue is high

```
>>> stats.ks_2samp(rvs1, rvs2)
(0.025999999999999995, 0.99541195173064878)
```

In the second example, with different location, i.e. means, we can reject the null hypothesis since the pvalue is below 1%

```
>>> stats.ks_2samp(rvs1, rvs3)
(0.11399999999999999, 0.0027132103661283141)
```

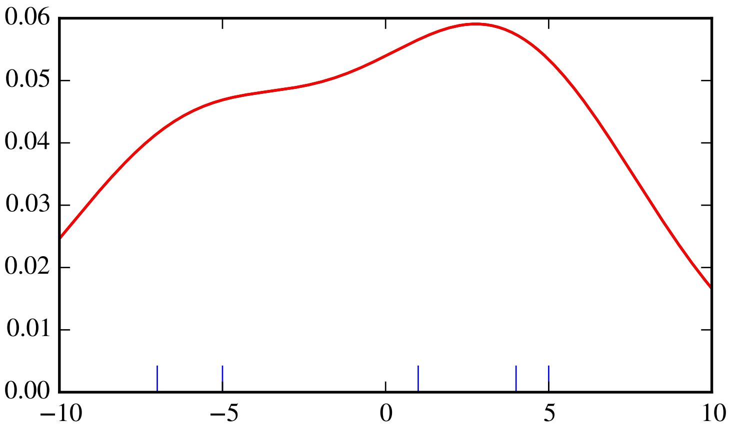
1.13.6 Kernel Density Estimation

A common task in statistics is to estimate the probability density function (PDF) of a random variable from a set of data samples. This task is called density estimation. The most well-known tool to do this is the histogram. A histogram is a useful tool for visualization (mainly because everyone understands it), but doesn't use the available data very efficiently. Kernel density estimation (KDE) is a more efficient tool for the same task. The `gaussian_kde` estimator can be used to estimate the PDF of univariate as well as multivariate data. It works best if the data is unimodal.

Univariate estimation

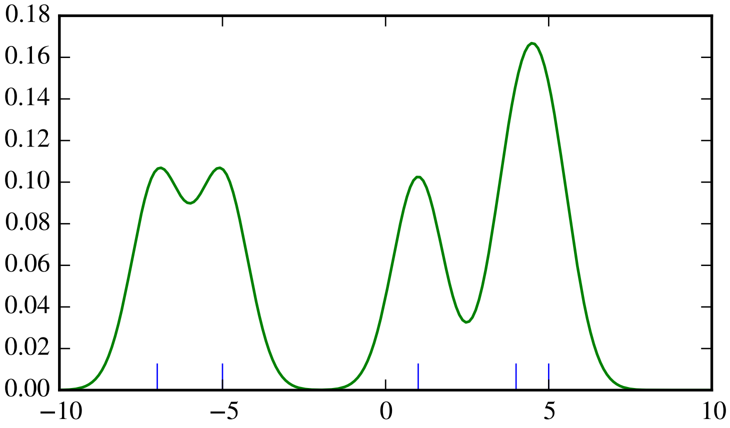
We start with a minimal amount of data in order to see how `gaussian_kde` works, and what the different options for bandwidth selection do. The data sampled from the PDF is show as blue dashes at the bottom of the figure (this is called a rug plot):

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

>>> x1 = np.array([-7, -5, 1, 4, 5], dtype=np.float)
>>> kde1 = stats.gaussian_kde(x1)
>>> kde2 = stats.gaussian_kde(x1, bw_method='silverman')

>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)

>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
>>> x_eval = np.linspace(-10, 10, num=200)
>>> ax.plot(x_eval, kde1(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde1(x_eval), 'r-', label="Silverman's Rule")

>>> plt.show()
```



We see that there is very little difference between Scott's Rule and Silverman's Rule, and that the bandwidth selection with a limited amount of data is probably a bit too wide. We can define our own bandwidth function to get a less smoothed out result.

```
>>> def my_kde_bandwidth(obj, fac=1./5):
...     """We use Scott's Rule, multiplied by a constant factor."""
...     return np.power(obj.n, -1./(obj.d+4)) * fac

>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)

>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
>>> kde3 = stats.gaussian_kde(x1, bw_method=my_kde_bandwidth)
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="With smaller BW")

>>> plt.show()
```

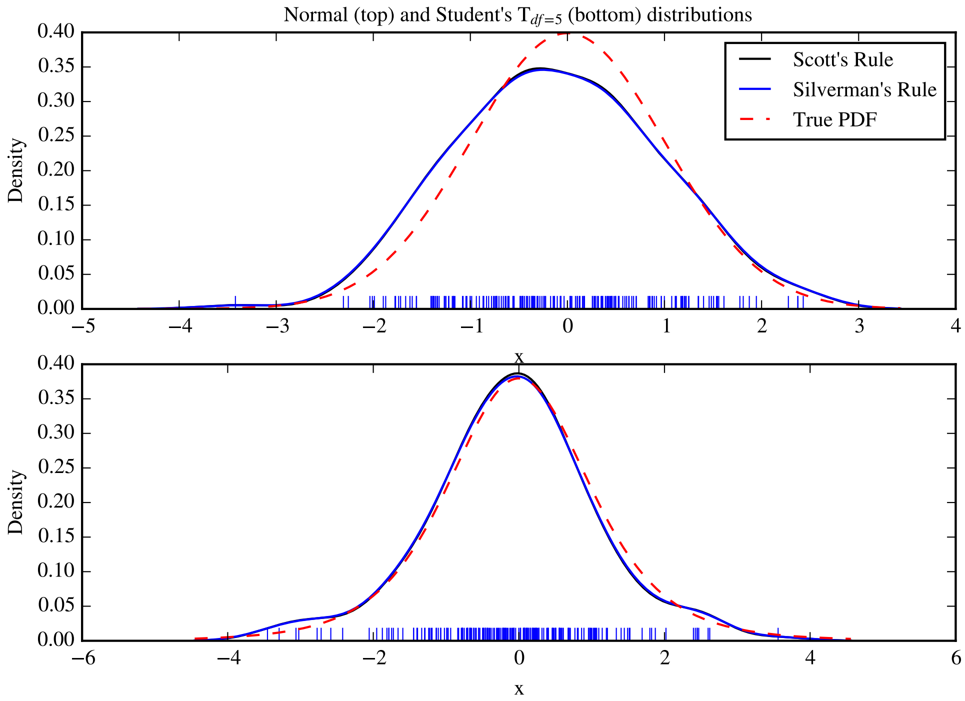


We see that if we set bandwidth to be very narrow, the obtained estimate for the probability density function (PDF) is simply the sum of Gaussians around each data point.

We now take a more realistic example, and look at the difference between the two available bandwidth selection rules. Those rules are known to work well for (close to) normal distributions, but even for unimodal distributions that are quite strongly non-normal they work reasonably well. As a non-normal distribution we take a Student's T distribution with 5 degrees of freedom.

```
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats


np.random.seed(12456)
x1 = np.random.normal(size=200)  # random data, normal distribution
xs = np.linspace(x1.min()-1, x1.max()+1, 200)

kde1 = stats.gaussian_kde(x1)
kde2 = stats.gaussian_kde(x1, bw_method='silverman')

fig = plt.figure(figsize=(8, 6))
```

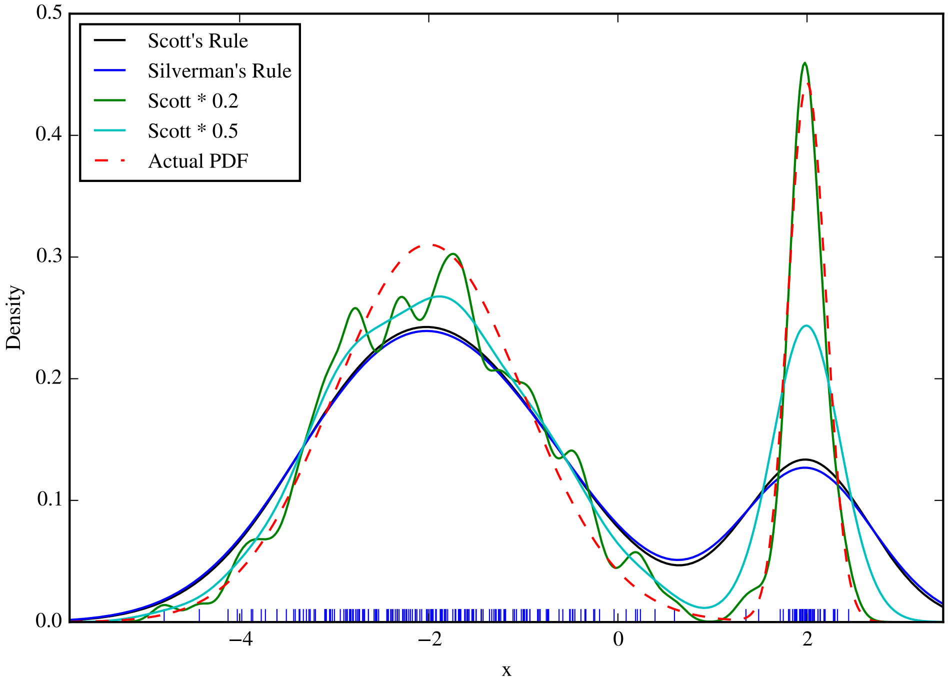
```
ax1 = fig.add_subplot(211)
ax1.plot(x1, np.zeros(x1.shape), 'b+', ms=12)  # rug plot
ax1.plot(xs, kde1(xs), 'k-', label="Scott's Rule")
ax1.plot(xs, kde2(xs), 'b-', label="Silverman's Rule")
ax1.plot(xs, stats.norm.pdf(xs), 'r--', label="True PDF")

ax1.set_xlabel('x')
ax1.set_ylabel('Density')
ax1.set_title("Normal (top) and Student's T$_{df=5}$ (bottom) distributions")
ax1.legend(loc=1)

x2 = stats.t.rvs(5, size=200)  # random data, T distribution
xs = np.linspace(x2.min() - 1, x2.max() + 1, 200)

kde3 = stats.gaussian_kde(x2)
kde4 = stats.gaussian_kde(x2, bw_method='silverman')

ax2 = fig.add_subplot(212)
ax2.plot(x2, np.zeros(x2.shape), 'b+', ms=12)  # rug plot
ax2.plot(xs, kde3(xs), 'k-', label="Scott's Rule")
ax2.plot(xs, kde4(xs), 'b-', label="Silverman's Rule")
ax2.plot(xs, stats.t.pdf(xs, 5), 'r--', label="True PDF")

ax2.set_xlabel('x')
ax2.set_ylabel('Density')

plt.show()
```



We now take a look at a bimodal distribution with one wider and one narrower Gaussian feature. We expect that this will be a more difficult density to approximate, due to the different bandwidths required to accurately resolve each feature.

```
>>> from functools import partial

>>> loc1, scale1, size1 = (-2, 1, 175)
>>> loc2, scale2, size2 = (2, 0.2, 50)
>>> x2 = np.concatenate([np.random.normal(loc=loc1, scale=scale1, size=size1),
...                      np.random.normal(loc=loc2, scale=scale2, size=size2)])

>>> x_eval = np.linspace(x2.min() - 1, x2.max() + 1, 500)

>>> kde = stats.gaussian_kde(x2)
>>> kde2 = stats.gaussian_kde(x2, bw_method='silverman')
>>> kde3 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.2))
>>> kde4 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.5))

>>> pdf = stats.norm.pdf
>>> bimodal_pdf = pdf(x_eval, loc=loc1, scale=scale1) * float(size1) / x2.size + \
...               pdf(x_eval, loc=loc2, scale=scale2) * float(size2) / x2.size

>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)
```

```
>>> ax.plot(x2, np.zeros(x2.shape), 'b+', ms=12)
>>> ax.plot(x_eval, kde(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde2(x_eval), 'b-', label="Silverman's Rule")
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="Scott * 0.2")
>>> ax.plot(x_eval, kde4(x_eval), 'c-', label="Scott * 0.5")
>>> ax.plot(x_eval, bimodal_pdf, 'r--', label="Actual PDF")

>>> ax.set_xlim([x_eval.min(), x_eval.max()])
>>> ax.legend(loc=2)
>>> ax.set_xlabel('x')
>>> ax.set_ylabel('Density')
>>> plt.show()
```



As expected, the KDE is not as close to the true PDF as we would like due to the different characteristic size of the two features of the bimodal distribution. By halving the default bandwidth (`Scott * 0.5`) we can do somewhat better, while using a factor 5 smaller bandwidth than the default doesn't smooth enough. What we really need though in this case is a non-uniform (adaptive) bandwidth.

Multivariate estimation

With `gaussian_kde` we can perform multivariate as well as univariate estimation. We demonstrate the bivariate case. First we generate some random data with a model in which the two variates are correlated.

```
>>> def measure(n):
...     """Measurement model, return two coupled measurements."""
```

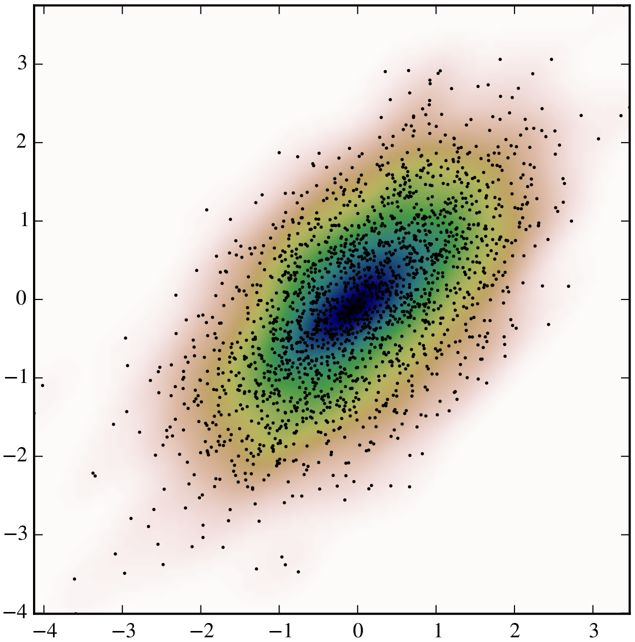
```
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2

>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()
```

Then we apply the KDE to the data:

```
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel.evaluate(positions).T, X.shape)
```

Finally we plot the estimated bivariate distribution as a colormap, and plot the individual data points on top.

```
>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)

>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r,
...           extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)

>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])

>>> plt.show()
```



1.14 Multidimensional image processing (`scipy.ndimage`)

1.14.1 Introduction

Image processing and analysis are generally seen as operations on two-dimensional arrays of values. There are however a number of fields where images of higher dimensionality must be analyzed. Good examples of these are medical imaging and biological imaging. `numpy` is suited very well for this type of applications due its inherent multidimensional nature. The `scipy.ndimage` packages provides a number of general image processing and analysis functions that are designed to operate with arrays of arbitrary dimensionality. The packages currently includes functions for linear and non-linear filtering, binary morphology, B-spline interpolation, and object measurements.

1.14.2 Properties shared by all functions

All functions share some common properties. Notably, all functions allow the specification of an output array with the *output* argument. With this argument you can specify an array that will be changed in-place with the result with the operation. In this case the result is not returned. Usually, using the *output* argument is more efficient, since an existing array is used to store the result.

The type of arrays returned is dependent on the type of operation, but it is in most cases equal to the type of the input. If, however, the *output* argument is used, the type of the result is equal to the type of the specified output argument.

If no output argument is given, it is still possible to specify what the result of the output should be. This is done by simply assigning the desired `numpy` type object to the output argument. For example:

```
>>> correlate(np.arange(10), [1, 2.5])
array([ 0,  2,  6,  9, 13, 16, 20, 23, 27, 30])
>>> correlate(np.arange(10), [1, 2.5], output=np.float64)
array([  0. ,   2.5,   6. ,   9.5,  13. ,  16.5,  20. ,  23.5,  27. ,  30.5])
```

1.14.3 Filter functions

The functions described in this section all perform some type of spatial filtering of the input array: the elements in the output are some function of the values in the neighborhood of the corresponding input element. We refer to this neighborhood of elements as the filter kernel, which is often rectangular in shape but may also have an arbitrary footprint. Many of the functions described below allow you to define the footprint of the kernel, by passing a mask through the *footprint* parameter. For example a cross shaped kernel can be defined as follows:

```
>>> footprint = array([[0,1,0],[1,1,1],[0,1,0]])
>>> footprint
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
```

Usually the origin of the kernel is at the center calculated by dividing the dimensions of the kernel shape by two. For instance, the origin of a one-dimensional kernel of length three is at the second element. Take for example the correlation of a one-dimensional array with a filter of length 3 consisting of ones:

```
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1])
array([0, 0, 1, 1, 1, 0, 0])
```

Sometimes it is convenient to choose a different origin for the kernel. For this reason most functions support the *origin* parameter which gives the origin of the filter relative to its center. For example:

```
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1], origin = -1)
array([0 1 1 1 0 0 0])
```

The effect is a shift of the result towards the left. This feature will not be needed very often, but it may be useful especially for filters that have an even size. A good example is the calculation of backward and forward differences:

```
>>> a = [0, 0, 1, 1, 1, 0, 0]
>>> correlate1d(a, [-1, 1])               # backward difference
array([ 0  0  1  0  0 -1  0])
>>> correlate1d(a, [-1, 1], origin = -1)  # forward difference
array([ 0  1  0  0 -1  0  0])
```

We could also have calculated the forward difference as follows:

```
>>> correlate1d(a, [0, -1, 1])
array([ 0  1  0  0 -1  0  0])
```

However, using the origin parameter instead of a larger kernel is more efficient. For multidimensional kernels *origin* can be a number, in which case the origin is assumed to be equal along all axes, or a sequence giving the origin along each axis.

Since the output elements are a function of elements in the neighborhood of the input elements, the borders of the array need to be dealt with appropriately by providing the values outside the borders. This is done by assuming that the arrays are extended beyond their boundaries according certain boundary conditions. In the functions described below, the boundary conditions can be selected using the *mode* parameter which must be a string with the name of the boundary condition. Following boundary conditions are currently supported:

"nearest"	Use the value at the boundary	[1 2 3]->[1 1 2 3 3]
"wrap"	Periodically replicate the array	[1 2 3]->[3 1 2 3 1]
"reflect"	Reflect the array at the boundary	[1 2 3]->[1 1 2 3 3]
"constant"	Use a constant value, default is 0.0	[1 2 3]->[0 1 2 3 0]

The "constant" mode is special since it needs an additional parameter to specify the constant value that should be used.

Note: The easiest way to implement such boundary conditions would be to copy the data to a larger array and extend the data at the borders according to the boundary conditions. For large arrays and large filter kernels, this would be very memory consuming, and the functions described below therefore use a different approach that does not require allocating large temporary buffers.

Correlation and convolution

The `correlate1d` function calculates a one-dimensional correlation along the given axis. The lines of the array along the given axis are correlated with the given *weights*. The *weights* parameter must be a one-dimensional sequences of numbers.

The function `correlate` implements multidimensional correlation of the input array with a given kernel.

The `convolve1d` function calculates a one-dimensional convolution along the given axis. The lines of the array along the given axis are convoluted with the given *weights*. The *weights* parameter must be a one-dimensional sequences of numbers.

Note: A convolution is essentially a correlation after mirroring the kernel. As a result, the *origin* parameter behaves differently than in the case of a correlation: the result is shifted in the opposite directions.

The function `convolve` implements multidimensional convolution of the input array with a given kernel.

Note: A convolution is essentially a correlation after mirroring the kernel. As a result, the *origin* parameter behaves differently than in the case of a correlation: the results is shifted in the opposite direction.

Smoothing filters

The `gaussian_filter1d` function implements a one-dimensional Gaussian filter. The standard-deviation of the Gaussian filter is passed through the parameter *sigma*. Setting *order* = 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented.

The `gaussian_filter` function implements a multidimensional Gaussian filter. The standard-deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions. The order of the filter can be specified separately for each axis. An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented. The *order* parameter must be a number, to specify the same order for all axes, or a sequence of numbers to specify a different order for each axis.

Note: The multidimensional filter is implemented as a sequence of one-dimensional Gaussian filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

The `uniform_filter1d` function calculates a one-dimensional uniform filter of the given *size* along the given axis.
The `uniform_filter` implements a multidimensional uniform filter. The sizes of the uniform filter are given for each axis as a sequence of integers by the *size* parameter. If *size* is not a sequence, but a single number, the sizes along all axis are assumed to be equal.

Note: The multidimensional filter is implemented as a sequence of one-dimensional uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

Filters based on order statistics

The `minimum_filter1d` function calculates a one-dimensional minimum filter of given *size* along the given axis.
The `maximum_filter1d` function calculates a one-dimensional maximum filter of given *size* along the given axis.
The `minimum_filter` function calculates a multidimensional minimum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
The `maximum_filter` function calculates a multidimensional maximum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
The `rank_filter` function calculates a multidimensional rank filter. The *rank* may be less then zero, i.e., *rank* = -1 indicates the largest element. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
The `percentile_filter` function calculates a multidimensional percentile filter. The *percentile* may be less then zero, i.e., *percentile* = -20 equals *percentile* = 80. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
The `median_filter` function calculates a multidimensional median filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint* if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Derivatives

Derivative filters can be constructed in several ways. The function `gaussian_filter1d` described in *Smoothing filters* can be used to calculate derivatives along a given axis using the *order* parameter. Other derivative filters are the Prewitt and Sobel filters:

The `prewitt` function calculates a derivative along the given axis.
The `sobel` function calculates a derivative along the given axis.

The Laplace filter is calculated by the sum of the second derivatives along all axes. Thus, different Laplace filters can be constructed using different second derivative functions. Therefore we provide a general function that takes a function argument to calculate the second derivative along a given direction and to construct the Laplace filter:

The function `generic_laplace` calculates a laplace filter using the function passed through `derivative2` to calculate second derivatives. The function `derivative2` should have the following signature:

```
derivative2(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)
```

It should calculate the second derivative along the dimension *axis*. If *output* is not None it should use that for the output and return None, otherwise it should return the result. *mode*, *cval* have the usual meaning.

The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to `derivative2` at each call.

For example:

```
>>> def d2(input, axis, output, mode, cval):
...     return correlate1d(input, [1, -2, 1], axis, output, mode, cval, 0)
...
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> generic_laplace(a, d2)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

To demonstrate the use of the *extra_arguments* argument we could do:

```
>>> def d2(input, axis, output, mode, cval, weights):
...     return correlate1d(input, weights, axis, output, mode, cval, 0,)
...
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> generic_laplace(a, d2, extra_arguments = ([1, -2, 1],))
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

or:

```
>>> generic_laplace(a, d2, extra_keywords = {'weights': [1, -2, 1]})
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

The following two functions are implemented using `generic_laplace` by providing appropriate functions for the second derivative function:

The function `laplace` calculates the Laplace using discrete differentiation for the second derivative (i.e. convolution with `[1, -2, 1]`).

The function `gaussian_laplace` calculates the Laplace using `gaussian_filter` to calculate the second derivatives. The standard-deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

The gradient magnitude is defined as the square root of the sum of the squares of the gradients in all directions. Similar to the generic Laplace function there is a `generic_gradient_magnitude` function that calculated the gradient magnitude of an array:

The function `generic_gradient_magnitude` calculates a gradient magnitude using the function passed through `derivative` to calculate first derivatives. The function `derivative` should have the following signature:

```
derivative(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)
```

It should calculate the derivative along the dimension *axis*. If *output* is not None it should use that for the output and return None, otherwise it should return the result. *mode*, *cval* have the usual meaning.
The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to *derivative* at each call.
For example, the `sobel` function fits the required signature:

```
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> generic_gradient_magnitude(a, sobel)
array([[ 0.        ,  0.        ,  0.        ,  0.        ,  0.        ],
       [ 0.        ,  1.41421356,  2.        ,  1.41421356,  0.        ],
       [ 0.        ,  2.        ,  0.        ,  2.        ,  0.        ],
       [ 0.        ,  1.41421356,  2.        ,  1.41421356,  0.        ],
       [ 0.        ,  0.        ,  0.        ,  0.        ,  0.        ]])
```

See the documentation of `generic_laplace` for examples of using the *extra_arguments* and *extra_keywords* arguments.

The `sobel` and `prewitt` functions fit the required signature and can therefore directly be used with `generic_gradient_magnitude`. The following function implements the gradient magnitude using Gaussian derivatives:

The function `gaussian_gradient_magnitude` calculates the gradient magnitude using `gaussian_filter` to calculate the first derivatives. The standard-deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

Generic filter functions

To implement filter functions, generic functions can be used that accept a callable object that implements the filtering operation. The iteration over the input and output arrays is handled by these generic functions, along with such details as the implementation of the boundary conditions. Only a callable object implementing a callback function that does the actual filtering work must be provided. The callback function can also be written in C and passed using a `PyCObject` (see *Extending ndimage in C* for more information).

The `generic_filter1d` function implements a generic one-dimensional filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The `generic_filter1d` function iterates over the lines of an array and calls `function` at each line. The arguments that are passed to `function` are one-dimensional arrays of the `tFloat64` type. The first contains the values of the current line. It is extended at the beginning end the end, according to the *filter_size* and *origin* arguments. The second array should be modified in-place to provide the output values of the line. For example consider a correlation along one dimension:

```
>>> a = arange(12).reshape(3,4)
>>> correlate1d(a, [1, 2, 3])
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

The same operation can be implemented using `generic_filter1d` as follows:

```
>>> def fnc(iline, oline):
...     oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...
>>> generic_filter1d(a, fnc, 3)
array([[ 3,  8, 14, 17],
```

```
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

Here the origin of the kernel was (by default) assumed to be in the middle of the filter of length 3. Therefore, each input line was extended by one value at the beginning and at the end, before the function was called.

Optionally extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the parameters of our filter as an argument:

```
>>> def fnc(iline, oline, a, b):
...     oline[...] = iline[:-2] + a * iline[1:-1] + b * iline[2:]
...
>>> generic_filter1d(a, fnc, 3, extra_arguments = (2, 3))
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

or:

```
>>> generic_filter1d(a, fnc, 3, extra_keywords = {'a':2, 'b':3})
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

The `generic_filter` function implements a generic filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The `generic_filter` function iterates over the array and calls `function` at each element. The argument of `function` is a one-dimensional array of the `tFloat64` type, that contains the values around the current element that are within the footprint of the filter. The function should return a single value that can be converted to a double precision number. For example consider a correlation:

```
>>> a = arange(12).reshape(3,4)
>>> correlate(a, [[1, 0], [0, 3]])
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

The same operation can be implemented using *generic_filter* as follows:

```
>>> def fnc(buffer):
...     return (buffer * array([1, 3])).sum()
...
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]])
array([[ 0  3  7 11],
       [12 15 19 23],
       [28 31 35 39]])
```

Here a kernel footprint was specified that contains only two elements. Therefore the filter function receives a buffer of length equal to two, which was multiplied with the proper weights and the result summed.

When calling `generic_filter`, either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Optionally extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the parameters of our filter as an argument:

```
>>> def fnc(buffer, weights):
...     weights = asarray(weights)
...     return (buffer * weights).sum()
...
```

```
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_arguments = ([1, 3],))
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

or:

```
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_keywords= {'weights': [1, 3]})
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

These functions iterate over the lines or elements starting at the last axis, i.e. the last index changes the fastest. This order of iteration is guaranteed for the case that it is important to adapt the filter depending on spatial location. Here is an example of using a class that implements the filter and keeps track of the current coordinates while iterating. It performs the same filter operation as described above for `generic_filter`, but additionally prints the current coordinates:

```
>>> a = arange(12).reshape(3,4)
>>>
>>> class fnc_class:
...     def __init__(self, shape):
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...
...     def filter(self, buffer):
...         result = (buffer * array([1, 3])).sum()
...         print self.coordinates
...         # calculate the next coordinates:
...         axes = range(len(self.shape))
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 self.coordinates[jj] += 1
...                 break
...             else:
...                 self.coordinates[jj] = 0
...         return result
...
>>> fnc = fnc_class(shape = (3,4))
>>> generic_filter(a, fnc.filter, footprint = [[1, 0], [0, 1]])
[0, 0]
[0, 1]
[0, 2]
[0, 3]
[1, 0]
[1, 1]
[1, 2]
[1, 3]
[2, 0]
[2, 1]
[2, 2]
[2, 3]
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

For the `generic_filter1d` function the same approach works, except that this function does not iterate over the axis that is being filtered. The example for `generic_filter1d` then becomes this:

```
>>> a = arange(12).reshape(3,4)
>>>
>>> class fnc1d_class:
...     def __init__(self, shape, axis = -1):
...         # store the filter axis:
...         self.axis = axis
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...
...     def filter(self, iline, oline):
...         oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...         print self.coordinates
...         # calculate the next coordinates:
...         axes = range(len(self.shape))
...         # skip the filter axis:
...         del axes[self.axis]
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 self.coordinates[jj] += 1
...                 break
...             else:
...                 self.coordinates[jj] = 0
...
>>> fnc = fnc1d_class(shape = (3,4))
>>> generic_filter1d(a, fnc.filter, 3)
[0, 0]
[1, 0]
[2, 0]
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

Fourier domain filters

The functions described in this section perform filtering operations in the Fourier domain. Thus, the input array of such a function should be compatible with an inverse Fourier transform function, such as the functions from the `numpy.fft` module. We therefore have to deal with arrays that may be the result of a real or a complex Fourier transform. In the case of a real Fourier transform only half of the of the symmetric complex transform is stored. Additionally, it needs to be known what the length of the axis was that was transformed by the real fft. The functions described here provide a parameter *n* that in the case of a real transform must be equal to the length of the real transform axis before transformation. If this parameter is less than zero, it is assumed that the input array was the result of a complex Fourier transform. The parameter *axis* can be used to indicate along which axis the real transform was executed.

> The `fourier_shift` function multiplies the input array with the multidimensional Fourier transform of a shift operation for the given shift. The *shift* parameter is a sequences of shifts for each dimension, or a single value for all dimensions.
> The `fourier_gaussian` function multiplies the input array with the multidimensional Fourier transform of a Gaussian filter with given standard-deviations *sigma*. The *sigma* parameter is a sequences of values for each dimension, or a single value for all dimensions.

The `fourier_uniform` function multiplies the input array with the multidimensional Fourier transform of a uniform filter with given sizes *size*. The *size* parameter is a sequences of values for each dimension, or a single value for all dimensions.

The `fourier_ellipsoid` function multiplies the input array with the multidimensional Fourier transform of a elliptically shaped filter with given sizes *size*. The *size* parameter is a sequences of values for each dimension, or a single value for all dimensions. This function is only implemented for dimensions 1, 2, and 3.

1.14.4 Interpolation functions

This section describes various interpolation functions that are based on B-spline theory. A good introduction to B-splines can be found in: M. Unser, "Splines: A Perfect Fit for Signal and Image Processing," IEEE Signal Processing Magazine, vol. 16, no. 6, pp. 22-38, November 1999.

Spline pre-filters

Interpolation using splines of an order larger than 1 requires a pre- filtering step. The interpolation functions described in section *Interpolation functions* apply pre-filtering by calling `spline_filter`, but they can be instructed not to do this by setting the *prefilter* keyword equal to False. This is useful if more than one interpolation operation is done on the same array. In this case it is more efficient to do the pre-filtering only once and use a prefiltered array as the input of the interpolation functions. The following two functions implement the pre-filtering:

The `spline_filter1d` function calculates a one-dimensional spline filter along the given axis. An output array can optionally be provided. The order of the spline must be larger then 1 and less than 6.

The `spline_filter` function calculates a multidimensional spline filter.

Note: The multidimensional filter is implemented as a sequence of one-dimensional spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, if an output with a limited precision is requested, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a output type of high precision.

Interpolation functions

Following functions all employ spline interpolation to effect some type of geometric transformation of the input array. This requires a mapping of the output coordinates to the input coordinates, and therefore the possibility arises that input values outside the boundaries are needed. This problem is solved in the same way as described in *Filter functions* for the multidimensional filter functions. Therefore these functions all support a *mode* parameter that determines how the boundaries are handled, and a *cval* parameter that gives a constant value in case that the 'constant' mode is used.

The `geometric_transform` function applies an arbitrary geometric transform to the input. The given *mapping* function is called at each point in the output to find the corresponding coordinates in the input. *mapping* must be a callable object that accepts a tuple of length equal to the output array rank and returns the corresponding input coordinates as a tuple of length equal to the input array rank. The output shape and output type can optionally be provided. If not given they are equal to the input shape and type.

For example:

```
>>> a = arange(12).reshape(4,3).astype(np.float64)
>>> def shift_func(output_coordinates):
...     return (output_coordinates[0] - 0.5, output_coordinates[1] - 0.5)
...
>>> geometric_transform(a, shift_func)
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
```

```
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

Optionally extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the shifts in our example as arguments:

```
>>> def shift_func(output_coordinates, s0, s1):
...     return (output_coordinates[0] - s0, output_coordinates[1] - s1)
...
>>> geometric_transform(a, shift_func, extra_arguments = (0.5, 0.5))
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

or:

```
>>> geometric_transform(a, shift_func, extra_keywords = {'s0': 0.5, 's1': 0.5})
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

Note: The mapping function can also be written in C and passed using a `PyCObject`. See *Extending ndimage in C* for more information.

The function `map_coordinates` applies an arbitrary coordinate transformation using the given array of coordinates. The shape of the output is derived from that of the coordinate array by dropping the first axis. The parameter *coordinates* is used to find for each point in the output the corresponding coordinates in the input. The values of *coordinates* along the first axis are the coordinates in the input array at which the output value is found. (See also the numarray *coordinates* function.) Since the coordinates may be non- integer coordinates, the value of the input at these coordinates is determined by spline interpolation of the requested order. Here is an example that interpolates a 2D array at (0.5, 0.5) and (1, 2):

```
>>> a = arange(12).reshape(4,3).astype(np.float64)
>>> a
array([[  0.,   1.,   2.],
       [  3.,   4.,   5.],
       [  6.,   7.,   8.],
       [  9.,  10.,  11.]])
>>> map_coordinates(a, [[0.5, 2], [0.5, 1]])
array([ 1.3625  7.    ])
```

The `affine_transform` function applies an affine transformation to the input array. The given transformation *matrix* and *offset* are used to find for each point in the output the corresponding coordinates in the input. The value of the input at the calculated coordinates is determined by spline interpolation of the requested order. The transformation *matrix* must be two-dimensional or can also be given as a one-dimensional sequence or array. In the latter case, it is assumed that the matrix is diagonal. A more efficient interpolation algorithm is then applied that exploits the separability of the problem. The output shape and output type can optionally be provided. If not given they are equal to the input shape and type.
The `shift` function returns a shifted version of the input, using spline interpolation of the requested *order*.
The `zoom` function returns a rescaled version of the input, using spline interpolation of the requested *order*.
The `rotate` function returns the input array rotated in the plane defined by the two axes given by the parameter *axes*, using spline interpolation of the requested *order*. The angle must be given in degrees. If *reshape* is true, then the size of the output array is adapted to contain the rotated input.

1.14.5 Morphology

Binary morphology

Binary morphology (need something to put here).

> The `generate_binary_structure` functions generates a binary structuring element for use in binary morphology operations. The *rank* of the structure must be provided. The size of the structure that is returned is equal to three in each direction. The value of each element is equal to one if the square of the Euclidean distance from the element to the center is less or equal to *connectivity*. For instance, two dimensional 4-connected and 8-connected structures are generated as follows:

```
>>> generate_binary_structure(2, 1)
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> generate_binary_structure(2, 2)
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
```

Most binary morphology functions can be expressed in terms of the basic operations erosion and dilation:

> The `binary_erosion` function implements binary erosion of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The *border_value* parameter gives the value of the array outside boundaries. The erosion is repeated *iterations* times. If *iterations* is less than one, the erosion is repeated until the result does not change anymore. If a *mask* array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.
>
> The `binary_dilation` function implements binary dilation of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The *border_value* parameter gives the value of the array outside boundaries. The dilation is repeated *iterations* times. If *iterations* is less than one, the dilation is repeated until the result does not change anymore. If a *mask* array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.
>
> Here is an example of using `binary_dilation` to find all elements that touch the border, by repeatedly dilating an empty array from the border using the data array as the mask:

```
>>> struct = array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
>>> a = array([[1,0,0,0,0], [1,1,0,1,0], [0,0,1,1,0], [0,0,0,0,0]])
>>> a
array([[1, 0, 0, 0, 0],
       [1, 1, 0, 1, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> binary_dilation(zeros(a.shape), struct, -1, a, border_value=1)
array([[ True, False, False, False, False],
       [ True,  True, False, False, False],
       [False, False, False, False, False],
       [False, False, False, False, False]], dtype=bool)
```

The `binary_erosion` and `binary_dilation` functions both have an *iterations* parameter which allows the erosion or dilation to be repeated a number of times. Repeating an erosion or a dilation with a given structure *n* times is equivalent to an erosion or a dilation with a structure that is *n-1* times dilated with itself. A function is provided that allows the calculation of a structure that is dilated a number of times with itself:

The `iterate_structure` function returns a structure by dilation of the input structure *iteration* - 1 times with itself. For instance:

```
>>> struct = generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> iterate_structure(struct, 2)
array([[False, False,  True, False, False],
       [False,  True,  True,  True, False],
       [ True,  True,  True,  True,  True],
       [False,  True,  True,  True, False],
       [False, False,  True, False, False]], dtype=bool)
```

If the origin of the original structure is equal to 0, then it is also equal to 0 for the iterated structure. If not, the origin must also be adapted if the equivalent of the *iterations* erosions or dilations must be achieved with the iterated structure. The adapted origin is simply obtained by multiplying with the number of iterations. For convenience the `iterate_structure` also returns the adapted origin if the *origin* parameter is not None:

```
>>> iterate_structure(struct, 2, -1)
(array([[False, False,  True, False, False],
       [False,  True,  True,  True, False],
       [ True,  True,  True,  True,  True],
       [False,  True,  True,  True, False],
       [False, False,  True, False, False]], dtype=bool), [-2, -2])
```

Other morphology operations can be defined in terms of erosion and d dilation. Following functions provide a few of these operations for convenience:

The `binary_opening` function implements binary opening of arrays of arbitrary rank with the given structuring element. Binary opening is equivalent to a binary erosion followed by a binary dilation with the same structuring element. The origin parameter controls the placement of the structuring element as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The *iterations* parameter gives the number of erosions that is performed followed by the same number of dilations.

The `binary_closing` function implements binary closing of arrays of arbitrary rank with the given structuring element. Binary closing is equivalent to a binary dilation followed by a binary erosion with the same structuring element. The origin parameter controls the placement of the structuring element as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The *iterations* parameter gives the number of dilations that is performed followed by the same number of erosions.

The `binary_fill_holes` function is used to close holes in objects in a binary image, where the structure defines the connectivity of the holes. The origin parameter controls the placement of the structuring element as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`.

The `binary_hit_or_miss` function implements a binary hit-or-miss transform of arrays of arbitrary rank with the given structuring elements. The hit-or-miss transform is calculated by erosion of the input with the first structure, erosion of the logical *not* of the input with the second structure, followed by the logical *and* of these two erosions. The origin parameters control the placement of the structuring elements as described in *Filter functions*. If *origin2* equals None it is set equal to the *origin1* parameter. If the first structuring element is not provided, a structuring element with connectivity equal to one is generated using `generate_binary_structure`, if *structure2* is not provided, it is set equal to the logical *not* of *structure1*.

Grey-scale morphology

Grey-scale morphology operations are the equivalents of binary morphology operations that operate on arrays with arbitrary values. Below we describe the grey-scale equivalents of erosion, dilation, opening and closing. These operations are implemented in a similar fashion as the filters described in *Filter functions*, and we refer to this section for the description of filter kernels and footprints, and the handling of array borders. The grey-scale morphology operations optionally take a *structure* parameter that gives the values of the structuring element. If this parameter is not given the structuring element is assumed to be flat with a value equal to zero. The shape of the structure can optionally be defined by the *footprint* parameter. If this parameter is not given, the structure is assumed to be rectangular, with sizes equal to the dimensions of the *structure* array, or by the *size* parameter if *structure* is not given. The *size* parameter is only used if both *structure* and *footprint* are not given, in which case the structuring element is assumed to be rectangular and flat with the dimensions given by *size*. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint* parameter, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Similar to binary erosion and dilation there are operations for grey-scale erosion and dilation:

> The `grey_erosion` function calculates a multidimensional grey- scale erosion.
> The `grey_dilation` function calculates a multidimensional grey- scale dilation.

Grey-scale opening and closing operations can be defined similar to their binary counterparts:

> The `grey_opening` function implements grey-scale opening of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale erosion followed by a grey-scale dilation.
> The `grey_closing` function implements grey-scale closing of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale dilation followed by a grey-scale erosion.
> The `morphological_gradient` function implements a grey-scale morphological gradient of arrays of arbitrary rank. The grey-scale morphological gradient is equal to the difference of a grey-scale dilation and a grey-scale erosion.
> The `morphological_laplace` function implements a grey-scale morphological laplace of arrays of arbitrary rank. The grey-scale morphological laplace is equal to the sum of a grey-scale dilation and a grey-scale erosion minus twice the input.
> The `white_tophat` function implements a white top-hat filter of arrays of arbitrary rank. The white top-hat is equal to the difference of the input and a grey-scale opening.
> The `black_tophat` function implements a black top-hat filter of arrays of arbitrary rank. The black top-hat is equal to the difference of the a grey-scale closing and the input.

1.14.6 Distance transforms

Distance transforms are used to calculate the minimum distance from each element of an object to the background. The following functions implement distance transforms for three different distance metrics: Euclidean, City Block, and Chessboard distances.

> The function `distance_transform_cdt` uses a chamfer type algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The structure determines the type of chamfering that is done. If the structure is equal to 'cityblock' a structure is generated using `generate_binary_structure` with a squared distance equal to 1. If the structure is equal to 'chessboard', a structure is generated using `generate_binary_structure` with a squared distance equal to the rank of the array. These choices correspond to the common interpretations of the cityblock and the chessboard distancemetrics in two dimensions.
> In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The *return_distances*, and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.
> The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (both `Int32`).

The basics of the algorithm used to implement this function is described in: G. Borgefors, "Distance transformations in arbitrary dimensions.", Computer Vision, Graphics, and Image Processing, 27:321-345, 1984.

The function `distance_transform_edt` calculates the exact euclidean distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest euclidean distance to the background (all non-object elements).

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The *return_distances*, and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

Optionally the sampling along each axis can be given by the *sampling* parameter which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes.

The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (`Float64` and `Int32`).

The algorithm used to implement this function is described in: C. R. Maurer, Jr., R. Qi, and V. Raghavan, "A linear time algorithm for computing exact euclidean distance transforms of binary images in arbitrary dimensions. IEEE Trans. PAMI 25, 265-270, 2003.

The function `distance_transform_bf` uses a brute-force algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The metric must be one of "euclidean", "cityblock", or "chessboard".

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The *return_distances*, and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

Optionally the sampling along each axis can be given by the *sampling* parameter which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes. This parameter is only used in the case of the euclidean distance transform.

The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (`Float64` and `Int32`).

Note: This function uses a slow brute-force algorithm, the function `distance_transform_cdt` can be used to more efficiently calculate cityblock and chessboard distance transforms. The function `distance_transform_edt` can be used to more efficiently calculate the exact euclidean distance transform.

1.14.7 Segmentation and labeling

Segmentation is the process of separating objects of interest from the background. The most simple approach is probably intensity thresholding, which is easily done with `numpy` functions:

```
>>> a = array([[1,2,2,1,1,0],
...            [0,2,3,1,2,0],
...            [1,1,1,3,3,2],
...            [1,1,1,1,2,1]])
>>> where(a > 1, 1, 0)
array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 1, 0]])
```

The result is a binary image, in which the individual objects still need to be identified and labeled. The function `label` generates an array where each object is assigned a unique number:

The `label` function generates an array where the objects in the input are labeled with an integer index. It returns a tuple consisting of the array of object labels and the number of objects found, unless the *output* parameter is given, in which case only the number of objects is returned. The connectivity of the objects is defined by a structuring element. For instance, in two dimensions using a four-connected structuring element gives:

```
>>> a = array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
>>> s = [[0, 1, 0], [1,1,1], [0,1,0]]
>>> label(a, s)
(array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 2, 0],
       [0, 0, 0, 2, 2, 2],
       [0, 0, 0, 0, 2, 0]]), 2)
```

These two objects are not connected because there is no way in which we can place the structuring element such that it overlaps with both objects. However, an 8-connected structuring element results in only a single object:

```
>>> a = array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
>>> s = [[1,1,1], [1,1,1], [1,1,1]]
>>> label(a, s)[0]
array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 1, 0]])
```

If no structuring element is provided, one is generated by calling `generate_binary_structure` (see *Binary morphology*) using a connectivity of one (which in 2D is the 4-connected structure of the first example). The input can be of any type, any value not equal to zero is taken to be part of an object. This is useful if you need to 're-label' an array of object indices, for instance after removing unwanted objects. Just apply the label function again to the index array. For instance:

```
>>> l, n = label([1, 0, 1, 0, 1])
>>> l
array([1 0 2 0 3])
>>> l = where(l != 2, l, 0)
>>> l
array([1 0 0 0 3])
>>> label(l)[0]
array([1 0 0 0 2])
```

Note: The structuring element used by `label` is assumed to be symmetric.

There is a large number of other approaches for segmentation, for instance from an estimation of the borders of the objects that can be obtained for instance by derivative filters. One such an approach is watershed segmentation. The function `watershed_ift` generates an array where each object is assigned a unique label, from an array that localizes the object borders, generated for instance by a gradient magnitude filter. It uses an array containing initial markers for the objects:

The `watershed_ift` function applies a watershed from markers algorithm, using an Iterative Forest Transform, as described in: P. Felkel, R. Wegenkittl, and M. Bruckschwaiger, "Implementation and Complexity of the Watershed-from-Markers Algorithm Computed as a Minimal Cost Forest.", Eurographics 2001, pp. C:26-35. The inputs of this function are the array to which the transform is applied, and an array of markers that designate the objects by a unique label, where any non-zero value is a marker. For instance:

```
>>> input = array([[0, 0, 0, 0, 0, 0, 0],
...                [0, 1, 1, 1, 1, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 1, 1, 1, 1, 0],
...                [0, 0, 0, 0, 0, 0, 0]], np.uint8)
>>> markers = array([[1, 0, 0, 0, 0, 0, 0],
...                  [0, 0, 0, 0, 0, 0, 0],
...                  [0, 0, 0, 0, 0, 0, 0],
...                  [0, 0, 0, 2, 0, 0, 0],
```

```
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0]], np.int8)
>>> watershed_ift(input, markers)
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 1, 1, 1, 1, 1]], dtype=int8)
```

Here two markers were used to designate an object (*marker* = 2) and the background (*marker* = 1). The order in which these are processed is arbitrary: moving the marker for the background to the lower right corner of the array yields a different result:

```
>>> markers = array([[0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 2, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 1]], np.int8)
>>> watershed_ift(input, markers)
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1, 1, 1]], dtype=int8)
```

The result is that the object (*marker* = 2) is smaller because the second marker was processed earlier. This may not be the desired effect if the first marker was supposed to designate a background object. Therefore `watershed_ift` treats markers with a negative value explicitly as background markers and processes them after the normal markers. For instance, replacing the first marker by a negative marker gives a result similar to the first example:

```
>>> markers = array([[0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 2, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, -1]], np.int8)
>>> watershed_ift(input, markers)
array([[-1, -1, -1, -1, -1, -1, -1],
       [-1, -1,  2,  2,  2, -1, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1, -1,  2,  2,  2, -1, -1],
       [-1, -1, -1, -1, -1, -1, -1]], dtype=int8)
```

The connectivity of the objects is defined by a structuring element. If no structuring element is provided, one is generated by calling `generate_binary_structure` (see *Binary morphology*) using a connectivity of one (which in 2D is a 4-connected structure.) For example, using an 8-connected structure with the last example yields a different object:

```
>>> watershed_ift(input, markers,
...               structure = [[1,1,1], [1,1,1], [1,1,1]])
array([[-1, -1, -1, -1, -1, -1, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1, -1, -1, -1, -1, -1, -1]], dtype=int8)
```

Note: The implementation of `watershed_ift` limits the data types of the input to `UInt8` and `UInt16`.

1.14.8 Object measurements

Given an array of labeled objects, the properties of the individual objects can be measured. The `find_objects` function can be used to generate a list of slices that for each object, give the smallest sub-array that fully contains the object:

> The `find_objects` function finds all objects in a labeled array and returns a list of slices that correspond to the smallest regions in the array that contains the object. For instance:
>
> ```
> >>> a = array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
> >>> l, n = label(a)
> >>> f = find_objects(l)
> >>> a[f[0]]
> array([[1 1],
>        [1 1]])
> >>> a[f[1]]
> array([[0, 1, 0],
>        [1, 1, 1],
>        [0, 1, 0]])
> ```
>
> `find_objects` returns slices for all objects, unless the *max_label* parameter is larger then zero, in which case only the first *max_label* objects are returned. If an index is missing in the *label* array, None is return instead of a slice. For example:
>
> ```
> >>> find_objects([1, 0, 3, 4], max_label = 3)
> [(slice(0, 1, None),), None, (slice(2, 3, None),)]
> ```

The list of slices generated by `find_objects` is useful to find the position and dimensions of the objects in the array, but can also be used to perform measurements on the individual objects. Say we want to find the sum of the intensities of an object in image:

```
>>> image = arange(4 * 6).reshape(4, 6)
>>> mask = array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
>>> labels = label(mask)[0]
>>> slices = find_objects(labels)
```

Then we can calculate the sum of the elements in the second object:

```
>>> where(labels[slices[1]] == 2, image[slices[1]], 0).sum()
80
```

That is however not particularly efficient, and may also be more complicated for other types of measurements. Therefore a few measurements functions are defined that accept the array of object labels and the index of the object to be measured. For instance calculating the sum of the intensities can be done by:

```
>>> sum(image, labels, 2)
80
```

For large arrays and small objects it is more efficient to call the measurement functions after slicing the array:

```
>>> sum(image[slices[1]], labels[slices[1]], 2)
80
```

Alternatively, we can do the measurements for a number of labels with a single function call, returning a list of results. For instance, to measure the sum of the values of the background and the second object in our example we give a list of labels:

```
>>> sum(image, labels, [0, 2])
array([178.0, 80.0])
```

The measurement functions described below all support the *index* parameter to indicate which object(s) should be measured. The default value of *index* is None. This indicates that all elements where the label is larger than zero should be treated as a single object and measured. Thus, in this case the *labels* array is treated as a mask defined by the elements that are larger than zero. If *index* is a number or a sequence of numbers it gives the labels of the objects that are measured. If *index* is a sequence, a list of the results is returned. Functions that return more than one result, return their result as a tuple if *index* is a single number, or as a tuple of lists, if *index* is a sequence.

> The `sum` function calculates the sum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `mean` function calculates the mean of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `variance` function calculates the variance of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `standard_deviation` function calculates the standard deviation of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `minimum` function calculates the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `maximum` function calculates the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `minimum_position` function calculates the position of the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `maximum_position` function calculates the position of the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.
> The `extrema` function calculates the minimum, the maximum, and their positions, of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation. The result is a tuple giving the minimum, the maximum, the position of the minimum and the postition of the maximum. The result is the same as a tuple formed by the results of the functions *minimum*, *maximum*, *minimum_position*, and *maximum_position* that are described above.
> The `center_of_mass` function calculates the center of mass of the of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `histogram` function calculates a histogram of the of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation. Histograms are defined by their minimum (*min*), maximum (*max*) and the number of bins (*bins*). They are returned as one-dimensional arrays of type `Int32`.

1.14.9 Extending `ndimage` in C

A few functions in the `scipy.ndimage` take a call-back argument. This can be a python function, but also a `PyCObject` containing a pointer to a C function. To use this feature, you must write your own C extension that defines the function, and define a Python function that returns a `PyCObject` containing a pointer to this function.

An example of a function that supports this is `geometric_transform` (see *Interpolation functions*). You can pass it a python callable object that defines a mapping from all output coordinates to corresponding coordinates in the input array. This mapping function can also be a C function, which generally will be much more efficient, since the overhead of calling a python function at each element is avoided.

For example to implement a simple shift function we define the following function:

```
static int
_shift_function(int *output_coordinates, double* input_coordinates,
                int output_rank, int input_rank, void *callback_data)
{
  int ii;
  /* get the shift from the callback data pointer: */
  double shift = *(double*)callback_data;
  /* calculate the coordinates: */
  for(ii = 0; ii < irank; ii++)
    icoor[ii] = ocoor[ii] - shift;
  /* return OK status: */
  return 1;
}
```

This function is called at every element of the output array, passing the current coordinates in the *output_coordinates* array. On return, the *input_coordinates* array must contain the coordinates at which the input is interpolated. The ranks of the input and output array are passed through *output_rank* and *input_rank*. The value of the shift is passed through the *callback_data* argument, which is a pointer to void. The function returns an error status, in this case always 1, since no error can occur.

A pointer to this function and a pointer to the shift value must be passed to `geometric_transform`. Both are passed by a single `PyCObject` which is created by the following python extension function:

```
static PyObject *
py_shift_function(PyObject *obj, PyObject *args)
{
  double shift = 0.0;
  if (!PyArg_ParseTuple(args, "d", &shift)) {
    PyErr_SetString(PyExc_RuntimeError, "invalid parameters");
    return NULL;
  } else {
    /* assign the shift to a dynamically allocated location: */
    double *cdata = (double*)malloc(sizeof(double));
    *cdata = shift;
    /* wrap function and callback_data in a CObject: */
    return PyCObject_FromVoidPtrAndDesc(_shift_function, cdata,
                                        _destructor);
  }
}
```

The value of the shift is obtained and then assigned to a dynamically allocated memory location. Both this data pointer and the function pointer are then wrapped in a `PyCObject`, which is returned. Additionally, a pointer to a destructor function is given, that will free the memory we allocated for the shift value when the `PyCObject` is destroyed. This destructor is very simple:

```
static void
_destructor(void* cobject, void *cdata)
{
  if (cdata)
    free(cdata);
}
```

To use these functions, an extension module is built:

```
static PyMethodDef methods[] = {
  {"shift_function", (PyCFunction)py_shift_function, METH_VARARGS, ""},
  {NULL, NULL, 0, NULL}
};

void
initexample(void)
{
  Py_InitModule("example", methods);
}
```

This extension can then be used in Python, for example:

```
>>> import example
>>> array = arange(12).reshape=(4, 3).astype(np.float64)
>>> fnc = example.shift_function(0.5)
>>> geometric_transform(array, fnc)
array([[ 0.      0.      0.    ],
       [ 0.      1.3625  2.7375],
       [ 0.      4.8125  6.1875],
       [ 0.      8.2625  9.6375]])
```

C callback functions for use with `ndimage` functions must all be written according to this scheme. The next section lists the `ndimage` functions that acccept a C callback function and gives the prototype of the callback function.

1.14.10 Functions that support C callback functions

The `ndimage` functions that support C callback functions are described here. Obviously, the prototype of the function that is provided to these functions must match exactly that what they expect. Therefore we give here the prototypes of the callback functions. All these callback functions accept a void *callback_data* pointer that must be wrapped in a `PyCObject` using the Python `PyCObject_FromVoidPtrAndDesc` function, which can also accept a pointer to a destructor function to free any memory allocated for *callback_data*. If *callback_data* is not needed, `PyCObject_FromVoidPtr` may be used instead. The callback functions must return an integer error status that is equal to zero if something went wrong, or 1 otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise, a default error message is set by the calling function.

The function `generic_filter` (see *Generic filter functions*) accepts a callback function with the following prototype:

> The calling function iterates over the elements of the input and output arrays, calling the callback function at each element. The elements within the footprint of the filter at the current element are passed through the *buffer* parameter, and the number of elements within the footprint through *filter_size*. The calculated valued should be returned in the *return_value* argument.

The function `generic_filter1d` (see *Generic filter functions*) accepts a callback function with the following prototype:

> The calling function iterates over the lines of the input and output arrays, calling the callback function at each line. The current line is extended according to the border conditions set by the calling function, and the result is copied into the array that is passed through the *input_line* array. The length of the input line (after extension) is passed through *input_length*. The callback function should apply the 1D filter and store the result in the array passed through *output_line*. The length of the output line is passed through *output_length*.

The function `geometric_transform` (see *Interpolation functions*) expects a function with the following prototype:

> The calling function iterates over the elements of the output array, calling the callback function at each element. The coordinates of the current output element are passed through *output_coordinates*. The callback function must return the coordinates at which the input must be interpolated in *input_coordinates*. The rank of the input and output arrays are given by *input_rank* and *output_rank* respectively.

1.15 File IO (`scipy.io`)

See also:

numpy-reference.routines.io (in numpy)

1.15.1 MATLAB files

`loadmat`(file_name[, mdict, appendmat])	Load MATLAB file
`savemat`(file_name, mdict[, appendmat, ...])	Save a dictionary of names and arrays into a MATLAB-style .mat file.
`whosmat`(file_name[, appendmat])	List variables inside a MATLAB file

The basic functions

We'll start by importing `scipy.io` and calling it `sio` for convenience:

```
>>> import scipy.io as sio
```

If you are using IPython, try tab completing on `sio`. Among the many options, you will find:

```
sio.loadmat
sio.savemat
sio.whosmat
```

These are the high-level functions you will most likely use when working with MATLAB files. You'll also find:

```
sio.matlab
```

This is the package from which `loadmat`, `savemat` and `whosmat` are imported. Within `sio.matlab`, you will find the `mio` module This module contains the machinery that `loadmat` and `savemat` use. From time to time you may find yourself re-using this machinery.

How do I start?

You may have a `.mat` file that you want to read into Scipy. Or, you want to pass some variables from Scipy / Numpy into MATLAB.

To save us using a MATLAB license, let's start in Octave. Octave has MATLAB-compatible save and load functions. Start Octave (`octave` at the command line for me):

```
octave:1> a = 1:12
a =

   1   2   3   4   5   6   7   8   9  10  11  12

octave:2> a = reshape(a, [1 3 4])
a =

ans(:,:,1) =

   1   2   3

ans(:,:,2) =

   4   5   6

ans(:,:,3) =

   7   8   9

ans(:,:,4) =

   10   11   12

octave:3> save -6 octave_a.mat a % MATLAB 6 compatible
octave:4> ls octave_a.mat
octave_a.mat
```

Now, to Python:

```
>>> mat_contents = sio.loadmat('octave_a.mat')
>>> mat_contents
{'a': array([[[  1.,   4.,   7.,  10.],
        [  2.,   5.,   8.,  11.],
        [  3.,   6.,   9.,  12.]]]),
 '__version__': '1.0',
 '__header__': 'MATLAB 5.0 MAT-file, written by
 Octave 3.6.3, 2013-02-17 21:02:11 UTC',
 '__globals__': []}
>>> oct_a = mat_contents['a']
>>> oct_a
array([[[  1.,   4.,   7.,  10.],
        [  2.,   5.,   8.,  11.],
        [  3.,   6.,   9.,  12.]]])
>>> oct_a.shape
(1, 3, 4)
```

Now let's try the other way round:

```
>>> import numpy as np
>>> vect = np.arange(10)
>>> vect.shape
(10,)
>>> sio.savemat('np_vector.mat', {'vect':vect})
```

Then back to Octave:

```
octave:8> load np_vector.mat
octave:9> vect
vect =

  0  1  2  3  4  5  6  7  8  9

octave:10> size(vect)
ans =

    1   10
```

If you want to inspect the contents of a MATLAB file without reading the data into memory, use the `whosmat` command:

```
>>> sio.whosmat('octave_a.mat')
[('a', (1, 3, 4), 'double')]
```

`whosmat` returns a list of tuples, one for each array (or other object) in the file. Each tuple contains the name, shape and data type of the array.

MATLAB structs

MATLAB structs are a little bit like Python dicts, except the field names must be strings. Any MATLAB object can be a value of a field. As for all objects in MATLAB, structs are in fact arrays of structs, where a single struct is an array of shape (1, 1).

```
octave:11> my_struct = struct('field1', 1, 'field2', 2)
my_struct =
{
  field1 =  1
  field2 =  2
}

octave:12> save -6 octave_struct.mat my_struct
```

We can load this in Python:

```
>>> mat_contents = sio.loadmat('octave_struct.mat')
>>> mat_contents
{'my_struct': array([[([[1.0]], [[2.0]])]],
      dtype=[('field1', 'O'), ('field2', 'O')]), '__version__': '1.0', '__header__': 'MATLAB 5.0 MAT-
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape
(1, 1)
>>> val = oct_struct[0,0]
>>> val
([[1.0]], [[2.0]])
>>> val['field1']
array([[ 1.]])
>>> val['field2']
array([[ 2.]])
>>> val.dtype
dtype([('field1', 'O'), ('field2', 'O')])
```

In versions of Scipy from 0.12.0, MATLAB structs come back as numpy structured arrays, with fields named for the struct fields. You can see the field names in the `dtype` output above. Note also:

```
>>> val = oct_struct[0,0]
```

and:

```
octave:13> size(my_struct)
ans =

   1   1
```

So, in MATLAB, the struct array must be at least 2D, and we replicate that when we read into Scipy. If you want all length 1 dimensions squeezed out, try this:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape
()
```

Sometimes, it's more convenient to load the MATLAB structs as python objects rather than numpy structured arrays - it can make the access syntax in python a bit more similar to that in MATLAB. In order to do this, use the `struct_as_record=False` parameter setting to `loadmat`.

```
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct[0,0].field1
array([[ 1.]])
```

`struct_as_record=False` works nicely with `squeeze_me`:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False, squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape # but no - it's a scalar
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
AttributeError: 'mat_struct' object has no attribute 'shape'
>>> type(oct_struct)
<class 'scipy.io.matlab.mio5_params.mat_struct'>
>>> oct_struct.field1
1.0
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
AttributeError: 'mat_struct' object has no attribute 'shape'
```

Saving struct arrays can be done in various ways. One simple method is to use dicts:

```
>>> a_dict = {'field1': 0.5, 'field2': 'a string'}
>>> sio.savemat('saved_struct.mat', {'a_dict': a_dict})
```

loaded as:

```
octave:21> load saved_struct
octave:22> a_dict
a_dict =

  scalar structure containing the fields:

    field2 = a string
    field1 =  0.50000
```

You can also save structs back again to MATLAB (or Octave in our case) like this:

```
>>> dt = [('f1', 'f8'), ('f2', 'S10')]
>>> arr = np.zeros((2,), dtype=dt)
>>> arr
array([(0.0, ''), (0.0, '')],
      dtype=[('f1', '<f8'), ('f2', 'S10')])
>>> arr[0]['f1'] = 0.5
>>> arr[0]['f2'] = 'python'
>>> arr[1]['f1'] = 99
>>> arr[1]['f2'] = 'not perl'
>>> sio.savemat('np_struct_arr.mat', {'arr': arr})
```

MATLAB cell arrays

Cell arrays in MATLAB are rather like python lists, in the sense that the elements in the arrays can contain any type of MATLAB object. In fact they are most similar to numpy object arrays, and that is how we load them into numpy.

```
octave:14> my_cells = {1, [2, 3]}
my_cells =
{
  [1,1] =  1
  [1,2] =

     2   3

}

octave:15> save -6 octave_cells.mat my_cells
```

Back to Python:

```
>>> mat_contents = sio.loadmat('octave_cells.mat')
>>> oct_cells = mat_contents['my_cells']
>>> print(oct_cells.dtype)
object
>>> val = oct_cells[0,0]
>>> val
array([[ 1.]])
>>> print(val.dtype)
float64
```

Saving to a MATLAB cell array just involves making a numpy object array:

```
>>> obj_arr = np.zeros((2,), dtype=np.object)
>>> obj_arr[0] = 1
>>> obj_arr[1] = 'a string'
>>> obj_arr
array([1, 'a string'], dtype=object)
>>> sio.savemat('np_cells.mat', {'obj_arr':obj_arr})

octave:16> load np_cells.mat
octave:17> obj_arr
obj_arr =
{
  [1,1] = 1
  [2,1] = a string
}
```

1.15.2 IDL files

`readsav`(file_name[, idict, python_dict, ...])	Read an IDL .sav file

1.15.3 Matrix Market files

`mminfo`(source)	Queries the contents of the Matrix Market file 'filename' to extract size and storag
`mmread`(source)	Reads the contents of a Matrix Market file 'filename' into a matrix.
`mmwrite`(target, a[, comment, field, precision])	Writes the sparse or dense array *a* to a Matrix Market formatted file.

1.15.4 Wav sound files (`scipy.io.wavfile`)

`read`(filename[, mmap])	Return the sample rate (in samples/sec) and data from a WAV file
`write`(filename, rate, data)	Write a numpy array as a WAV file

1.15.5 Arff files (`scipy.io.arff`)

Module to read ARFF files, which are the standard data format for WEKA.

ARFF is a text file format which support numerical, string and data values. The format can also represent missing data and sparse data.

See the WEKA website for more details about arff format and available datasets.

Examples

```
>>> from scipy.io import arff
>>> from cStringIO import StringIO
>>> content = """
... @relation foo
... @attribute width  numeric
... @attribute height numeric
... @attribute color  {red,green,blue,yellow,black}
... @data
... 5.0,3.25,blue
... 4.5,3.75,green
... 3.0,4.00,red
... """
>>> f = StringIO(content)
>>> data, meta = arff.loadarff(f)
>>> data
array([(5.0, 3.25, 'blue'), (4.5, 3.75, 'green'), (3.0, 4.0, 'red')],
      dtype=[('width', '<f8'), ('height', '<f8'), ('color', '|S6')])
>>> meta
Dataset: foo
        width's type is numeric
        height's type is numeric
        color's type is nominal, range is ('red', 'green', 'blue', 'yellow', 'black')
```

`loadarff`(f)	Read an arff file.

1.15.6 Netcdf (`scipy.io.netcdf`)

`netcdf_file`(filename[, mode, mmap, version])	A file object for NetCDF data.

Allows reading of NetCDF files (version of pupynere package)

1.16 Weave (`scipy.weave`)

1.16.1 Outline

Contents

1.16.2 Introduction

The `scipy.weave` (below just `weave`) package provides tools for including C/C++ code within in Python code. This offers both another level of optimization to those who need it, and an easy way to modify and extend any supported extension libraries such as wxPython and hopefully VTK soon. Inlining C/C++ code within Python generally results in speed ups of 1.5x to 30x speed-up over algorithms written in pure Python (However, it is also possible to slow things down...). Generally algorithms that require a large number of calls to the Python API don't benefit as much from the conversion to C/C++ as algorithms that have inner loops completely convertable to C.

There are three basic ways to use `weave`. The `weave.inline()` function executes C code directly within Python, and `weave.blitz()` translates Python NumPy expressions to C++ for fast execution. `blitz()` was the original reason `weave` was built. For those interested in building extension libraries, the `ext_tools` module provides classes for building extension modules within Python.

Most of `weave's` functionality should work on Windows and Unix, although some of its functionality requires `gcc` or a similarly modern C++ compiler that handles templates well. Up to now, most testing has been done on Windows 2000 with Microsoft's C++ compiler (MSVC) and with gcc (mingw32 2.95.2 and 2.95.3-6). All tests also pass on Linux (RH 7.1 with gcc 2.96), and I've had reports that it works on Debian also (thanks Pearu).

The `inline` and `blitz` provide new functionality to Python (although I've recently learned about the PyInline project which may offer similar functionality to `inline`). On the other hand, tools for building Python extension modules already exists (SWIG, SIP, pycpp, CXX, and others). As of yet, I'm not sure where `weave` fits in this spectrum. It is closest in flavor to CXX in that it makes creating new C/C++ extension modules pretty easy. However, if you're wrapping a gaggle of legacy functions or classes, SWIG and friends are definitely the better choice. `weave` is set up so that you can customize how Python types are converted to C types in `weave`. This is great for `inline()`, but, for wrapping legacy code, it is more flexible to specify things the other way around – that is how C types map to Python types. This `weave` does not do. I guess it would be possible to build such a tool on top of `weave`, but with good tools like SWIG around, I'm not sure the effort produces any new capabilities. Things like function overloading are probably easily implemented in `weave` and it might be easier to mix Python/C code in function calls, but nothing beyond this comes to mind. So, if you're developing new extension modules or optimizing Python functions in C, `weave.ext_tools()` might be the tool for you. If you're wrapping legacy code, stick with SWIG.

The next several sections give the basics of how to use `weave`. We'll discuss what's happening under the covers in more detail later on. Serious users will need to at least look at the type conversion section to understand how Python variables map to C/C++ types and how to customize this behavior. One other note. If you don't know C or C++ then these docs are probably of very little help to you. Further, it'd be helpful if you know something about writing Python extensions. `weave` does quite a bit for you, but for anything complex, you'll need to do some conversions, reference counting, etc.

Note: `weave` is actually part of the SciPy package. However, it also works fine as a standalone package (you can install from scipy/weave with `python setup.py install`). The examples here are given as if it is used as a stand alone package. If you are using from within scipy, you can use `from scipy import weave` and the examples will work identically.

1.16.3 Requirements

- Python

  I use 2.1.1. Probably 2.0 or higher should work.

- C++ compiler

  `weave` uses `distutils` to actually build extension modules, so it uses whatever compiler was originally used to build Python. `weave` itself requires a C++ compiler. If you used a C++ compiler to build Python, your probably fine.

On Unix gcc is the preferred choice because I've done a little testing with it. All testing has been done with gcc, but I expect the majority of compilers should work for `inline` and `ext_tools`. The one issue I'm not sure about is that I've hard coded things so that compilations are linked with the `stdc++` library. *Is this standard across Unix compilers, or is this a gcc-ism?*

For `blitz()`, you'll need a reasonably recent version of gcc. 2.95.2 works on windows and 2.96 looks fine on Linux. Other versions are likely to work. Its likely that KAI's C++ compiler and maybe some others will work, but I haven't tried. My advice is to use gcc for now unless your willing to tinker with the code some.

On Windows, either MSVC or gcc (mingw32) should work. Again, you'll need gcc for `blitz()` as the MSVC compiler doesn't handle templates well.

I have not tried Cygwin, so please report success if it works for you.

- NumPy

  The python NumPy module is required for `blitz()` to work and for numpy.distutils which is used by weave.

1.16.4 Installation

There are currently two ways to get `weave`. First, `weave` is part of SciPy and installed automatically (as a sub-package) whenever SciPy is installed. Second, since `weave` is useful outside of the scientific community, it has been setup so that it can be used as a stand-alone module.

The stand-alone version can be downloaded from here. Instructions for installing should be found there as well. setup.py file to simplify installation.

1.16.5 Testing

Once `weave` is installed, fire up python and run its unit tests.

```
>>> import weave
>>> weave.test()
runs long time... spews tons of output and a few warnings
.
.
.
..............................................................
................................................................
..................................................
----------------------------------------------------------------------
Ran 184 tests in 158.418s
OK
>>>
```

This takes a while, usually several minutes. On Unix with remote file systems, I've had it take 15 or so minutes. In the end, it should run about 180 tests and spew some speed results along the way. If you get errors, they'll be reported at the end of the output. Please report errors that you find. Some tests are known to fail at this point.

If you only want to test a single module of the package, you can do this by running test() for that specific module.

```
>>> import weave.scalar_spec
>>> weave.scalar_spec.test()
.......
 ----------------------------------------------------------------------
Ran 7 tests in 23.284s
```

Testing Notes:

- Windows 1

  I've had some test fail on windows machines where I have msvc, gcc-2.95.2 (in c:gcc-2.95.2), and gcc-2.95.3-6 (in c:gcc) all installed. My environment has c:gcc in the path and does not have c:gcc-2.95.2 in the path. The test process runs very smoothly until the end where several test using gcc fail with cpp0 not found by g++. If I check os.system('gcc -v') before running tests, I get gcc-2.95.3-6. If I check after running tests (and after failure), I get gcc-2.95.2. ??huh??. The os.environ['PATH'] still has c:gcc first in it and is not corrupted (msvc/distutils messes with the environment variables, so we have to undo its work in some places). If anyone else sees this, let me know - - it may just be an quirk on my machine (unlikely). Testing with the gcc- 2.95.2 installation always works.

- Windows 2

  If you run the tests from PythonWin or some other GUI tool, you'll get a ton of DOS windows popping up periodically as `weave` spawns the compiler multiple times. Very annoying. Anyone know how to fix this?

- wxPython

  wxPython tests are not enabled by default because importing wxPython on a Unix machine without access to a X-term will cause the program to exit. Anyone know of a safe way to detect whether wxPython can be imported and whether a display exists on a machine?

1.16.6 Benchmarks

This section has not been updated from old scipy weave and Numeric....

This section has a few benchmarks – thats all people want to see anyway right? These are mostly taken from running files in the `weave/example` directory and also from the test scripts. Without more information about what the test actually do, their value is limited. Still, their here for the curious. Look at the example scripts for more specifics about what problem was actually solved by each run. These examples are run under windows 2000 using Microsoft Visual C++ and python2.1 on a 850 MHz PIII laptop with 320 MB of RAM. Speed up is the improvement (degredation) factor of `weave` compared to conventional Python functions. `The blitz()` comparisons are shown compared to NumPy.

Table 1.7: inline and ext_tools

Algorithm	Speed up
binary search	1.50
fibonacci (recursive)	82.10
fibonacci (loop)	9.17
return None	0.14
map	1.20
dictionary sort	2.54
vector quantization	37.40

Table 1.8: blitz – double precision

Algorithm	Speed up
a = b + c 512x512	3.05
a = b + c + d 512x512	4.59
5 pt avg. filter, 2D Image 512x512	9.01
Electromagnetics (FDTD) 100x100x100	8.61

The benchmarks shown `blitz` in the best possible light. NumPy (at least on my machine) is significantly worse for double precision than it is for single precision calculations. If your interested in single precision results, you can pretty much divide the double precision speed up by 3 and you'll be close.

1.16.7 Inline

`inline()` compiles and executes C/C++ code on the fly. Variables in the local and global Python scope are also available in the C/C++ code. Values are passed to the C/C++ code by assignment much like variables are passed into a standard Python function. Values are returned from the C/C++ code through a special argument called return_val. Also, the contents of mutable objects can be changed within the C/C++ code and the changes remain after the C code exits and returns to Python. (more on this later)

Here's a trivial `printf` example using `inline()`:

```
>>> import weave
>>> a  = 1
>>> weave.inline('printf("%d\\n",a);',['a'])
1
```

In this, its most basic form, `inline(c_code, var_list)` requires two arguments. `c_code` is a string of valid C/C++ code. `var_list` is a list of variable names that are passed from Python into C/C++. Here we have a simple `printf` statement that writes the Python variable `a` to the screen. The first time you run this, there will be a pause while the code is written to a .cpp file, compiled into an extension module, loaded into Python, cataloged for future use, and executed. On windows (850 MHz PIII), this takes about 1.5 seconds when using Microsoft's C++ compiler (MSVC) and 6-12 seconds using gcc (mingw32 2.95.2). All subsequent executions of the code will happen very quickly because the code only needs to be compiled once. If you kill and restart the interpreter and then execute the same code fragment again, there will be a much shorter delay in the fractions of seconds range. This is because `weave` stores a catalog of all previously compiled functions in an on disk cache. When it sees a string that has been compiled, it loads the already compiled module and executes the appropriate function.

Note: If you try the `printf` example in a GUI shell such as IDLE, PythonWin, PyShell, etc., you're unlikely to see the output. This is because the C code is writing to stdout, instead of to the GUI window. This doesn't mean that inline doesn't work in these environments – it only means that standard out in C is not the same as the standard out for Python in these cases. Non input/output functions will work as expected.

Although effort has been made to reduce the overhead associated with calling inline, it is still less efficient for simple code snippets than using equivalent Python code. The simple `printf` example is actually slower by 30% or so than using Python `print` statement. And, it is not difficult to create code fragments that are 8-10 times slower using inline than equivalent Python. However, for more complicated algorithms, the speedup can be worthwhile – anywhere from 1.5-30 times faster. Algorithms that have to manipulate Python objects (sorting a list) usually only see a factor of 2 or so improvement. Algorithms that are highly computational or manipulate NumPy arrays can see much larger improvements. The examples/vq.py file shows a factor of 30 or more improvement on the vector quantization algorithm that is used heavily in information theory and classification problems.

More with printf

MSVC users will actually see a bit of compiler output that distutils does not suppress the first time the code executes:

```
>>> weave.inline(r'printf("%d\n",a);',['a'])
sc_e013937dbc8c647ac62438874e5795131.cpp
   Creating library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp
   \Release\sc_e013937dbc8c647ac62438874e5795131.lib and
   object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_e013937dbc8c647ac62438874e
1
```

Nothing bad is happening, its just a bit annoying. * Anyone know how to turn this off?*

This example also demonstrates using 'raw strings'. The `r` preceding the code string in the last example denotes that this is a 'raw string'. In raw strings, the backslash character is not interpreted as an escape character, and so it isn't necessary to use a double backslash to indicate that the 'n' is meant to be interpreted in the C `printf` statement instead of by Python. If your C code contains a lot of strings and control characters, raw strings might make things easier. Most of the time, however, standard strings work just as well.

The `printf` statement in these examples is formatted to print out integers. What happens if `a` is a string? `inline` will happily, compile a new version of the code to accept strings as input, and execute the code. The result?

```
>>> a = 'string'
>>> weave.inline(r'printf("%d\n",a);',['a'])
32956972
```

In this case, the result is non-sensical, but also non-fatal. In other situations, it might produce a compile time error because `a` is required to be an integer at some point in the code, or it could produce a segmentation fault. Its possible to protect against passing `inline` arguments of the wrong data type by using asserts in Python.

```
>>> a = 'string'
>>> def protected_printf(a):
...     assert(type(a) == type(1))
...     weave.inline(r'printf("%d\n",a);',['a'])
>>> protected_printf(1)
 1
>>> protected_printf('string')
AssertError...
```

For printing strings, the format statement needs to be changed. Also, weave doesn't convert strings to char*. Instead it uses CXX Py::String type, so you have to do a little more work. Here we convert it to a C++ std::string and then ask cor the char* version.

```
>>> a = 'string'
>>> weave.inline(r'printf("%s\n",std::string(a).c_str());',['a'])
string
```

XXX

This is a little convoluted. Perhaps strings should convert to `std::string` objects instead of CXX objects. Or maybe to `char*`.

As in this case, C/C++ code fragments often have to change to accept different types. For the given printing task, however, C++ streams provide a way of a single statement that works for integers and strings. By default, the stream objects live in the std (standard) namespace and thus require the use of `std::`.

```
>>> weave.inline('std::cout << a << std::endl;',['a'])
1
>>> a = 'string'
>>> weave.inline('std::cout << a << std::endl;',['a'])
string
```

Examples using `printf` and `cout` are included in examples/print_example.py.

More examples

This section shows several more advanced uses of `inline`. It includes a few algorithms from the Python Cookbook that have been re-written in inline C to improve speed as well as a couple examples using NumPy and wxPython.

Binary search

Lets look at the example of searching a sorted list of integers for a value. For inspiration, we'll use Kalle Svensson's binary_search() algorithm from the Python Cookbook. His recipe follows:

```
def binary_search(seq, t):
    min = 0; max = len(seq) - 1
    while 1:
        if max < min:
            return -1
        m = (min  + max)  / 2
        if seq[m] < t:
            min = m  + 1
        elif seq[m] > t:
            max = m  - 1
        else:
            return m
```

This Python version works for arbitrary Python data types. The C version below is specialized to handle integer values. There is a little type checking done in Python to assure that we're working with the correct data types before heading into C. The variables `seq` and `t` don't need to be declared because `weave` handles converting and declaring them in the C code. All other temporary variables such as `min, max`, etc. must be declared – it is C after all. Here's the new mixed Python/C function:

```
def c_int_binary_search(seq,t):
    # do a little type checking in Python
    assert(type(t) == type(1))
    assert(type(seq) == type([]))

    # now the C code
    code = """
           #line 29 "binary_search.py"
           int val, m, min = 0;
           int max = seq.length() - 1;
           PyObject *py_val;
           for(;;)
           {
               if (max < min  )
               {
                   return_val =  Py::new_reference_to(Py::Int(-1));
                   break;
               }
               m =  (min + max) /2;
               val = py_to_int(PyList_GetItem(seq.ptr(),m),"val");
               if (val  < t)
                   min = m  + 1;
               else if (val >  t)
                   max = m - 1;
               else
               {
                   return_val = Py::new_reference_to(Py::Int(m));
                   break;
               }
           }
           """
    return inline(code,['seq','t'])
```

We have two variables `seq` and `t` passed in. `t` is guaranteed (by the `assert`) to be an integer. Python integers are converted to C int types in the transition from Python to C. `seq` is a Python list. By default, it is translated to a CXX list object. Full documentation for the CXX library can be found at its website. The basics are that the CXX provides C++ class equivalents for Python objects that simplify, or at least object orientify, working with Python objects in C/C++. For example, `seq.length()` returns the length of the list. A little more about CXX and its class methods, etc. is in the *Type Conversions* section.

Note: CXX uses templates and therefore may be a little less portable than another alternative by Gordan McMillan called SCXX which was inspired by CXX. It doesn't use templates so it should compile faster and be more portable. SCXX has a few less features, but it appears to me that it would mesh with the needs of weave quite well. Hopefully xxx_spec files will be written for SCXX in the future, and we'll be able to compare on a more empirical basis. Both sets of spec files will probably stick around, it just a question of which becomes the default.

Most of the algorithm above looks similar in C to the original Python code. There are two main differences. The first is the setting of `return_val` instead of directly returning from the C code with a `return` statement. `return_val` is an automatically defined variable of type `PyObject*` that is returned from the C code back to Python. You'll have to handle reference counting issues when setting this variable. In this example, CXX classes and functions handle the dirty work. All CXX functions and classes live in the namespace `Py::`. The following code converts the integer `m` to a CXX `Int()` object and then to a `PyObject*` with an incremented reference count using `Py::new_reference_to()`.

```
return_val = Py::new_reference_to(Py::Int(m));
```

The second big differences shows up in the retrieval of integer values from the Python list. The simple Python `seq[i]` call balloons into a C Python API call to grab the value out of the list and then a separate call to `py_to_int()` that converts the PyObject* to an integer. `py_to_int()` includes both a NULL cheack and a `PyInt_Check()` call as well as the conversion call. If either of the checks fail, an exception is raised. The entire C++ code block is executed with in a `try/catch` block that handles exceptions much like Python does. This removes the need for most error checking code.

It is worth note that CXX lists do have indexing operators that result in code that looks much like Python. However, the overhead in using them appears to be relatively high, so the standard Python API was used on the `seq.ptr()` which is the underlying `PyObject*` of the List object.

The `#line` directive that is the first line of the C code block isn't necessary, but it's nice for debugging. If the compilation fails because of the syntax error in the code, the error will be reported as an error in the Python file "binary_search.py" with an offset from the given line number (29 here).

So what was all our effort worth in terms of efficiency? Well not a lot in this case. The examples/binary_search.py file runs both Python and C versions of the functions As well as using the standard `bisect` module. If we run it on a 1 million element list and run the search 3000 times (for 0- 2999), here are the results we get:

```
C:\home\ej\wrk\scipy\weave\examples> python binary_search.py
Binary search for 3000 items in 1000000 length list of integers:
speed in python: 0.159999966621
speed of bisect: 0.121000051498
speed up: 1.32
speed in c: 0.110000014305
speed up: 1.45
speed in c(no asserts): 0.0900000333786
speed up: 1.78
```

So, we get roughly a 50-75% improvement depending on whether we use the Python asserts in our C version. If we move down to searching a 10000 element list, the advantage evaporates. Even smaller lists might result in the Python version being faster. I'd like to say that moving to NumPy lists (and getting rid of the GetItem() call) offers a substantial speed up, but my preliminary efforts didn't produce one. I think the log(N) algorithm is to blame. Because the algorithm is nice, there just isn't much time spent computing things, so moving to C isn't that big of a win. If there are ways to reduce conversion overhead of values, this may improve the C/Python speed up. Anyone have other explanations or faster code, please let me know.

Dictionary Sort

The demo in examples/dict_sort.py is another example from the Python CookBook. This submission, by Alex Martelli, demonstrates how to return the values from a dictionary sorted by their keys:

```
def sortedDictValues3(adict):
    keys = adict.keys()
    keys.sort()
    return map(adict.get, keys)
```

Alex provides 3 algorithms and this is the 3rd and fastest of the set. The C version of this same algorithm follows:

```
def c_sort(adict):
    assert(type(adict) == type({}))
    code = """
    #line 21 "dict_sort.py"
    Py::List keys = adict.keys();
    Py::List items(keys.length()); keys.sort();
    PyObject* item = NULL;
    for(int i = 0;  i < keys.length();i++)
    {
        item = PyList_GET_ITEM(keys.ptr(),i);
        item = PyDict_GetItem(adict.ptr(),item);
        Py_XINCREF(item);
        PyList_SetItem(items.ptr(),i,item);
    }
    return_val = Py::new_reference_to(items);
    """
    return inline_tools.inline(code,['adict'],verbose=1)
```

Like the original Python function, the C++ version can handle any Python dictionary regardless of the key/value pair types. It uses CXX objects for the most part to declare python types in C++, but uses Python API calls to manipulate their contents. Again, this choice is made for speed. The C++ version, while more complicated, is about a factor of 2 faster than Python.

```
C:\home\ej\wrk\scipy\weave\examples> python dict_sort.py
Dict sort of 1000 items for 300 iterations:
 speed in python: 0.319999933243
[0, 1, 2, 3, 4]
 speed in c: 0.151000022888
 speed up: 2.12
[0, 1, 2, 3, 4]
```

NumPy – cast/copy/transpose

CastCopyTranspose is a function called quite heavily by Linear Algebra routines in the NumPy library. Its needed in part because of the row-major memory layout of multi-demensional Python (and C) arrays vs. the col-major order of the underlying Fortran algorithms. For small matrices (say 100x100 or less), a significant portion of the common routines such as LU decompisition or singular value decompostion are spent in this setup routine. This shouldn't happen. Here is the Python version of the function using standard NumPy operations.

```
def _castCopyAndTranspose(type, array):
    if a.typecode() == type:
        cast_array = copy.copy(NumPy.transpose(a))
    else:
        cast_array = copy.copy(NumPy.transpose(a).astype(type))
    return cast_array
```

And the following is a inline C version of the same function:

```
from weave.blitz_tools import blitz_type_factories
from weave import scalar_spec
from weave import inline
def _cast_copy_transpose(type,a_2d):
```

```
    assert(len(shape(a_2d)) == 2)
    new_array = zeros(shape(a_2d),type)
    NumPy_type = scalar_spec.NumPy_to_blitz_type_mapping[type]
    code = \
    """
    for(int i = 0;i < _Na_2d[0]; i++)
        for(int j = 0;  j < _Na_2d[1]; j++)
            new_array(i,j) = (%s) a_2d(j,i);
    """ % NumPy_type
    inline(code,['new_array','a_2d'],
           type_factories = blitz_type_factories,compiler='gcc')
    return new_array
```

This example uses blitz++ arrays instead of the standard representation of NumPy arrays so that indexing is simpler to write. This is accomplished by passing in the blitz++ "type factories" to override the standard Python to C++ type conversions. Blitz++ arrays allow you to write clean, fast code, but they also are sloooow to compile (20 seconds or more for this snippet). This is why they aren't the default type used for Numeric arrays (and also because most compilers can't compile blitz arrays...). `inline()` is also forced to use 'gcc' as the compiler because the default compiler on Windows (MSVC) will not compile blitz code. ('gcc' I think will use the standard compiler on Unix machine instead of explicitly forcing gcc (check this)) Comparisons of the Python vs inline C++ code show a factor of 3 speed up. Also shown are the results of an "inplace" transpose routine that can be used if the output of the linear algebra routine can overwrite the original matrix (this is often appropriate). This provides another factor of 2 improvement.

```
#C:\home\ej\wrk\scipy\weave\examples> python cast_copy_transpose.py
# Cast/Copy/Transposing (150,150)array 1 times
#  speed in python: 0.870999932289
#  speed in c: 0.25
#  speed up: 3.48
#  inplace transpose c: 0.129999995232
#  speed up: 6.70
```

wxPython

`inline` knows how to handle wxPython objects. Thats nice in and of itself, but it also demonstrates that the type conversion mechanism is reasonably flexible. Chances are, it won't take a ton of effort to support special types you might have. The examples/wx_example.py borrows the scrolled window example from the wxPython demo, accept that it mixes inline C code in the middle of the drawing function.

```
def DoDrawing(self, dc):

    red = wxNamedColour("RED");
    blue = wxNamedColour("BLUE");
    grey_brush = wxLIGHT_GREY_BRUSH;
    code = \
    """
    #line 108 "wx_example.py"
    dc->BeginDrawing();
    dc->SetPen(wxPen(*red,4,wxSOLID));
    dc->DrawRectangle(5,5,50,50);
    dc->SetBrush(*grey_brush);
    dc->SetPen(wxPen(*blue,4,wxSOLID));
    dc->DrawRectangle(15, 15, 50, 50);
    """
    inline(code,['dc','red','blue','grey_brush'])

    dc.SetFont(wxFont(14, wxSWISS, wxNORMAL, wxNORMAL))
    dc.SetTextForeground(wxColour(0xFF, 0x20, 0xFF))
```

```
    te = dc.GetTextExtent("Hello World")
    dc.DrawText("Hello World", 60, 65)

    dc.SetPen(wxPen(wxNamedColour('VIOLET'), 4))
    dc.DrawLine(5, 65+te[1], 60+te[0], 65+te[1])
    ...
```

Here, some of the Python calls to wx objects were just converted to C++ calls. There isn't any benefit, it just demonstrates the capabilities. You might want to use this if you have a computationally intensive loop in your drawing code that you want to speed up. On windows, you'll have to use the MSVC compiler if you use the standard wxPython DLLs distributed by Robin Dunn. Thats because MSVC and gcc, while binary compatible in C, are not binary compatible for C++. In fact, its probably best, no matter what platform you're on, to specify that `inline` use the same compiler that was used to build wxPython to be on the safe side. There isn't currently a way to learn this info from the library – you just have to know. Also, at least on the windows platform, you'll need to install the wxWindows libraries and link to them. I think there is a way around this, but I haven't found it yet – I get some linking errors dealing with wxString. One final note. You'll probably have to tweak weave/wx_spec.py or weave/wx_info.py for your machine's configuration to point at the correct directories etc. There. That should sufficiently scare people into not even looking at this... :)

Keyword Option

The basic definition of the `inline()` function has a slew of optional variables. It also takes keyword arguments that are passed to `distutils` as compiler options. The following is a formatted cut/paste of the argument section of `inline's` doc-string. It explains all of the variables. Some examples using various options will follow.

```
def inline(code,arg_names,local_dict = None, global_dict = None,
           force = 0,
           compiler='',
           verbose = 0,
           support_code = None,
           customize=None,
           type_factories = None,
           auto_downcast=1,
           **kw):
```

`inline` has quite a few options as listed below. Also, the keyword arguments for distutils extension modules are accepted to specify extra information needed for compiling.

Inline Arguments

code string. A string of valid C++ code. It should not specify a return statement. Instead it should assign results that need to be returned to Python in the return_val. arg_names list of strings. A list of Python variable names that should be transferred from Python into the C/C++ code. local_dict optional. dictionary. If specified, it is a dictionary of values that should be used as the local scope for the C/C++ code. If local_dict is not specified the local dictionary of the calling function is used. global_dict optional. dictionary. If specified, it is a dictionary of values that should be used as the global scope for the C/C++ code. If global_dict is not specified the global dictionary of the calling function is used. force optional. 0 or 1. default 0. If 1, the C++ code is compiled every time inline is called. This is really only useful for debugging, and probably only useful if you're editing support_code a lot. compiler optional. string. The name of compiler to use when compiling. On windows, it understands 'msvc' and 'gcc' as well as all the compiler names understood by distutils. On Unix, it'll only understand the values understoof by distutils. (I should add 'gcc' though to this).

On windows, the compiler defaults to the Microsoft C++ compiler. If this isn't available, it looks for mingw32 (the gcc compiler).

On Unix, it'll probably use the same compiler that was used when compiling Python. Cygwin's behavior should be similar.

verbose optional. 0,1, or 2. defualt 0. Speficies how much much information is printed during the compile phase of inlining code. 0 is silent (except on windows with msvc where it still prints some garbage). 1 informs you when compiling starts, finishes, and how long it took. 2 prints out the command lines for the compilation process and can be useful if you're having problems getting code to work. Its handy for finding the name of the .cpp file if you need to examine it. verbose has no affect if the compilation isn't necessary. support_code optional. string. A string of valid C++ code declaring extra code that might be needed by your compiled function. This could be declarations of functions, classes, or structures. customize optional. base_info.custom_info object. An alternative way to specifiy support_code, headers, etc. needed by the function see the weave.base_info module for more details. (not sure this'll be used much). type_factories optional. list of type specification factories. These guys are what convert Python data types to C/C++ data types. If you'd like to use a different set of type conversions than the default, specify them here. Look in the type conversions section of the main documentation for examples. auto_downcast optional. 0 or 1. default 1. This only affects functions that have Numeric arrays as input variables. Setting this to 1 will cause all floating point values to be cast as float instead of double if all the NumPy arrays are of type float. If even one of the arrays has type double or double complex, all variables maintain there standard types.

Distutils keywords

`inline()` also accepts a number of `distutils` keywords for controlling how the code is compiled. The following descriptions have been copied from Greg Ward's `distutils.extension.Extension` class doc- strings for convenience: sources [string] list of source filenames, relative to the distribution root (where the setup script lives), in Unix form (slash- separated) for portability. Source files may be C, C++, SWIG (.i), platform- specific resource files, or whatever else is recognized by the "build_ext" command as source for a Python extension. Note: The module_path file is always appended to the front of this list include_dirs [string] list of directories to search for C/C++ header files (in Unix form for portability) define_macros [(name : string, value : string|None)] list of macros to define; each macro is defined using a 2-tuple, where 'value' is either the string to define it to or None to define it without a particular value (equivalent of "#define FOO" in source or -DFOO on Unix C compiler command line) undef_macros [string] list of macros to undefine explicitly library_dirs [string] list of directories to search for C/C++ libraries at link time libraries [string] list of library names (not filenames or paths) to link against runtime_library_dirs [string] list of directories to search for C/C++ libraries at run time (for shared extensions, this is when the extension is loaded) extra_objects [string] list of extra files to link with (eg. object files not implied by 'sources', static library that must be explicitly specified, binary resource files, etc.) extra_compile_args [string] any extra platform- and compiler-specific information to use when compiling the source files in 'sources'. For platforms and compilers where "command line" makes sense, this is typically a list of command-line arguments, but for other platforms it could be anything. extra_link_args [string] any extra platform- and compiler-specific information to use when linking object files together to create the extension (or to create a new static Python interpreter). Similar interpretation as for 'extra_compile_args'. export_symbols [string] list of symbols to be exported from a shared extension. Not used on all platforms, and not generally necessary for Python extensions, which typically export exactly one symbol: "init" + extension_name.

Keyword Option Examples

We'll walk through several examples here to demonstrate the behavior of `inline` and also how the various arguments are used. In the simplest (most) cases, `code` and `arg_names` are the only arguments that need to be specified. Here's a simple example run on Windows machine that has Microsoft VC++ installed.

```
>>> from weave import inline
>>> a = 'string'
>>> code = """
...        int l = a.length();
...        return_val = Py::new_reference_to(Py::Int(l));
...        """
>>> inline(code,['a'])
 sc_86e98826b65b047ffd2cd5f479c627f12.cpp
```

```
Creating
   library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f4
and object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ff
d2cd5f479c627f12.exp
6
>>> inline(code,['a'])
6
```

When `inline` is first run, you'll notice that pause and some trash printed to the screen. The "trash" is actually part of the compiler's output that distutils does not supress. The name of the extension file, `sc_bighonkingnumber.cpp`, is generated from the SHA-256 check sum of the C/C++ code fragment. On Unix or windows machines with only gcc installed, the trash will not appear. On the second call, the code fragment is not compiled since it already exists, and only the answer is returned. Now kill the interpreter and restart, and run the same code with a different string.

```
>>> from weave import inline
>>> a = 'a longer string'
>>> code = """
...        int l = a.length();
...        return_val = Py::new_reference_to(Py::Int(l));
...        """
>>> inline(code,['a'])
15
```

Notice this time, `inline()` did not recompile the code because it found the compiled function in the persistent catalog of functions. There is a short pause as it looks up and loads the function, but it is much shorter than compiling would require.

You can specify the local and global dictionaries if you'd like (much like `exec` or `eval()` in Python), but if they aren't specified, the "expected" ones are used – i.e. the ones from the function that called `inline()`. This is accomplished through a little call frame trickery. Here is an example where the local_dict is specified using the same code example from above:

```
>>> a = 'a longer string'
>>> b = 'an even  longer string'
>>> my_dict = {'a':b}
>>> inline(code,['a'])
15
>>> inline(code,['a'],my_dict)
21
```

Every time the `code` is changed, `inline` does a recompile. However, changing any of the other options in inline does not force a recompile. The `force` option was added so that one could force a recompile when tinkering with other variables. In practice, it is just as easy to change the `code` by a single character (like adding a space some place) to force the recompile.

Note: It also might be nice to add some methods for purging the cache and on disk catalogs.

I use `verbose` sometimes for debugging. When set to 2, it'll output all the information (including the name of the .cpp file) that you'd expect from running a make file. This is nice if you need to examine the generated code to see where things are going haywire. Note that error messages from failed compiles are printed to the screen even if `verbose` is set to 0.

The following example demonstrates using gcc instead of the standard msvc compiler on windows using same code fragment as above. Because the example has already been compiled, the `force=1` flag is needed to make `inline()` ignore the previously compiled version and recompile using gcc. The verbose flag is added to show what is printed out:

```
>>>inline(code,['a'],compiler='gcc',verbose=2,force=1)
running build_ext
building 'sc_86e98826b65b047ffd2cd5f479c627f13' extension
c:\gcc-2.95.2\bin\g++.exe -mno-cygwin -mdll -O2 -w -Wstrict-prototypes -IC:
\home\ej\wrk\scipy\weave -IC:\Python21\Include -c C:\DOCUME~1\eric\LOCAL
S~1\Temp\python21_compiled\sc_86e98826b65b047ffd2cd5f479c627f13.cpp
-o C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b04ffd2cd5f479c627f13
skipping C:\home\ej\wrk\scipy\weave\CXX\cxxextensions.c
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxextensions.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\cxxsupport.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxsupport.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\IndirectPythonInterface.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\indirectpythoninterface.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\cxx_extensions.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxx_extensions.o
up-to-date)
writing C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f479c
c:\gcc-2.95.2\bin\dllwrap.exe --driver-name g++ -mno-cygwin
-mdll -static --output-lib
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\libsc_86e98826b65b047ffd2cd5f479c627f1
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f479c627f13.d
-sC:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f479c627f13
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxextensions.o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxsupport.o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\indirectpythoninterface.o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxx_extensions.o -LC:\Python21\libs
-lpython21 -o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\sc_86e98826b65b047ffd2cd5f479c627f13.pyd
15
```

That's quite a bit of output. `verbose=1` just prints the compile time.

```
>>>inline(code,['a'],compiler='gcc',verbose=1,force=1)
Compiling code...
finished compiling (sec):  6.00800001621
15
```

Note: I've only used the `compiler` option for switching between 'msvc' and 'gcc' on windows. It may have use on Unix also, but I don't know yet.

The `support_code` argument is likely to be used a lot. It allows you to specify extra code fragments such as function, structure or class definitions that you want to use in the `code` string. Note that changes to `support_code` do *not* force a recompile. The catalog only relies on `code` (for performance reasons) to determine whether recompiling is necessary. So, if you make a change to support_code, you'll need to alter `code` in some way or use the `force` argument to get the code to recompile. I usually just add some inocuous whitespace to the end of one of the lines in `code` somewhere. Here's an example of defining a separate method for calculating the string length:

```
>>> from weave import inline
>>> a = 'a longer string'
>>> support_code = """
...                PyObject* length(Py::String a)
...                {
...                    int l = a.length();
...                    return Py::new_reference_to(Py::Int(l));
...                }
...                """
>>> inline("return_val = length(a);",['a'],
...        support_code = support_code)
```

```
15
```

`customize` is a left over from a previous way of specifying compiler options. It is a `custom_info` object that can specify quite a bit of information about how a file is compiled. These `info` objects are the standard way of defining compile information for type conversion classes. However, I don't think they are as handy here, especially since we've exposed all the keyword arguments that distutils can handle. Between these keywords, and the `support_code` option, I think `customize` may be obsolete. We'll see if anyone cares to use it. If not, it'll get axed in the next version.

The `type_factories` variable is important to people who want to customize the way arguments are converted from Python to C. We'll talk about this in the next chapter **xx** of this document when we discuss type conversions.

`auto_downcast` handles one of the big type conversion issues that is common when using NumPy arrays in conjunction with Python scalar values. If you have an array of single precision values and multiply that array by a Python scalar, the result is upcast to a double precision array because the scalar value is double precision. This is not usually the desired behavior because it can double your memory usage. `auto_downcast` goes some distance towards changing the casting precedence of arrays and scalars. If your only using single precision arrays, it will automatically downcast all scalar values from double to single precision when they are passed into the C++ code. This is the default behavior. If you want all values to keep there default type, set `auto_downcast` to 0.

Returning Values

Python variables in the local and global scope transfer seemlessly from Python into the C++ snippets. And, if `inline` were to completely live up to its name, any modifications to variables in the C++ code would be reflected in the Python variables when control was passed back to Python. For example, the desired behavior would be something like:

```
# THIS DOES NOT WORK
>>> a = 1
>>> weave.inline("a++;",['a'])
>>> a
2
```

Instead you get:

```
>>> a = 1
>>> weave.inline("a++;",['a'])
>>> a
1
```

Variables are passed into C++ as if you are calling a Python function. Python's calling convention is sometimes called "pass by assignment". This means its as if a `c_a = a` assignment is made right before `inline` call is made and the `c_a` variable is used within the C++ code. Thus, any changes made to `c_a` are not reflected in Python's `a` variable. Things do get a little more confusing, however, when looking at variables with mutable types. Changes made in C++ to the contents of mutable types *are* reflected in the Python variables.

```
>>> a= [1,2]
>>> weave.inline("PyList_SetItem(a.ptr(),0,PyInt_FromLong(3));",['a'])
>>> print a
[3, 2]
```

So modifications to the contents of mutable types in C++ are seen when control is returned to Python. Modifications to immutable types such as tuples, strings, and numbers do not alter the Python variables. If you need to make changes to an immutable variable, you'll need to assign the new value to the "magic" variable `return_val` in C++. This value is returned by the `inline()` function:

```
>>> a = 1
>>> a = weave.inline("return_val = Py::new_reference_to(Py::Int(a+1));",['a'])
>>> a
2
```

The `return_val` variable can also be used to return newly created values. This is possible by returning a tuple. The following trivial example illustrates how this can be done:

```
# python version
def multi_return():
    return 1, '2nd'

# C version.
def c_multi_return():
    code =  """
              py::tuple results(2);
              results[0] = 1;
              results[1] = "2nd";
              return_val = results;
            """
    return inline_tools.inline(code)
```

The example is available in `examples/tuple_return.py`. It also has the dubious honor of demonstrating how much `inline()` can slow things down. The C version here is about 7-10 times slower than the Python version. Of course, something so trivial has no reason to be written in C anyway.

The issue with `locals()` `inline` passes the `locals()` and `globals()` dictionaries from Python into the C++ function from the calling function. It extracts the variables that are used in the C++ code from these dictionaries, converts then to C++ variables, and then calculates using them. It seems like it would be trivial, then, after the calculations were finished to then insert the new values back into the `locals()` and `globals()` dictionaries so that the modified values were reflected in Python. Unfortunately, as pointed out by the Python manual, the locals() dictionary is not writable.

I suspect `locals()` is not writable because there are some optimizations done to speed lookups of the local namespace. I'm guessing local lookups don't always look at a dictionary to find values. Can someone "in the know" confirm or correct this? Another thing I'd like to know is whether there is a way to write to the local namespace of another stack frame from C/C++. If so, it would be possible to have some clean up code in compiled functions that wrote final values of variables in C++ back to the correct Python stack frame. I think this goes a long way toward making `inline` truly live up to its name. I don't think we'll get to the point of creating variables in Python for variables created in C – although I suppose with a C/C++ parser you could do that also.

A quick look at the code

`weave` generates a C++ file holding an extension function for each `inline` code snippet. These file names are generated using from the SHA-256 signature of the code snippet and saved to a location specified by the PYTHONCOMPILED environment variable (discussed later). The cpp files are generally about 200-400 lines long and include quite a few functions to support type conversions, etc. However, the actual compiled function is pretty simple. Below is the familiar `printf` example:

```
>>> import weave
>>> a = 1
>>> weave.inline('printf("%d\\n",a);',['a'])
1
```

And here is the extension function generated by `inline`:

```
static PyObject* compiled_func(PyObject*self, PyObject* args)
{
    py::object return_val;
    int exception_occured = 0;
    PyObject *py__locals = NULL;
    PyObject *py__globals = NULL;
    PyObject *py_a;
```

```
    py_a = NULL;

    if(!PyArg_ParseTuple(args,"OO:compiled_func",&py__locals,&py__globals))
        return NULL;
    try
    {
        PyObject* raw_locals = py_to_raw_dict(py__locals,"_locals");
        PyObject* raw_globals = py_to_raw_dict(py__globals,"_globals");
        /* argument conversion code */
        py_a = get_variable("a",raw_locals,raw_globals);
        int a = convert_to_int(py_a,"a");
        /* inline code */
        /* NDARRAY API VERSION 90907 */
        printf("%d\n",a);    /*I would like to fill in changed locals and globals here...*/
    }
    catch(...)
    {
        return_val =  py::object();
        exception_occured = 1;
    }
    /* cleanup code */
    if(!(PyObject*)return_val && !exception_occured)
    {
        return_val = Py_None;
    }
    return return_val.disown();
}
```

Every inline function takes exactly two arguments – the local and global dictionaries for the current scope. All variable values are looked up out of these dictionaries. The lookups, along with all `inline` code execution, are done within a C++ `try` block. If the variables aren't found, or there is an error converting a Python variable to the appropriate type in C++, an exception is raised. The C++ exception is automatically converted to a Python exception by SCXX and returned to Python. The `py_to_int()` function illustrates how the conversions and exception handling works. py_to_int first checks that the given PyObject* pointer is not NULL and is a Python integer. If all is well, it calls the Python API to convert the value to an `int`. Otherwise, it calls `handle_bad_type()` which gathers information about what went wrong and then raises a SCXX TypeError which returns to Python as a TypeError.

```
int py_to_int(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyInt_Check(py_obj))
        handle_bad_type(py_obj,"int", name);
    return (int) PyInt_AsLong(py_obj);
}

void handle_bad_type(PyObject* py_obj, char* good_type, char* var_name)
{
    char msg[500];
    sprintf(msg,"received '%s' type instead of '%s' for variable '%s'",
            find_type(py_obj),good_type,var_name);
    throw Py::TypeError(msg);
}

char* find_type(PyObject* py_obj)
{
    if(py_obj == NULL) return "C NULL value";
    if(PyCallable_Check(py_obj)) return "callable";
    if(PyString_Check(py_obj)) return "string";
    if(PyInt_Check(py_obj)) return "int";
```

```
    if(PyFloat_Check(py_obj)) return "float";
    if(PyDict_Check(py_obj)) return "dict";
    if(PyList_Check(py_obj)) return "list";
    if(PyTuple_Check(py_obj)) return "tuple";
    if(PyFile_Check(py_obj)) return "file";
    if(PyModule_Check(py_obj)) return "module";

    //should probably do more interagation (and thinking) on these.
    if(PyCallable_Check(py_obj) && PyInstance_Check(py_obj)) return "callable";
    if(PyInstance_Check(py_obj)) return "instance";
    if(PyCallable_Check(py_obj)) return "callable";
    return "unknown type";
}
```

Since the `inline` is also executed within the `try/catch` block, you can use CXX exceptions within your code. It is usually a bad idea to directly `return` from your code, even if an error occurs. This skips the clean up section of the extension function. In this simple example, there isn't any clean up code, but in more complicated examples, there may be some reference counting that needs to be taken care of here on converted variables. To avoid this, either uses exceptions or set `return_val` to NULL and use `if/then's` to skip code after errors.

Technical Details

There are several main steps to using C/C++ code within Python:

1. Type conversion
2. Generating C/C++ code
3. Compile the code to an extension module
4. Catalog (and cache) the function for future use

Items 1 and 2 above are related, but most easily discussed separately. Type conversions are customizable by the user if needed. Understanding them is pretty important for anything beyond trivial uses of `inline`. Generating the C/C++ code is handled by `ext_function` and `ext_module` classes and . For the most part, compiling the code is handled by distutils. Some customizations were needed, but they were relatively minor and do not require changes to distutils itself. Cataloging is pretty simple in concept, but surprisingly required the most code to implement (and still likely needs some work). So, this section covers items 1 and 4 from the list. Item 2 is covered later in the chapter covering the `ext_tools` module, and distutils is covered by a completely separate document xxx.

Passing Variables in/out of the C/C++ code

Note: Passing variables into the C code is pretty straight forward, but there are subtlties to how variable modifications in C are returned to Python. see Returning Values for a more thorough discussion of this issue.

Type Conversions

Note: Maybe `xxx_converter` instead of `xxx_specification` is a more descriptive name. Might change in future version?

By default, `inline()` makes the following type conversions between Python and C++ types.

Table 1.9: Default Data Type Conversions

Python	C++
int	int
float	double
complex	std::complex
string	py::string
list	py::list
dict	py::dict
tuple	py::tuple
file	FILE*
callable	py::object
instance	py::object
numpy.ndarray	PyArrayObject*
wxXXX	wxXXX*

The `Py::` namespace is defined by the SCXX library which has C++ class equivalents for many Python types. `std::` is the namespace of the standard library in C++.

Note:

- I haven't figured out how to handle `long int` yet (I think they are currenlty converted to int - - check this).
- Hopefully VTK will be added to the list soon

Python to C++ conversions fill in code in several locations in the generated `inline` extension function. Below is the basic template for the function. This is actually the exact code that is generated by calling `weave.inline("")`.

The `/* inline code */` section is filled with the code passed to the `inline()` function call. The `/*argument conversion code*/` and `/* cleanup code */` sections are filled with code that handles conversion from Python to C++ types and code that deallocates memory or manipulates reference counts before the function returns. The following sections demonstrate how these two areas are filled in by the default conversion methods. * Note: I'm not sure I have reference counting correct on a few of these. The only thing I increase/decrease the ref count on is NumPy arrays. If you see an issue, please let me know.

NumPy Argument Conversion

Integer, floating point, and complex arguments are handled in a very similar fashion. Consider the following inline function that has a single integer variable passed in:

```
>>> a = 1
>>> inline("",['a'])
```

The argument conversion code inserted for `a` is:

```
/* argument conversion code */
int a = py_to_int (get_variable("a",raw_locals,raw_globals),"a");
```

`get_variable()` reads the variable `a` from the local and global namespaces. `py_to_int()` has the following form:

```
static int py_to_int(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyInt_Check(py_obj))
        handle_bad_type(py_obj,"int", name);
    return (int) PyInt_AsLong(py_obj);
}
```

Similarly, the float and complex conversion routines look like:

```
static double py_to_float(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyFloat_Check(py_obj))
        handle_bad_type(py_obj,"float", name);
    return PyFloat_AsDouble(py_obj);
}

static std::complex py_to_complex(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyComplex_Check(py_obj))
        handle_bad_type(py_obj,"complex", name);
    return std::complex(PyComplex_RealAsDouble(py_obj),
                                PyComplex_ImagAsDouble(py_obj));
}
```

NumPy conversions do not require any clean up code.

String, List, Tuple, and Dictionary Conversion

Strings, Lists, Tuples and Dictionary conversions are all converted to SCXX types by default. For the following code,

```
>>> a = [1]
>>> inline("",['a'])
```

The argument conversion code inserted for `a` is:

```
/* argument conversion code */
Py::List a = py_to_list(get_variable("a",raw_locals,raw_globals),"a");
```

`get_variable()` reads the variable `a` from the local and global namespaces. `py_to_list()` and its friends have the following form:

```
static Py::List py_to_list(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyList_Check(py_obj))
        handle_bad_type(py_obj,"list", name);
    return Py::List(py_obj);
}

static Py::String py_to_string(PyObject* py_obj,char* name)
{
    if (!PyString_Check(py_obj))
        handle_bad_type(py_obj,"string", name);
    return Py::String(py_obj);
}

static Py::Dict py_to_dict(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyDict_Check(py_obj))
        handle_bad_type(py_obj,"dict", name);
    return Py::Dict(py_obj);
}

static Py::Tuple py_to_tuple(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyTuple_Check(py_obj))
        handle_bad_type(py_obj,"tuple", name);
```

```
    return Py::Tuple(py_obj);
}
```

SCXX handles reference counts on for strings, lists, tuples, and dictionaries, so clean up code isn't necessary.

File Conversion

For the following code,

```
>>> a = open("bob",'w')
>>> inline("",['a'])
```

The argument conversion code is:

```
/* argument conversion code */
PyObject* py_a = get_variable("a",raw_locals,raw_globals);
FILE* a = py_to_file(py_a,"a");
```

`get_variable()` reads the variable a from the local and global namespaces. `py_to_file()` converts PyObject* to a FILE* and increments the reference count of the PyObject*:

```
FILE* py_to_file(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyFile_Check(py_obj))
        handle_bad_type(py_obj,"file", name);

    Py_INCREF(py_obj);
    return PyFile_AsFile(py_obj);
}
```

Because the PyObject* was incremented, the clean up code needs to decrement the counter

```
/* cleanup code */
Py_XDECREF(py_a);
```

Its important to understand that file conversion only works on actual files – i.e. ones created using the `open()` command in Python. It does not support converting arbitrary objects that support the file interface into C `FILE*` pointers. This can affect many things. For example, in initial `printf()` examples, one might be tempted to solve the problem of C and Python IDE's (PythonWin, PyCrust, etc.) writing to different stdout and stderr by using `fprintf()` and passing in `sys.stdout` and `sys.stderr`. For example, instead of

```
>>> weave.inline('printf("hello\\n");')
```

You might try:

```
>>> buf = sys.stdout
>>> weave.inline('fprintf(buf,"hello\\n");',['buf'])
```

This will work as expected from a standard python interpreter, but in PythonWin, the following occurs:

```
>>> buf = sys.stdout
>>> weave.inline('fprintf(buf,"hello\\n");',['buf'])
Traceback (most recent call last):
    File "", line 1, in ?
    File "C:\Python21\weave\inline_tools.py", line 315, in inline
        auto_downcast = auto_downcast,
    File "C:\Python21\weave\inline_tools.py", line 386, in compile_function
        type_factories = type_factories)
    File "C:\Python21\weave\ext_tools.py", line 197, in __init__
        auto_downcast, type_factories)
```

```
    File "C:\Python21\weave\ext_tools.py", line 390, in assign_variable_types
        raise TypeError, format_error_msg(errors)
    TypeError: {'buf': "Unable to convert variable 'buf' to a C++ type."}
```

The traceback tells us that `inline()` was unable to convert 'buf' to a C++ type (If instance conversion was implemented, the error would have occurred at runtime instead). Why is this? Let's look at what the `buf` object really is:

```
>>> buf
pywin.framework.interact.InteractiveView instance at 00EAD014
```

PythonWin has reassigned `sys.stdout` to a special object that implements the Python file interface. This works great in Python, but since the special object doesn't have a FILE* pointer underlying it, `fprintf` doesn't know what to do with it (well this will be the problem when instance conversion is implemented...).

Callable, Instance, and Module Conversion

Note: Need to look into how ref counts should be handled. Also, Instance and Module conversion are not currently implemented.

```
>>> def a():
    pass
>>> inline("",['a'])
```

Callable and instance variables are converted to PyObject*. Nothing is done to their reference counts.

```
/* argument conversion code */
PyObject* a = py_to_callable(get_variable("a",raw_locals,raw_globals),"a");
```

`get_variable()` reads the variable `a` from the local and global namespaces. The `py_to_callable()` and `py_to_instance()` don't currently increment the ref count.

```
PyObject* py_to_callable(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyCallable_Check(py_obj))
        handle_bad_type(py_obj,"callable", name);
    return py_obj;
}

PyObject* py_to_instance(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyFile_Check(py_obj))
        handle_bad_type(py_obj,"instance", name);
    return py_obj;
}
```

There is no cleanup code for callables, modules, or instances.

Customizing Conversions

Converting from Python to C++ types is handled by `xxx_specification` classes. A type specification class actually serve in two related but different roles. The first is in determining whether a Python variable that needs to be converted should be represented by the given class. The second is as a code generator that generates C++ code needed to convert from Python to C++ types for a specific variable.

When

```
>>> a = 1
>>> weave.inline('printf("%d",a);',['a'])
```

is called for the first time, the code snippet has to be compiled. In this process, the variable ‘a’ is tested against a list of type specifications (the default list is stored in weave/ext_tools.py). The *first* specification in the list is used to represent the variable.

Examples of `xxx_specification` are scattered throughout numerous “xxx_spec.py” files in the `weave` package. Closely related to the `xxx_specification` classes are `yyy_info` classes. These classes contain compiler, header, and support code information necessary for including a certain set of capabilities (such as blitz++ or CXX support) in a compiled module. `xxx_specification` classes have one or more `yyy_info` classes associated with them. If you’d like to define your own set of type specifications, the current best route is to examine some of the existing spec and info files. Maybe looking over sequence_spec.py and cxx_info.py are a good place to start. After defining specification classes, you’ll need to pass them into `inline` using the `type_factories` argument. A lot of times you may just want to change how a specific variable type is represented. Say you’d rather have Python strings converted to `std::string` or maybe `char*` instead of using the CXX string object, but would like all other type conversions to have default behavior. This requires that a new specification class that handles strings is written and then prepended to a list of the default type specifications. Since it is closer to the front of the list, it effectively overrides the default string specification. The following code demonstrates how this is done: ...

The Catalog

`catalog.py` has a class called `catalog` that helps keep track of previously compiled functions. This prevents `inline()` and related functions from having to compile functions every time they are called. Instead, catalog will check an in memory cache to see if the function has already been loaded into python. If it hasn’t, then it starts searching through persisent catalogs on disk to see if it finds an entry for the given function. By saving information about compiled functions to disk, it isn’t necessary to re-compile functions every time you stop and restart the interpreter. Functions are compiled once and stored for future use.

When `inline(cpp_code)` is called the following things happen:

1. A fast local cache of functions is checked for the last function called for `cpp_code`. If an entry for `cpp_code` doesn’t exist in the cache or the cached function call fails (perhaps because the function doesn’t have compatible types) then the next step is to check the catalog.

2. The catalog class also keeps an in-memory cache with a list of all the functions compiled for `cpp_code`. If `cpp_code` has ever been called, then this cache will be present (loaded from disk). If the cache isn’t present, then it is loaded from disk.

   If the cache is present, each function in the cache is called until one is found that was compiled for the correct argument types. If none of the functions work, a new function is compiled with the given argument types. This function is written to the on-disk catalog as well as into the in-memory cache.

3. When a lookup for `cpp_code` fails, the catalog looks through the on-disk function catalogs for the entries. The PYTHONCOMPILED variable determines where to search for these catalogs and in what order. If PYTHONCOMPILED is not present several platform dependent locations are searched. All functions found for `cpp_code` in the path are loaded into the in-memory cache with functions found earlier in the search path closer to the front of the call list.

   If the function isn’t found in the on-disk catalog, then the function is compiled, written to the first writable directory in the PYTHONCOMPILED path, and also loaded into the in-memory cache.

Function Storage

Function caches are stored as dictionaries where the key is the entire C++ code string and the value is either a single function (as in the “level 1” cache) or a list of functions (as in the main catalog cache). On disk catalogs are stored in the same manor using standard Python shelves.

Early on, there was a question as to whether md5 checksums of the C++ code strings should be used instead of the actual code strings. I think this is the route inline Perl took. Some (admittedly quick) tests of the md5 vs. the entire string showed that using the entire string was at least a factor of 3 or 4 faster for Python. I think this is because it is more time consuming to compute the md5 value than it is to do look-ups of long strings in the dictionary. Look at the examples/md5_speed.py file for the test run.

Catalog search paths and the PYTHONCOMPILED variable

The default location for catalog files on Unix is ~/.pythonXX_compiled where XX is version of Python being used. If this directory doesn't exist, it is created the first time a catalog is used. The directory must be writable. If, for any reason it isn't, then the catalog attempts to create a directory based on your user id in the /tmp directory. The directory permissions are set so that only you have access to the directory. If this fails, I think you're out of luck. I don't think either of these should ever fail though. On Windows, a directory called pythonXX_compiled is created in the user's temporary directory.

The actual catalog file that lives in this directory is a Python shelf with a platform specific name such as "nt21compiled_catalog" so that multiple OSes can share the same file systems without trampling on each other. Along with the catalog file, the .cpp and .so or .pyd files created by inline will live in this directory. The catalog file simply contains keys which are the C++ code strings with values that are lists of functions. The function lists point at functions within these compiled modules. Each function in the lists executes the same C++ code string, but compiled for different input variables.

You can use the PYTHONCOMPILED environment variable to specify alternative locations for compiled functions. On Unix this is a colon (':') separated list of directories. On windows, it is a (';') separated list of directories. These directories will be searched prior to the default directory for a compiled function catalog. Also, the first writable directory in the list is where all new compiled function catalogs, .cpp and .so or .pyd files are written. Relative directory paths ('.' and '..') should work fine in the PYTHONCOMPILED variable as should environement variables.

There is a "special" path variable called MODULE that can be placed in the PYTHONCOMPILED variable. It specifies that the compiled catalog should reside in the same directory as the module that called it. This is useful if an admin wants to build a lot of compiled functions during the build of a package and then install them in site-packages along with the package. User's who specify MODULE in their PYTHONCOMPILED variable will have access to these compiled functions. Note, however, that if they call the function with a set of argument types that it hasn't previously been built for, the new function will be stored in their default directory (or some other writable directory in the PYTHONCOMPILED path) because the user will not have write access to the site-packages directory.

An example of using the PYTHONCOMPILED path on bash follows:

```
PYTHONCOMPILED=MODULE:/some/path;export PYTHONCOMPILED;
```

If you are using python21 on linux, and the module bob.py in site-packages has a compiled function in it, then the catalog search order when calling that function for the first time in a python session would be:

```
/usr/lib/python21/site-packages/linuxpython_compiled
/some/path/linuxpython_compiled
~/.python21_compiled/linuxpython_compiled
```

The default location is always included in the search path.

Note: hmmm. see a possible problem here. I should probably make a sub- directory such as /usr/lib/python21/site-packages/python21_compiled/linuxpython_compiled so that library files compiled with python21 are tried to link with python22 files in some strange scenarios. Need to check this.

The in-module cache (in `weave.inline_tools` reduces the overhead of calling inline functions by about a factor of 2. It can be reduced a little more for type loop calls where the same function is called over and over again if the cache was a single value instead of a dictionary, but the benefit is very small (less than 5%) and the utility is quite a bit less. So, we'll stick with a dictionary as the cache.

1.16.8 Blitz

Note: most of this section is lifted from old documentation. It should be pretty accurate, but there may be a few discrepancies.

`weave.blitz()` compiles NumPy Python expressions for fast execution. For most applications, compiled expressions should provide a factor of 2-10 speed-up over NumPy arrays. Using compiled expressions is meant to be as unobtrusive as possible and works much like pythons exec statement. As an example, the following code fragment takes a 5 point average of the 512x512 2d image, b, and stores it in array, a:

```
from scipy import *  # or from NumPy import *
a = ones((512,512), Float64)
b = ones((512,512), Float64)
# ...do some stuff to fill in b...
# now average
a[1:-1,1:-1] =  (b[1:-1,1:-1] + b[2:,1:-1] + b[:-2,1:-1] \
               + b[1:-1,2:] + b[1:-1,:-2]) / 5.
```

To compile the expression, convert the expression to a string by putting quotes around it and then use `weave.blitz`:

```
import weave
expr = "a[1:-1,1:-1] =  (b[1:-1,1:-1] + b[2:,1:-1] + b[:-2,1:-1]" \
                      "+ b[1:-1,2:] + b[1:-1,:-2]) / 5."
weave.blitz(expr)
```

The first time `weave.blitz` is run for a given expression and set of arguments, C++ code that accomplishes the exact same task as the Python expression is generated and compiled to an extension module. This can take up to a couple of minutes depending on the complexity of the function. Subsequent calls to the function are very fast. Furthermore, the generated module is saved between program executions so that the compilation is only done once for a given expression and associated set of array types. If the given expression is executed with a new set of array types, the code most be compiled again. This does not overwrite the previously compiled function – both of them are saved and available for exectution.

The following table compares the run times for standard NumPy code and compiled code for the 5 point averaging.

Method Run Time (seconds) Standard NumPy 0.46349 blitz (1st time compiling) 78.95526 blitz (subsequent calls) 0.05843 (factor of 8 speedup)

These numbers are for a 512x512 double precision image run on a 400 MHz Celeron processor under RedHat Linux 6.2.

Because of the slow compile times, its probably most effective to develop algorithms as you usually do using the capabilities of scipy or the NumPy module. Once the algorithm is perfected, put quotes around it and execute it using `weave.blitz`. This provides the standard rapid prototyping strengths of Python and results in algorithms that run close to that of hand coded C or Fortran.

Requirements

Currently, the `weave.blitz` has only been tested under Linux with gcc-2.95-3 and on Windows with Mingw32 (2.95.2). Its compiler requirements are pretty heavy duty (see the blitz++ home page), so it won't work with just any compiler. Particularly MSVC++ isn't up to snuff. A number of other compilers such as KAI++ will also work, but my suspicions are that gcc will get the most use.

Limitations

1. Currently, `weave.blitz` handles all standard mathematical operators except for the ** power operator. The built-in trigonmetric, log, floor/ceil, and fabs functions might work (but haven't been tested). It also handles all

types of array indexing supported by the NumPy module. numarray's NumPy compatible array indexing modes are likewise supported, but numarray's enhanced (array based) indexing modes are not supported.

`weave.blitz` does not currently support operations that use array broadcasting, nor have any of the special purpose functions in NumPy such as take, compress, etc. been implemented. Note that there are no obvious reasons why most of this functionality cannot be added to scipy.weave, so it will likely trickle into future versions. Using `slice()` objects directly instead of `start:stop:step` is also not supported.

2. Currently Python only works on expressions that include assignment such as

```
>>> result = b + c + d
```

This means that the result array must exist before calling `weave.blitz`. Future versions will allow the following:

```
>>> result = weave.blitz_eval("b + c + d")
```

3. `weave.blitz` works best when algorithms can be expressed in a "vectorized" form. Algorithms that have a large number of if/thens and other conditions are better hand-written in C or Fortran. Further, the restrictions imposed by requiring vectorized expressions sometimes preclude the use of more efficient data structures or algorithms. For maximum speed in these cases, hand-coded C or Fortran code is the only way to go.

4. `weave.blitz` can produce different results than NumPy in certain situations. It can happen when the array receiving the results of a calculation is also used during the calculation. The NumPy behavior is to carry out the entire calculation on the right hand side of an equation and store it in a temporary array. This temprorary array is assigned to the array on the left hand side of the equation. blitz, on the other hand, does a "running" calculation of the array elements assigning values from the right hand side to the elements on the left hand side immediately after they are calculated. Here is an example, provided by Prabhu Ramachandran, where this happens:

```
# 4 point average.
>>> expr = "u[1:-1, 1:-1] = (u[0:-2, 1:-1] + u[2:, 1:-1] + \
...                 "u[1:-1,0:-2] + u[1:-1, 2:])*0.25"
>>> u = zeros((5, 5), 'd'); u[0,:] = 100
>>> exec (expr)
>>> u
array([[ 100.,  100.,  100.,  100.,  100.],
       [   0.,   25.,   25.,   25.,    0.],
       [   0.,    0.,    0.,    0.,    0.],
       [   0.,    0.,    0.,    0.,    0.],
       [   0.,    0.,    0.,    0.,    0.]])

>>> u = zeros((5, 5), 'd'); u[0,:] = 100
>>> weave.blitz (expr)
>>> u
array([[ 100.  ,  100.       ,  100.       ,  100.       , 100. ],
       [   0.  ,   25.       ,   31.25     ,   32.8125   , 0. ],
       [   0.  ,    6.25     ,    9.375    ,   10.546875 , 0. ],
       [   0.  ,    1.5625   ,    2.734375 ,    3.3203125, 0. ],
       [   0.  ,    0.       ,    0.       ,    0.       , 0. ]])
```

You can prevent this behavior by using a temporary array.

```
>>> u = zeros((5, 5), 'd'); u[0,:] = 100
>>> temp = zeros((4, 4), 'd');
>>> expr = "temp = (u[0:-2, 1:-1] + u[2:, 1:-1] + "\
...        "u[1:-1,0:-2] + u[1:-1, 2:])*0.25;"\
...        "u[1:-1,1:-1] = temp"
>>> weave.blitz (expr)
>>> u
array([[ 100.,  100.,  100.,  100.,  100.],
```

```
[   0.,   25.,   25.,   25.,    0.],
[   0.,    0.,    0.,    0.,    0.],
[   0.,    0.,    0.,    0.,    0.],
[   0.,    0.,    0.,    0.,    0.]])
```

5. One other point deserves mention lest people be confused. `weave.blitz` is not a general purpose Python->C compiler. It only works for expressions that contain NumPy arrays and/or Python scalar values. This focused scope concentrates effort on the compuationally intensive regions of the program and sidesteps the difficult issues associated with a general purpose Python->C compiler.

NumPy efficiency issues: What compilation buys you

Some might wonder why compiling NumPy expressions to C++ is beneficial since operations on NumPy array operations are already executed within C loops. The problem is that anything other than the simplest expression are executed in less than optimal fashion. Consider the following NumPy expression:

```
a = 1.2 * b + c * d
```

When NumPy calculates the value for the 2d array, `a`, it does the following steps:

```
temp1 = 1.2 * b
temp2 = c * d
a = temp1 + temp2
```

Two things to note. Since `c` is an (perhaps large) array, a large temporary array must be created to store the results of `1.2 * b`. The same is true for `temp2`. Allocation is slow. The second thing is that we have 3 loops executing, one to calculate `temp1`, one for `temp2` and one for adding them up. A C loop for the same problem might look like:

```
for(int i = 0; i < M; i++)
    for(int j = 0; j < N; j++)
        a[i,j] = 1.2 * b[i,j] + c[i,j] * d[i,j]
```

Here, the 3 loops have been fused into a single loop and there is no longer a need for a temporary array. This provides a significant speed improvement over the above example (write me and tell me what you get).

So, converting NumPy expressions into C/C++ loops that fuse the loops and eliminate temporary arrays can provide big gains. The goal, then, is to convert NumPy expression to C/C++ loops, compile them in an extension module, and then call the compiled extension function. The good news is that there is an obvious correspondence between the NumPy expression above and the C loop. The bad news is that NumPy is generally much more powerful than this simple example illustrates and handling all possible indexing possibilities results in loops that are less than straightforward to write. (Take a peek at NumPy for confirmation). Luckily, there are several available tools that simplify the process.

The Tools

`weave.blitz` relies heavily on several remarkable tools. On the Python side, the main facilitators are Jermey Hylton's parser module and Travis Oliphant's NumPy module. On the compiled language side, Todd Veldhuizen's blitz++ array library, written in C++ (shhhh. don't tell David Beazley), does the heavy lifting. Don't assume that, because it's C++, it's much slower than C or Fortran. Blitz++ uses a jaw dropping array of template techniques (metaprogramming, template expression, etc) to convert innocent-looking and readable C++ expressions into to code that usually executes within a few percentage points of Fortran code for the same problem. This is good. Unfortunately all the template raz-ma-taz is very expensive to compile, so the 200 line extension modules often take 2 or more minutes to compile. This isn't so good. `weave.blitz` works to minimize this issue by remembering where compiled modules live and reusing them instead of re-compiling every time a program is re-run.

Parser

Tearing NumPy expressions apart, examining the pieces, and then rebuilding them as C++ (blitz) expressions requires a parser of some sort. I can imagine someone attacking this problem with regular expressions, but it'd likely be ugly and fragile. Amazingly, Python solves this problem for us. It actually exposes its parsing engine to the world through the `parser` module. The following fragment creates an Abstract Syntax Tree (AST) object for the expression and then converts to a (rather unpleasant looking) deeply nested list representation of the tree.

```
>>> import parser
>>> import scipy.weave.misc
>>> ast = parser.suite("a = b * c + d")
>>> ast_list = ast.tolist()
>>> sym_list = scipy.weave.misc.translate_symbols(ast_list)
>>> pprint.pprint(sym_list)
['file_input',
 ['stmt',
  ['simple_stmt',
   ['small_stmt',
    ['expr_stmt',
     ['testlist',
      ['test',
       ['and_test',
        ['not_test',
         ['comparison',
          ['expr',
           ['xor_expr',
            ['and_expr',
             ['shift_expr',
              ['arith_expr',
               ['term',
                ['factor', ['power', ['atom', ['NAME', 'a']]]]]]]]]]]]]]]],
     ['EQUAL', '='],
     ['testlist',
      ['test',
       ['and_test',
        ['not_test',
         ['comparison',
          ['expr',
           ['xor_expr',
            ['and_expr',
             ['shift_expr',
              ['arith_expr',
               ['term',
                ['factor', ['power', ['atom', ['NAME', 'b']]]]],
                ['STAR', '*'],
                ['factor', ['power', ['atom', ['NAME', 'c']]]]]],
               ['PLUS', '+'],
               ['term',
                ['factor', ['power', ['atom', ['NAME', 'd']]]]]]]]]]]]]]]]]],
   ['NEWLINE', '']]],
 ['ENDMARKER', '']]
```

Despite its looks, with some tools developed by Jermey H., it's possible to search these trees for specific patterns (sub-trees), extract the sub-tree, manipulate them converting python specific code fragments to blitz code fragments, and then re-insert it in the parse tree. The parser module documentation has some details on how to do this. Traversing the new blitzified tree, writing out the terminal symbols as you go, creates our new blitz++ expression string.

Blitz and NumPy

The other nice discovery in the project is that the data structure used for NumPy arrays and blitz arrays is nearly identical. NumPy stores "strides" as byte offsets and blitz stores them as element offsets, but other than that, they are the same. Further, most of the concept and capabilities of the two libraries are remarkably similar. It is satisfying that two completely different implementations solved the problem with similar basic architectures. It is also fortuitous. The work involved in converting NumPy expressions to blitz expressions was greatly diminished. As an example, consider the code for slicing an array in Python with a stride:

```
>>> a = b[0:4:2] + c
>>> a
[0,2,4]
```

In Blitz it is as follows:

```
Array<2,int> b(10);
Array<2,int> c(3);
// ...
Array<2,int> a = b(Range(0,3,2)) + c;
```

Here the range object works exactly like Python slice objects with the exception that the top index (3) is inclusive where as Python's (4) is exclusive. Other differences include the type declarations in C++ and parentheses instead of brackets for indexing arrays. Currently, `weave.blitz` handles the inclusive/exclusive issue by subtracting one from upper indices during the translation. An alternative that is likely more robust/maintainable in the long run is to write a `PyRange` class that behaves like Python's `range`. This is likely very easy.

The stock blitz also doesn't handle negative indices in ranges. The current implementation of the `blitz()` has a partial solution to this problem. It calculates and index that starts with a '-' sign by subtracting it from the maximum index in the array so that:

```
                upper index limit
                    /-----\
b[:-1] -> b(Range(0,Nb[0]-1-1))
```

This approach fails, however, when the top index is calculated from other values. In the following scenario, if `i+j` evaluates to a negative value, the compiled code will produce incorrect results and could even core-dump. Right now, all calculated indices are assumed to be positive.

```
b[:i-j] -> b(Range(0,i+j))
```

A solution is to calculate all indices up front using if/then to handle the +/- cases. This is a little work and results in more code, so it hasn't been done. I'm holding out to see if blitz++ can be modified to handle negative indexing, but haven't looked into how much effort is involved yet. While it needs fixin', I don't think there is a ton of code where this is an issue.

The actual translation of the Python expressions to blitz expressions is currently a two part process. First, all x:y:z slicing expression are removed from the AST, converted to slice(x,y,z) and re-inserted into the tree. Any math needed on these expressions (subtracting from the maximum index, etc.) are also preformed here. _beg and _end are used as special variables that are defined as blitz::fromBegin and blitz::toEnd.

```
a[i+j:i+j+1,:] = b[2:3,:]
```

becomes a more verbose:

```
a[slice(i+j,i+j+1),slice(_beg,_end)] = b[slice(2,3),slice(_beg,_end)]
```

The second part does a simple string search/replace to convert to a blitz expression with the following translations:

```
slice(_beg,_end) -> _all  # not strictly needed, but cuts down on code.
slice            -> blitz::Range
```

```
[                 -> (
]                 -> )
_stp              -> 1
```

`_all` is defined in the compiled function as `blitz::Range.all()`. These translations could of course happen directly in the syntax tree. But the string replacement is slightly easier. Note that namespaces are maintained in the C++ code to lessen the likelihood of name clashes. Currently no effort is made to detect name clashes. A good rule of thumb is don't use values that start with '_' or 'py_' in compiled expressions and you'll be fine.

Type definitions and coersion

So far we've glossed over the dynamic vs. static typing issue between Python and C++. In Python, the type of value that a variable holds can change through the course of program execution. C/C++, on the other hand, forces you to declare the type of value a variables will hold prior at compile time. `weave.blitz` handles this issue by examining the types of the variables in the expression being executed, and compiling a function for those explicit types. For example:

```
a = ones((5,5),Float32)
b = ones((5,5),Float32)
weave.blitz("a = a + b")
```

When compiling this expression to C++, `weave.blitz` sees that the values for a and b in the local scope have type `Float32`, or 'float' on a 32 bit architecture. As a result, it compiles the function using the float type (no attempt has been made to deal with 64 bit issues).

What happens if you call a compiled function with array types that are different than the ones for which it was originally compiled? No biggie, you'll just have to wait on it to compile a new version for your new types. This doesn't overwrite the old functions, as they are still accessible. See the catalog section in the inline() documentation to see how this is handled. Suffice to say, the mechanism is transparent to the user and behaves like dynamic typing with the occasional wait for compiling newly typed functions.

When working with combined scalar/array operations, the type of the array is *always* used. This is similar to the savespace flag that was recently added to NumPy. This prevents issues with the following expression perhaps unexpectedly being calculated at a higher (more expensive) precision that can occur in Python:

```
>>> a = array((1,2,3),typecode = Float32)
>>> b = a * 2.1 # results in b being a Float64 array.
```

In this example,

```
>>> a = ones((5,5),Float32)
>>> b = ones((5,5),Float32)
>>> weave.blitz("b = a * 2.1")
```

the `2.1` is cast down to a `float` before carrying out the operation. If you really want to force the calculation to be a `double`, define `a` and `b` as `double` arrays.

One other point of note. Currently, you must include both the right hand side and left hand side (assignment side) of your equation in the compiled expression. Also, the array being assigned to must be created prior to calling `weave.blitz`. I'm pretty sure this is easily changed so that a compiled_eval expression can be defined, but no effort has been made to allocate new arrays (and decern their type) on the fly.

Cataloging Compiled Functions

See The Catalog section in the `weave.inline()` documentation.

Checking Array Sizes

Surprisingly, one of the big initial problems with compiled code was making sure all the arrays in an operation were of compatible type. The following case is trivially easy:

```
a = b + c
```

It only requires that arrays `a`, `b`, and `c` have the same shape. However, expressions like:

```
a[i+j:i+j+1,:] = b[2:3,:] + c
```

are not so trivial. Since slicing is involved, the size of the slices, not the input arrays, must be checked. Broadcasting complicates things further because arrays and slices with different dimensions and shapes may be compatible for math operations (broadcasting isn't yet supported by `weave.blitz`). Reductions have a similar effect as their results are different shapes than their input operand. The binary operators in NumPy compare the shapes of their two operands just before they operate on them. This is possible because NumPy treats each operation independently. The intermediate (temporary) arrays created during sub-operations in an expression are tested for the correct shape before they are combined by another operation. Because `weave.blitz` fuses all operations into a single loop, this isn't possible. The shape comparisons must be done and guaranteed compatible before evaluating the expression.

The solution chosen converts input arrays to "dummy arrays" that only represent the dimensions of the arrays, not the data. Binary operations on dummy arrays check that input array sizes are comptible and return a dummy array with the size correct size. Evaluating an expression of dummy arrays traces the changing array sizes through all operations and fails if incompatible array sizes are ever found.

The machinery for this is housed in `weave.size_check`. It basically involves writing a new class (dummy array) and overloading its math operators to calculate the new sizes correctly. All the code is in Python and there is a fair amount of logic (mainly to handle indexing and slicing) so the operation does impose some overhead. For large arrays (ie. 50x50x50), the overhead is negligible compared to evaluating the actual expression. For small arrays (ie. 16x16), the overhead imposed for checking the shapes with this method can cause the `weave.blitz` to be slower than evaluating the expression in Python.

What can be done to reduce the overhead? (1) The size checking code could be moved into C. This would likely remove most of the overhead penalty compared to NumPy (although there is also some calling overhead), but no effort has been made to do this. (2) You can also call `weave.blitz` with `check_size=0` and the size checking isn't done. However, if the sizes aren't compatible, it can cause a core-dump. So, foregoing size_checking isn't advisable until your code is well debugged.

Creating the Extension Module

`weave.blitz` uses the same machinery as `weave.inline` to build the extension module. The only difference is the code included in the function is automatically generated from the NumPy array expression instead of supplied by the user.

1.16.9 Extension Modules

`weave.inline` and `weave.blitz` are high level tools that generate extension modules automatically. Under the covers, they use several classes from `weave.ext_tools` to help generate the extension module. The main two classes are `ext_module` and `ext_function` (I'd like to add `ext_class` and `ext_method` also). These classes simplify the process of generating extension modules by handling most of the "boiler plate" code automatically.

Note: `inline` actually sub-classes `weave.ext_tools.ext_function` to generate slightly different code than the standard `ext_function`. The main difference is that the standard class converts function arguments to C types, while inline always has two arguments, the local and global dicts, and the grabs the variables that need to be convereted to C from these.

A Simple Example

The following simple example demonstrates how to build an extension module within a Python function:

```
# examples/increment_example.py
from weave import ext_tools

def build_increment_ext():
    """ Build a simple extension with functions that increment numbers.
        The extension will be built in the local directory.
    """
    mod = ext_tools.ext_module('increment_ext')

    a = 1 # effectively a type declaration for 'a' in the
          # following functions.

    ext_code = "return_val = Py::new_reference_to(Py::Int(a+1));"
    func = ext_tools.ext_function('increment',ext_code,['a'])
    mod.add_function(func)

    ext_code = "return_val = Py::new_reference_to(Py::Int(a+2));"
    func = ext_tools.ext_function('increment_by_2',ext_code,['a'])
    mod.add_function(func)

    mod.compile()
```

The function `build_increment_ext()` creates an extension module named `increment_ext` and compiles it to a shared library (.so or .pyd) that can be loaded into Python.. `increment_ext` contains two functions, `increment` and `increment_by_2`. The first line of `build_increment_ext()`,

> mod = ext_tools.ext_module('increment_ext')

creates an `ext_module` instance that is ready to have `ext_function` instances added to it. `ext_function` instances are created much with a calling convention similar to `weave.inline()`. The most common call includes a C/C++ code snippet and a list of the arguments for the function. The following:

```
ext_code = "return_val = Py::new_reference_to(Py::Int(a+1));"
func = ext_tools.ext_function('increment',ext_code,['a'])
```

creates a C/C++ extension function that is equivalent to the following Python function:

```
def increment(a):
    return a + 1
```

A second method is also added to the module and then,

```
mod.compile()
```

is called to build the extension module. By default, the module is created in the current working directory. This example is available in the `examples/increment_example.py` file found in the `weave` directory. At the bottom of the file in the module's "main" program, an attempt to import `increment_ext` without building it is made. If this fails (the module doesn't exist in the PYTHONPATH), the module is built by calling `build_increment_ext()`. This approach only takes the time-consuming (a few seconds for this example) process of building the module if it hasn't been built before.

```
if __name__ == "__main__":
    try:
        import increment_ext
    except ImportError:
        build_increment_ext()
```

```
        import increment_ext
    a = 1
    print 'a, a+1:', a, increment_ext.increment(a)
    print 'a, a+2:', a, increment_ext.increment_by_2(a)
```

Note: If we were willing to always pay the penalty of building the C++ code for a module, we could store the SHA-256 checksum of the C++ code along with some information about the compiler, platform, etc. Then, `ext_module.compile()` could try importing the module before it actually compiles it, check the SHA-256 checksum and other meta-data in the imported module with the meta-data of the code it just produced and only compile the code if the module didn't exist or the meta-data didn't match. This would reduce the above code to:

```
if __name__ == "__main__":
    build_increment_ext()

    a = 1
    print 'a, a+1:', a, increment_ext.increment(a)
    print 'a, a+2:', a, increment_ext.increment_by_2(a)
```

Note: There would always be the overhead of building the C++ code, but it would only actually compile the code once. You pay a little in overhead and get cleaner "import" code. Needs some thought.

If you run `increment_example.py` from the command line, you get the following:

```
[eric@n0]$ python increment_example.py
a, a+1: 1 2
a, a+2: 1 3
```

If the module didn't exist before it was run, the module is created. If it did exist, it is just imported and used.

Fibonacci Example

`examples/fibonacci.py` provides a little more complex example of how to use `ext_tools`. Fibonacci numbers are a series of numbers where each number in the series is the sum of the previous two: 1, 1, 2, 3, 5, 8, etc. Here, the first two numbers in the series are taken to be 1. One approach to calculating Fibonacci numbers uses recursive function calls. In Python, it might be written as:

```
def fib(a):
    if a <= 2:
        return 1
    else:
        return fib(a-2) + fib(a-1)
```

In C, the same function would look something like this:

```
int fib(int a)
{
    if(a <= 2)
        return 1;
    else
        return fib(a-2) + fib(a-1);
}
```

Recursion is much faster in C than in Python, so it would be beneficial to use the C version for fibonacci number calculations instead of the Python version. We need an extension function that calls this C function to do this. This is possible by including the above code snippet as "support code" and then calling it from the extension function.

Support code snippets (usually structure definitions, helper functions and the like) are inserted into the extension module C/C++ file before the extension function code. Here is how to build the C version of the fibonacci number generator:

```
def build_fibonacci():
    """ Builds an extension module with fibonacci calculators.
    """
    mod = ext_tools.ext_module('fibonacci_ext')
    a = 1 # this is effectively a type declaration

    # recursive fibonacci in C
    fib_code = """
                   int fib1(int a)
                   {
                       if(a <= 2)
                           return 1;
                       else
                           return fib1(a-2) + fib1(a-1);
                   }
               """
    ext_code = """
                   int val = fib1(a);
                   return_val = Py::new_reference_to(Py::Int(val));
               """
    fib = ext_tools.ext_function('fib',ext_code,['a'])
    fib.customize.add_support_code(fib_code)
    mod.add_function(fib)

    mod.compile()
```

XXX More about custom_info, and what xxx_info instances are good for.

Note: recursion is not the fastest way to calculate fibonacci numbers, but this approach serves nicely for this example.

1.16.10 Customizing Type Conversions – Type Factories

not written

1.16.11 Things I wish `weave` did

It is possible to get name clashes if you uses a variable name that is already defined in a header automatically included (such as `stdio.h`) For instance, if you try to pass in a variable named `stdout`, you'll get a cryptic error report due to the fact that `stdio.h` also defines the name. `weave` should probably try and handle this in some way. Other things...

CHAPTER

TWO

CONTRIBUTING TO SCIPY

This document aims to give an overview of how to contribute to SciPy. It tries to answer commonly asked questions, and provide some insight into how the community process works in practice. Readers who are familiar with the SciPy community and are experienced Python coders may want to jump straight to the git workflow documentation.

Note: You may want to check the latest version of this guide, which is available at: https://github.com/scipy/scipy/blob/master/HACKING.rst.txt

---

2.1 Contributing new code

If you have been working with the scientific Python toolstack for a while, you probably have some code lying around of which you think "this could be useful for others too". Perhaps it's a good idea then to contribute it to SciPy or another open source project. The first question to ask is then, where does this code belong? That question is hard to answer here, so we start with a more specific one: *what code is suitable for putting into SciPy?* Almost all of the new code added to scipy has in common that it's potentially useful in multiple scientific domains and it fits in the scope of existing scipy submodules. In principle new submodules can be added too, but this is far less common. For code that is specific to a single application, there may be an existing project that can use the code. Some scikits (scikit-learn, scikit-image, statsmodels, etc.) are good examples here; they have a narrower focus and because of that more domain-specific code than SciPy.

Now if you have code that you would like to see included in SciPy, how do you go about it? After checking that your code can be distributed in SciPy under a compatible license (see FAQ for details), the first step is to discuss on the scipy-dev mailing list. All new features, as well as changes to existing code, are discussed and decided on there. You can, and probably should, already start this discussion before your code is finished.

Assuming the outcome of the discussion on the mailing list is positive and you have a function or piece of code that does what you need it to do, what next? Before code is added to SciPy, it at least has to have good documentation, unit tests and correct code style.

1. ***Unit tests*** In principle you should aim to create unit tests that exercise all the code that you are adding. This gives some degree of confidence that your code runs correctly, also on Python versions and hardware or OSes that you don't have available yourself. An extensive description of how to write unit tests is given in the NumPy testing guidelines.

2. ***Documentation***
   Clear and complete documentation is essential in order for users to be able to find and understand the code. Documentation for individual functions and classes – which includes at least a basic description, type and meaning of all parameters and returns values, and usage examples in doctest format – is put in docstrings. Those docstrings can be read within the interpreter, and are compiled into a reference guide in html and pdf format. Higher-level documentation for key (areas of) functionality is provided in tutorial format and/or in module docstrings. A guide on how to write documentation is given in how to document.

3. ***Code style*** Uniformity of style in which code is written is important to others trying to understand the code. SciPy follows the standard Python guidelines for code style, PEP8. In order to check that your code conforms to PEP8, you can use the pep8 package style checker. Most IDEs and text editors have settings that can help you follow PEP8, for example by translating tabs by four spaces. Using pyflakes to check your code is also a good idea.

At the end of this document a checklist is given that may help to check if your code fulfills all requirements for inclusion in SciPy.

Another question you may have is: *where exactly do I put my code*? To answer this, it is useful to understand how the SciPy public API (application programming interface) is defined. For most modules the API is two levels deep, which means your new function should appear as `scipy.submodule.my_new_func`. `my_new_func` can be put in an existing or new file under `/scipy/<submodule>/`, its name is added to the `__all__` list in that file (which lists all public functions in the file), and those public functions are then imported in `/scipy/<submodule>/__init__.py`. Any private functions/classes should have a leading underscore (_) in their name. A more detailed description of what the public API of SciPy is, is given in SciPy API.

Once you think your code is ready for inclusion in SciPy, you can send a pull request (PR) on Github. We won't go into the details of how to work with git here, this is described well in the git workflow section of the NumPy documentation and on the Github help pages. When you send the PR for a new feature, be sure to also mention this on the scipy-dev mailing list. This can prompt interested people to help review your PR. Assuming that you already got positive feedback before on the general idea of your code/feature, the purpose of the code review is to ensure that the code is correct, efficient and meets the requirements outlined above. In many cases the code review happens relatively quickly, but it's possible that it stalls. If you have addressed all feedback already given, it's perfectly fine to ask on the mailing list again for review (after a reasonable amount of time, say a couple of weeks, has passed). Once the review is completed, the PR is merged into the "master" branch of SciPy.

The above describes the requirements and process for adding code to SciPy. It doesn't yet answer the question though how decisions are made exactly. The basic answer is: decisions are made by consensus, by everyone who chooses to participate in the discussion on the mailing list. This includes developers, other users and yourself. Aiming for consensus in the discussion is important – SciPy is a project by and for the scientific Python community. In those rare cases that agreement cannot be reached, the maintainers of the module in question can decide the issue.

2.2 Contributing by helping maintain existing code

The previous section talked specifically about adding new functionality to SciPy. A large part of that discussion also applies to maintenance of existing code. Maintenance means fixing bugs, improving code quality or style, documenting existing functionality better, adding missing unit tests, keeping build scripts up-to-date, etc. The SciPy issue list contains all reported bugs, build/documentation issues, etc. Fixing issues helps improve the overall quality of SciPy, and is also a good way of getting familiar with the project. You may also want to fix a bug because you ran into it and need the function in question to work correctly.

The discussion on code style and unit testing above applies equally to bug fixes. It is usually best to start by writing a unit test that shows the problem, i.e. it should pass but doesn't. Once you have that, you can fix the code so that the test does pass. That should be enough to send a PR for this issue. Unlike when adding new code, discussing this on the mailing list may not be necessary - if the old behavior of the code is clearly incorrect, no one will object to having it fixed. It may be necessary to add some warning or deprecation message for the changed behavior. This should be part of the review process.

2.3 Other ways to contribute

There are many ways to contribute other than contributing code. Participating in discussions on the scipy-user and scipy-dev *mailing lists* is a contribution in itself. The scipy.org *website* contains a lot of information on the SciPy community and can always use a new pair of hands.

2.4 Recommended development setup

Since Scipy contains parts written in C, C++, and Fortran that need to be compiled before use, make sure you have the necessary compilers and Python development headers installed. Having compiled code also means that importing Scipy from the development sources needs some additional steps, which are explained below.

First fork a copy of the main Scipy repository in Github onto your own account and then create your local repository via:

```
$ git clone git@github.com:YOURUSERNAME/scipy.git scipy
$ cd scipy
$ git remote add upstream git://github.com/scipy/scipy.git
```

To build the development version of Scipy and run tests, spawn interactive shells with the Python import paths properly set up etc., do one of:

```
$ python runtests.py -v
$ python runtests.py -v -s optimize
$ python runtests.py -v -t scipy/special/tests/test_basic.py:test_xlogy
$ python runtests.py --ipython
$ python runtests.py --python somescript.py
$ python runtests.py --bench
```

This builds Scipy first, so the first time it may take some time. If you specify `-n`, the tests are run against the version of Scipy (if any) found on current PYTHONPATH.

Using `runtests.py` is the recommended approach to running tests. There are also a number of alternatives to it, for example in-place build or installing to a virtualenv. See the FAQ below for details.

Some of the tests in Scipy are very slow and need to be separately enabled. See the FAQ below for details.

2.5 SciPy structure

All SciPy modules should follow the following conventions. In the following, a *SciPy module* is defined as a Python package, say `yyy`, that is located in the scipy/ directory.

- Ideally, each SciPy module should be as self-contained as possible. That is, it should have minimal dependencies on other packages or modules. Even dependencies on other SciPy modules should be kept to a minimum. A dependency on NumPy is of course assumed.
- Directory `yyy/` contains:
  - A file `setup.py` that defines `configuration(parent_package='',top_path=None)` function for `numpy.distutils`.
  - A directory `tests/` that contains files `test_<name>.py` corresponding to modules `yyy/<name>{.py,.so,/}`.
- Private modules should be prefixed with an underscore _, for instance `yyy/_somemodule.py`.
- User-visible functions should have good documentation following the Numpy documentation style, see how to document
- The `__init__.py` of the module should contain the main reference documentation in its docstring. This is connected to the Sphinx documentation under `doc/` via Sphinx's automodule directive.

> The reference documentation should first give a categorized list of the contents of the module using `autosummary::` directives, and after that explain points essential for understanding the use of the module.
>
> Tutorial-style documentation with extensive examples should be separate, and put under `doc/source/tutorial/`

See the existing Scipy submodules for guidance.

For further details on Numpy distutils, see:

> https://github.com/numpy/numpy/blob/master/doc/DISTUTILS.rst.txt

2.6 Useful links, FAQ, checklist

2.6.1 Checklist before submitting a PR

- Are there unit tests with good code coverage?
- Do all public function have docstrings including examples?
- Is the code style correct (PEP8, pyflakes)
- Is the new functionality tagged with `.. versionadded:: X.Y.Z` (with X.Y.Z the version number of the next release - can be found in setup.py)?
- Is the new functionality mentioned in the release notes of the next release?
- Is the new functionality added to the reference guide?
- In case of larger additions, is there a tutorial or more extensive module-level description?
- In case compiled code is added, is it integrated correctly via setup.py (and preferably also Bento configuration files - bento.info and bscript)?
- If you are a first-time contributor, did you add yourself to THANKS.txt? Please note that this is perfectly normal and desirable - the aim is to give every single contributor credit, and if you don't add yourself it's simply extra work for the reviewer (or worse, the reviewer may forget).
- Did you check that the code can be distributed under a BSD license?

2.6.2 Useful SciPy documents

- The how to document guidelines
- NumPy/SciPy testing guidelines
- SciPy API
- SciPy maintainers
- NumPy/SciPy git workflow

2.6.3 FAQ

I based my code on existing Matlab/R/... code I found online, is this OK?

It depends. SciPy is distributed under a BSD license, so if the code that you based your code on is also BSD licensed or has a BSD-compatible license (MIT, Apache, ...) then it's OK. Code which is GPL-licensed, has no clear license, requires citation or is free for academic use only can't be included in SciPy. Therefore if you copied existing code with such a license or made a direct translation to Python of it, your code can't be included. See also license compatibility.

Why is SciPy under the BSD license and not, say, the GPL?

Like Python, SciPy uses a "permissive" open source license, which allows proprietary re-use. While this allows companies to use and modify the software without giving anything back, it is felt that the larger user base results in more contributions overall, and companies often publish their modifications anyway, without being required to. See John Hunter's BSD pitch.

How do I set up a development version of SciPy in parallel to a released version that I use to do my job/research?

One simple way to achieve this is to install the released version in site-packages, by using a binary installer or pip for example, and set up the development version in a virtualenv. First install virtualenv (optionally use virtualenvwrapper), then create your virtualenv (named scipy-dev here) with:

```
$ virtualenv scipy-dev
```

Now, whenever you want to switch to the virtual environment, you can use the command `source scipy-dev/bin/activate`, and `deactivate` to exit from the virtual environment and back to your previous shell. With scipy-dev activated, install first Scipy's dependencies:

```
$ pip install Numpy Nose Cython
```

After that, you can install a development version of Scipy, for example via:

```
$ python setup.py install
```

The installation goes to the virtual environment.

How do I set up an in-place build for development

For development, you can set up an in-place build so that changes made to `.py` files have effect without rebuild. First, run:

```
$ python setup.py build_ext -i
```

Then you need to point your PYTHONPATH environment variable to this directory. Some IDEs (Spyder for example) have utilities to manage PYTHONPATH. On Linux and OSX, you can run the command:

```
$ export PYTHONPATH=$PWD
```

and on Windows

> $ set PYTHONPATH=/path/to/scipy

Now editing a Python source file in SciPy allows you to immediately test and use your changes (in `.py` files), by simply restarting the interpreter.

Can I use a programming language other than Python to speed up my code?

Yes. The languages used in SciPy are Python, Cython, C, C++ and Fortran. All of these have their pros and cons. If Python really doesn't offer enough performance, one of those languages can be used. Important concerns when using compiled languages are maintainability and portability. For maintainability, Cython is clearly preferred over C/C++/Fortran. Cython and C are more portable than C++/Fortran. A lot of the existing C and Fortran code in SciPy is older, battle-tested code that was only wrapped in (but not specifically written for) Python/SciPy. Therefore the basic advice is: use Cython. If there's specific reasons why C/C++/Fortran should be preferred, please discuss those reasons first.

How do I debug code written in C/C++/Fortran inside Scipy?

The easiest way to do this is to first write a Python script that invokes the C code whose execution you want to debug. For instance `mytest.py`:

```
from scipy.special import hyp2f1
print(hyp2f1(5.0, 1.0, -1.8, 0.95))
```

Now, you can run:

```
gdb --args python runtests.py -g --python mytest.py
```

If you didn't compile with debug symbols enabled before, remove the `build` directory first. While in the debugger:

```
(gdb) break cephes_hyp2f1
(gdb) run
```

The execution will now stop at the corresponding C function and you can step through it as usual. Instead of plain `gdb` you can of course use your favourite alternative debugger; run it on the `python` binary with arguments `runtests.py -g --python mytest.py`.

How do I enable additional tests in Scipy?

Some of the tests in Scipy's test suite are very slow and not enabled by default. You can run the full suite via:

```
$ python runtests.py -g -m full
```

This invokes the test suite `import scipy; scipy.test("full")`, enabling also slow tests.

There is an additional level of very slow tests (several minutes), which are disabled also in this case. They can be enabled by setting the environment variable `SCIPY_XSLOW=1` before running the test suite.

How do I write tests with test generators?

The Nose test framework supports so-called test generators, which can come useful if you need to have multiple tests where just a parameter changes. Using test generators so that they are more useful than harmful is tricky, and we recommend the following pattern:

```
def test_something():
    some_array = (...)

    def check(some_param):
        c = compute_result(some_array, some_param)
        known_result = (...)
        assert_allclose(c, known_result)

    for some_param in ['a', 'b', 'c']:
        yield check, some_param
```

We require the following:

- All asserts and all computation that is tested must only be reached after a yield. (Rationale: the generator body is part of no test, and a failure in it will show neither the test name nor for what parameters the test failed.)
- Arrays must not be passed as yield parameters. Either use variables from outer scope (eg. with some index passed to yield), or capsulate test data to a class with a sensible `__repr__`. (Rationale: Nose truncates the printed form of arrays in test output, and this makes it impossible to know for what parameters a test failed. Arrays are big, and clutter test output unnecessarily.)
- Test generators cannot be used in test classes inheriting from unittest.TestCase; either use object as base class, or use standalone test functions. (Rationale: Nose does not run test generators in TestCase-inheriting classes.)

If in doubt, do not use test generators. You can track for what parameter things failed also by passing `err_msg=repr((param1, param2, ...))` to the various assert functions.

CHAPTER

THREE

API - IMPORTING FROM SCIPY

In Python the distinction between what is the public API of a library and what are private implementation details is not always clear. Unlike in other languages like Java, it is possible in Python to access "private" function or objects. Occasionally this may be convenient, but be aware that if you do so your code may break without warning in future releases. Some widely understood rules for what is and isn't public in Python are:

- Methods / functions / classes and module attributes whose names begin with a leading underscore are private.
- If a class name begins with a leading underscore none of its members are public, whether or not they begin with a leading underscore.
- If a module name in a package begins with a leading underscore none of its members are public, whether or not they begin with a leading underscore.
- If a module or package defines `__all__` that authoritatively defines the public interface.
- If a module or package doesn't define `__all__` then all names that don't start with a leading underscore are public.

Note: Reading the above guidelines one could draw the conclusion that every private module or object starts with an underscore. This is not the case; the presence of underscores do mark something as private, but the absence of underscores do not mark something as public.

In Scipy there are modules whose names don't start with an underscore, but that should be considered private. To clarify which modules these are we define below what the public API is for Scipy, and give some recommendations for how to import modules/functions/objects from Scipy.

3.1 Guidelines for importing functions from Scipy

The scipy namespace itself only contains functions imported from numpy. These functions still exist for backwards compatibility, but should be imported from numpy directly.

Everything in the namespaces of scipy submodules is public. In general, it is recommended to import functions from submodule namespaces. For example, the function `curve_fit` (defined in scipy/optimize/minpack.py) should be imported like this:

```python
from scipy import optimize
result = optimize.curve_fit(...)
```

This form of importing submodules is preferred for all submodules except `scipy.io` (because `io` is also the name of a module in the Python stdlib):

```
from scipy import interpolate
from scipy import integrate
import scipy.io as spio
```

In some cases, the public API is one level deeper. For example the `scipy.sparse.linalg` module is public, and the functions it contains are not available in the `scipy.sparse` namespace. Sometimes it may result in more easily understandable code if functions are imported from one level deeper. For example, in the following it is immediately clear that `lomax` is a distribution if the second form is chosen:

```
# first form
from scipy import stats
stats.lomax(...)

# second form
from scipy.stats import distributions
distributions.lomax(...)
```

In that case the second form can be chosen, **if** it is documented in the next section that the submodule in question is public.

3.2 API definition

Every submodule listed below is public. That means that these submodules are unlikely to be renamed or changed in an incompatible way, and if that is necessary a deprecation warning will be raised for one Scipy release before the change is made.

- scipy.cluster
  - vq
  - hierarchy
- scipy.constants
- scipy.fftpack
- scipy.integrate
- scipy.interpolate
- scipy.io
  - arff
  - harwell_boeing
  - idl
  - matlab
  - netcdf
  - wavfile
- scipy.linalg
  - scipy.linalg.blas
  - scipy.linalg.lapack
  - scipy.linalg.interpolative
- scipy.misc

- scipy.ndimage
- scipy.odr
- scipy.optimize
- scipy.signal
- scipy.sparse
  - linalg
  - csgraph
- scipy.spatial
  - distance
- scipy.special
- scipy.stats
  - distributions
  - mstats
- scipy.weave

CHAPTER

FOUR

RELEASE NOTES

4.1 SciPy 0.16.0 Release Notes

Contents

SciPy 0.16.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.6.2 or greater.

Highlights of this release include:

- A Cython API for BLAS/LAPACK in `scipy.linalg`
- A new benchmark suite. It's now straightforward to add new benchmarks, and they're routinely included with performance enhancement PRs.
- Support for the second order sections (SOS) format in `scipy.signal`.

4.1.1 New features

Benchmark suite

The benchmark suite has switched to using Airspeed Velocity for benchmarking. You can run the suite locally via `python runtests.py --bench`. For more details, see `benchmarks/README.rst`.

`scipy.linalg` improvements

A full set of Cython wrappers for BLAS and LAPACK has been added in the modules `scipy.linalg.cython_blas` and `scipy.linalg.cython_lapack`. In Cython, these wrappers can now be cimported from their corresponding modules and used without linking directly against BLAS or LAPACK.

The functions `scipy.linalg.qr_delete`, `scipy.linalg.qr_insert` and `scipy.linalg.qr_update` for updating QR decompositions were added.

The function `scipy.linalg.solve_circulant` solves a linear system with a circulant coefficient matrix.

The function `scipy.linalg.invpascal` computes the inverse of a Pascal matrix.

The function `scipy.linalg.solve_toeplitz`, a Levinson-Durbin Toeplitz solver, was added.

Added wrapper for potentially useful LAPACK function `*lasd4`. It computes the square root of the i-th updated eigenvalue of a positive symmetric rank-one modification to a positive diagonal matrix. See its LAPACK documentation and unit tests for it to get more info.

Added two extra wrappers for LAPACK least-square solvers. Namely, they are `*gelsd` and `*gelsy`.

Wrappers for the LAPACK `*lange` functions, which calculate various matrix norms, were added.

Wrappers for `*gtsv` and `*ptsv`, which solve `A*X = B` for tri-diagonal matrix `A`, were added.

`scipy.signal` improvements

Support for second order sections (SOS) as a format for IIR filters was added. The new functions are:

- `scipy.signal.sosfilt`
- `scipy.signal.sosfilt_zi`,
- `scipy.signal.sos2tf`
- `scipy.signal.sos2zpk`
- `scipy.signal.tf2sos`
- `scipy.signal.zpk2sos`.

Additionally, the filter design functions *iirdesign*, *iirfilter*, *butter*, *cheby1*, *cheby2*, *ellip*, and *bessel* can return the filter in the SOS format.

The function `scipy.signal.place_poles`, which provides two methods to place poles for linear systems, was added.

The option to use Gustafsson's method for choosing the initial conditions of the forward and backward passes was added to `scipy.signal.filtfilt`.

New classes `TransferFunction`, `StateSpace` and `ZerosPolesGain` were added. These classes are now returned when instantiating `scipy.signal.lti`. Conversion between those classes can be done explicitly now.

An exponential (Poisson) window was added as `scipy.signal.exponential`, and a Tukey window was added as `scipy.signal.tukey`.

The function for computing digital filter group delay was added as `scipy.signal.group_delay`.

The functionality for spectral analysis and spectral density estimation has been significantly improved: `scipy.signal.welch` became ~8x faster and the functions `scipy.signal.spectrogram`, `scipy.signal.coherence` and `scipy.signal.csd` (cross-spectral density) were added.

`scipy.signal.lsim` was rewritten - all known issues are fixed, so this function can now be used instead of `lsim2`; `lsim` is orders of magnitude faster than `lsim2` in most cases.

`scipy.sparse` improvements

The function *scipy.sparse.norm*, which computes sparse matrix norms, was added.

The function `scipy.sparse.random`, which allows to draw random variates from an arbitrary distribution, was added.

`scipy.spatial` improvements

`scipy.spatial.cKDTree` has seen a major rewrite, which improved the performance of the `query` method significantly, added support for parallel queries, pickling, and options that affect the tree layout. See pull request 4374 for more details.

The function `scipy.spatial.procrustes` for Procrustes analysis (statistical shape analysis) was added.

`scipy.stats` improvements

The Wishart distribution and its inverse have been added, as `scipy.stats.wishart` and `scipy.stats.invwishart`.

The Exponentially Modified Normal distribution has been added as `scipy.stats.exponnorm`.

The Generalized Normal distribution has been added as `scipy.stats.gennorm`.

All distributions now contain a `random_state` property and allow specifying a specific `numpy.random.RandomState` random number generator when generating random variates.

Many statistical tests and other `scipy.stats` functions that have multiple return values now return `namedtuples`. See pull request 4709 for details.

`scipy.optimize` improvements

A new derivative-free method DF-SANE has been added to the nonlinear equation system solving function `scipy.optimize.root`.

4.1.2 Deprecated features

`scipy.stats.pdf_fromgamma` is deprecated. This function was undocumented, untested and rarely used. Statsmodels provides equivalent functionality with `statsmodels.distributions.ExpandedNormal`.

`scipy.stats.fastsort` is deprecated. This function is unnecessary, `numpy.argsort` can be used instead.

`scipy.stats.signaltonoise` and `scipy.stats.mstats.signaltonoise` are deprecated. These functions did not belong in `scipy.stats` and are rarely used. See issue #609 for details.

`scipy.stats.histogram2` is deprecated. This function is unnecessary, `numpy.histogram2d` can be used instead.

4.1.3 Backwards incompatible changes

The deprecated global optimizer `scipy.optimize.anneal` was removed.

The following deprecated modules have been removed: `scipy.lib.blas`, `scipy.lib.lapack`, `scipy.linalg.cblas`, `scipy.linalg.fblas`, `scipy.linalg.clapack`, `scipy.linalg.flapack`. They had been deprecated since Scipy 0.12.0, the functionality should be accessed as `scipy.linalg.blas` and `scipy.linalg.lapack`.

The deprecated function `scipy.special.all_mat` has been removed.

The deprecated functions `fprob`, `ksprob`, `zprob`, `randwcdf` and `randwppf` have been removed from `scipy.stats`.

4.1.4 Other changes

The version numbering for development builds has been updated to comply with PEP 440.

Building with `python setup.py develop` is now supported.

4.1.5 Authors

- @axiru +
- @endolith
- Elliott Sales de Andrade +
- Anne Archibald
- Yoshiki Vázquez Baeza +
- Sylvain Bellemare
- Felix Berkenkamp +
- Raoul Bourquin +
- Matthew Brett
- Per Brodtkorb
- Christian Brueffer
- Lars Buitinck
- Evgeni Burovski
- Steven Byrnes
- CJ Carey
- George Castillo +
- Alex Conley +
- Liam Damewood +
- Rupak Das +
- Abraham Escalante +
- Matthias Feurer +
- Eric Firing +

- Clark Fitzgerald
- Chad Fulton
- André Gaul
- Andreea Georgescu +
- Christoph Gohlke
- Andrey Golovizin +
- Ralf Gommers
- J.J. Green +
- Alex Griffing
- Alexander Grigorievskiy +
- Hans Moritz Gunther +
- Jonas Hahnfeld +
- Charles Harris
- Ian Henriksen
- Andreas Hilboll
- Åsmund Hjulstad +
- Jan Schlüter +
- Janko Slavič +
- Daniel Jensen +
- Johannes Ballé +
- Terry Jones +
- Amato Kasahara +
- Eric Larson
- Denis Laxalde
- Antony Lee
- Gregory R. Lee
- Perry Lee +
- Loïc Estève
- Martin Manns +
- Eric Martin +
- Matěj Kocián +
- Andreas Mayer +
- Nikolay Mayorov +
- Robert McGibbon +
- Sturla Molden
- Nicola Montecchio +

- Eric Moore
- Jamie Morton +
- Nikolas Moya +
- Maniteja Nandana +
- Andrew Nelson
- Joel Nothman
- Aldrian Obaja
- Regina Ongowarsito +
- Paul Ortyl +
- Pedro López-Adeva Fernández-Layos +
- Stefan Peterson +
- Irvin Probst +
- Eric Quintero +
- John David Reaver +
- Juha Remes +
- Thomas Robitaille
- Clancy Rowley +
- Tobias Schmidt +
- Skipper Seabold
- Aman Singh +
- Eric Soroos
- Valentine Svensson +
- Julian Taylor
- Aman Thakral +
- Helmut Toplitzer +
- Fukumu Tsutsumi +
- Anastasiia Tsyplia +
- Jacob Vanderplas
- Pauli Virtanen
- Matteo Visconti +
- Warren Weckesser
- Florian Wilhelm +
- Nathan Woods
- Haochen Wu +
- Daan Wynen +

A total of 93 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.16.0

- #1063: Implement a whishart distribution (Trac #536)
- #1885: Rbf: floating point warnings - possible bug (Trac #1360)
- #2020: Rbf default epsilon too large (Trac #1495)
- #2325: extending distributions, hypergeom, to degenerate cases (Trac...
- #3502: [ENH] linalg.hessenberg should use ORGHR for calc_q=True
- #3603: Passing array as window into signal.resample() fails
- #3675: Intermittent failures for signal.slepian on Windows
- #3742: Pchipinterpolator inconvenient as ppoly
- #3786: add procrustes?
- #3798: scipy.io.savemat fails for empty dicts
- #3975: Use RandomState in scipy.stats
- #4022: savemat incorrectly saves logical arrays
- #4028: scipy.stats.geom.logpmf(1,1) returns nan. The correct value is...
- #4030: simplify scipy.stats.betaprime.cdf
- #4031: improve accuracy of scipy.stats.gompertz distribution for small...
- #4033: improve accuracy of scipy.stats.lomax distribution for small...
- #4034: improve accuracy of scipy.stats.rayleigh distribution for large...
- #4035: improve accuracy of scipy.stats.truncexpon distribution for small...
- #4081: Error when reading matlab file: buffer is too small for requested...
- #4100: Why does qr(a, lwork=0) not fail?
- #4134: scipy.stats: rv_frozen has no expect() method
- #4204: Please add docstring to scipy.optimize.RootResults
- #4206: Wrap LAPACK tridiagonal solve routine *gtsv*
- #4208: Empty sparse matrices written to MAT file cannot be read by MATLAB
- #4217: use a TravisCI configuration with numpy built with NPY_RELAXED_STRIDES_CHECKING=1
- #4282: integrate.odeint raises an exception when full_output=1 and the...
- #4301: scipy and numpy version names do not follow pep 440
- #4355: PPoly.antiderivative() produces incorrect output
- #4391: spsolve becomes extremely slow with large b matrix
- #4393: Documentation glitsch in sparse.linalg.spilu
- #4408: Vector-valued constraints in minimize() et al
- #4412: Documentation of scipy.signal.cwt error

- #4428: dok.__setitem__ problem with negative indices
- #4434: Incomplete documentation for sparse.linalg.spsolve
- #4438: linprog() documentation example wrong
- #4445: Typo in scipy.special.expit doc
- #4467: Documentation Error in scipy.optimize options for TNC
- #4492: solve_toeplitz benchmark is bitrotting already
- #4506: lobpcg/sparse performance regression Jun 2014?
- #4520: g77_abi_wrappers needed on Linux for MKL as well
- #4521: Broken check in uses_mkl for newer versions of the library
- #4523: rbf with gaussian kernel seems to produce more noise than original...
- #4526: error in site documentation for poisson.pmf() method
- #4527: KDTree example doesn't work in Python 3
- #4550: `scipy.stats.mode` - UnboundLocalError on empty sequence
- #4554: filter out convergence warnings in optimization tests
- #4565: odeint messages
- #4569: remez: "ValueError: Failure to converge after 25 iterations....
- #4582: DOC: optimize: _minimize_scalar_brent does not have a disp option
- #4585: DOC: Erroneous latex-related characters in tutorial.
- #4590: sparse.linalg.svds should throw an exception if which not in...
- #4594: scipy.optimize.linprog IndexError when a callback is providen
- #4596: scipy.linalg.block_diag misbehavior with empty array inputs (v0.13.3)
- #4599: scipy.integrate.nquad should call _OptFunc when called with only...
- #4612: Crash in signal.lfilter on nd input with wrong shaped zi
- #4613: scipy.io.readsav error on reading sav file
- #4673: scipy.interpolate.RectBivariateSpline construction locks PyQt...
- #4681: Broadcasting in signal.lfilter still not quite right.
- #4705: kmeans k_or_guess parameter error if guess is not square array
- #4719: Build failure on 14.04.2
- #4724: GenGamma _munp function fails due to overflow
- #4726: FAIL: test_cobyla.test_vector_constraints
- #4734: Failing tests in stats with numpy master.
- #4736: qr_update bug or incompatibility with numpy 1.10?
- #4746: linprog returns solution violating equality constraint
- #4757: optimize.leastsq docstring mismatch
- #4774: Update contributor list for v0.16
- #4779: circmean and others do not appear in the documentation

- #4788: problems with scipy sparse linalg isolve iterative.py when complex
- #4791: BUG: scipy.spatial: incremental Voronoi doesn't increase size...

Pull requests for 0.16.0

- #3116: sparse: enhancements for DIA format
- #3157: ENH: linalg: add the function 'solve_circulant' for solving a...
- #3442: ENH: signal: Add Gustafsson's method as an option for the filtfilt...
- #3679: WIP: fix sporadic slepian failures
- #3680: Some cleanups in stats
- #3717: ENH: Add second-order sections filtering
- #3741: Dltisys changes
- #3956: add note to scipy.signal.resample about prime sample numbers
- #3980: Add check_finite flag to UnivariateSpline
- #3996: MAINT: stricter linalg argument checking
- #4001: BUG: numerical precision in dirichlet
- #4012: ENH: linalg: Add a function to compute the inverse of a Pascal...
- #4021: ENH: Cython api for lapack and blas
- #4089: Fixes for various PEP8 issues.
- #4116: MAINT: fitpack: trim down compiler warnings (unused labels, variables)
- #4129: ENH: stats: add a random_state property to distributions
- #4135: ENH: Add Wishart and inverse Wishart distributions
- #4195: improve the interpolate docs
- #4200: ENH: Add t-test from descriptive stats function.
- #4202: Dendrogram threshold color
- #4205: BLD: fix a number of Bento build warnings.
- #4211: add an ufunc for the inverse Box-Cox transfrom
- #4212: MRG:fix for gh-4208
- #4213: ENH: specific warning if matlab file is empty
- #4215: Issue #4209: splprep documentation updated to reflect dimensional...
- #4219: DOC: silence several Sphinx warnings when building the docs
- #4223: MAINT: remove two redundant lines of code
- #4226: try forcing the numpy rebuild with relaxed strides
- #4228: BLD: some updates to Bento config files and docs. Closes gh-3978.
- #4232: wrong references in the docs
- #4242: DOC: change example sample spacing
- #4245: Arff fixes

- #4246: MAINT: C fixes
- #4247: MAINT: remove some unused code
- #4249: Add routines for updating QR decompositions
- #4250: MAINT: Some pyflakes-driven cleanup in linalg and sparse
- #4252: MAINT trim away >10 kLOC of generated C code
- #4253: TST: stop shadowing ellip* tests vs boost data
- #4254: MAINT: special: use NPY_PI, not M_PI
- #4255: DOC: INSTALL: use Py3-compatible print syntax, and don't mention...
- #4256: ENH: spatial: reimplement cdist_cosine using np.dot
- #4258: BUG: io.arff #4429 #2088
- #4261: MAINT: signal: PEP8 and related style clean up.
- #4262: BUG: newton_krylov() was ignoring norm_tol argument, closes #4259
- #4263: MAINT: clean up test noise and optimize tests for docstrings...
- #4266: MAINT: io: Give an informative error when attempting to read...
- #4268: MAINT: fftpack benchmark integer division vs true division
- #4269: MAINT: avoid shadowing the eigvals function
- #4272: BUG: sparse: Fix bench_sparse.py
- #4276: DOC: remove confusing parts of the documentation related to writing...
- #4281: Sparse matrix multiplication: only convert array if needed (with...
- #4284: BUG: integrate: odeint crashed when the integration time was...
- #4286: MRG: fix matlab output type of logical array
- #4287: DEP: deprecate stats.pdf_fromgamma. Closes gh-699.
- #4291: DOC: linalg: fix layout in cholesky_banded docstring
- #4292: BUG: allow empty dict as proxy for empty struct
- #4293: MAINT: != -> not_equal in hamming distance implementation
- #4295: Pole placement
- #4296: MAINT: some cleanups in tests of several modules
- #4302: ENH: Solve toeplitz linear systems
- #4306: Add benchmark for conjugate gradient solver.
- #4307: BLD: PEP 440
- #4310: BUG: make stats.geom.logpmf(1,1) return 0.0 instead of nan
- #4311: TST: restore a test that uses slogdet now that we have dropped...
- #4313: Some minor fixes for stats.wishart addition.
- #4315: MAINT: drop numpy 1.5 compatibility code in sparse matrix tests
- #4318: ENH: Add random_state to multivariate distributions
- #4319: MAINT: fix hamming distance regression for exotic arrays, with...

- #4320: TST: a few changes like self.assertTrue(x == y, message) -> assert_equal(x,...
- #4321: TST: more changes like self.assertTrue(x == y, message) -> assert_equal(x,...
- #4322: TST: in test_signaltools, changes like self.assertTrue(x == y,...
- #4323: MAINT: clean up benchmarks so they can all be run as single files.
- #4324: Add more detailed committer guidelines, update MAINTAINERS.txt
- #4326: TST: use numpy.testing in test_hierarchy.py
- #4329: MAINT: stats: rename check_random_state test function
- #4330: Update distance tests
- #4333: MAINT: import comb, factorial from scipy.special, not scipy.misc
- #4338: TST: more conversions from nose to numpy.testing
- #4339: MAINT: remove the deprecated all_mat function from special_matrices.py
- #4340: add several features to frozen distributions
- #4344: BUG: Fix/test invalid lwork param in qr
- #4345: Fix test noise visible with Python 3.x
- #4347: Remove deprecated blas/lapack imports, rename lib to _lib
- #4349: DOC: add a nontrivial example to stats.binned_statistic.
- #4350: MAINT: remove optimize.anneal for 0.16.0 (was deprecated in 0.14.0).
- #4351: MAINT: fix usage of deprecated Numpy C API in optimize...
- #4352: MAINT: fix a number of special test failures
- #4353: implement cdf for betaprime distribution
- #4357: BUG: piecewise polynomial antiderivative
- #4358: BUG: integrate: fix handling of banded Jacobians in odeint, plus...
- #4359: MAINT: remove a code path taken for Python version < 2.5
- #4360: MAINT: stats.mstats: Remove some unused variables (thanks, pyflakes).
- #4362: Removed erroneous reference to smoothing parameter #4072
- #4363: MAINT: interpolate: clean up in fitpack.py
- #4364: MAINT: lib: don’t export “partial” from decorator
- #4365: svdvals now returns a length-0 sequence of singular values given...
- #4367: DOC: slightly improve TeX rendering of wishart/invwishart docstring
- #4373: ENH: wrap gtsv and ptsv for solve_banded and solveh_banded.
- #4374: ENH: Enhancements to spatial.cKDTree
- #4376: BF: fix reading off-spec matlab logical sparse
- #4377: MAINT: integrate: Clean up some Fortran test code.
- #4378: MAINT: fix usage of deprecated Numpy C API in signal
- #4380: MAINT: scipy.optimize, removing further anneal references
- #4381: ENH: Make DCT and DST accept int and complex types like fft

- #4392: ENH: optimize: add DF-SANE nonlinear derivative-free solver
- #4394: Make reordering algorithms 64-bit clean
- #4396: BUG: bundle cblas.h in Accelerate ABI wrappers to enable compilation...
- #4398: FIX pdist bug where wminkowski's w.dtype != double
- #4402: BUG: fix stat.hypergeom argcheck
- #4404: MAINT: Fill in the full symmetric squareform in the C loop
- #4405: BUG: avoid X += X.T (refs #4401)
- #4407: improved accuracy of gompertz distribution for small x
- #4414: DOC:fix error in scipy.signal.cwt documentation.
- #4415: ENH: Improve accuracy of lomax for small x.
- #4416: DOC: correct a parameter name in docstring of SuperLU.solve....
- #4419: Restore scipy.linalg.calc_lwork also in master
- #4420: fix a performance issue with a sparse solver
- #4423: ENH: improve rayleigh accuracy for large x.
- #4424: BUG: optimize.minimize: fix overflow issue with integer x0 input.
- #4425: ENH: Improve accuracy of truncexpon for small x
- #4426: ENH: improve rayleigh accuracy for large x.
- #4427: MAINT: optimize: cleanup of TNC code
- #4429: BLD: fix build failure with numpy 1.7.x and 1.8.x.
- #4430: BUG: fix a sparse.dok_matrix set/get copy-paste bug
- #4433: Update _minimize.py
- #4435: ENH: release GIL around batch distance computations
- #4436: Fixed incomplete documentation for spsolve
- #4439: MAINT: integrate: Some clean up in the tests.
- #4440: Fast permutation t-test
- #4442: DOC: optimize: fix wrong result in docstring
- #4447: DOC: signal: Some additional documentation to go along with the...
- #4448: DOC: tweak the docstring of lapack.linalg module
- #4449: fix a typo in the expit docstring
- #4451: ENH: vectorize distance loops with gcc
- #4456: MAINT: don't fail large data tests on MemoryError
- #4461: CI: use travis_retry to deal with network timeouts
- #4462: DOC: rationalize minimize() et al. documentation
- #4470: MAINT: sparse: inherit dok_matrix.toarray from spmatrix
- #4473: BUG: signal: Fix validation of the zi shape in sosfilt.
- #4475: BLD: setup.py: update min numpy version and support "setup.py...

- #4481: ENH: add a new linalg special matrix: the Helmert matrix
- #4485: MRG: some changes to allow reading bad mat files
- #4490: [ENH] linalg.hessenberg: use orghr - rebase
- #4491: ENH: linalg: Adding wrapper for potentially useful LAPACK function...
- #4493: BENCH: the solve_toeplitz benchmark used outdated syntax and...
- #4494: MAINT: stats: remove duplicated code
- #4496: References added for watershed_ift algorithm
- #4499: DOC: reshuffle stats distributions documentation
- #4501: Replace benchmark suite with airspeed velocity
- #4502: SLSQP should strictly satisfy bound constraints
- #4503: DOC: forward port 0.15.x release notes and update author name...
- #4504: ENH: option to avoid computing possibly unused svd matrix
- #4505: Rebase of PR 3303 (sparse matrix norms)
- #4507: MAINT: fix lobpcg performance regression
- #4509: DOC: sparse: replace dead link
- #4511: Fixed differential evolution bug
- #4512: Change to fully PEP440 compliant dev version numbers (always...
- #4525: made tiny style corrections (pep8)
- #4533: Add exponentially modified gaussian distribution (scipy.stats.expongauss)
- #4534: MAINT: benchmarks: make benchmark suite importable on all scipy...
- #4535: BUG: Changed zip() to list(zip()) so that it could work in Python...
- #4536: Follow up to pr 4348 (exponential window)
- #4540: ENH: spatial: Add procrustes analysis
- #4541: Bench fixes
- #4542: TST: NumpyVersion dev -> dev0
- #4543: BUG: Overflow in savgol_coeffs
- #4544: pep8 fixes for stats
- #4546: MAINT: use reduction axis arguments in one-norm estimation
- #4549: ENH : Added group_delay to scipy.signal
- #4553: ENH: Significantly faster moment function
- #4556: DOC: document the changes of the sparse.linalg.svds (optional...
- #4559: DOC: stats: describe loc and scale parameters in the docstring...
- #4563: ENH: rewrite of stats.ppcc_plot
- #4564: Be more (or less) forgiving when user passes +-inf instead of...
- #4566: DEP: remove a bunch of deprecated function from scipy.stats,...
- #4570: MNT: Suppress LineSearchWarning's in scipy.optimize tests

- #4572: ENH: Extract inverse hessian information from L-BFGS-B
- #4576: ENH: Split signal.lti into subclasses, part of #2912
- #4578: MNT: Reconcile docstrings and function signatures
- #4581: Fix build with Intel MKL on Linux
- #4583: DOC: optimize: remove references to unused disp kwarg
- #4584: ENH: scipy.signal - Tukey window
- #4587: Hermite asymptotic
- #4593: DOC - add example to RegularGridInterpolator
- #4595: DOC: Fix erroneous latex characters in tutorial/optimize.
- #4600: Add return codes to optimize.tnc docs
- #4603: ENH: Wrap LAPACK `*lange` functions for matrix norms
- #4604: scipy.stats: generalized normal distribution
- #4609: MAINT: interpolate: fix a few inconsistencies between docstrings...
- #4610: MAINT: make runtest.py –bench-compare use asv continuous and...
- #4611: DOC: stats: explain rice scaling; add a note to the tutorial...
- #4614: BUG: lfilter, the size of zi was not checked correctly for nd...
- #4617: MAINT: integrate: Clean the C code behind odeint.
- #4618: FIX: Raise error when window length != data length
- #4619: Issue #4550: `scipy.stats.mode` - UnboundLocalError on empty...
- #4620: Fixed a problem (#4590) with svds accepting wrong eigenvalue...
- #4621: Speed up special.ai_zeros/bi_zeros by 10x
- #4623: MAINT: some tweaks to spatial.procrustes (private file, html...
- #4628: Speed up signal.lfilter and add a convolution path for FIR filters
- #4629: Bug: integrate.nquad; resolve issue #4599
- #4631: MAINT: integrate: Remove unused variables in a Fortran test function.
- #4633: MAINT: Fix convergence message for remez
- #4635: PEP8: indentation (so that pep8 bot does not complain)
- #4637: MAINT: generalize a sign function to do the right thing for complex...
- #4639: Amended typo in apple_sgemv_fix.c
- #4642: MAINT: use lapack for scipy.linalg.norm
- #4643: RBF default epsilon too large 2020
- #4646: Added atleast_1d around poly in invres and invresz
- #4647: fix doc pdf build
- #4648: BUG: Fixes #4408: Vector-valued constraints in minimize() et...
- #4649: Vonmisesfix
- #4650: Signal example clean up in Tukey and place_poles

- #4652: DOC: Fix the error in convolve for same mode
- #4653: improve erf performance
- #4655: DEP: deprecate scipy.stats.histogram2 in favour of np.histogram2d
- #4656: DEP: deprecate scipy.stats.signaltonoise
- #4660: Avoid extra copy for sparse compressed [:, seq] and [seq, :]...
- #4661: Clean, rebase of #4478, adding ?gelsy and ?gelsd wrappers
- #4662: MAINT: Correct odeint messages
- #4664: Update _monotone.py
- #4672: fix behavior of scipy.linalg.block_diag for empty input
- #4675: Fix lsim
- #4676: Added missing colon to :math: directive in docstring.
- #4679: ENH: sparse randn
- #4682: ENH: scipy.signal - Addition of CSD, coherence; Enhancement of...
- #4684: BUG: various errors in weight calculations in orthogonal.py
- #4685: BUG: Fixes #4594: optimize.linprog IndexError when a callback...
- #4686: MAINT: cluster: Clean up duplicated exception raising code.
- #4688: Improve is_distance_dm exception message
- #4692: MAINT: stats: Simplify the calculation in tukeylambda._ppf
- #4693: ENH: added functionality to handle scalars in *stats._chk_asarray*
- #4694: Vectorization of Anderson-Darling computations.
- #4696: Fix singleton expansion in lfilter.
- #4698: MAINT: quiet warnings from cephes.
- #4701: add Bpoly.antiderivatives / integrals
- #4703: Add citation of published paper
- #4706: MAINT: special: avoid out-of-bounds access in specfun
- #4707: MAINT: fix issues with np.matrix as input to functions related...
- #4709: ENH: `scipy.stats` now returns namedtuples.
- #4710: scipy.io.idl: make reader more robust to missing variables in...
- #4711: Fix crash for unknown chunks at the end of file
- #4712: Reduce onenormest memory usage
- #4713: MAINT: interpolate: no need to pass dtype around if it can be...
- #4714: BENCH: Add benchmarks for stats module
- #4715: MAINT: polish signal.place_poles and signal/test_ltisys.py
- #4716: DEP: deprecate mstats.signaltonoise ...
- #4717: MAINT: basinhopping: fix error in tests, silence /0 warning,...
- #4718: ENH: stats: can specify f-shapes to fix in fitting by name

- #4721: Document that imresize converts the input to a PIL image
- #4722: MAINT: PyArray_BASE is not an lvalue unless the deprecated API...
- #4725: Fix gengamma _nump failure
- #4728: DOC: add poch to the list of scipy special function descriptions
- #4735: MAINT: stats: avoid (a spurious) division-by-zero in skew
- #4738: TST: silence runtime warnings for some corner cases in *stats*...
- #4739: BLD: try to build numpy instead of using the one on TravisCI
- #4740: DOC: Update some docstrings with 'versionadded'.
- #4742: BLD: make sure that relaxed strides checking is in effect on...
- #4750: DOC: special: TeX typesetting of rel_entr, kl_div and pseudo_huber
- #4751: BENCH: add sparse null slice benchmark
- #4753: BUG: Fixed compilation with recent Cython versions.
- #4756: BUG: Fixes #4733: optimize.brute finish option is not compatible...
- #4758: DOC: optimize.leastsq default maxfev clarification
- #4759: improved stats mle fit
- #4760: MAINT: count bfgs updates more carefully
- #4762: BUGS: Fixes #4746 and #4594: linprog returns solution violating...
- #4763: fix small linprog bugs
- #4766: BENCH: add signal.lsim benchmark
- #4768: fix python syntax errors in docstring examples
- #4769: Fixes #4726: test_cobyla.test_vector_constraints
- #4770: Mark FITPACK functions as thread safe.
- #4771: edited scipy/stats/stats.py to fix doctest for fisher_exact
- #4773: DOC: update 0.16.0 release notes.
- #4775: DOC: linalg: add funm_psd as a docstring example
- #4778: Use a dictionary for function name synonyms
- #4780: Include apparently-forgotten functions in docs
- #4783: Added many missing special functions to docs
- #4784: add an axis attribute to PPoly and friends
- #4785: Brief note about origin of Lena image
- #4786: DOC: reformat the Methods section of the KDE docstring
- #4787: Add rice cdf and ppf.
- #4792: CI: add a kludge for detecting test failures which try to disguise...
- #4795: Make refguide_check smarter about false positives
- #4797: BUG/TST: numpoints not updated for incremental Voronoi
- #4799: BUG: spatial: Fix a couple edge cases for the Mahalanobis metric...

- #4801: BUG: Fix TypeError in scipy.optimize._trust-region.py when disp=True.
- #4803: Issues with relaxed strides in QR updating routines
- #4806: MAINT: use an informed initial guess for cauchy fit
- #4810: PEP8ify codata.py
- #4812: BUG: Relaxed strides cleanup in decomp_update.pyx.in
- #4820: BLD: update Bento build for sgemv fix and install cython blas/lapack...
- #4823: ENH: scipy.signal - Addition of spectrogram function
- #4827: DOC: add csd and coherence to __init__.py
- #4833: BLD: fix issue in linalg `*lange` wrappers for g77 builds.
- #4841: TST: fix test failures in scipy.special with mingw32 due to test...
- #4842: DOC: update site.cfg.example. Mostly taken over from Numpy
- #4845: BUG: signal: Make spectrogram's return values order match the...
- #4849: DOC:Fix error in ode docstring example
- #4856: BUG: fix typo causing memleak

4.2 SciPy 0.15.0 Release Notes

Contents

SciPy 0.15.0 is the culmination of 6 months of hard work. It contains several new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

4.2.1 New features

Linear Programming Interface

The new function `scipy.optimize.linprog` provides a generic linear programming similar to the way `scipy.optimize.minimize` provides a generic interface to nonlinear programming optimizers. Currently the only method supported is *simplex* which provides a two-phase, dense-matrix-based simplex algorithm. Callbacks functions are supported, allowing the user to monitor the progress of the algorithm.

Differential evolution, a global optimizer

A new `scipy.optimize.differential_evolution` function has been added to the `optimize` module. Differential Evolution is an algorithm used for finding the global minimum of multivariate functions. It is stochastic in nature (does not use gradient methods), and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

`scipy.signal` improvements

The function `scipy.signal.max_len_seq` was added, which computes a Maximum Length Sequence (MLS) signal.

`scipy.integrate` improvements

It is now possible to use `scipy.integrate` routines to integrate multivariate ctypes functions, thus avoiding callbacks to Python and providing better performance.

`scipy.linalg` improvements

The function `scipy.linalg.orthogonal_procrustes` for solving the procrustes linear algebra problem was added.

BLAS level 2 functions `her`, `syr`, `her2` and `syr2` are now wrapped in `scipy.linalg`.

`scipy.sparse` improvements

`scipy.sparse.linalg.svds` can now take a `LinearOperator` as its main input.

`scipy.special` improvements

Values of ellipsoidal harmonic (i.e. Lame) functions and associated normalization constants can be now computed using `ellip_harm`, `ellip_harm_2`, and `ellip_normal`.

New convenience functions `entr`, `rel_entr` `kl_div`, `huber`, and `pseudo_huber` were added.

`scipy.sparse.csgraph` improvements

Routines `reverse_cuthill_mckee` and `maximum_bipartite_matching` for computing reorderings of sparse graphs were added.

`scipy.stats` improvements

Added a Dirichlet multivariate distribution, `scipy.stats.dirichlet`.

The new function `scipy.stats.median_test` computes Mood's median test.

The new function `scipy.stats.combine_pvalues` implements Fisher's and Stouffer's methods for combining p-values.

`scipy.stats.describe` returns a namedtuple rather than a tuple, allowing users to access results by index or by name.

4.2.2 Deprecated features

The `scipy.weave` module is deprecated. It was the only module never ported to Python 3.x, and is not recommended to be used for new code - use Cython instead. In order to support existing code, `scipy.weave` has been packaged separately: https://github.com/scipy/weave. It is a pure Python package, and can easily be installed with `pip install weave`.

`scipy.special.bessel_diff_formula` is deprecated. It is a private function, and therefore will be removed from the public API in a following release.

`scipy.stats.nanmean`, `nanmedian` and `nanstd` functions are deprecated in favor of their numpy equivalents.

4.2.3 Backwards incompatible changes

The functions *scipy.ndimage.minimum_positions*, *scipy.ndimage.maximum_positions*‘ and `scipy.ndimage.extrema` return positions as ints instead of floats.

The format of banded Jacobians in `scipy.integrate.ode` solvers is changed. Note that the previous documentation of this feature was erroneous.

4.2.4 Authors

- Abject +
- Ankit Agrawal +
- Sylvain Bellemare +
- Matthew Brett
- Christian Brodbeck
- Christian Brueffer
- Lars Buitinck
- Evgeni Burovski
- Pierre de Buyl +
- Greg Caporaso +
- CJ Carey
- Jacob Carey +
- Thomas A Caswell
- Helder Cesar +

- Björn Dahlgren +
- Kevin Davies +
- Yotam Doron +
- Marcos Duarte +
- endolith
- Jesse Engel +
- Rob Falck +
- Corey Farwell +
- Jaime Fernandez del Rio +
- Clark Fitzgerald +
- Tom Flannaghan +
- Chad Fulton +
- Jochen Garcke +
- François Garillot +
- André Gaul
- Christoph Gohlke
- Ralf Gommers
- Alex Griffing
- Blake Griffith
- Olivier Grisel
- Charles Harris
- Trent Hauck +
- Ian Henriksen +
- Jinhyok Heo +
- Matt Hickford +
- Andreas Hilboll
- Danilo Horta +
- David Menéndez Hurtado +
- Gert-Ludwig Ingold
- Thouis (Ray) Jones
- Chris Kerr +
- Carl Kleffner +
- Andreas Kloeckner
- Thomas Kluyver +
- Adrian Kretz +
- Johannes Kulick +

- Eric Larson
- Brianna Laugher +
- Denis Laxalde
- Antony Lee +
- Gregory R. Lee +
- Brandon Liu
- Alex Loew +
- Loïc Estève +
- Jaakko Luttinen +
- Benny Malengier
- Tobias Megies +
- Sturla Molden
- Eric Moore
- Brett R. Murphy +
- Paul Nation +
- Andrew Nelson
- Brian Newsom +
- Joel Nothman
- Sergio Oller +
- Janani Padmanabhan +
- Tiago M.D. Pereira +
- Nicolas Del Piano +
- Manuel Reinhardt +
- Thomas Robitaille
- Mike Romberg +
- Alex Rothberg +
- Sebastian Pölsterl +
- Maximilian Singh +
- Brigitta Sipocz +
- Alex Stewart +
- Julian Taylor
- Collin Tokheim +
- James Tomlinson +
- Benjamin Trendelkamp-Schroer +
- Richard Tsai
- Alexey Umnov +

- Jacob Vanderplas
- Joris Vankerschaver
- Bastian Venthur +
- Pauli Virtanen
- Stefan van der Walt
- Yuxiang Wang +
- James T. Webber
- Warren Weckesser
- Axl West +
- Nathan Woods
- Benda Xu +
- Víctor Zabalza +
- Tiziano Zito +

A total of 99 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed

- #1431: ellipk(x) extending its domain for x<0 (Trac #904)
- #1727: consistency of std interface (Trac #1200)
- #1851: Shape parameter negated in genextreme (relative to R, MATLAB,...
- #1889: interp2d is weird (Trac #1364)
- #2188: splev gives wrong values or crashes outside of support when der...
- #2343: scipy.insterpolate's splrep function fails with certain combinations...
- #2669: .signal.ltisys.ss2tf should only apply to MISO systems in current...
- #2911: interpolate.splder() failure on Fedora
- #3171: future of weave in scipy
- #3176: Suggestion to improve error message in scipy.integrate.odeint
- #3198: pdf() and logpdf() methods for scipy.stats.gaussian_kde
- #3318: Travis CI is breaking on test("full")
- #3329: scipy.stats.scoreatpercentile backward-incompatible change not...
- #3362: Reference cycle in scipy.sparse.linalg.eigs with shift-invert...
- #3364: BUG: linalg.hessenberg broken (wrong results)
- #3376: stats f_oneway needs floats
- #3379: Installation of scipy 0.13.3 via zc.buildout fails
- #3403: hierarchy.linkage raises an ugly exception for a compressed 2x2...
- #3422: optimize.curve_fit() handles NaN by returning all parameters...

- #3457: linalg.fractional_matrix_power has no docstring
- #3469: DOC: *ndimage.find_object* ignores zero-values
- #3491: optimize.leastsq() documentation should mention it does not work...
- #3499: cluster.vq.whiten return nan for all zeros column in observations
- #3503: minimize attempts to do vector addition when numpy arrays are...
- #3508: exponweib.logpdf fails for valid parameters
- #3509: libatlas3-base-dev does not exist
- #3550: BUG: anomalous values computed by special.ellipkinc
- #3555: `scipy.ndimage` positions are float instead of int
- #3557: UnivariateSpline.__call__ should pass all relevant args through...
- #3569: No license statement for test data imported from boost?
- #3576: mstats test failure (too sensitive?)
- #3579: Errors on scipy 0.14.x branch using MKL, Ubuntu 14.04 x86_64
- #3580: Operator overloading with sparse matrices
- #3587: Wrong alphabetical order in continuous statistical distribution...
- #3596: scipy.signal.fftconvolve no longer threadsafe
- #3623: BUG: signal.convolve takes longer than it needs to
- #3655: Integer returned from integer data in scipy.signal.periodogram...
- #3662: Travis failure on Numpy 1.5.1 (not reproducible?)
- #3668: dendogram(orientation='foo')
- #3669: KroghInterpolator doesn't pass through points
- #3672: Inserting a knot in a spline
- #3682: misleading documentation of scipy.optimize.curve_fit
- #3699: BUG?: minor problem with scipy.signal.lfilter w/initial conditions
- #3700: Inconsistent exceptions raised by scipy.io.loadmat
- #3703: TypeError for RegularGridInterpolator with big-endian data
- #3714: Misleading error message in eigsh: k must be between 1 and rank(A)-1
- #3720: coo_matrix.setdiag() fails
- #3740: Scipy.Spatial.KdTree (Query) Return Type?
- #3761: Invalid result from scipy.special.btdtri
- #3784: DOC - Special Functions - Drum example fix for higher modes
- #3785: minimize() should have friendlier args=
- #3787: BUG: signal: Division by zero in lombscargle
- #3800: BUG: scipy.sparse.csgraph.shortest_path overwrites input matrix
- #3817: Warning in calculating moments from Binomial distribution for...
- #3821: review scipy usage of *np.ma.is_masked*

- #3829: Linear algebra function documentation doesn't mention default...
- #3830: A bug in Docstring of scipy.linalg.eig
- #3844: Issue with shape parameter returned by genextreme
- #3858: "ImportError: No module named Cython.Compiler.Main" on install
- #3876: savgol_filter not in release notes and has no versionadded
- #3884: scipy.stats.kendalltau empty array error
- #3895: ValueError: illegal value in 12-th argument of internal gesdd...
- #3898: skimage test broken by minmax filter change
- #3901: scipy sparse errors with numpy master
- #3905: DOC: optimize: linprog docstring has two "Returns" sections
- #3915: DOC: sphinx warnings because of ***kwds* in the stats distributions...
- #3935: Split stats.distributions files in tutorial
- #3969: gh-3607 breaks backward compatibility in ode solver banded jacobians
- #4025: DOC: signal: The return value of find_peaks_cwt is not documented.
- #4029: scipy.stats.nbinom.logpmf(0,1,1) returns nan. Correct value is...
- #4032: ERROR: test_imresize (test_pilutil.TestPILUtil)
- #4038: errors do not propagate through scipy.integrate.odeint properly
- #4171: orthogonal_procrustes always returns scale.
- #4176: Solving the Discrete Lyapunov Equation does not work with matrix...

Pull requests

- #3109: ENH Added Fisher's method and Stouffer's Z-score method
- #3225: Add the limiting distributions to generalized Pareto distribution...
- #3262: Implement back end of faster multivariate integration
- #3266: ENH: signal: add type=False as parameter for periodogram and...
- #3273: Add PEP8 check to Travis-CI
- #3342: ENH: linprog function for linear programming
- #3348: BUG: add proper error handling when using interp2d on regular...
- #3351: ENH: Add MLS method
- #3382: ENH: scipy.special information theory functions
- #3396: ENH: improve stats.nanmedian more by assuming nans are rare
- #3398: Added two wrappers to the gaussian_kde class.
- #3405: BUG: cluster.linkage array conversion to double dtype
- #3407: MAINT: use assert_warns instead of a more complicated mechanism
- #3409: ENH: change to use array view in signal/_peak_finding.py
- #3416: Issue 3376 : stats f_oneway needs floats

- #3419: BUG: tools: Fix list of FMA instructions in detect_cpu_extensions_wine.py
- #3420: DOC: stats: Add 'entropy' to the stats package-level documentation.
- #3429: BUG: close intermediate file descriptor right after it is used...
- #3430: MAINT: Fix some cython variable declarations to avoid warnings...
- #3433: Correcting the normalization of chebwin window function
- #3435: Add more precise link to R's quantile documentation
- #3446: ENH: scipy.optimize - adding differential_evolution
- #3450: MAINT: remove unused function scipy.stats.mstats_basic._kolmog1
- #3458: Reworked version of PR-3084 (mstats-stats comparison)
- #3462: MAINT : Returning a warning for low attenuation values of chebwin...
- #3463: DOC: linalg: Add examples to functions in matfuncs.py
- #3477: ENH: sparse: release GIL in sparsetools routines
- #3480: DOC: Add more details to deconvolve docstring
- #3484: BLD: fix Qhull build issue with MinGW-w64. Closes gh-3237.
- #3498: MAINT: io: remove old warnings from idl.py
- #3504: BUG: cluster.vq.whiten returns nan or inf when std==0
- #3510: MAINT: stats: Reimplement the pdf and logpdf methods of exponweib.
- #3512: Fix PEP8 errors showing up on TravisCI after pep8 1.5 release
- #3514: DOC: libatlas3-base-dev seems to have never been a thing
- #3516: DOC improve scipy.sparse docstrings
- #3517: ENH: speed-up ndimage.filters.min(max)imum_filter1d
- #3518: Issues in scipy.misc.logsumexp
- #3526: DOC: graphical example for cwt, and use a more interesting signal
- #3527: ENH: Implement min(max)imum_filter1d using the MINLIST algorithm
- #3537: STY: reduce number of C compiler warnings
- #3540: DOC: linalg: add docstring to fractional_matrix_power
- #3542: kde.py Doc Typo
- #3545: BUG: stats: stats.levy.cdf with small arguments loses precision.
- #3547: BUG: special: erfcinv with small arguments loses precision.
- #3553: DOC: Convolve examples
- #3561: FIX: in ndimage.measurements return positions as int instead...
- #3564: Fix test failures with numpy master. Closes gh-3554
- #3565: ENH: make interp2d accept unsorted arrays for interpolation.
- #3566: BLD: add numpy requirement to metadata if it can't be imported.
- #3567: DOC: move matfuncs docstrings to user-visible functions
- #3574: Fixes multiple bugs in mstats.theilslopes

- #3577: TST: decrease sensitivity of an mstats test
- #3585: Cleanup of code in scipy.constants
- #3589: BUG: sparse: allow operator overloading
- #3594: BUG: lobpcg returned wrong values for small matrices (n < 10)
- #3598: MAINT: fix coverage and coveralls
- #3599: MAINT: symeig – now that’s a name I’ve not heard in a long time
- #3602: MAINT: clean up the new optimize.linprog and add a few more tests
- #3607: BUG: integrate: Fix some bugs and documentation errors in the...
- #3609: MAINT integrate/odepack: kill dead Fortran code
- #3616: FIX: Invalid values
- #3617: Sort netcdf variables in a Python-3 compatible way
- #3622: DOC: Added 0.15.0 release notes entry for linprog function.
- #3625: Fix documentation for cKDTree.sparse_distance_matrix
- #3626: MAINT: linalg.orth memory efficiency
- #3627: MAINT: stats: A bit of clean up
- #3628: MAINT: signal: remove a useless function from wavelets.py
- #3632: ENH: stats: Add Mood’s median test.
- #3636: MAINT: cluster: some clean up
- #3638: DOC: docstring of optimize.basinhopping confuses singular and...
- #3639: BUG: change ddof default to 1 in mstats.sem, consistent with...
- #3640: Weave: deprecate the module and disable slow tests on TravisCI
- #3641: ENH: Added support for date attributes to io.arff.arffread
- #3644: MAINT: stats: remove superfluous alias in mstats_basic.py
- #3646: ENH: adding *sum_duplicates* method to COO sparse matrix
- #3647: Fix for #3596: Make fftconvolve threadsafe
- #3650: BUG: sparse: smarter random index selection
- #3652: fix wrong option name in power_divergence dosctring example
- #3654: Changing EPD to Canopy
- #3657: BUG: signal.welch: ensure floating point dtype regardless of...
- #3660: TST: mark a test as known fail
- #3661: BLD: ignore pep8 E302 (expected 2 blank lines, found 1)
- #3663: BUG: fix leaking errstate, and ignore invalid= errors in a test
- #3664: BUG: correlate was extremely slow when in2.size > in1.size
- #3667: ENH: Adds default params to pdfs of multivariate_norm
- #3670: ENH: Small speedup of FFT size check
- #3671: DOC: adding differential_evolution function to 0.15 release notes

- #3673: BUG: interpolate/fitpack: arguments to fortran routines may not...
- #3674: Add support for appending to existing netcdf files
- #3681: Speed up test('full'), solve Travis CI timeout issues
- #3683: ENH: cluster: rewrite and optimize *vq* in Cython
- #3684: Update special docs
- #3688: Spacing in special docstrings
- #3692: ENH: scipy.special: Improving sph_harm function
- #3693: Update refguide entries for signal and fftpack
- #3695: Update continuous.rst
- #3696: ENH: check for valid 'orientation' kwarg in dendrogram()
- #3701: make 'a' and 'b' coefficients atleast_1d array in filtfilt
- #3702: BUG: cluster: _vq unable to handle large features
- #3704: BUG: special: ellip(k,e)inc nan and double expected value
- #3707: BUG: handle fill_value dtype checks correctly in RegularGridInterpolator
- #3708: Reraise exception on failure to read mat file.
- #3709: BUG: cast 'x' to correct dtype in KroghInterpolator._evaluate
- #3712: ENH: cluster: reimplement the update-step of K-means in Cython
- #3713: FIX: Check type of lfiltic
- #3718: Changed INSTALL file extension to rst
- #3719: address svds returning nans for zero input matrix
- #3722: MAINT: spatial: static, unused code, sqrt(sqeuclidean)
- #3725: ENH: use numpys nanmedian if available
- #3727: TST: add a new fixed_point test and change some test function...
- #3731: BUG: fix romb in scipy.integrate.quadrature
- #3734: DOC: simplify examples with semilogx
- #3735: DOC: Add minimal docstrings to lti.impulse/step
- #3736: BUG: cast pchip arguments to floats
- #3744: stub out inherited methods of Akima1DInterpolator
- #3746: DOC: Fix formatting for Raises section
- #3748: ENH: Added discrete Lyapunov transformation solve
- #3750: Enable automated testing with Python 3.4
- #3751: Reverse Cuthill-McKee and Maximum Bipartite Matching reorderings...
- #3759: MAINT: avoid indexing with a float array
- #3762: TST: filter out RuntimeWarning in vq tests
- #3766: TST: cluster: some cleanups in test_hierarchy.py
- #3767: ENH/BUG: support negative m in elliptic integrals

- #3769: ENH: avoid repeated matrix inverse
- #3770: BUG: signal: In lfilter_zi, b was not rescaled correctly when...
- #3772: STY avoid unnecessary transposes in csr_matrix.getcol/row
- #3773: ENH: Add ext parameter to UnivariateSpline call
- #3774: BUG: in integrate/quadpack.h, put all declarations before statements.
- #3779: Incbet fix
- #3788: BUG: Fix lombscargle ZeroDivisionError
- #3791: Some maintenance for doc builds
- #3795: scipy.special.legendre docstring
- #3796: TYPO: sheroidal -> spheroidal
- #3801: BUG: shortest_path overwrite
- #3803: TST: lombscargle regression test related to atan vs atan2
- #3809: ENH: orthogonal procrustes solver
- #3811: ENH: scipy.special, Implemented Ellipsoidal harmonic function:...
- #3819: BUG: make a fully connected csgraph from an ndarray with no zeros
- #3820: MAINT: avoid spurious warnings in binom(n, p=0).mean() etc
- #3825: Don’t claim scipy.cluster does distance matrix calculations.
- #3827: get and set diagonal of coo_matrix, and related csgraph laplacian...
- #3832: DOC: Minor additions to integrate/nquad docstring.
- #3845: Bug fix for #3842: Bug in scipy.optimize.line_search
- #3848: BUG: edge case where the covariance matrix is exactly zero
- #3850: DOC: typo
- #3851: DOC: document default argument values for some arpack functions
- #3860: DOC: sparse: add the function ‘find’ to the module-level docstring
- #3861: BUG: Removed unnecessary storage of args as instance variables...
- #3862: BUG: signal: fix handling of multi-output systems in ss2tf.
- #3865: Feature request: ability to read heterogeneous types in FortranFile
- #3866: MAINT: update pip wheelhouse for installs
- #3871: MAINT: linalg: get rid of calc_lwork.f
- #3872: MAINT: use scipy.linalg instead of np.dual
- #3873: BLD: show a more informative message if Cython wasn’t installed.
- #3874: TST: cluster: cleanup the hierarchy test data
- #3877: DOC: Savitzky-Golay filter version added
- #3878: DOC: move versionadded to notes
- #3879: small tweaks to the docs
- #3881: FIX incorrect sorting during fancy assignment

- #3885: kendalltau function now returns a nan tuple if empty arrays used...
- #3886: BUG: fixing linprog's kwarg order to match docs
- #3888: BUG: optimize: In _linprog_simplex, handle the case where the...
- #3891: BUG: stats: Fix ValueError message in chi2_contingency.
- #3892: DOC: sparse.linalg: Fix lobpcg docstring.
- #3894: DOC: stats: Assorted docstring edits.
- #3896: Fix 2 mistakes in MatrixMarket format parsing
- #3897: BUG: associated Legendre function of second kind for 1<x<1.0001
- #3899: BUG: fix undefined behavior in alngam
- #3906: MAINT/DOC: Whitespace tweaks in several docstrings.
- #3907: TST: relax bounds of interpolate test to accomodate rounding...
- #3909: MAINT: Create a common version of *count_nonzero* for compatibility...
- #3910: Fix a couple of test errors in master
- #3911: Use MathJax for the html docs
- #3914: Rework the _roots functions and document them.
- #3916: Remove all linpack_lite code and replace with LAPACK routines
- #3917: splines, constant extrapolation
- #3918: DOC: tweak the rv_discrete docstring example
- #3919: Quadrature speed-up: scipy.special.orthogonal.p_roots with cache
- #3920: DOC: Clarify docstring for *sigma* parameter for *curve_fit*
- #3922: Fixed Docstring issues in linprog (Fixes #3905).
- #3924: Coerce args into tuple if necessary.
- #3926: DOC: Surround stats class methods in docstrings with backticks.
- #3927: Changed doc for romb's dx parameter to int.
- #3928: check FITPACK conditions in LSQUnivariateSpline
- #3929: Added a warning about leastsq using with NaNs.
- #3930: ENH: optimize: curve_fit now warns if pcov is undetermined
- #3932: Clarified the k > n case.
- #3933: DOC: remove *import scipy as sp* abbreviation here and there
- #3936: Add license and copyright holders to test data imported from...
- #3938: DOC: Corrected documentation for return types.
- #3939: DOC: fitpack: add a note about Sch-W conditions to splrep docstring
- #3940: TST: integrate: Remove an invalid test of odeint.
- #3942: FIX: Corrected error message of eigsh.
- #3943: ENH: release GIL for filter and interpolation of ndimage
- #3944: FIX: Raise value error if window data-type is unsupported

- #3946: Fixed signal.get_window with unicode window name
- #3947: MAINT: some docstring fixes and style cleanups in stats.mstats
- #3949: DOC: fix a couple of issues in stats docstrings.
- #3950: TST: sparse: remove known failure that doesn't fail
- #3951: TST: switch from Rackspace wheelhouse to numpy/cython source...
- #3952: DOC: stats: Small formatting correction to the 'chi' distribution...
- #3953: DOC: stats: Several corrections and small additions to docstrings.
- #3955: signal.__init__.py: remove duplicated *get_window* entry
- #3959: TST: sparse: more "known failures" for DOK that don't fail
- #3960: BUG: io.netcdf: do not close mmap if there are references left...
- #3965: DOC: Fix a few more sphinx warnings that occur when building...
- #3966: DOC: add guidelines for using test generators in HACKING
- #3968: BUG: sparse.linalg: make Inv objects in arpack garbage-collectable...
- #3971: Remove all linpack_lite code and replace with LAPACK routines
- #3972: fix typo in error message
- #3973: MAINT: better error message for multivariate normal.
- #3981: turn the cryptically named scipy.special information theory functions...
- #3984: Wrap her, syr, her2, syr2 blas routines
- #3990: improve UnivariateSpline docs
- #3991: ENH: stats: return namedtuple for describe output
- #3993: DOC: stats: percentileofscore references np.percentile
- #3997: BUG: linalg: pascal(35) was incorrect: last element overflowed...
- #3998: MAINT: use isMaskedArray instead of is_masked to check type
- #3999: TST: test against all of boost data files.
- #4000: BUG: stats: Fix edge-case handling in a few distributions.
- #4003: ENH: using python's warnings instead of prints in fitpack.
- #4004: MAINT: optimize: remove a couple unused variables in zeros.c
- #4006: BUG: Fix C90 compiler warnings in *NI_MinOrMaxFilter1D*
- #4007: MAINT/DOC: Fix spelling of 'decomposition' in several files.
- #4008: DOC: stats: Split the descriptions of the distributions in the...
- #4015: TST: logsumexp regression test
- #4016: MAINT: remove some inf-related warnings from logsumexp
- #4020: DOC: stats: fix whitespace in docstrings of several distributions
- #4023: Exactly one space required before assignments
- #4024: In dendrogram(): Correct an argument name and a grammar issue...
- #4041: BUG: misc: Ensure that the 'size' argument of PIL's 'resize'...

- #4049: BUG: Return of _logpmf
- #4051: BUG: expm of integer matrices
- #4052: ENH: integrate: odeint: Handle exceptions in the callback functions.
- #4053: BUG: stats: Refactor argument validation to avoid a unicode issue.
- #4057: Added newline to scipy.sparse.linalg.svds documentation for correct...
- #4058: MAINT: stats: Add note about change to scoreatpercentile in release...
- #4059: ENH: interpolate: Allow splev to accept an n-dimensional array.
- #4064: Documented the return value for scipy.signal.find_peaks_cwt
- #4074: ENH: Support LinearOperator as input to svds
- #4084: BUG: Match exception declarations in scipy/io/matlab/streams.pyx...
- #4091: DOC: special: more clear instructions on how to evaluate polynomials
- #4105: BUG: Workaround for SGEMV segfault in Accelerate
- #4107: DOC: get rid of 'import *' in examples
- #4113: DOC: fix typos in distance.yule
- #4114: MAINT C fixes
- #4117: deprecate nanmean, nanmedian and nanstd in favor of their numpy...
- #4126: scipy.io.idl: support description records and fix bug with null...
- #4131: ENH: release GIL in more ndimage functions
- #4132: MAINT: stats: fix a typo [skip ci]
- #4145: DOC: Fix documentation error for nc chi-squared dist
- #4150: Fix _nd_image.geometric_transform endianness bug
- #4153: MAINT: remove use of deprecated numpy API in lib/lapack/ f2py...
- #4156: MAINT: optimize: remove dead code
- #4159: MAINT: optimize: clean up Zeros code
- #4165: DOC: add missing special functions to __doc__
- #4172: DOC: remove misleading procrustes docstring line
- #4175: DOC: sparse: clarify CSC and CSR constructor usage
- #4177: MAINT: enable np.matrix inputs to solve_discrete_lyapunov
- #4179: TST: fix an intermittently failing test case for special.legendre
- #4181: MAINT: remove unnecessary null checks before free
- #4182: Ellipsoidal harmonics
- #4183: Skip Cython build in Travis-CI
- #4184: Pr 4074
- #4187: Pr/3923
- #4190: BUG: special: fix up ellip_harm build
- #4193: BLD: fix msvc compiler errors

- #4194: BUG: fix buffer dtype mismatch on win-amd64
- #4199: ENH: Changed scipy.stats.describe output from datalen to nobs
- #4201: DOC: add blas2 and nan* deprecations to the release notes
- #4243: TST: bump test tolerances

4.3 SciPy 0.14.0 Release Notes

Contents

SciPy 0.14.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.14.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

4.3.1 New features

`scipy.interpolate` improvements

A new wrapper function `scipy.interpolate.interpn` for interpolation on regular grids has been added. *interpn* supports linear and nearest-neighbor interpolation in arbitrary dimensions and spline interpolation in two dimensions.

Faster implementations of piecewise polynomials in power and Bernstein polynomial bases have been added as `scipy.interpolate.PPoly` and `scipy.interpolate.BPoly`. New users should use these in favor of `scipy.interpolate.PiecewisePolynomial`.

`scipy.interpolate.interp1d` now accepts non-monotonic inputs and sorts them. If performance is critical, sorting can be turned off by using the new `assume_sorted` keyword.

Functionality for evaluation of bivariate spline derivatives in `scipy.interpolate` has been added.

The new class `scipy.interpolate.Akima1DInterpolator` implements the piecewise cubic polynomial interpolation scheme devised by H. Akima.

Functionality for fast interpolation on regular, unevenly spaced grids in arbitrary dimensions has been added as `scipy.interpolate.RegularGridInterpolator` .

`scipy.linalg` improvements

The new function `scipy.linalg.dft` computes the matrix of the discrete Fourier transform.

A condition number estimation function for matrix exponential, `scipy.linalg.expm_cond`, has been added.

`scipy.optimize` improvements

A set of benchmarks for optimize, which can be run with `optimize.bench()`, has been added.

`scipy.optimize.curve_fit` now has more controllable error estimation via the `absolute_sigma` keyword.

Support for passing custom minimization methods to `optimize.minimize()` and `optimize.minimize_scalar()` has been added, currently useful especially for combining `optimize.basinhopping()` with custom local optimizer routines.

`scipy.stats` improvements

A new class `scipy.stats.multivariate_normal` with functionality for multivariate normal random variables has been added.

A lot of work on the `scipy.stats` distribution framework has been done. Moment calculations (skew and kurtosis mainly) are fixed and verified, all examples are now runnable, and many small accuracy and performance improvements for individual distributions were merged.

The new function `scipy.stats.anderson_ksamp` computes the k-sample Anderson-Darling test for the null hypothesis that k samples come from the same parent population.

`scipy.signal` improvements

`scipy.signal.iirfilter` and related functions to design Butterworth, Chebyshev, elliptical and Bessel IIR filters now all use pole-zero ("zpk") format internally instead of using transformations to numerator/denominator format. The accuracy of the produced filters, especially high-order ones, is improved significantly as a result.

The Savitzky-Golay filter was added with the new functions `scipy.signal.savgol_filter` and `scipy.signal.savgol_coeffs`.

The new function `scipy.signal.vectorstrength` computes the vector strength, a measure of phase synchrony, of a set of events.

`scipy.special` improvements

The functions `scipy.special.boxcox` and `scipy.special.boxcox1p`, which compute the Box-Cox transformation, have been added.

`scipy.sparse` improvements

- Significant performance improvement in CSR, CSC, and DOK indexing speed.
- When using Numpy >= 1.9 (to be released in MM 2014), sparse matrices function correctly when given to arguments of `np.dot`, `np.multiply` and other ufuncs. With earlier Numpy and Scipy versions, the results of such operations are undefined and usually unexpected.
- Sparse matrices are no longer limited to `2^31` nonzero elements. They automatically switch to using 64-bit index data type for matrices containing more elements. User code written assuming the sparse matrices use int32 as the index data type will continue to work, except for such large matrices. Code dealing with larger matrices needs to accept either int32 or int64 indices.

4.3.2 Deprecated features

`anneal`

The global minimization function *scipy.optimize.anneal* is deprecated. All users should use the `scipy.optimize.basinhopping` function instead.

`scipy.stats`

`randwcdf` and `randwppf` functions are deprecated. All users should use distribution-specific `rvs` methods instead.

Probability calculation aliases `zprob`, `fprob` and `ksprob` are deprecated. Use instead the `sf` methods of the corresponding distributions or the `special` functions directly.

`scipy.interpolate`

`PiecewisePolynomial` class is deprecated.

4.3.3 Backwards incompatible changes

`lpmn` no longer accepts complex-valued arguments. A new function `clpmn` with uniform complex analytic behavior has been added, and it should be used instead.

Eigenvectors in the case of generalized eigenvalue problem are normalized to unit vectors in 2-norm, rather than following the LAPACK normalization convention.

The deprecated UMFPACK wrapper in `scipy.sparse.linalg` has been removed due to license and install issues. If available, `scikits.umfpack` is still used transparently in the `spsolve` and `factorized` functions. Otherwise, SuperLU is used instead in these functions.

The deprecated functions `glm`, `oneway` and `cmedian` have been removed from `scipy.stats`.

`stats.scoreatpercentile` now returns an array instead of a list of percentiles.

The API for computing derivatives of a monotone piecewise interpolation has changed: if *p* is a `PchipInterpolator` object, *p.derivative(der)* returns a callable object representing the derivative of *p*. For in-place derivatives use the second argument of the *__call__* method: *p(0.1, der=2)* evaluates the second derivative of *p* at *x=0.1*.

The method *p.derivatives* has been removed.

4.3.4 Other changes

4.3.5 Authors

- Marc Abramowitz +
- Anders Bech Borchersen +
- Vincent Arel-Bundock +
- Petr Baudis +
- Max Bolingbroke
- François Boulogne
- Matthew Brett
- Lars Buitinck
- Evgeni Burovski
- CJ Carey +
- Thomas A Caswell +
- Pawel Chojnacki +
- Phillip Cloud +
- Stefano Costa +
- David Cournapeau
- David Menendez Hurtado +
- Matthieu Dartiailh +
- Christoph Deil +
- Jörg Dietrich +
- endolith
- Francisco de la Peña +
- Ben FrantzDale +
- Jim Garrison +
- André Gaul
- Christoph Gohlke
- Ralf Gommers
- Robert David Grant
- Alex Griffing

- Blake Griffith
- Yaroslav Halchenko
- Andreas Hilboll
- Kat Huang
- Gert-Ludwig Ingold
- James T. Webber +
- Dorota Jarecka +
- Todd Jennings +
- Thouis (Ray) Jones
- Juan Luis Cano Rodríguez
- ktritz +
- Jacques Kvam +
- Eric Larson +
- Justin Lavoie +
- Denis Laxalde
- Jussi Leinonen +
- lemonlaug +
- Tim Leslie
- Alain Leufroy +
- George Lewis +
- Max Linke +
- Brandon Liu +
- Benny Malengier +
- Matthias Kümmerer +
- Cimarron Mittelsteadt +
- Eric Moore
- Andrew Nelson +
- Niklas Hambüchen +
- Joel Nothman +
- Clemens Novak
- Emanuele Olivetti +
- Stefan Otte +
- peb +
- Josef Perktold
- pjwerneck
- poolio

- Jérôme Roy +
- Carl Sandrock +
- Andrew Sczesnak +
- Shauna +
- Fabrice Silva
- Daniel B. Smith
- Patrick Snape +
- Thomas Spura +
- Jacob Stevenson
- Julian Taylor
- Tomas Tomecek
- Richard Tsai
- Jacob Vanderplas
- Joris Vankerschaver +
- Pauli Virtanen
- Warren Weckesser

A total of 80 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed

- #1325: add custom axis keyword to dendrogram function in scipy.cluster.hierarchy...
- #1437: Wrong pochhammer symbol for negative integers (Trac #910)
- #1555: scipy.io.netcdf leaks file descriptors (Trac #1028)
- #1569: sparse matrix failed with element-wise multiplication using numpy.multiply()...
- #1833: Sparse matrices are limited to 2^32 non-zero elements (Trac #1307)
- #1834: scipy.linalg.eig does not normalize eigenvector if B is given...
- #1866: stats for invgamma (Trac #1340)
- #1886: stats.zipf floating point warnings (Trac #1361)
- #1887: Stats continuous distributions - floating point warnings (Trac...
- #1897: scoreatpercentile() does not handle empty list inputs (Trac #1372)
- #1918: splint returns incorrect results (Trac #1393)
- #1949: kurtosistest fails in mstats with type error (Trac #1424)
- #2092: scipy.test leaves darwin27compiled_catalog, cpp and so files...
- #2106: stats ENH: shape parameters in distribution docstrings (Trac...
- #2123: Bad behavior of sparse matrices in a binary ufunc (Trac #1598)
- #2152: Fix mmio/fromfile on gzip on Python 3 (Trac #1627)

- #2164: stats.rice.pdf(x, 0) returns nan (Trac #1639)
- #2169: scipy.optimize.fmin_bfgs not handling functions with boundaries...
- #2177: scipy.cluster.hierarchy.ClusterNode.pre_order returns IndexError...
- #2179: coo.todense() segfaults (Trac #1654)
- #2185: Precision of scipy.ndimage.gaussian_filter*() limited (Trac #1660)
- #2186: scipy.stats.mstats.kurtosistest crashes on 1d input (Trac #1661)
- #2238: Negative p-value on hypergeom.cdf (Trac #1719)
- #2283: ascending order in interpolation routines (Trac #1764)
- #2288: mstats.kurtosistest is incorrectly converting to float, and fails...
- #2396: lpmn wrong results for `|z| > 1` (Trac #1877)
- #2398: ss2tf returns num as 2D array instead of 1D (Trac #1879)
- #2406: linkage does not take Unicode strings as method names (Trac #1887)
- #2443: IIR filter design should not transform to tf representation internally
- #2572: class method solve of splu return object corrupted or falsely...
- #2667: stats endless loop ?
- #2671: .stats.hypergeom documentation error in the note about pmf
- #2691: BUG scipy.linalg.lapack: potrf/ptroi interpret their 'lower'...
- #2721: Allow use of ellipsis in scipy.sparse slicing
- #2741: stats: deprecate and remove alias for special functions
- #2742: stats add rvs to rice distribution
- #2765: bugs stats entropy
- #2832: argrelextrema returns tuple of 2 empty arrays when no peaks found...
- #2861: scipy.stats.scoreatpercentile broken for vector *per*
- #2891: COBYLA successful termination when constraints violated
- #2919: test failure with the current master
- #2922: ndimage.percentile_filter ignores origin argument for multidimensional...
- #2938: Sparse/dense matrix inplace operations fail due to __numpy_ufunc__
- #2944: MacPorts builds yield 40Mb worth of build warnings
- #2945: FAIL: test_random_complex (test_basic.TestDet)
- #2947: FAIL: Test some trivial edge cases for savgol_filter()
- #2953: Scipy Delaunay triangulation is not oriented
- #2971: scipy.stats.mstats.winsorize documentation error
- #2980: Problems running what seems a perfectly valid example
- #2996: entropy for rv_discrete is incorrect?!
- #2998: Fix numpy version comparisons
- #3002: python setup.py install fails

- #3014: Bug in stats.fisher_exact
- #3030: relative entropy using scipy.stats.distribution.entropy when...
- #3037: scipy.optimize.curve_fit leads to unexpected behavior when input...
- #3047: mstats.ttest_rel axis=None, requires masked array
- #3059: BUG: Slices of sparse matrices return incorrect dtype
- #3063: range keyword in binned_statistics incorrect
- #3067: cumtrapz not working as expected
- #3069: sinc
- #3086: standard error calculation inconsistent between 'stats' and 'mstats'
- #3094: Add a *perm* function into `scipy.misc` and an enhancement of...
- #3111: scipy.sparse.[hv]stack don't respect anymore the dtype parameter
- #3172: optimize.curve_fit uses different nomenclature from optimize.leastsq
- #3196: scipy.stats.mstats.gmean does not actually take dtype
- #3212: Dot product of csr_matrix causes segmentation fault
- #3227: ZeroDivisionError in broyden1 when initial guess is the right...
- #3238: lbfgsb output not suppressed by disp=0
- #3249: Sparse matrix min/max/etc don't support axis=-1
- #3251: cdist performance issue with 'sqeuclidean' metric
- #3279: logm fails for singular matrix
- #3285: signal.chirp(method='hyp') disallows hyperbolic upsweep
- #3299: MEMORY LEAK: fmin_tnc
- #3330: test failures with the current master
- #3345: scipy and/or numpy change is causing tests to fail in another...
- #3363: splu does not work for non-vector inputs
- #3385: expit does not handle large arguments well
- #3395: specfun.f doesn't compile with MinGW
- #3399: Error message bug in scipy.cluster.hierarchy.linkage
- #3404: interpolate._ppoly doesn't build with MinGW
- #3412: Test failures in signal
- #3466: ``scipy.sparse.csgraph.shortest_path`` does not work on ``scipy.sparse.csr_matrix`` or ``lil_matrix``

Pull requests

- #442: ENH: sparse: enable 64-bit index arrays & nnz > 2**31
- #2766: DOC: remove doc/seps/technology-preview.rst
- #2772: TST: stats: Added a regression test for stats.wilcoxon. Closes...

- #2778: Clean up stats._support, close statistics review issues
- #2792: BUG io: fix file descriptor closing for netcdf variables
- #2847: Rice distribution: extend to b=0, add an explicit rvs method.
- #2878: [stats] fix formulas for higher moments of dweibull distribution
- #2904: ENH: moments for the zipf distribution
- #2907: ENH: add coverage info with coveralls.io for Travis runs.
- #2932: BUG+TST: setdiag implementation for dia_matrix (Close #2931)...
- #2942: Misc fixes pointed out by Eclipse PyDev static code analysis
- #2946: ENH: allow non-monotonic input in interp1d
- #2986: BUG: runtests: chdir away from root when running tests
- #2987: DOC: linalg: don't recommend np.linalg.norm
- #2992: ENH: Add "limit" parameter to dijkstra calculation
- #2995: ENH: Use int shape
- #3006: DOC: stats: add a log base note to the docstring
- #3007: DEP: stats: Deprecate randwppf and randwcdf
- #3008: Fix mstats.kurtosistest, and test coverage for skewtest/normaltest
- #3009: Minor reST typo
- #3010: Add *scipy.optimize.Result* to API docs
- #3012: Corrects documentation error
- #3052: PEP-8 conformance improvements
- #3064: Binned statistic
- #3068: Fix Issue #3067 fix cumptrapz that was raising an exception when...
- #3073: Arff reader with nominal value of 1 character
- #3074: Some maintenance work
- #3080: Review and clean up all Box-Cox functions
- #3083: Bug: should return 0 if no regions found
- #3085: BUG: Use zpk in IIR filter design to improve accuracy
- #3101: refactor stats tests a bit
- #3112: ENH: implement Akima interpolation in 1D
- #3123: MAINT: an easier way to make ranges from slices
- #3124: File object support for imread and imsave
- #3126: pep8ify stats/distributions.py
- #3134: MAINT: split distributions.py into three files
- #3138: clean up tests for discrete distributions
- #3155: special: handle the edge case lambda=0 in pdtr, pdtrc and pdtrik
- #3156: Rename optimize.Result to OptimizeResult

- #3166: BUG: make curve_fit() work with array_like input. Closes gh-3037.
- #3170: Fix numpy version checks
- #3175: use numpy sinc
- #3177: Update numpy version warning, remove oldnumeric import
- #3178: DEP: remove deprecated umfpack wrapper. Closes gh-3002.
- #3179: DOC: add BPoly to the docs
- #3180: Suppress warnings when running stats.test()
- #3181: altered sem func in mstats to match stats
- #3182: Make weave tests behave
- #3183: ENH: Add k-sample Anderson-Darling test to stats module
- #3186: Fix stats.scoreatpercentile
- #3187: DOC: make curve_fit nomenclature same as leastsq
- #3201: Added axis keyword to dendrogram function
- #3207: Make docstring examples in stats.distributions docstrings runnable
- #3218: BUG: integrate: Fix banded jacobian handling in the “vode” and...
- #3222: BUG: limit input ranges in special.nctdtr
- #3223: Fix test errors with numpy master
- #3224: Fix int32 overflows in sparsetools
- #3228: DOC: tf2ss zpk2ss note controller canonical form
- #3234: Add See Also links and Example graphs to filter design `*ord` functions
- #3235: Updated the buttord function to be consistent with the other...
- #3239: correct doc for pchip interpolation
- #3240: DOC: fix ReST errors in the BPoly docstring
- #3241: RF: check write attr of fileobject without writing
- #3243: a bit of maintanence work in stats
- #3245: BUG/ENH: stats: make frozen distributions hold separate instances
- #3247: ENH function to return nnz per row/column in some sparse matrices
- #3248: ENH much more efficient sparse min/max with axis
- #3252: Fast sqeuclidean
- #3253: FIX support axis=-1 and -2 for sparse reduce methods
- #3254: TST tests for non-canonical input to sparse matrix operations
- #3272: BUG: sparse: fix bugs in dia_matrix.setdiag
- #3278: Also generate a tar.xz when running paver sdist
- #3286: DOC: update 0.14.0 release notes.
- #3289: TST: remove insecure mktemp use in tests
- #3292: MAINT: fix a backwards incompatible change to stats.distributions.__all__

- #3293: ENH: signal: Allow upsweeps of frequency in the ‘hyperbolic’...
- #3302: ENH: add dtype arg to stats.mstats.gmean and stats.mstats.hmean
- #3307: DOC: add note about different ba forms in tf2zpk
- #3309: doc enhancements to scipy.stats.mstats.winsorize
- #3310: DOC: clarify matrix vs array in mmio docstrings
- #3314: BUG: fix scipy.io.mmread() of gzipped files under Python3
- #3323: ENH: Efficient interpolation on regular grids in arbitrary dimensions
- #3332: DOC: clean up scipy.special docs
- #3335: ENH: improve nanmedian performance
- #3347: BUG: fix use of np.max in stats.fisher_exact
- #3356: ENH: sparse: speed up LIL indexing + assignment via Cython
- #3357: Fix “imresize does not work with size = int”
- #3358: MAINT: rename AkimaInterpolator to Akima1DInterpolator
- #3366: WHT: sparse: reindent `dsolve/*.c *.h`
- #3367: BUG: sparse/dsolve: fix dense matrix fortran order bugs in superlu...
- #3369: ENH minimize, minimize_scalar: Add support for user-provided...
- #3371: scipy.stats.sigmaclip doesn’t appear in the html docs.
- #3373: BUG: sparse/dsolve: detect invalid LAPACK parameters in superlu...
- #3375: ENH: sparse/dsolve: make the L and U factors of splu and spilu...
- #3377: MAINT: make travis build one target against Numpy 1.5
- #3378: MAINT: fftpack: Remove the use of `'import *'` in a couple test...
- #3381: MAINT: replace np.isinf(x) & (x>0) -> np.isposinf(x) to avoid...
- #3383: MAINT: skip float96 tests on platforms without float96
- #3384: MAINT: add pyflakes to Travis-CI
- #3386: BUG: stable evaluation of expit
- #3388: BUG: SuperLU: fix missing declaration of dlamch
- #3389: BUG: sparse: downcast 64-bit indices safely to intp when required
- #3390: BUG: nonlinear solvers are not confused by lucky guess
- #3391: TST: fix sparse test errors due to axis=-1,-2 usage in np.matrix.sum().
- #3392: BUG: sparse/lil: fix up Cython bugs in fused type lookup
- #3393: BUG: sparse/compressed: work around bug in np.unique in earlier...
- #3394: BUG: allow ClusterNode.pre_order() for non-root nodes
- #3400: BUG: cluster.linkage ValueError typo bug
- #3402: BUG: special: In specfun.f, replace the use of CMPLX with DCMPLX,...
- #3408: MAINT: sparse: Numpy 1.5 compatibility fixes
- #3410: MAINT: interpolate: fix blas defs in _ppoly

- #3411: MAINT: Numpy 1.5 fixes in interpolate
- #3413: Fix more test issues with older numpy versions
- #3414: TST: signal: loosen some error tolerances in the filter tests....
- #3415: MAINT: tools: automated close issue + pr listings for release...
- #3440: MAINT: wrap sparsetools manually instead via SWIG
- #3460: TST: open image file in binary mode
- #3467: BUG: fix validation in csgraph.shortest_path

4.4 SciPy 0.13.2 Release Notes

SciPy 0.13.2 is a bug-fix release with no new features compared to 0.13.1.

4.4.1 Issues fixed

- 3096: require Cython 0.19, earlier versions have memory leaks in fused types
- 3079: `ndimage.label` fix swapped 64-bitness test
- 3108: `optimize.fmin_slsqp` constraint violation

4.5 SciPy 0.13.1 Release Notes

SciPy 0.13.1 is a bug-fix release with no new features compared to 0.13.0. The only changes are several fixes in `ndimage`, one of which was a serious regression in `ndimage.label` (Github issue 3025), which gave incorrect results in 0.13.0.

4.5.1 Issues fixed

- 3025: `ndimage.label` returns incorrect results in scipy 0.13.0
- 1992: `ndimage.label` return type changed from int32 to uint32
- 1992: `ndimage.find_objects` doesn't work with int32 input in some cases

4.6 SciPy 0.13.0 Release Notes

Contents

SciPy 0.13.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.13.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Highlights of this release are:

- support for fancy indexing and boolean comparisons with sparse matrices
- interpolative decompositions and matrix functions in the linalg module
- two new trust-region solvers for unconstrained minimization

4.6.1 New features

`scipy.integrate` improvements

N-dimensional numerical integration

A new function `scipy.integrate.nquad`, which provides N-dimensional integration functionality with a more flexible interface than `dblquad` and `tplquad`, has been added.

`dopri*` improvements

The intermediate results from the `dopri` family of ODE solvers can now be accessed by a *solout* callback function.

`scipy.linalg` improvements

Interpolative decompositions

Scipy now includes a new module `scipy.linalg.interpolative` containing routines for computing interpolative matrix decompositions (ID). This feature is based on the ID software package by P.G. Martinsson, V. Rokhlin, Y. Shkolnisky, and M. Tygert, previously adapted for Python in the PymatrixId package by K.L. Ho.

Polar decomposition

A new function `scipy.linalg.polar`, to compute the polar decomposition of a matrix, was added.

BLAS level 3 functions

The BLAS functions `symm`, `syrk`, `syr2k`, `hemm`, `herk` and `her2k` are now wrapped in `scipy.linalg`.

Matrix functions

Several matrix function algorithms have been implemented or updated following detailed descriptions in recent papers of Nick Higham and his co-authors. These include the matrix square root (`sqrtm`), the matrix logarithm (`logm`), the matrix exponential (`expm`) and its Frechet derivative (`expm_frechet`), and fractional matrix powers (`fractional_matrix_power`).

`scipy.optimize` improvements

Trust-region unconstrained minimization algorithms

The `minimize` function gained two trust-region solvers for unconstrained minimization: `dogleg` and `trust-ncg`.

`scipy.sparse` improvements

Boolean comparisons and sparse matrices

All sparse matrix types now support boolean data, and boolean operations. Two sparse matrices A and B can be compared in all the expected ways $A < B$, $A >= B$, $A \,!= B$, producing similar results as dense Numpy arrays. Comparisons with dense matrices and scalars are also supported.

CSR and CSC fancy indexing

Compressed sparse row and column sparse matrix types now support fancy indexing with boolean matrices, slices, and lists. So where A is a (CSC or CSR) sparse matrix, you can do things like:

```
>>> A[A > 0.5] = 1  # since Boolean sparse matrices work
>>> A[:2, :3] = 2
>>> A[[1,2], 2] = 3
```

`scipy.sparse.linalg` improvements

The new function `onenormest` provides a lower bound of the 1-norm of a linear operator and has been implemented according to Higham and Tisseur (2000). This function is not only useful for sparse matrices, but can also be used to estimate the norm of products or powers of dense matrices without explicitly building the intermediate matrix.

The multiplicative action of the matrix exponential of a linear operator (`expm_multiply`) has been implemented following the description in Al-Mohy and Higham (2011).

Abstract linear operators (`scipy.sparse.linalg.LinearOperator`) can now be multiplied, added to each other, and exponentiated, producing new linear operators. This enables easier construction of composite linear operations.

`scipy.spatial` improvements

The vertices of a *ConvexHull* can now be accessed via the *vertices* attribute, which gives proper orientation in 2-D.

`scipy.signal` improvements

The cosine window function `scipy.signal.cosine` was added.

`scipy.special` improvements

New functions `scipy.special.xlogy` and `scipy.special.xlog1py` were added. These functions can simplify and speed up code that has to calculate `x * log(y)` and give 0 when `x == 0`.

`scipy.io` improvements

Unformatted Fortran file reader

The new class `scipy.io.FortranFile` facilitates reading unformatted sequential files written by Fortran code.

`scipy.io.wavfile` *enhancements*

`scipy.io.wavfile.write` now accepts a file buffer. Previously it only accepted a filename.

`scipy.io.wavfile.read` and `scipy.io.wavfile.write` can now handle floating point WAV files.

`scipy.interpolate` improvements

B-spline derivatives and antiderivatives

`scipy.interpolate.splder` and `scipy.interpolate.splantider` functions for computing B-splines that represent derivatives and antiderivatives of B-splines were added. These functions are also available in the class-based FITPACK interface as `UnivariateSpline.derivative` and `UnivariateSpline.antiderivative`.

`scipy.stats` improvements

Distributions now allow using keyword parameters in addition to positional parameters in all methods.

The function `scipy.stats.power_divergence` has been added for the Cressie-Read power divergence statistic and goodness of fit test. Included in this family of statistics is the "G-test" (http://en.wikipedia.org/wiki/G-test).

`scipy.stats.mood` now accepts multidimensional input.

An option was added to `scipy.stats.wilcoxon` for continuity correction.

`scipy.stats.chisquare` now has an *axis* argument.

`scipy.stats.mstats.chisquare` now has *axis* and *ddof* arguments.

4.6.2 Deprecated features

`expm2` and `expm3`

The matrix exponential functions `scipy.linalg.expm2` and `scipy.linalg.expm3` are deprecated. All users should use the numerically more robust `scipy.linalg.expm` function instead.

`scipy.stats` functions

scipy.stats.oneway is deprecated; `scipy.stats.f_oneway` should be used instead.

scipy.stats.glm is deprecated. `scipy.stats.ttest_ind` is an equivalent function; more full-featured general (and generalized) linear model implementations can be found in statsmodels.

scipy.stats.cmedian is deprecated; `numpy.median` should be used instead.

4.6.3 Backwards incompatible changes

LIL matrix assignment

Assigning values to LIL matrices with two index arrays now works similarly as assigning into ndarrays:

```
>>> x = lil_matrix((3, 3))
>>> x[[0,1,2],[0,1,2]]=[0,1,2]
>>> x.todense()
matrix([[ 0.,  0.,  0.],
        [ 0.,  1.,  0.],
        [ 0.,  0.,  2.]])
```

rather than giving the result:

```
>>> x.todense()
matrix([[ 0.,  1.,  2.],
        [ 0.,  1.,  2.],
        [ 0.,  1.,  2.]])
```

Users relying on the previous behavior will need to revisit their code. The previous behavior is obtained by `x[numpy.ix_([0,1,2],[0,1,2])] = ...`.

Deprecated `radon` function removed

The `misc.radon` function, which was deprecated in scipy 0.11.0, has been removed. Users can find a more full-featured `radon` function in scikit-image.

Removed deprecated keywords `xa` and `xb` from `stats.distributions`

The keywords `xa` and `xb`, which were deprecated since 0.11.0, have been removed from the distributions in `scipy.stats`.

Changes to MATLAB file readers / writers

The major change is that 1D arrays in numpy now become row vectors (shape 1, N) when saved to a MATLAB 5 format file. Previously 1D arrays saved as column vectors (N, 1). This is to harmonize the behavior of writing MATLAB 4 and 5 formats, and adapt to the defaults of numpy and MATLAB - for example `np.atleast_2d` returns 1D arrays as row vectors.

Trying to save arrays of greater than 2 dimensions in MATLAB 4 format now raises an error instead of silently reshaping the array as 2D.

`scipy.io.loadmat('afile')` used to look for *afile* on the Python system path (`sys.path`); now `loadmat` only looks in the current directory for a relative path filename.

4.6.4 Other changes

Security fix: `scipy.weave` previously used temporary directories in an insecure manner under certain circumstances.

Cython is now required to build *unreleased* versions of scipy. The C files generated from Cython sources are not included in the git repo anymore. They are however still shipped in source releases.

The code base received a fairly large PEP8 cleanup. A `tox pep8` command has been added; new code should pass this test command.

Scipy cannot be compiled with gfortran 4.1 anymore (at least on RH5), likely due to that compiler version not supporting entry constructs well.

4.6.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jorge Cañardo Alastuey +
- Tom Aldcroft +
- Max Bolingbroke +
- Joseph Jon Booker +
- François Boulogne
- Matthew Brett
- Christian Brodbeck +
- Per Brodtkorb +

- Christian Brueffer +
- Lars Buitinck
- Evgeni Burovski +
- Tim Cera
- Lawrence Chan +
- David Cournapeau
- Drazen Lucanin +
- Alexander J. Dunlap +
- endolith
- André Gaul +
- Christoph Gohlke
- Ralf Gommers
- Alex Griffing +
- Blake Griffith +
- Charles Harris
- Bob Helmbold +
- Andreas Hilboll
- Kat Huang +
- Oleksandr (Sasha) Huziy +
- Gert-Ludwig Ingold +
- Thouis (Ray) Jones
- Juan Luis Cano Rodríguez +
- Robert Kern
- Andreas Kloeckner +
- Sytse Knypstra +
- Gustav Larsson +
- Denis Laxalde
- Christopher Lee
- Tim Leslie
- Wendy Liu +
- Clemens Novak +
- Takuya Oshima +
- Josef Perktold
- Illia Polosukhin +
- Przemek Porebski +
- Steve Richardson +

- Branden Rolston +
- Skipper Seabold
- Fazlul Shahriar
- Leo Singer +
- Rohit Sivaprasad +
- Daniel B. Smith +
- Julian Taylor
- Louis Thibault +
- Tomas Tomecek +
- John Travers
- Richard Tsai +
- Jacob Vanderplas
- Patrick Varilly
- Pauli Virtanen
- Stefan van der Walt
- Warren Weckesser
- Pedro Werneck +
- Nils Werner +
- Michael Wimmer +
- Nathan Woods +
- Tony S. Yu +

A total of 65 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

4.7 SciPy 0.12.1 Release Notes

SciPy 0.12.1 is a bug-fix release with no new features compared to 0.12.0. The single issue fixed by this release is a security issue in `scipy.weave`, which was previously using temporary directories in an insecure manner under certain circumstances.

4.8 SciPy 0.12.0 Release Notes

Contents

SciPy 0.12.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.12.x branch, and on adding new features on the master branch.

Some of the highlights of this release are:

- Completed QHull wrappers in scipy.spatial.
- cKDTree now a drop-in replacement for KDTree.
- A new global optimizer, basinhopping.
- Support for Python 2 and Python 3 from the same code base (no more 2to3).

This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Support for Python 2.4 and 2.5 has been dropped as of this release.

4.8.1 New features

`scipy.spatial` improvements

cKDTree feature-complete

Cython version of KDTree, cKDTree, is now feature-complete. Most operations (construction, query, query_ball_point, query_pairs, count_neighbors and sparse_distance_matrix) are between 200 and 1000 times faster in cKDTree than in KDTree. With very minor caveats, cKDTree has exactly the same interface as KDTree, and can be used as a drop-in replacement.

Voronoi diagrams and convex hulls

`scipy.spatial` now contains functionality for computing Voronoi diagrams and convex hulls using the Qhull library. (Delaunay triangulation was available since Scipy 0.9.0.)

Delaunay improvements

It's now possible to pass in custom Qhull options in Delaunay triangulation. Coplanar points are now also recorded, if present. Incremental construction of Delaunay triangulations is now also possible.

Spectral estimators (`scipy.signal`)

The functions `scipy.signal.periodogram` and `scipy.signal.welch` were added, providing DFT-based spectral estimators.

`scipy.optimize` improvements

Callback functions in L-BFGS-B and TNC

A callback mechanism was added to L-BFGS-B and TNC minimization solvers.

Basin hopping global optimization (`scipy.optimize.basinhopping`)

A new global optimization algorithm. Basinhopping is designed to efficiently find the global minimum of a smooth function.

`scipy.special` improvements

Revised complex error functions

The computation of special functions related to the error function now uses a new Faddeeva library from MIT which increases their numerical precision. The scaled and imaginary error functions `erfcx` and `erfi` were also added, and the Dawson integral `dawsn` can now be evaluated for a complex argument.

Faster orthogonal polynomials

Evaluation of orthogonal polynomials (the `eval_*` routines) in now faster in `scipy.special`, and their `out=` argument functions properly.

`scipy.sparse.linalg` features

- In `scipy.sparse.linalg.spsolve`, the `b` argument can now be either a vector or a matrix.
- `scipy.sparse.linalg.inv` was added. This uses `spsolve` to compute a sparse matrix inverse.
- `scipy.sparse.linalg.expm` was added. This computes the exponential of a sparse matrix using a similar algorithm to the existing dense array implementation in `scipy.linalg.expm`.

Listing Matlab(R) file contents in `scipy.io`

A new function `whosmat` is available in `scipy.io` for inspecting contents of MAT files without reading them to memory.

Documented BLAS and LAPACK low-level interfaces (`scipy.linalg`)

The modules `scipy.linalg.blas` and `scipy.linalg.lapack` can be used to access low-level BLAS and LAPACK functions.

Polynomial interpolation improvements (`scipy.interpolate`)

The barycentric, Krogh, piecewise and pchip polynomial interpolators in `scipy.interpolate` accept now an `axis` argument.

4.8.2 Deprecated features

`scipy.lib.lapack`

The module `scipy.lib.lapack` is deprecated. You can use `scipy.linalg.lapack` instead. The module `scipy.lib.blas` was deprecated earlier in Scipy 0.10.0.

fblas and *cblas*

Accessing the modules `scipy.linalg.fblas`, *cblas*, *flapack*, *clapack* is deprecated. Instead, use the modules `scipy.linalg.lapack` and `scipy.linalg.blas`.

4.8.3 Backwards incompatible changes

Removal of `scipy.io.save_as_module`

The function `scipy.io.save_as_module` was deprecated in Scipy 0.11.0, and is now removed.

Its private support modules `scipy.io.dumbdbm_patched` and `scipy.io.dumb_shelve` are also removed.

axis argument added to `scipy.stats.scoreatpercentile`

The function `scipy.stats.scoreatpercentile` has been given an *axis* argument. The default argument is *axis=None*, which means the calculation is done on the flattened array. Before this change, *scoreatpercentile* would act as if *axis=0* had been given. Code using *scoreatpercentile* with a multidimensional array will need to add *axis=0* to the function call to preserve the old behavior. (This API change was not noticed until long after the release of 0.12.0.)

4.8.4 Authors

- Anton Akhmerov +
- Alexander Eberspächer +
- Anne Archibald
- Jisk Attema +
- K.-Michael Aye +
- bemasc +
- Sebastian Berg +

- François Boulogne +
- Matthew Brett
- Lars Buitinck
- Steven Byrnes +
- Tim Cera +
- Christian +
- Keith Clawson +
- David Cournapeau
- Nathan Crock +
- endolith
- Bradley M. Froehle +
- Matthew R Goodman
- Christoph Gohlke
- Ralf Gommers
- Robert David Grant +
- Yaroslav Halchenko
- Charles Harris
- Jonathan Helmus
- Andreas Hilboll
- Hugo +
- Oleksandr Huziy
- Jeroen Demeyer +
- Johannes Schönberger +
- Steven G. Johnson +
- Chris Jordan-Squire
- Jonathan Taylor +
- Niklas Kroeger +
- Jerome Kieffer +
- kingson +
- Josh Lawrence
- Denis Laxalde
- Alex Leach +
- Tim Leslie
- Richard Lindsley +
- Lorenzo Luengo +
- Stephen McQuay +

- MinRK
- Sturla Molden +
- Eric Moore +
- mszep +
- Matt Newville +
- Vlad Niculae
- Travis Oliphant
- David Parker +
- Fabian Pedregosa
- Josef Perktold
- Zach Ploskey +
- Alex Reinhart +
- Gilles Rochefort +
- Ciro Duran Santillli +
- Jan Schlueter +
- Jonathan Scholz +
- Anthony Scopatz
- Skipper Seabold
- Fabrice Silva +
- Scott Sinclair
- Jacob Stevenson +
- Sturla Molden +
- Julian Taylor +
- thorstenkranz +
- John Travers +
- True Price +
- Nicky van Foreest
- Jacob Vanderplas
- Patrick Varilly
- Daniel Velkov +
- Pauli Virtanen
- Stefan van der Walt
- Warren Weckesser

A total of 75 people contributed to this release. People with a “+” by their names contributed a patch for the first time.

4.9 SciPy 0.11.0 Release Notes

Contents

SciPy 0.11.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. Highlights of this release are:

- A new module has been added which provides a number of common sparse graph algorithms.
- New unified interfaces to the existing optimization and root finding functions have been added.

All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Our development attention will now shift to bug-fix releases on the 0.11.x branch, and on adding new features on the master branch.

This release requires Python 2.4-2.7 or 3.1-3.2 and NumPy 1.5.1 or greater.

4.9.1 New features

Sparse Graph Submodule

The new submodule `scipy.sparse.csgraph` implements a number of efficient graph algorithms for graphs stored as sparse adjacency matrices. Available routines are:

- `connected_components` - determine connected components of a graph
- `laplacian` - compute the laplacian of a graph
- `shortest_path` - compute the shortest path between points on a positive graph
- `dijkstra` - use Dijkstra's algorithm for shortest path

- `floyd_warshall` - use the Floyd-Warshall algorithm for shortest path
- `breadth_first_order` - compute a breadth-first order of nodes
- `depth_first_order` - compute a depth-first order of nodes
- `breadth_first_tree` - construct the breadth-first tree from a given node
- `depth_first_tree` - construct a depth-first tree from a given node
- `minimum_spanning_tree` - construct the minimum spanning tree of a graph

`scipy.optimize` improvements

The optimize module has received a lot of attention this release. In addition to added tests, documentation improvements, bug fixes and code clean-up, the following improvements were made:

- A unified interface to minimizers of univariate and multivariate functions has been added.
- A unified interface to root finding algorithms for multivariate functions has been added.
- The L-BFGS-B algorithm has been updated to version 3.0.

Unified interfaces to minimizers

Two new functions `scipy.optimize.minimize` and `scipy.optimize.minimize_scalar` were added to provide a common interface to minimizers of multivariate and univariate functions respectively. For multivariate functions, `scipy.optimize.minimize` provides an interface to methods for unconstrained optimization (*fmin*, *fmin_powell*, *fmin_cg*, *fmin_ncg*, *fmin_bfgs* and *anneal*) or constrained optimization (*fmin_l_bfgs_b*, *fmin_tnc*, *fmin_cobyla* and *fmin_slsqp*). For univariate functions, `scipy.optimize.minimize_scalar` provides an interface to methods for unconstrained and bounded optimization (*brent*, *golden*, *fminbound*). This allows for easier comparing and switching between solvers.

Unified interface to root finding algorithms

The new function `scipy.optimize.root` provides a common interface to root finding algorithms for multivariate functions, embeding *fsolve*, *leastsq* and *nonlin* solvers.

`scipy.linalg` improvements

New matrix equation solvers

Solvers for the Sylvester equation (`scipy.linalg.solve_sylvester`, discrete and continuous Lyapunov equations (`scipy.linalg.solve_lyapunov`, `scipy.linalg.solve_discrete_lyapunov`) and discrete and continuous algebraic Riccati equations (`scipy.linalg.solve_continuous_are`, `scipy.linalg.solve_discrete_are`) have been added to `scipy.linalg`. These solvers are often used in the field of linear control theory.

QZ and QR Decomposition

It is now possible to calculate the QZ, or Generalized Schur, decomposition using `scipy.linalg.qz`. This function wraps the LAPACK routines sgges, dgges, cgges, and zgges.

The function `scipy.linalg.qr_multiply`, which allows efficient computation of the matrix product of Q (from a QR decomposition) and a vector, has been added.

Pascal matrices

A function for creating Pascal matrices, `scipy.linalg.pascal`, was added.

Sparse matrix construction and operations

Two new functions, `scipy.sparse.diags` and `scipy.sparse.block_diag`, were added to easily construct diagonal and block-diagonal sparse matrices respectively.

`scipy.sparse.csc_matrix` and `csr_matrix` now support the operations `sin`, `tan`, `arcsin`, `arctan`, `sinh`, `tanh`, `arcsinh`, `arctanh`, `rint`, `sign`, `expm1`, `log1p`, `deg2rad`, `rad2deg`, `floor`, `ceil` and `trunc`. Previously, these operations had to be performed by operating on the matrices' `data` attribute.

LSMR iterative solver

LSMR, an iterative method for solving (sparse) linear and linear least-squares systems, was added as `scipy.sparse.linalg.lsmr`.

Discrete Sine Transform

Bindings for the discrete sine transform functions have been added to `scipy.fftpack`.

`scipy.interpolate` improvements

For interpolation in spherical coordinates, the three classes `scipy.interpolate.SmoothSphereBivariateSpline`, `scipy.interpolate.LSQSphereBivariateSpline`, and `scipy.interpolate.RectSphereBivariateSpline` have been added.

Binned statistics (`scipy.stats`)

The stats module has gained functions to do binned statistics, which are a generalization of histograms, in 1-D, 2-D and multiple dimensions: `scipy.stats.binned_statistic`, `scipy.stats.binned_statistic_2d` and `scipy.stats.binned_statistic_dd`.

4.9.2 Deprecated features

`scipy.sparse.cs_graph_components` has been made a part of the sparse graph submodule, and renamed to `scipy.sparse.csgraph.connected_components`. Calling the former routine will result in a deprecation warning.

`scipy.misc.radon` has been deprecated. A more full-featured radon transform can be found in scikits-image.

`scipy.io.save_as_module` has been deprecated. A better way to save multiple Numpy arrays is the `numpy.savez` function.

The *xa* and *xb* parameters for all distributions in `scipy.stats.distributions` already weren't used; they have now been deprecated.

4.9.3 Backwards incompatible changes

Removal of `scipy.maxentropy`

The `scipy.maxentropy` module, which was deprecated in the 0.10.0 release, has been removed. Logistic regression in scikits.learn is a good and modern alternative for this functionality.

Minor change in behavior of `splev`

The spline evaluation function now behaves similarly to `interp1d` for size-1 arrays. Previous behavior:

```
>>> from scipy.interpolate import splev, splrep, interp1d
>>> x = [1,2,3,4,5]
>>> y = [4,5,6,7,8]
>>> tck = splrep(x, y)
>>> splev([1], tck)
4.
>>> splev(1, tck)
4.
```

Corrected behavior:

```
>>> splev([1], tck)
array([ 4.])
>>> splev(1, tck)
array(4.)
```

This affects also the `UnivariateSpline` classes.

Behavior of `scipy.integrate.complex_ode`

The behavior of the `y` attribute of `complex_ode` is changed. Previously, it expressed the complex-valued solution in the form:

```
z = ode.y[::2] + 1j * ode.y[1::2]
```

Now, it is directly the complex-valued solution:

```
z = ode.y
```

Minor change in behavior of T-tests

The T-tests `scipy.stats.ttest_ind`, `scipy.stats.ttest_rel` and `scipy.stats.ttest_1samp` have been changed so that 0 / 0 now returns NaN instead of 1.

4.9.4 Other changes

The SuperLU sources in `scipy.sparse.linalg` have been updated to version 4.3 from upstream.

The function `scipy.signal.bode`, which calculates magnitude and phase data for a continuous-time system, has been added.

The two-sample T-test `scipy.stats.ttest_ind` gained an option to compare samples with unequal variances, i.e. Welch's T-test.

`scipy.misc.logsumexp` now takes an optional `axis` keyword argument.

4.9.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jeff Armstrong

- Chad Baker
- Brandon Beacher +
- behrisch +
- borishim +
- Matthew Brett
- Lars Buitinck
- Luis Pedro Coelho +
- Johann Cohen-Tanugi
- David Cournapeau
- dougal +
- Ali Ebrahim +
- endolith +
- Bjørn Forsman +
- Robert Gantner +
- Sebastian Gassner +
- Christoph Gohlke
- Ralf Gommers
- Yaroslav Halchenko
- Charles Harris
- Jonathan Helmus +
- Andreas Hilboll +
- Marc Honnorat +
- Jonathan Hunt +
- Maxim Ivanov +
- Thouis (Ray) Jones
- Christopher Kuster +
- Josh Lawrence +
- Denis Laxalde +
- Travis Oliphant
- Joonas Paalasmaa +
- Fabian Pedregosa
- Josef Perktold
- Gavin Price +
- Jim Radford +
- Andrew Schein +
- Skipper Seabold

- Jacob Silterra +
- Scott Sinclair
- Alexis Tabary +
- Martin Teichmann
- Matt Terry +
- Nicky van Foreest +
- Jacob Vanderplas
- Patrick Varilly +
- Pauli Virtanen
- Nils Wagner +
- Darryl Wally +
- Stefan van der Walt
- Liming Wang +
- David Warde-Farley +
- Warren Weckesser
- Sebastian Werk +
- Mike Wimmer +
- Tony S Yu +

A total of 55 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

4.10 SciPy 0.10.1 Release Notes

Contents

SciPy 0.10.1 is a bug-fix release with no new features compared to 0.10.0.

4.10.1 Main changes

The most important changes are:

1. The single precision routines of `eigs` and `eigsh` in `scipy.sparse.linalg` have been disabled (they internally use double precision now).
2. A compatibility issue related to changes in NumPy macros has been fixed, in order to make scipy 0.10.1 compile with the upcoming numpy 1.7.0 release.

4.10.2 Other issues fixed

- #835: stats: nan propagation in stats.distributions
- #1202: io: netcdf segfault
- #1531: optimize: make curve_fit work with method as callable.
- #1560: linalg: fixed mistake in eig_banded documentation.
- #1565: ndimage: bug in ndimage.variance
- #1457: ndimage: standard_deviation does not work with sequence of indexes
- #1562: cluster: segfault in linkage function
- #1568: stats: One-sided fisher_exact() returns $p < 1$ for 0 successful attempts
- #1575: stats: zscore and zmap handle the axis keyword incorrectly

4.11 SciPy 0.10.0 Release Notes

Contents

SciPy 0.10.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a limited number of deprecations and backwards-incompatible changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.10.x branch, and on adding new features on the development master branch.

Release highlights:

- Support for Bento as optional build system.
- Support for generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

This release requires Python 2.4-2.7 or 3.1- and NumPy 1.5 or greater.

4.11.1 New features

Bento: new optional build system

Scipy can now be built with Bento. Bento has some nice features like parallel builds and partial rebuilds, that are not possible with the default build system (distutils). For usage instructions see BENTO_BUILD.txt in the scipy top-level directory.

Currently Scipy has three build systems, distutils, numscons and bento. Numscons is deprecated and is planned and will likely be removed in the next release.

Generalized and shift-invert eigenvalue problems in `scipy.sparse.linalg`

The sparse eigenvalue problem solver functions `scipy.sparse.eigs/eigh` now support generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

Discrete-Time Linear Systems (`scipy.signal`)

Support for simulating discrete-time linear systems, including `scipy.signal.dlsim`, `scipy.signal.dimpulse`, and `scipy.signal.dstep`, has been added to SciPy. Conversion of linear systems from continuous-time to discrete-time representations is also present via the `scipy.signal.cont2discrete` function.

Enhancements to `scipy.signal`

A Lomb-Scargle periodogram can now be computed with the new function `scipy.signal.lombscargle`.

The forward-backward filter function `scipy.signal.filtfilt` can now filter the data in a given axis of an n-dimensional numpy array. (Previously it only handled a 1-dimensional array.) Options have been added to allow more control over how the data is extended before filtering.

FIR filter design with `scipy.signal.firwin2` now has options to create filters of type III (zero at zero and Nyquist frequencies) and IV (zero at zero frequency).

Additional decomposition options (`scipy.linalg`)

A sort keyword has been added to the Schur decomposition routine (`scipy.linalg.schur`) to allow the sorting of eigenvalues in the resultant Schur form.

Additional special matrices (`scipy.linalg`)

The functions `hilbert` and `invhilbert` were added to `scipy.linalg`.

Enhancements to `scipy.stats`

- The *one-sided form* of Fisher's exact test is now also implemented in `stats.fisher_exact`.
- The function `stats.chi2_contingency` for computing the chi-square test of independence of factors in a contingency table has been added, along with the related utility functions `stats.contingency.margins` and `stats.contingency.expected_freq`.

Enhancements to `scipy.special`

The functions `logit(p) = log(p/(1-p))` and `expit(x) = 1/(1+exp(-x))` have been implemented as `scipy.special.logit` and `scipy.special.expit` respectively.

Basic support for Harwell-Boeing file format for sparse matrices

Both read and write are support through a simple function-based API, as well as a more complete API to control number format. The functions may be found in scipy.sparse.io.

The following features are supported:

- Read and write sparse matrices in the CSC format
- Only real, symmetric, assembled matrix are supported (RUA format)

4.11.2 Deprecated features

`scipy.maxentropy`

The maxentropy module is unmaintained, rarely used and has not been functioning well for several releases. Therefore it has been deprecated for this release, and will be removed for scipy 0.11. Logistic regression in scikits.learn is a good alternative for this functionality. The `scipy.maxentropy.logsumexp` function has been moved to `scipy.misc`.

`scipy.lib.blas`

There are similar BLAS wrappers in `scipy.linalg` and `scipy.lib`. These have now been consolidated as `scipy.linalg.blas`, and `scipy.lib.blas` is deprecated.

Numscons build system

The numscons build system is being replaced by Bento, and will be removed in one of the next scipy releases.

4.11.3 Backwards-incompatible changes

The deprecated name *invnorm* was removed from `scipy.stats.distributions`, this distribution is available as *invgauss*.

The following deprecated nonlinear solvers from `scipy.optimize` have been removed:

```
- ``broyden_modified`` (bad performance)
- ``broyden1_modified`` (bad performance)
- ``broyden_generalized`` (equivalent to ``anderson``)
- ``anderson2`` (equivalent to ``anderson``)
- ``broyden3`` (obsoleted by new limited-memory broyden methods)
- ``vackar`` (renamed to ``diagbroyden``)
```

4.11.4 Other changes

`scipy.constants` has been updated with the CODATA 2010 constants.

`__all__` dicts have been added to all modules, which has cleaned up the namespaces (particularly useful for interactive work).

An API section has been added to the documentation, giving recommended import guidelines and specifying which submodules are public and which aren't.

4.11.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jeff Armstrong +
- Matthew Brett
- Lars Buitinck +
- David Cournapeau
- FI$H 2000 +
- Michael McNeil Forbes +
- Matty G +
- Christoph Gohlke
- Ralf Gommers
- Yaroslav Halchenko
- Charles Harris
- Thouis (Ray) Jones +
- Chris Jordan-Squire +
- Robert Kern
- Chris Lasher +
- Wes McKinney +
- Travis Oliphant
- Fabian Pedregosa
- Josef Perktold
- Thomas Robitaille +
- Pim Schellart +
- Anthony Scopatz +
- Skipper Seabold +
- Fazlul Shahriar +
- David Simcha +
- Scott Sinclair +

- Andrey Smirnov +
- Collin RM Stocks +
- Martin Teichmann +
- Jake Vanderplas +
- Gaël Varoquaux +
- Pauli Virtanen
- Stefan van der Walt
- Warren Weckesser
- Mark Wiebe +

A total of 35 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

4.12 SciPy 0.9.0 Release Notes

Contents

SciPy 0.9.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.9.x branch, and on adding new features on the development trunk.

This release requires Python 2.4 - 2.7 or 3.1 - and NumPy 1.5 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

4.12.1 Python 3

Scipy 0.9.0 is the first SciPy release to support Python 3. The only module that is not yet ported is `scipy.weave`.

4.12.2 Scipy source code location to be changed

Soon after this release, Scipy will stop using SVN as the version control system, and move to Git. The development source code for Scipy can from then on be found at

> http://github.com/scipy/scipy

4.12.3 New features

Delaunay tesselations (`scipy.spatial`)

Scipy now includes routines for computing Delaunay tesselations in N dimensions, powered by the Qhull computational geometry library. Such calculations can now make use of the new `scipy.spatial.Delaunay` interface.

N-dimensional interpolation (`scipy.interpolate`)

Support for scattered data interpolation is now significantly improved. This version includes a `scipy.interpolate.griddata` function that can perform linear and nearest-neighbour interpolation for N-dimensional scattered data, in addition to cubic spline (C1-smooth) interpolation in 2D and 1D. An object-oriented interface to each interpolator type is also available.

Nonlinear equation solvers (`scipy.optimize`)

Scipy includes new routines for large-scale nonlinear equation solving in `scipy.optimize`. The following methods are implemented:

- Newton-Krylov (`scipy.optimize.newton_krylov`)
- (Generalized) secant methods:
  - Limited-memory Broyden methods (`scipy.optimize.broyden1`, `scipy.optimize.broyden2`)
  - Anderson method (`scipy.optimize.anderson`)
- Simple iterations (`scipy.optimize.diagbroyden`, `scipy.optimize.excitingmixing`, `scipy.optimize.linearmixing`)

The `scipy.optimize.nonlin` module was completely rewritten, and some of the functions were deprecated (see above).

New linear algebra routines (`scipy.linalg`)

Scipy now contains routines for effectively solving triangular equation systems (`scipy.linalg.solve_triangular`).

Improved FIR filter design functions (`scipy.signal`)

The function `scipy.signal.firwin` was enhanced to allow the design of highpass, bandpass, bandstop and multi-band FIR filters.

The function `scipy.signal.firwin2` was added. This function uses the window method to create a linear phase FIR filter with an arbitrary frequency response.

The functions `scipy.signal.kaiser_atten` and `scipy.signal.kaiser_beta` were added.

Improved statistical tests (`scipy.stats`)

A new function `scipy.stats.fisher_exact` was added, that provides Fisher's exact test for 2x2 contingency tables.

The function `scipy.stats.kendalltau` was rewritten to make it much faster (O(n log(n)) vs O(n^2)).

4.12.4 Deprecated features

Obsolete nonlinear solvers (in `scipy.optimize`)

The following nonlinear solvers from `scipy.optimize` are deprecated:

- `broyden_modified` (bad performance)
- `broyden1_modified` (bad performance)
- `broyden_generalized` (equivalent to `anderson`)
- `anderson2` (equivalent to `anderson`)
- `broyden3` (obsoleted by new limited-memory broyden methods)
- `vackar` (renamed to `diagbroyden`)

4.12.5 Removed features

The deprecated modules `helpmod`, `pexec` and `ppimport` were removed from `scipy.misc`.

The `output_type` keyword in many `scipy.ndimage` interpolation functions has been removed.

The `econ` keyword in `scipy.linalg.qr` has been removed. The same functionality is still available by specifying `mode='economic'`.

Old correlate/convolve behavior (in `scipy.signal`)

The old behavior for `scipy.signal.convolve`, `scipy.signal.convolve2d`, `scipy.signal.correlate` and `scipy.signal.correlate2d` was deprecated in 0.8.0 and has now been removed. Convolve and correlate used to swap their arguments if the second argument has dimensions larger than the first one, and the mode was relative to the input with the largest dimension. The current behavior is to never swap the inputs, which is what most people expect, and is how correlation is usually defined.

`scipy.stats`

Many functions in `scipy.stats` that are either available from numpy or have been superseded, and have been deprecated since version 0.7, have been removed: *std*, *var*, *mean*, *median*, *cov*, *corrcoef*, *z*, *zs*, *stderr*, *samplestd*, *samplevar*, *pdfapprox*, *pdf_moments* and *erfc*. These changes are mirrored in `scipy.stats.mstats`.

`scipy.sparse`

Several methods of the sparse matrix classes in `scipy.sparse` which had been deprecated since version 0.7 were removed: *save*, *rowcol*, *getdata*, *listprint*, *ensure_sorted_indices*, *matvec*, *matmat* and *rmatvec*.

The functions `spkron`, `speye`, `spidentity`, `lil_eye` and `lil_diags` were removed from `scipy.sparse`. The first three functions are still available as `scipy.sparse.kron`, `scipy.sparse.eye` and `scipy.sparse.identity`.

The *dims* and *nzmax* keywords were removed from the sparse matrix constructor. The *colind* and *rowind* attributes were removed from CSR and CSC matrices respectively.

`scipy.sparse.linalg.arpack.speigs`

A duplicated interface to the ARPACK library was removed.

4.12.6 Other changes

ARPACK interface changes

The interface to the ARPACK eigenvalue routines in `scipy.sparse.linalg` was changed for more robustness.

The eigenvalue and SVD routines now raise `ArpackNoConvergence` if the eigenvalue iteration fails to converge. If partially converged results are desired, they can be accessed as follows:

```
import numpy as np
from scipy.sparse.linalg import eigs, ArpackNoConvergence

m = np.random.randn(30, 30)
try:
    w, v = eigs(m, 6)
except ArpackNoConvergence, err:
    partially_converged_w = err.eigenvalues
    partially_converged_v = err.eigenvectors
```

Several bugs were also fixed.

The routines were moreover renamed as follows:

- eigen –> eigs
- eigen_symmetric –> eigsh
- svd –> svds

4.13 SciPy 0.8.0 Release Notes

Contents

SciPy 0.8.0 is the culmination of 17 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.8.x branch, and on adding new features on the development trunk. This release requires Python 2.4 - 2.6 and NumPy 1.4.1 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

4.13.1 Python 3

Python 3 compatibility is planned and is currently technically feasible, since Numpy has been ported. However, since the Python 3 compatible Numpy 1.5 has not been released yet, support for Python 3 in Scipy is not yet included in Scipy 0.8. SciPy 0.9, planned for fall 2010, will very likely include experimental support for Python 3.

4.13.2 Major documentation improvements

SciPy documentation is greatly improved.

4.13.3 Deprecated features

Swapping inputs for correlation functions (scipy.signal)

Concern correlate, correlate2d, convolve and convolve2d. If the second input is larger than the first input, the inputs are swapped before calling the underlying computation routine. This behavior is deprecated, and will be removed in scipy 0.9.0.

Obsolete code deprecated (scipy.misc)

The modules *helpmod*, *ppimport* and *pexec* from `scipy.misc` are deprecated. They will be removed from SciPy in version 0.9.

Additional deprecations

- linalg: The function *solveh_banded* currently returns a tuple containing the Cholesky factorization and the solution to the linear system. In SciPy 0.9, the return value will be just the solution.
- The function *constants.codata.find* will generate a DeprecationWarning. In Scipy version 0.8.0, the keyword argument ‘disp’ was added to the function, with the default value ‘True’. In 0.9.0, the default will be ‘False’.
- The *qshape* keyword argument of *signal.chirp* is deprecated. Use the argument *vertex_zero* instead.
- Passing the coefficients of a polynomial as the argument *f0* to *signal.chirp* is deprecated. Use the function *signal.sweep_poly* instead.
- The *io.recaster* module has been deprecated and will be removed in 0.9.0.

4.13.4 New features

DCT support (scipy.fftpack)

New realtransforms have been added, namely dct and idct for Discrete Cosine Transform; type I, II and III are available.

Single precision support for fft functions (scipy.fftpack)

fft functions can now handle single precision inputs as well: fft(x) will return a single precision array if x is single precision.

At the moment, for FFT sizes that are not composites of 2, 3, and 5, the transform is computed internally in double precision to avoid rounding error in FFTPACK.

Correlation functions now implement the usual definition (scipy.signal)

The outputs should now correspond to their matlab and R counterparts, and do what most people expect if the old_behavior=False argument is passed:

- correlate, convolve and their 2d counterparts do not swap their inputs depending on their relative shape anymore;

- correlation functions now conjugate their second argument while computing the slided sum-products, which correspond to the usual definition of correlation.

Additions and modification to LTI functions (scipy.signal)

- The functions *impulse2* and *step2* were added to `scipy.signal`. They use the function `scipy.signal.lsim2` to compute the impulse and step response of a system, respectively.
- The function `scipy.signal.lsim2` was changed to pass any additional keyword arguments to the ODE solver.

Improved waveform generators (scipy.signal)

Several improvements to the *chirp* function in `scipy.signal` were made:

- The waveform generated when *method=”logarithmic”* was corrected; it now generates a waveform that is also known as an “exponential” or “geometric” chirp. (See http://en.wikipedia.org/wiki/Chirp.)
- A new *chirp* method, “hyperbolic”, was added.
- Instead of the keyword *qshape*, *chirp* now uses the keyword *vertex_zero*, a boolean.
- *chirp* no longer handles an arbitrary polynomial. This functionality has been moved to a new function, *sweep_poly*.

A new function, *sweep_poly*, was added.

New functions and other changes in scipy.linalg

The functions *cho_solve_banded*, *circulant*, *companion*, *hadamard* and *leslie* were added to `scipy.linalg`.

The function *block_diag* was enhanced to accept scalar and 1D arguments, along with the usual 2D arguments.

New function and changes in scipy.optimize

The *curve_fit* function has been added; it takes a function and uses non-linear least squares to fit that to the provided data.

The *leastsq* and *fsolve* functions now return an array of size one instead of a scalar when solving for a single parameter.

New sparse least squares solver

The *lsqr* function was added to `scipy.sparse`. This routine finds a least-squares solution to a large, sparse, linear system of equations.

ARPACK-based sparse SVD

A naive implementation of SVD for sparse matrices is available in scipy.sparse.linalg.eigen.arpack. It is based on using an symmetric solver on <A, A>, and as such may not be very precise.

Alternative behavior available for `scipy.constants.find`

The keyword argument *disp* was added to the function `scipy.constants.find`, with the default value *True*. When *disp* is *True*, the behavior is the same as in Scipy version 0.7. When *False*, the function returns the list of keys instead of printing them. (In SciPy version 0.9, the default will be reversed.)

Incomplete sparse LU decompositions

Scipy now wraps SuperLU version 4.0, which supports incomplete sparse LU decompositions. These can be accessed via `scipy.sparse.linalg.spilu`. Upgrade to SuperLU 4.0 also fixes some known bugs.

Faster matlab file reader and default behavior change

We've rewritten the matlab file reader in Cython and it should now read matlab files at around the same speed that Matlab does.

The reader reads matlab named and anonymous functions, but it can't write them.

Until scipy 0.8.0 we have returned arrays of matlab structs as numpy object arrays, where the objects have attributes named for the struct fields. As of 0.8.0, we return matlab structs as numpy structured arrays. You can get the older behavior by using the optional `struct_as_record=False` keyword argument to `scipy.io.loadmat` and friends.

There is an inconsistency in the matlab file writer, in that it writes numpy 1D arrays as column vectors in matlab 5 files, and row vectors in matlab 4 files. We will change this in the next version, so both write row vectors. There is a *FutureWarning* when calling the writer to warn of this change; for now we suggest using the `oned_as='row'` keyword argument to `scipy.io.savemat` and friends.

Faster evaluation of orthogonal polynomials

Values of orthogonal polynomials can be evaluated with new vectorized functions in `scipy.special`: *eval_legendre*, *eval_chebyt*, *eval_chebyu*, *eval_chebyc*, *eval_chebys*, *eval_jacobi*, *eval_laguerre*, *eval_genlaguerre*, *eval_hermite*, *eval_hermitenorm*, *eval_gegenbauer*, *eval_sh_legendre*, *eval_sh_chebyt*, *eval_sh_chebyu*, *eval_sh_jacobi*. This is faster than constructing the full coefficient representation of the polynomials, which was previously the only available way.

Note that the previous orthogonal polynomial routines will now also invoke this feature, when possible.

Lambert W function

`scipy.special.lambertw` can now be used for evaluating the Lambert W function.

Improved hypergeometric 2F1 function

Implementation of `scipy.special.hyp2f1` for real parameters was revised. The new version should produce accurate values for all real parameters.

More flexible interface for Radial basis function interpolation

The `scipy.interpolate.Rbf` class now accepts a callable as input for the "function" argument, in addition to the built-in radial basis functions which can be selected with a string argument.

4.13.5 Removed features

scipy.stsci: the package was removed

The module *scipy.misc.limits* was removed.

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` are removed in the 0.8.0 release including: *npfile*, *save*, *load*, *create_module*, *create_shelf*, *objload*, *objsave*, *fopen*, *read_array*, *write_array*, *fread*, *fwrite*, *bswap*, *packbits*, *unpackbits*, and *convert_objectarray*. Some of these functions have been replaced by NumPy's raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

4.14 SciPy 0.7.2 Release Notes

Contents

SciPy 0.7.2 is a bug-fix release with no new features compared to 0.7.1. The only change is that all C sources from Cython code have been regenerated with Cython 0.12.1. This fixes the incompatibility between binaries of SciPy 0.7.1 and NumPy 1.4.

4.15 SciPy 0.7.1 Release Notes

Contents

SciPy 0.7.1 is a bug-fix release with no new features compared to 0.7.0.

Bugs fixed:

- Several fixes in Matlab file IO

Bugs fixed:

- Work around a failure with Python 2.6

Memory leak in lfilter have been fixed, as well as support for array object

Bugs fixed:

- #880, #925: lfilter fixes
- #871: bicgstab fails on Win32

Bugs fixed:

- #883: scipy.io.mmread with scipy.sparse.lil_matrix broken
- lil_matrix and csc_matrix reject now unexpected sequences, cf. http://thread.gmane.org/gmane.comp.python.scientific.user/19996

Several bugs of varying severity were fixed in the special functions:

- #503, #640: iv: problems at large arguments fixed by new implementation
- #623: jv: fix errors at large arguments
- #679: struve: fix wrong output for v < 0
- #803: pbdv produces invalid output
- #804: lqmn: fix crashes on some input
- #823: betainc: fix documentation
- #834: exp1 strange behavior near negative integer values
- #852: jn_zeros: more accurate results for large s, also in jnp/yn/ynp_zeros
- #853: jv, yv, iv: invalid results for non-integer v < 0, complex x
- #854: jv, yv, iv, kv: return nan more consistently when out-of-domain
- #927: ellipj: fix segfault on Windows
- #946: ellpj: fix segfault on Mac OS X/python 2.6 combination.
- ive, jve, yve, kv, kve: with real-valued input, return nan for out-of-domain instead of returning only the real part of the result.

Also, when `scipy.special.errprint(1)` has been enabled, warning messages are now issued as Python warnings instead of printing them to stderr.

- linregress, mannwhitneyu, describe: errors fixed
- kstwobign, norm, expon, exponweib, exponpow, frechet, genexpon, rdist, truncexpon, planck: improvements to numerical accuracy in distributions

4.15.1 Windows binaries for python 2.6

python 2.6 binaries for windows are now included. The binary for python 2.5 requires numpy 1.2.0 or above, and the one for python 2.6 requires numpy 1.3.0 or above.

4.15.2 Universal build for scipy

Mac OS X binary installer is now a proper universal build, and does not depend on gfortran anymore (libgfortran is statically linked). The python 2.5 version of scipy requires numpy 1.2.0 or above, the python 2.6 version requires numpy 1.3.0 or above.

4.16 SciPy 0.7.0 Release Notes

Contents

SciPy 0.7.0 is the culmination of 16 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.7.x branch, and on adding new features on the development trunk. This release requires Python 2.4 or 2.5 and NumPy 1.2 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible. For example, in addition to fixing numerous bugs in this release, we have also doubled the number of unit tests since the last release.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

Over the last year, we have seen a rapid increase in community involvement, and numerous infrastructure improvements to lower the barrier to contributions (e.g., more explicit coding standards, improved testing infrastructure, better documentation tools). Over the next year, we hope to see this trend continue and invite everyone to become more involved.

4.16.1 Python 2.6 and 3.0

A significant amount of work has gone into making SciPy compatible with Python 2.6; however, there are still some issues in this regard. The main issue with 2.6 support is NumPy. On UNIX (including Mac OS X), NumPy 1.2.1 mostly works, with a few caveats. On Windows, there are problems related to the compilation process. The upcoming

NumPy 1.3 release will fix these problems. Any remaining issues with 2.6 support for SciPy 0.7 will be addressed in a bug-fix release.

Python 3.0 is not supported at all; it requires NumPy to be ported to Python 3.0. This requires immense effort, since a lot of C code has to be ported. The transition to 3.0 is still under consideration; currently, we don't have any timeline or roadmap for this transition.

4.16.2 Major documentation improvements

SciPy documentation is greatly improved; you can view a HTML reference manual online or download it as a PDF file. The new reference guide was built using the popular Sphinx tool.

This release also includes an updated tutorial, which hadn't been available since SciPy was ported to NumPy in 2005. Though not comprehensive, the tutorial shows how to use several essential parts of Scipy. It also includes the `ndimage` documentation from the `numarray` manual.

Nevertheless, more effort is needed on the documentation front. Luckily, contributing to Scipy documentation is now easier than before: if you find that a part of it requires improvements, and want to help us out, please register a user name in our web-based documentation editor at http://docs.scipy.org/ and correct the issues.

4.16.3 Running Tests

NumPy 1.2 introduced a new testing framework based on nose. Starting with this release, SciPy now uses the new NumPy test framework as well. Taking advantage of the new testing framework requires `nose` version 0.10, or later. One major advantage of the new framework is that it greatly simplifies writing unit tests - which has all ready paid off, given the rapid increase in tests. To run the full test suite:

```
>>> import scipy
>>> scipy.test('full')
```

For more information, please see The NumPy/SciPy Testing Guide.

We have also greatly improved our test coverage. There were just over 2,000 unit tests in the 0.6.0 release; this release nearly doubles that number, with just over 4,000 unit tests.

4.16.4 Building SciPy

Support for NumScons has been added. NumScons is a tentative new build system for NumPy/SciPy, using SCons at its core.

SCons is a next-generation build system, intended to replace the venerable `Make` with the integrated functionality of `autoconf`/`automake` and `ccache`. Scons is written in Python and its configuration files are Python scripts. NumScons is meant to replace NumPy's custom version of `distutils` providing more advanced functionality, such as `autoconf`, improved fortran support, more tools, and support for `numpy.distutils`/`scons` cooperation.

4.16.5 Sandbox Removed

While porting SciPy to NumPy in 2005, several packages and modules were moved into `scipy.sandbox`. The sandbox was a staging ground for packages that were undergoing rapid development and whose APIs were in flux. It was also a place where broken code could live. The sandbox has served its purpose well, but was starting to create confusion. Thus `scipy.sandbox` was removed. Most of the code was moved into `scipy`, some code was made into a `scikit`, and the remaining code was just deleted, as the functionality had been replaced by other code.

4.16.6 Sparse Matrices

Sparse matrices have seen extensive improvements. There is now support for integer dtypes such `int8`, `uint32`, etc. Two new sparse formats were added:

- new class `dia_matrix` : the sparse DIAgonal format
- new class `bsr_matrix` : the Block CSR format

Several new sparse matrix construction functions were added:

- `sparse.kron` : sparse Kronecker product
- `sparse.bmat` : sparse version of `numpy.bmat`
- `sparse.vstack` : sparse version of `numpy.vstack`
- `sparse.hstack` : sparse version of `numpy.hstack`

Extraction of submatrices and nonzero values have been added:

- `sparse.tril` : extract lower triangle
- `sparse.triu` : extract upper triangle
- `sparse.find` : nonzero values and their indices

`csr_matrix` and `csc_matrix` now support slicing and fancy indexing (e.g., `A[1:3, 4:7]` and `A[[3,2,6,8],:]`). Conversions among all sparse formats are now possible:

- using member functions such as `.tocsr()` and `.tolil()`
- using the `.asformat()` member function, e.g. `A.asformat('csr')`
- using constructors `A = lil_matrix([[1,2]]); B = csr_matrix(A)`

All sparse constructors now accept dense matrices and lists of lists. For example:

- `A = csr_matrix( rand(3,3) )` and `B = lil_matrix( [[1,2],[3,4]] )`

The handling of diagonals in the `spdiags` function has been changed. It now agrees with the MATLAB(TM) function of the same name.

Numerous efficiency improvements to format conversions and sparse matrix arithmetic have been made. Finally, this release contains numerous bugfixes.

4.16.7 Statistics package

Statistical functions for masked arrays have been added, and are accessible through `scipy.stats.mstats`. The functions are similar to their counterparts in `scipy.stats` but they have not yet been verified for identical interfaces and algorithms.

Several bugs were fixed for statistical functions, of those, `kstest` and `percentileofscore` gained new keyword arguments.

Added deprecation warning for `mean`, `median`, `var`, `std`, `cov`, and `corrcoef`. These functions should be replaced by their numpy counterparts. Note, however, that some of the default options differ between the `scipy.stats` and numpy versions of these functions.

Numerous bug fixes to `stats.distributions`: all generic methods now work correctly, several methods in individual distributions were corrected. However, a few issues remain with higher moments (`skew`, `kurtosis`) and entropy. The maximum likelihood estimator, `fit`, does not work out-of-the-box for some distributions - in some cases, starting values have to be carefully chosen, in other cases, the generic implementation of the maximum likelihood method might not be the numerically appropriate estimation method.

We expect more bugfixes, increases in numerical precision and enhancements in the next release of scipy.

4.16.8 Reworking of IO package

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` have been deprecated and will be removed in the 0.8.0 release including `npfile`, `save`, `load`, `create_module`, `create_shelf`, `objload`, `objsave`, `fopen`, `read_array`, `write_array`, `fread`, `fwrite`, `bswap`, `packbits`, `unpackbits`, and `convert_objectarray`. Some of these functions have been replaced by NumPy's raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

The Matlab (TM) file readers/writers have a number of improvements:

- default version 5
- v5 writers for structures, cell arrays, and objects
- v5 readers/writers for function handles and 64-bit integers
- new struct_as_record keyword argument to `loadmat`, which loads struct arrays in matlab as record arrays in numpy
- string arrays have `dtype='U...'` instead of `dtype=object`
- `loadmat` no longer squeezes singleton dimensions, i.e. `squeeze_me=False` by default

4.16.9 New Hierarchical Clustering module

This module adds new hierarchical clustering functionality to the `scipy.cluster` package. The function interfaces are similar to the functions provided MATLAB(TM)'s Statistics Toolbox to help facilitate easier migration to the NumPy/SciPy framework. Linkage methods implemented include single, complete, average, weighted, centroid, median, and ward.

In addition, several functions are provided for computing inconsistency statistics, cophenetic distance, and maximum distance between descendants. The `fcluster` and `fclusterdata` functions transform a hierarchical clustering into a set of flat clusters. Since these flat clusters are generated by cutting the tree into a forest of trees, the `leaders` function takes a linkage and a flat clustering, and finds the root of each tree in the forest. The `ClusterNode` class represents a hierarchical clusterings as a field-navigable tree object. `to_tree` converts a matrix-encoded hierarchical clustering to a `ClusterNode` object. Routines for converting between MATLAB and SciPy linkage encodings are provided. Finally, a `dendrogram` function plots hierarchical clusterings as a dendrogram, using matplotlib.

4.16.10 New Spatial package

The new spatial package contains a collection of spatial algorithms and data structures, useful for spatial statistics and clustering applications. It includes rapidly compiled code for computing exact and approximate nearest neighbors, as well as a pure-python kd-tree with the same interface, but that supports annotation and a variety of other algorithms. The API for both modules may change somewhat, as user requirements become clearer.

It also includes a `distance` module, containing a collection of distance and dissimilarity functions for computing distances between vectors, which is useful for spatial statistics, clustering, and kd-trees. Distance and dissimilarity functions provided include Bray-Curtis, Canberra, Chebyshev, City Block, Cosine, Dice, Euclidean, Hamming, Jaccard, Kulsinski, Mahalanobis, Matching, Minkowski, Rogers-Tanimoto, Russell-Rao, Squared Euclidean, Standardized Euclidean, Sokal-Michener, Sokal-Sneath, and Yule.

The `pdist` function computes pairwise distance between all unordered pairs of vectors in a set of vectors. The `cdist` computes the distance on all pairs of vectors in the Cartesian product of two sets of vectors. Pairwise distance matrices are stored in condensed form; only the upper triangular is stored. `squareform` converts distance matrices between square and condensed forms.

4.16.11 Reworked fftpack package

FFTW2, FFTW3, MKL and DJBFFT wrappers have been removed. Only (NETLIB) fftpack remains. By focusing on one backend, we hope to add new features - like float32 support - more easily.

4.16.12 New Constants package

`scipy.constants` provides a collection of physical constants and conversion factors. These constants are taken from CODATA Recommended Values of the Fundamental Physical Constants: 2002. They may be found at physics.nist.gov/constants. The values are stored in the dictionary physical_constants as a tuple containing the value, the units, and the relative precision - in that order. All constants are in SI units, unless otherwise stated. Several helper functions are provided.

4.16.13 New Radial Basis Function module

`scipy.interpolate` now contains a Radial Basis Function module. Radial basis functions can be used for smoothing/interpolating scattered data in n-dimensions, but should be used with caution for extrapolation outside of the observed data range.

4.16.14 New complex ODE integrator

`scipy.integrate.ode` now contains a wrapper for the ZVODE complex-valued ordinary differential equation solver (by Peter N. Brown, Alan C. Hindmarsh, and George D. Byrne).

4.16.15 New generalized symmetric and hermitian eigenvalue problem solver

`scipy.linalg.eigh` now contains wrappers for more LAPACK symmetric and hermitian eigenvalue problem solvers. Users can now solve generalized problems, select a range of eigenvalues only, and choose to use a faster algorithm at the expense of increased memory usage. The signature of the `scipy.linalg.eigh` changed accordingly.

4.16.16 Bug fixes in the interpolation package

The shape of return values from `scipy.interpolate.interp1d` used to be incorrect, if interpolated data had more than 2 dimensions and the axis keyword was set to a non-default value. This has been fixed. Moreover, `interp1d` returns now a scalar (0D-array) if the input is a scalar. Users of `scipy.interpolate.interp1d` may need to revise their code if it relies on the previous behavior.

4.16.17 Weave clean up

There were numerous improvements to `scipy.weave`. `blitz++` was relicensed by the author to be compatible with the SciPy license. `wx_spec.py` was removed.

4.16.18 Known problems

Here are known problems with scipy 0.7.0:

- weave test failures on windows: those are known, and are being revised.
- weave test failure with gcc 4.3 (std::labs): this is a gcc 4.3 bug. A workaround is to add #include <cstdlib> in scipy/weave/blitz/blitz/funcs.h (line 27). You can make the change in the installed scipy (in site-packages).

CHAPTER

FIVE

REFERENCE

5.1 Clustering package (`scipy.cluster`)

`scipy.cluster.vq`

Clustering algorithms are useful in information theory, target detection, communications, compression, and other areas. The `vq` module only supports vector quantization and the k-means algorithms.

`scipy.cluster.hierarchy`

The `hierarchy` module provides functions for hierarchical and agglomerative clustering. Its features include generating hierarchical clusters from distance matrices, calculating statistics on clusters, cutting linkages to generate flat clusters, and visualizing clusters with dendrograms.

5.2 K-means clustering and vector quantization (`scipy.cluster.vq`)

Provides routines for k-means clustering, generating code books from k-means models, and quantizing vectors by comparing them with centroids in a code book.

`whiten`(obs[, check_finite])	Normalize a group of observations on a per feature basis.
`vq`(obs, code_book[, check_finite])	Assign codes from a code book to observations.
`kmeans`(obs, k_or_guess[, iter, thresh, ...])	Performs k-means on a set of observation vectors forming k clusters.
`kmeans2`(data, k[, iter, thresh, minit, ...])	Classify a set of observations into k clusters using the k-means algorithm.

`scipy.cluster.vq.`**`whiten`**(*obs*, *check_finite=True*)

Normalize a group of observations on a per feature basis.

Before running k-means, it is beneficial to rescale each feature dimension of the observation set with whitening. Each feature is divided by its standard deviation across all observations to give it unit variance.

Parameters **obs** : ndarray

Each row of the array is an observation. The columns are the features seen during each observation.

```
>>> #         f0    f1    f2
>>> obs = [[  1.,   1.,   1.],  #o0
...        [  2.,   2.,   2.],  #o1
...        [  3.,   3.,   3.],  #o2
...        [  4.,   4.,   4.]]  #o3
```

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns **result** : ndarray

Contains the values in *obs* scaled by the standard deviation of each column.

Examples

```
>>> from scipy.cluster.vq import whiten
>>> features  = np.array([[1.9, 2.3, 1.7],
...                       [1.5, 2.5, 2.2],
...                       [0.8, 0.6, 1.7,]])
>>> whiten(features)
array([[ 4.17944278,  2.69811351,  7.21248917],
       [ 3.29956009,  2.93273208,  9.33380951],
       [ 1.75976538,  0.7038557 ,  7.21248917]])
```

`scipy.cluster.vq.`**`vq`**`(`*obs*, *code_book*, *check_finite=True*`)`

Assign codes from a code book to observations.

Assigns a code from a code book to each observation. Each observation vector in the 'M' by 'N' *obs* array is compared with the centroids in the code book and assigned the code of the closest centroid.

The features in *obs* should have unit variance, which can be achieved by passing them through the whiten function. The code book can be created with the k-means algorithm or a different encoding algorithm.

Parameters **obs** : ndarray

Each row of the 'M' x 'N' array is an observation. The columns are the "features" seen during each observation. The features must be whitened first using the whiten function or something equivalent.

code_book : ndarray

The code book is usually generated using the k-means algorithm. Each row of the array holds a different code, and the columns are the features of the code.

```
>>> #              f0    f1    f2   f3
>>> code_book = [
...             [  1.,   2.,   3.,   4.],  #c0
...             [  1.,   2.,   3.,   4.],  #c1
...             [  1.,   2.,   3.,   4.]]  #c2
```

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns **code** : ndarray

A length M array holding the code book index for each observation.

dist : ndarray

The distortion (distance) between the observation and its nearest code.

Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import vq
>>> code_book = array([[1.,1.,1.],
...                    [2.,2.,2.]])
>>> features  = array([[  1.9,2.3,1.7],
...                    [  1.5,2.5,2.2],
...                    [  0.8,0.6,1.7]])
```

```
>>> vq(features,code_book)
(array([1, 1, 0],'i'), array([ 0.43588989,  0.73484692,  0.83066239]))
```

`scipy.cluster.vq.`**`kmeans`**(*obs*, *k_or_guess*, *iter=20*, *thresh=1e-05*, *check_finite=True*)

Performs k-means on a set of observation vectors forming k clusters.

The k-means algorithm adjusts the centroids until sufficient progress cannot be made, i.e. the change in distortion since the last iteration is less than some threshold. This yields a code book mapping centroids to codes and vice versa.

Distortion is defined as the sum of the squared differences between the observations and the corresponding centroid.

Parameters **obs** : ndarray

Each row of the M by N array is an observation vector. The columns are the features seen during each observation. The features must be whitened first with the `whiten` function.

k_or_guess : int or ndarray

The number of centroids to generate. A code is assigned to each centroid, which is also the row index of the centroid in the code_book matrix generated.

The initial k centroids are chosen by randomly selecting observations from the observation matrix. Alternatively, passing a k by N array specifies the initial k centroids.

iter : int, optional

The number of times to run k-means, returning the codebook with the lowest distortion. This argument is ignored if initial centroids are specified with an array for the `k_or_guess` parameter. This parameter does not represent the number of iterations of the k-means algorithm.

thresh : float, optional

Terminates the k-means algorithm if the change in distortion since the last k-means iteration is less than or equal to thresh.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns **codebook** : ndarray

A k by N array of k centroids. The i'th centroid codebook[i] is represented with the code i. The centroids and codes generated represent the lowest distortion seen, not necessarily the globally minimal distortion.

distortion : float

The distortion between the observations passed and the centroids generated.

See also:

`kmeans2`	a different implementation of k-means clustering with more methods for generating initial centroids but without using a distortion change threshold as a stopping criterion.
`whiten`	must be called prior to passing an observation matrix to kmeans.

Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import vq, kmeans, whiten
>>> features  = array([[ 1.9,2.3],
...                    [ 1.5,2.5],
...                    [ 0.8,0.6],
...                    [ 0.4,1.8],
...                    [ 0.1,0.1],
```

```
...                       [ 0.2,1.8],
...                       [ 2.0,0.5],
...                       [ 0.3,1.5],
...                       [ 1.0,1.0]])
>>> whitened = whiten(features)
>>> book = array((whitened[0],whitened[2]))
>>> kmeans(whitened,book)
(array([[ 2.3110306 ,  2.86287398],
       [ 0.93218041,  1.24398691]]), 0.85684700941625547)

>>> from numpy import random
>>> random.seed((1000,2000))
>>> codes = 3
>>> kmeans(whitened,codes)
(array([[ 2.3110306 ,  2.86287398],
       [ 1.32544402,  0.65607529],
       [ 0.40782893,  2.02786907]]), 0.5196582527686241)
```

`scipy.cluster.vq.`**`kmeans2`**(*data*, *k*, *iter=10*, *thresh=1e-05*, *minit='random'*, *missing='warn'*, *check_finite=True*)

Classify a set of observations into k clusters using the k-means algorithm.

The algorithm attempts to minimize the Euclidian distance between observations and centroids. Several initialization methods are included.

Parameters **data** : ndarray

A 'M' by 'N' array of 'M' observations in 'N' dimensions or a length 'M' array of 'M' one-dimensional observations.

k : int or ndarray

The number of clusters to form as well as the number of centroids to generate. If *minit* initialization string is 'matrix', or if a ndarray is given instead, it is interpreted as initial cluster to use instead.

iter : int, optional

Number of iterations of the k-means algrithm to run. Note that this differs in meaning from the iters parameter to the kmeans function.

thresh : float, optional

(not used yet)

minit : str, optional

Method for initialization. Available methods are 'random', 'points', 'uniform', and 'matrix':

'random': generate k centroids from a Gaussian with mean and variance estimated from the data.

'points': choose k observations (rows) at random from data for the initial centroids.

'uniform': generate k observations from the data from a uniform distribution defined by the data set (unsupported).

'matrix': interpret the k parameter as a k by M (or length k array for one-dimensional data) array of initial centroids.

missing : str, optional

Method to deal with empty clusters. Available methods are 'warn' and 'raise':

'warn': give a warning and continue.

'raise': raise an ClusterError and terminate the algorithm.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns **centroid** : ndarray

A 'k' by 'N' array of centroids found at the last iteration of k-means.

label : ndarray

label[i] is the code or index of the centroid the i'th observation is closest to.

5.2.1 Background information

The k-means algorithm takes as input the number of clusters to generate, k, and a set of observation vectors to cluster. It returns a set of centroids, one for each of the k clusters. An observation vector is classified with the cluster number or centroid index of the centroid closest to it.

A vector v belongs to cluster i if it is closer to centroid i than any other centroids. If v belongs to i, we say centroid i is the dominating centroid of v. The k-means algorithm tries to minimize distortion, which is defined as the sum of the squared distances between each observation vector and its dominating centroid. Each step of the k-means algorithm refines the choices of centroids to reduce distortion. The change in distortion is used as a stopping criterion: when the change is lower than a threshold, the k-means algorithm is not making sufficient progress and terminates. One can also define a maximum number of iterations.

Since vector quantization is a natural application for k-means, information theory terminology is often used. The centroid index or cluster index is also referred to as a "code" and the table mapping codes to centroids and vice versa is often referred as a "code book". The result of k-means, a set of centroids, can be used to quantize vectors. Quantization aims to find an encoding of vectors that reduces the expected distortion.

All routines expect obs to be a M by N array where the rows are the observation vectors. The codebook is a k by N array where the i'th row is the centroid of code word i. The observation vectors and centroids have the same feature dimension.

As an example, suppose we wish to compress a 24-bit color image (each pixel is represented by one byte for red, one for blue, and one for green) before sending it over the web. By using a smaller 8-bit encoding, we can reduce the amount of data by two thirds. Ideally, the colors for each of the 256 possible 8-bit encoding values should be chosen to minimize distortion of the color. Running k-means with k=256 generates a code book of 256 codes, which fills up all possible 8-bit sequences. Instead of sending a 3-byte value for each pixel, the 8-bit centroid index (or code word) of the dominating centroid is transmitted. The code book is also sent over the wire so each 8-bit code can be translated back to a 24-bit pixel value representation. If the image of interest was of an ocean, we would expect many 24-bit blues to be represented by 8-bit codes. If it was an image of a human face, more flesh tone colors would be represented in the code book.

5.3 Hierarchical clustering (`scipy.cluster.hierarchy`)

These functions cut hierarchical clusterings into flat clusterings or find the roots of the forest formed by a cut by providing the flat cluster ids of each observation.

`fcluster`(Z, t[, criterion, depth, R, monocrit])	Forms flat clusters from the hierarchical clustering defined by the linkage matrix `Z`
`fclusterdata`(X, t[, criterion, metric, ...])	Cluster observation data using a given metric.
`leaders`(Z, T)	Returns the root nodes in a hierarchical clustering.

`scipy.cluster.hierarchy.`**`fcluster`**(*Z*, *t*, *criterion='inconsistent'*, *depth=2*, *R=None*, *monocrit=None*)

Forms flat clusters from the hierarchical clustering defined by the linkage matrix `Z`.

Parameters **Z** : ndarray

The hierarchical clustering encoded with the matrix returned by the `linkage` function.

t : float

The threshold to apply when forming flat clusters.

criterion : str, optional

The criterion to use in forming flat clusters. This can be any of the following values:

`inconsistent`

[If a cluster node and all its] descendants have an inconsistent value less than or equal to *t* then all its leaf descendants belong to the same flat cluster. When no non-singleton cluster meets this criterion, every node is assigned to its own cluster. (Default)

`distance` [Forms flat clusters so that the original] observations in each flat cluster have no greater a cophenetic distance than *t*.

`maxclust` [Finds a minimum threshold `r` so that] the cophenetic distance between any two original observations in the same flat cluster is no more than `r` and no more than *t* flat clusters are formed.

`monocrit` [Forms a flat cluster from a cluster node c] with index i when `monocrit[j] <= t`.

For example, to threshold on the maximum mean distance as computed in the inconsistency matrix R with a threshold of 0.8 do:

MR = maxRstat(Z, R, 3)
cluster(Z, t=0.8, criterion='monocrit', monocrit=MR)

`maxclust_monocrit`

[Forms a flat cluster from a] non-singleton cluster node `c` when `monocrit[i] <= r` for all cluster indices `i` below and including `c`. `r` is minimized such that no more than `t` flat clusters are formed. monocrit must be monotonic. For example, to minimize the threshold t on maximum inconsistency values so that no more than 3 flat clusters are formed, do:

MI = maxinconsts(Z, R)
cluster(Z, t=3, criterion='maxclust_monocrit', monocrit=MI)

depth : int, optional

The maximum depth to perform the inconsistency calculation. It has no meaning for the other criteria. Default is 2.

R : ndarray, optional

The inconsistency matrix to use for the 'inconsistent' criterion. This matrix is computed if not provided.

monocrit : ndarray, optional

An array of length n-1. *monocrit[i]* is the statistics upon which non-singleton i is thresholded. The monocrit vector must be monotonic, i.e. given a node c with index i, for all node indices j corresponding to nodes below c, *monocrit[i] >= monocrit[j]*.

Returns **fcluster** : ndarray

An array of length n. T[i] is the flat cluster number to which original observation i belongs.

`scipy.cluster.hierarchy.`**`fclusterdata`**(*X*, *t*, *criterion='inconsistent'*, *metric='euclidean'*, *depth=2*, *method='single'*, *R=None*)

Cluster observation data using a given metric.

Clusters the original observations in the n-by-m data matrix X (n observations in m dimensions), using the euclidean distance metric to calculate distances between original observations, performs hierarchical clustering using the single linkage algorithm, and forms flat clusters using the inconsistency method with *t* as the cut-off threshold.

A one-dimensional array T of length n is returned. T[i] is the index of the flat cluster to which the original observation i belongs.

Parameters **X** : (N, M) ndarray

N by M data matrix with N observations in M dimensions.

t : float

The threshold to apply when forming flat clusters.

criterion : str, optional

Specifies the criterion for forming flat clusters. Valid values are 'inconsistent' (default), 'distance', or 'maxclust' cluster formation algorithms. See `fcluster` for descriptions.

metric : str, optional

The distance metric for calculating pairwise distances. See `distance.pdist` for descriptions and linkage to verify compatibility with the linkage method.

depth : int, optional

The maximum depth for the inconsistency calculation. See `inconsistent` for more information.

method : str, optional

The linkage method to use (single, complete, average, weighted, median centroid, ward). See `linkage` for more information. Default is "single".

R : ndarray, optional

The inconsistency matrix. It will be computed if necessary if it is not passed.

Returns **fclusterdata** : ndarray

A vector of length n. T[i] is the flat cluster number to which original observation i belongs.

Notes

This function is similar to the MATLAB function clusterdata.

`scipy.cluster.hierarchy.`**`leaders`**`(`Z, T`)`

Returns the root nodes in a hierarchical clustering.

Returns the root nodes in a hierarchical clustering corresponding to a cut defined by a flat cluster assignment vector `T`. See the `fcluster` function for more information on the format of `T`.

For each flat cluster j of the k flat clusters represented in the n-sized flat cluster assignment vector `T`, this function finds the lowest cluster node i in the linkage tree Z such that:

- leaf descendents belong only to flat cluster j (i.e. `T[p]==j` for all p in $S(i)$ where $S(i)$ is the set of leaf ids of leaf nodes descendent with cluster node i)
- there does not exist a leaf that is not descendent with i that also belongs to cluster j (i.e. `T[q]!=j` for all q not in $S(i)$). If this condition is violated, `T` is not a valid cluster assignment vector, and an exception will be thrown.

Parameters **Z** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

T : ndarray

The flat cluster assignment vector.

Returns **L** : ndarray

The leader linkage node id's stored as a k-element 1-D array where `k` is the number of flat clusters found in `T`.

`L[j]=i` is the linkage cluster node id that is the leader of flat cluster with id M[j]. If `i < n`, `i` corresponds to an original observation, otherwise it corresponds to a non-singleton cluster.

For example: if `L[3]=2` and `M[3]=8`, the flat cluster with id 8's leader is linkage node 2.

M : ndarray

The leader linkage node id's stored as a k-element 1-D array where `k` is the number of flat clusters found in `T`. This allows the set of flat cluster ids to be any arbitrary set of `k` integers.

These are routines for agglomerative clustering.

`linkage`(y[, method, metric])	Performs hierarchical/agglomerative clustering on the condensed distance matrix y.
`single`(y)	Performs single/min/nearest linkage on the condensed distance matrix `y`
`complete`(y)	Performs complete/max/farthest point linkage on a condensed distance matrix
`average`(y)	Performs average/UPGMA linkage on a condensed distance matrix
`weighted`(y)	Performs weighted/WPGMA linkage on the condensed distance matrix.
`centroid`(y)	Performs centroid/UPGMC linkage.
`median`(y)	Performs median/WPGMC linkage.
`ward`(y)	Performs Ward's linkage on a condensed or redundant distance matrix.

`scipy.cluster.hierarchy.`**`linkage`**(*y*, *method='single'*, *metric='euclidean'*)

Performs hierarchical/agglomerative clustering on the condensed distance matrix y.

y must be a $\binom{n}{2}$ sized vector where n is the number of original observations paired in the distance matrix. The behavior of this function is very similar to the MATLAB linkage function.

A 4 by $(n-1)$ matrix `Z` is returned. At the i-th iteration, clusters with indices `Z[i, 0]` and `Z[i, 1]` are combined to form cluster $n+i$. A cluster with an index less than n corresponds to one of the n original observations. The distance between clusters `Z[i, 0]` and `Z[i, 1]` is given by `Z[i, 2]`. The fourth value `Z[i, 3]` represents the number of original observations in the newly formed cluster.

The following linkage methods are used to compute the distance $d(s,t)$ between two clusters s and t. The algorithm begins with a forest of clusters that have yet to be used in the hierarchy being formed. When two clusters s and t from this forest are combined into a single cluster u, s and t are removed from the forest, and u is added to the forest. When only one cluster remains in the forest, the algorithm stops, and this cluster becomes the root.

A distance matrix is maintained at each iteration. The `d[i,j]` entry corresponds to the distance between cluster i and j in the original forest.

At each iteration, the algorithm must update the distance matrix to reflect the distance of the newly formed cluster u with the remaining clusters in the forest.

Suppose there are $|u|$ original observations $u[0],\ldots,u[|u|-1]$ in cluster u and $|v|$ original objects $v[0],\ldots,v[|v|-1]$ in cluster v. Recall s and t are combined to form cluster u. Let v be any remaining cluster in the forest that is not u.

The following are methods for calculating the distance between the newly formed cluster u and each v.

- method='single' assigns

  $$d(u,v) = \min(dist(u[i], v[j]))$$

  for all points i in cluster u and j in cluster v. This is also known as the Nearest Point Algorithm.

- method='complete' assigns

  $$d(u,v) = \max(dist(u[i], v[j]))$$

  for all points i in cluster u and j in cluster v. This is also known by the Farthest Point Algorithm or Voor Hees Algorithm.

- method='average' assigns

  $$d(u,v) = \sum_{ij} \frac{d(u[i], v[j])}{(|u| * |v|)}$$

  for all points i and j where $|u|$ and $|v|$ are the cardinalities of clusters u and v, respectively. This is also called the UPGMA algorithm.

- method='weighted' assigns

  $$d(u,v) = (dist(s,v) + dist(t,v))/2$$

  where cluster u was formed with cluster s and t and v is a remaining cluster in the forest. (also called WPGMA)

- method='centroid' assigns

  $$dist(s,t) = ||c_s - c_t||_2$$

  where c_s and c_t are the centroids of clusters s and t, respectively. When two clusters s and t are combined into a new cluster u, the new centroid is computed over all the original objects in clusters s and t. The distance then becomes the Euclidean distance between the centroid of u and the centroid of a remaining cluster v in the forest. This is also known as the UPGMC algorithm.

- method='median' assigns $d(s,t)$ like the `centroid` method. When two clusters s and t are combined into a new cluster u, the average of centroids s and t give the new centroid u. This is also known as the WPGMC algorithm.

- method='ward' uses the Ward variance minimization algorithm. The new entry $d(u,v)$ is computed as follows,

  $$d(u,v) = \sqrt{\frac{|v|+|s|}{T}d(v,s)^2 + \frac{|v|+|t|}{T}d(v,t)^2 - \frac{|v|}{T}d(s,t)^2}$$

  where u is the newly joined cluster consisting of clusters s and t, v is an unused cluster in the forest, $T = |v| + |s| + |t|$, and $| * |$ is the cardinality of its argument. This is also known as the incremental algorithm.

Warning: When the minimum distance pair in the forest is chosen, there may be two or more pairs with the same minimum distance. This implementation may chose a different minimum than the MATLAB version.

Parameters **y** : ndarray

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array.

method : str, optional

The linkage algorithm to use. See the `Linkage Methods` section below for full descriptions.

metric : str or function, optional

The distance metric to use. See the `distance.pdist` function for a list of valid distance metrics. The customized distance can also be used. See the `distance.pdist` function for details.

Returns **Z** : ndarray

The hierarchical clustering encoded as a linkage matrix.

`scipy.cluster.hierarchy.`**`single`**`(y)`

Performs single/min/nearest linkage on the condensed distance matrix `y`

Parameters **y** : ndarray

The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns **Z** : ndarray

The linkage matrix.

See also:

`linkage`	for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`complete`**`(`*y*`)`

Performs complete/max/farthest point linkage on a condensed distance matrix

Parameters **y** : ndarray

The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns **Z** : ndarray

A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

See also:

`linkage`

`scipy.cluster.hierarchy.`**`average`**`(`*y*`)`

Performs average/UPGMA linkage on a condensed distance matrix

Parameters **y** : ndarray

The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns **Z** : ndarray

A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

See also:

`linkage` for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`weighted`**`(`*y*`)`

Performs weighted/WPGMA linkage on the condensed distance matrix.

See `linkage` for more information on the return structure and algorithm.

Parameters **y** : ndarray

The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns **Z** : ndarray

A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

See also:

`linkage` for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`centroid`**`(`*y*`)`

Performs centroid/UPGMC linkage.

See `linkage` for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = centroid(y)`

   Performs centroid/UPGMC linkage on the condensed distance matrix `y`. See `linkage` for more information on the return structure and algorithm.

2. `Z = centroid(X)`

   Performs centroid/UPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric. See `linkage` for more information on the return structure and algorithm.

Parameters **y** : ndarray

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as a m by n array.

Returns **Z** : ndarray

A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

See also:

`linkage`	for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`median`**`(y)`

Performs median/WPGMC linkage.

See `linkage` for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = median(y)`
   Performs median/WPGMC linkage on the condensed distance matrix `y`. See `linkage` for more information on the return structure and algorithm.
2. `Z = median(X)`
   Performs median/WPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric. See linkage for more information on the return structure and algorithm.

Parameters **y** : ndarray

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as a m by n array.

Returns **Z** : ndarray

The hierarchical clustering encoded as a linkage matrix.

See also:

`linkage`	for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`ward`**`(y)`

Performs Ward's linkage on a condensed or redundant distance matrix.

See linkage for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = ward(y)` Performs Ward's linkage on the condensed distance matrix `Z`. See linkage for more information on the return structure and algorithm.

2. `Z = ward(X)` Performs Ward's linkage on the observation matrix `X` using Euclidean distance as the distance metric. See linkage for more information on the return structure and algorithm.

Parameters **y** : ndarray

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as a m by n array.

Returns **Z** : ndarray

The hierarchical clustering encoded as a linkage matrix.

See also:

linkage for advanced creation of hierarchical clusterings.

These routines compute statistics on hierarchies.

`cophenet`(Z[, Y])	Calculates the cophenetic distances between each observation in the hierarchical clustering defined by
`from_mlab_linkage`(Z)	Converts a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this
`inconsistent`(Z[, d])	Calculates inconsistency statistics on a linkage.
`maxinconsts`(Z, R)	Returns the maximum inconsistency coefficient for each non-singleton cluster and its descendents.
`maxdists`(Z)	Returns the maximum distance between any non-singleton cluster.
`maxRstat`(Z, R, i)	Returns the maximum statistic for each non-singleton cluster and its descendents.
`to_mlab_linkage`(Z)	Converts a linkage matrix to a MATLAB(TM) compatible one.

`scipy.cluster.hierarchy.`**`cophenet`**`(`*Z*, *Y=None*`)`

Calculates the cophenetic distances between each observation in the hierarchical clustering defined by the linkage `Z`.

Suppose `p` and `q` are original observations in disjoint clusters `s` and `t`, respectively and `s` and `t` are joined by a direct parent cluster `u`. The cophenetic distance between observations `i` and `j` is simply the distance between clusters `s` and `t`.

Parameters **Z** : ndarray

The hierarchical clustering encoded as an array (see `linkage` function).

Y : ndarray (optional)

Calculates the cophenetic correlation coefficient `c` of a hierarchical clustering defined by the linkage matrix *Z* of a set of n observations in m dimensions. *Y* is the condensed distance matrix from which *Z* was generated.

Returns **c** : ndarray

The cophentic correlation distance (if `y` is passed).

d : ndarray

The cophenetic distance matrix in condensed form. The ij th entry is the cophenetic distance between original observations i and j.

`scipy.cluster.hierarchy.`**`from_mlab_linkage`**`(`*Z*`)`

Converts a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this module.

The conversion does two things:

- the indices are converted from `1..N` to `0..(N-1)` form, and
- a fourth column Z[:,3] is added where Z[i,3] is represents the number of original observations (leaves) in the non-singleton cluster i.

This function is useful when loading in linkages from legacy data files generated by MATLAB.

Parameters **Z** : ndarray

A linkage matrix generated by MATLAB(TM).

Returns **ZS** : ndarray

A linkage matrix compatible with this library.

`scipy.cluster.hierarchy.`**`inconsistent`**`(`*Z*, *d=2*`)`

Calculates inconsistency statistics on a linkage.

Note: This function behaves similarly to the MATLAB(TM) inconsistent function.

Parameters **Z** : ndarray

The $(n-1)$ by 4 matrix encoding the linkage (hierarchical clustering). See `linkage` documentation for more information on its form.

d : int, optional

The number of links up to *d* levels below each non-singleton cluster.

Returns **R** : ndarray

A $(n-1)$ by 5 matrix where the `i`'th row contains the link statistics for the non-singleton cluster `i`. The link statistics are computed over the link heights for links d levels below the cluster `i`. `R[i,0]` and `R[i,1]` are the mean and standard deviation of the link heights, respectively; `R[i,2]` is the number of links included in the calculation; and `R[i,3]` is the inconsistency coefficient,

$$\frac{\mathtt{Z[i,2]}-\mathtt{R[i,0]}}{R[i,1]}$$

`scipy.cluster.hierarchy.`**`maxinconsts`**`(`*Z*, *R*`)`

Returns the maximum inconsistency coefficient for each non-singleton cluster and its descendents.

Parameters **Z** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

R : ndarray

The inconsistency matrix.

Returns **MI** : ndarray

A monotonic `(n-1)`-sized numpy array of doubles.

`scipy.cluster.hierarchy.`**`maxdists`**`(`*Z*`)`

Returns the maximum distance between any non-singleton cluster.

Parameters **Z** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

Returns **maxdists** : ndarray

A `(n-1)` sized numpy array of doubles; `MD[i]` represents the maximum distance between any cluster (including singletons) below and including the node with index i. More specifically, `MD[i] = Z[Q(i)-n, 2].max()` where `Q(i)` is the set of all node indices below and including node i.

`scipy.cluster.hierarchy.`**`maxRstat`**`(`*Z*, *R*, *i*`)`

Returns the maximum statistic for each non-singleton cluster and its descendents.

Parameters **Z** : array_like

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

R : array_like

The inconsistency matrix.

i : int

The column of *R* to use as the statistic.

Returns **MR** : ndarray

Calculates the maximum statistic for the i'th column of the inconsistency matrix *R* for each non-singleton cluster node. `MR[j]` is the maximum over `R[Q(j)-n, i]` where `Q(j)` the set of all node ids corresponding to nodes below and including `j`.

`scipy.cluster.hierarchy.`**`to_mlab_linkage`**`(`*Z*`)`

Converts a linkage matrix to a MATLAB(TM) compatible one.

Converts a linkage matrix `Z` generated by the linkage function of this module to a MATLAB(TM) compatible one. The return linkage matrix has the last column removed and the cluster indices are converted to `1..N` indexing.

Parameters **Z** : ndarray

A linkage matrix generated by this library.

Returns **to_mlab_linkage** : ndarray
A linkage matrix compatible with MATLAB(TM)'s hierarchical clustering functions. The return linkage matrix has the last column removed and the cluster indices are converted to `1..N` indexing.

Routines for visualizing flat clusters.

`dendrogram`(Z[, p, truncate_mode, ...])	Plots the hierarchical clustering as a dendrogram.

`scipy.cluster.hierarchy.`**`dendrogram`**(*Z*, *p=30*, *truncate_mode=None*, *color_threshold=None*, *get_leaves=True*, *orientation='top'*, *labels=None*, *count_sort=False*, *distance_sort=False*, *show_leaf_counts=True*, *no_plot=False*, *no_labels=False*, *color_list=None*, *leaf_font_size=None*, *leaf_rotation=None*, *leaf_label_func=None*, *no_leaves=False*, *show_contracted=False*, *link_color_func=None*, *ax=None*, *above_threshold_color='b'*)

Plots the hierarchical clustering as a dendrogram.

The dendrogram illustrates how each cluster is composed by drawing a U-shaped link between a non-singleton cluster and its children. The height of the top of the U-link is the distance between its children clusters. It is also the cophenetic distance between original observations in the two children clusters. It is expected that the distances in Z[:,2] be monotonic, otherwise crossings appear in the dendrogram.

Parameters **Z** : ndarray
The linkage matrix encoding the hierarchical clustering to render as a dendrogram. See the `linkage` function for more information on the format of `Z`.

p : int, optional
The `p` parameter for `truncate_mode`.

truncate_mode : str, optional
The dendrogram can be hard to read when the original observation matrix from which the linkage is derived is large. Truncation is used to condense the dendrogram. There are several modes:

`None/'none'`
No truncation is performed (Default).

`'lastp'` The last `p` non-singleton formed in the linkage are the only non-leaf nodes in the linkage; they correspond to rows `Z[n-p-2:end]` in `Z`. All other non-singleton clusters are contracted into leaf nodes.

`'mlab'` This corresponds to MATLAB(TM) behavior. (not implemented yet)

`'level'/'mtica'`
No more than `p` levels of the dendrogram tree are displayed. This corresponds to Mathematica(TM) behavior.

color_threshold : double, optional
For brevity, let t be the `color_threshold`. Colors all the descendent links below a cluster node k the same color if k is the first node below the cut threshold t. All links connecting nodes with distances greater than or equal to the threshold are colored blue. If t is less than or equal to zero, all nodes are colored blue. If `color_threshold` is None or 'default', corresponding with MATLAB(TM) behavior, the threshold is set to `0.7*max(Z[:,2])`.

get_leaves : bool, optional
Includes a list `R['leaves']=H` in the result dictionary. For each i, `H[i] == j`, cluster node `j` appears in position `i` in the left-to-right traversal of the leaves, where $j < 2n - 1$ and $i < n$.

orientation : str, optional

The direction to plot the dendrogram, which can be any of the following strings:

'top'	Plots the root at the top, and plot descendent links going downwards. (default).
'bottom'	Plots the root at the bottom, and plot descendent links going upwards.
'left'	Plots the root at the left, and plot descendent links going right.
'right'	Plots the root at the right, and plot descendent links going left.

labels : ndarray, optional

By default `labels` is None so the index of the original observation is used to label the leaf nodes. Otherwise, this is an n -sized list (or tuple). The `labels[i]` value is the text to put under the i th leaf node only if it corresponds to an original observation and not a non-singleton cluster.

count_sort : str or bool, optional

For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

False	Nothing is done.
'ascending' or True	The child with the minimum number of original objects in its cluster is plotted first.
'descendent'	The child with the maximum number of original objects in its cluster is plotted first.

Note `distance_sort` and `count_sort` cannot both be True.

distance_sort : str or bool, optional

For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

False	Nothing is done.
'ascending' or True	The child with the minimum distance between its direct descendents is plotted first.
'descending'	The child with the maximum distance between its direct descendents is plotted first.

Note `distance_sort` and `count_sort` cannot both be True.

show_leaf_counts : bool, optional

When True, leaf nodes representing $k > 1$ original observation are labeled with the number of observations they contain in parentheses.

no_plot : bool, optional

When True, the final rendering is not performed. This is useful if only the data structures computed for the rendering are needed or if matplotlib is not available.

no_labels : bool, optional

When True, no labels appear next to the leaf nodes in the rendering of the dendrogram.

leaf_rotation : double, optional

Specifies the angle (in degrees) to rotate the leaf labels. When unspecified, the rotation is based on the number of nodes in the dendrogram (default is 0).

leaf_font_size : int, optional

Specifies the font size (in points) of the leaf labels. When unspecified, the size based on the number of nodes in the dendrogram.

leaf_label_func : lambda or function, optional

When leaf_label_func is a callable function, for each leaf with cluster index $k < 2n - 1$. The function is expected to return a string with the label for the leaf.

Indices $k < n$ correspond to original observations while indices $k \geq n$ correspond to non-singleton clusters.

For example, to label singletons with their node id and non-singletons with their id, count, and inconsistency coefficient, simply do:

```
>>> # First define the leaf label function.
>>> def llf(id):
...       if id < n:
...           return str(id)
...       else:
>>>           return '[%d %d %1.2f]' % (id, count, R[n-id,3])
>>>
>>>  # The text for the leaf nodes is going to be big so force
>>>  # a rotation of 90 degrees.
>>>  dendrogram(Z, leaf_label_func=llf, leaf_rotation=90)
```

show_contracted : bool, optional

When True the heights of non-singleton nodes contracted into a leaf node are plotted as crosses along the link connecting that leaf node. This really is only useful when truncation is used (see `truncate_mode` parameter).

link_color_func : callable, optional

If given, *link_color_function* is called with each non-singleton id corresponding to each U-shaped link it will paint. The function is expected to return the color to paint the link, encoded as a matplotlib color string code. For example:

```
>>> dendrogram(Z, link_color_func=lambda k: colors[k])
```

colors the direct links below each untruncated non-singleton node `k` using `colors[k]`.

ax : matplotlib Axes instance, optional

If None and *no_plot* is not True, the dendrogram will be plotted on the current axes. Otherwise if *no_plot* is not True the dendrogram will be plotted on the given `Axes` instance. This can be useful if the dendrogram is part of a more complex figure.

above_threshold_color : str, optional

This matplotlib color string sets the color of the links above the color_threshold. The default is 'b'.

Returns **R** : dict

A dictionary of data structures computed to render the dendrogram. Its has the following keys:

'color_list'

A list of color names. The k'th element represents the color of the k'th link.

'icoord' and 'dcoord'

Each of them is a list of lists. Let `icoord = [I1, I2, ..., Ip]` where `Ik = [xk1, xk2, xk3, xk4]` and `dcoord = [D1, D2, ..., Dp]` where `Dk = [yk1, yk2, yk3, yk4]`, then the k'th link painted is `(xk1, yk1) - (xk2, yk2) - (xk3, yk3) - (xk4, yk4)`.

'ivl' A list of labels corresponding to the leaf nodes.

'leaves' For each i, `H[i] == j`, cluster node `j` appears in position `i` in the left-to-right traversal of the leaves, where $j < 2n-1$ and $i < n$. If `j` is less than `n`, the `i`-th leaf node corresponds to an original observation. Otherwise, it corresponds to a non-singleton cluster.

These are data structures and routines for representing hierarchies as tree objects.

`ClusterNode`(id[, left, right, dist, count])	A tree node class for representing a cluster.
`leaves_list`(Z)	Returns a list of leaf node ids
`to_tree`(Z[, rd])	Converts a hierarchical clustering encoded in the matrix `Z` (by linkage) into an easy-to-

class `scipy.cluster.hierarchy.`**`ClusterNode`**(*id*, *left=None*, *right=None*, *dist=0*, *count=1*)

A tree node class for representing a cluster.

Leaf nodes correspond to original observations, while non-leaf nodes correspond to non-singleton clusters.

The to_tree function converts a matrix returned by the linkage function into an easy-to-use tree representation.

See also:

`to_tree`	for converting a linkage matrix `Z` into a tree object.

Methods

`get_count`()	The number of leaf nodes (original observations) belonging to the cluster node nd.
`get_id`()	The identifier of the target node.
`get_left`()	Return a reference to the left child tree object.
`get_right`()	Returns a reference to the right child tree object.
`is_leaf`()	Returns True if the target node is a leaf.
`pre_order`([func])	Performs pre-order traversal without recursive function calls.

`ClusterNode.`**`get_count`**`()`

The number of leaf nodes (original observations) belonging to the cluster node nd. If the target node is a leaf, 1 is returned.

Returns **get_count** : int
The number of leaf nodes below the target node.

`ClusterNode.`**`get_id`**`()`

The identifier of the target node.

For `0 <= i < n`, *i* corresponds to original observation i. For `n <= i < 2n-1`, *i* corresponds to non-singleton cluster formed at iteration `i-n`.

Returns **id** : int
The identifier of the target node.

`ClusterNode.`**`get_left`**`()`

Return a reference to the left child tree object.

Returns **left** : ClusterNode
The left child of the target node. If the node is a leaf, None is returned.

`ClusterNode.`**`get_right`**`()`

Returns a reference to the right child tree object.

Returns **right** : ClusterNode
The left child of the target node. If the node is a leaf, None is returned.

`ClusterNode.`**`is_leaf`**`()`

Returns True if the target node is a leaf.

Returns **leafness** : bool
True if the target node is a leaf node.

`ClusterNode.`**`pre_order`**`(`*func=<function <lambda> at 0x7fa4127d22a8>*`)`

Performs pre-order traversal without recursive function calls.

When a leaf node is first encountered, `func` is called with the leaf node as its argument, and its result is appended to the list.

For example, the statement:

```
ids = root.pre_order(lambda x: x.id)
```

returns a list of the node ids corresponding to the leaf nodes of the tree as they appear from left to right.

Parameters **func** : function

Applied to each leaf ClusterNode object in the pre-order traversal. Given the i'th leaf node in the pre-ordeR traversal `n[i]`, the result of func(n[i]) is stored in L[i]. If not provided, the index of the original observation to which the node corresponds is used.

Returns **L** : list

The pre-order traversal.

`scipy.cluster.hierarchy.`**`leaves_list`**`(`*Z*`)`

Returns a list of leaf node ids

The return corresponds to the observation vector index as it appears in the tree from left to right. Z is a linkage matrix.

Parameters **Z** : ndarray

The hierarchical clustering encoded as a matrix. *Z* is a linkage matrix. See `linkage` for more information.

Returns **leaves_list** : ndarray

The list of leaf node ids.

`scipy.cluster.hierarchy.`**`to_tree`**`(`*Z*, *rd=False*`)`

Converts a hierarchical clustering encoded in the matrix `Z` (by linkage) into an easy-to-use tree object.

The reference r to the root ClusterNode object is returned.

Each ClusterNode object has a left, right, dist, id, and count attribute. The left and right attributes point to ClusterNode objects that were combined to generate the cluster. If both are None then the ClusterNode object is a leaf node, its count must be 1, and its distance is meaningless but set to 0.

Note: This function is provided for the convenience of the library user. ClusterNodes are not used as input to any of the functions in this library.

Parameters **Z** : ndarray

The linkage matrix in proper form (see the `linkage` function documentation).

rd : bool, optional

When False, a reference to the root ClusterNode object is returned. Otherwise, a tuple (r,d) is returned. `r` is a reference to the root node while `d` is a dictionary mapping cluster ids to ClusterNode references. If a cluster id is less than n, then it corresponds to a singleton cluster (leaf node). See `linkage` for more information on the assignment of cluster ids to clusters.

Returns **L** : list

The pre-order traversal.

These are predicates for checking the validity of linkage and inconsistency matrices as well as for checking isomorphism of two flat cluster assignments.

`is_valid_im`(R[, warning, throw, name])	Returns True if the inconsistency matrix passed is valid.
`is_valid_linkage`(Z[, warning, throw, name])	Checks the validity of a linkage matrix.
`is_isomorphic`(T1, T2)	Determines if two different cluster assignments are equivalent.
`is_monotonic`(Z)	Returns True if the linkage passed is monotonic.
`correspond`(Z, Y)	Checks for correspondence between linkage and condensed distance matrices
`num_obs_linkage`(Z)	Returns the number of original observations of the linkage matrix passed.

`scipy.cluster.hierarchy.`**`is_valid_im`**`(`*R*, *warning=False*, *throw=False*, *name=None*`)`

Returns True if the inconsistency matrix passed is valid.

It must be a n by 4 numpy array of doubles. The standard deviations `R[:,1]` must be nonnegative. The link counts `R[:,2]` must be positive and no greater than $n-1$.

Parameters **R** : ndarray
The inconsistency matrix to check for validity.
warning : bool, optional
When True, issues a Python warning if the linkage matrix passed is invalid.
throw : bool, optional
When True, throws a Python exception if the linkage matrix passed is invalid.
name : str, optional
This string refers to the variable name of the invalid linkage matrix.

Returns **b** : bool
True if the inconsistency matrix is valid.

`scipy.cluster.hierarchy.`**`is_valid_linkage`**`(`*Z*, *warning=False*, *throw=False*, *name=None*`)`
Checks the validity of a linkage matrix.

A linkage matrix is valid if it is a two dimensional ndarray (type double) with n rows and 4 columns. The first two columns must contain indices between 0 and $2n-1$. For a given row `i`, $0 \leq \mathtt{Z}[\mathtt{i}, 0] \leq i+n-1$ and $0 \leq Z[i, 1] \leq i+n-1$ (i.e. a cluster cannot join another cluster unless the cluster being joined has been generated.)

Parameters **Z** : array_like
Linkage matrix.
warning : bool, optional
When True, issues a Python warning if the linkage matrix passed is invalid.
throw : bool, optional
When True, throws a Python exception if the linkage matrix passed is invalid.
name : str, optional
This string refers to the variable name of the invalid linkage matrix.

Returns **b** : bool
True iff the inconsistency matrix is valid.

`scipy.cluster.hierarchy.`**`is_isomorphic`**`(`*T1*, *T2*`)`
Determines if two different cluster assignments are equivalent.

Parameters **T1** : array_like
An assignment of singleton cluster ids to flat cluster ids.
T2 : array_like
An assignment of singleton cluster ids to flat cluster ids.

Returns **b** : bool
Whether the flat cluster assignments *T1* and *T2* are equivalent.

`scipy.cluster.hierarchy.`**`is_monotonic`**`(`*Z*`)`
Returns True if the linkage passed is monotonic.

The linkage is monotonic if for every cluster s and t joined, the distance between them is no less than the distance between any previously joined clusters.

Parameters **Z** : ndarray
The linkage matrix to check for monotonicity.

Returns **b** : bool
A boolean indicating whether the linkage is monotonic.

`scipy.cluster.hierarchy.`**`correspond`**`(`*Z*, *Y*`)`
Checks for correspondence between linkage and condensed distance matrices

They must have the same number of original observations for the check to succeed.

This function is useful as a sanity check in algorithms that make extensive use of linkage and distance matrices that must correspond to the same set of original observations.

Parameters	**Z** : array_like The linkage matrix to check for correspondence. **Y** : array_like The condensed distance matrix to check for correspondence.
Returns	**b** : bool A boolean indicating whether the linkage matrix and distance matrix could possibly correspond to one another.

`scipy.cluster.hierarchy.`**`num_obs_linkage`**`(`*Z*`)`

Returns the number of original observations of the linkage matrix passed.

Parameters	**Z** : ndarray The linkage matrix on which to perform the operation.
Returns	**n** : int The number of original observations in the linkage.

Utility routines for plotting:

`set_link_color_palette`(palette)	Set list of matplotlib color codes for dendrogram color_threshold.

`scipy.cluster.hierarchy.`**`set_link_color_palette`**`(`*palette*`)`

Set list of matplotlib color codes for dendrogram color_threshold.

Parameters	**palette** : list A list of matplotlib color codes. The order of the color codes is the order in which the colors are cycled through when color thresholding in the dendrogram.

5.3.1 References

- MATLAB and MathWorks are registered trademarks of The MathWorks, Inc.
- Mathematica is a registered trademark of The Wolfram Research, Inc.

5.4 Constants (`scipy.constants`)

Physical and mathematical constants and units.

5.4.1 Mathematical constants

`pi`	Pi
`golden`	Golden ratio

5.4.2 Physical constants

`c`	speed of light in vacuum
`mu_0`	the magnetic constant μ_0
`epsilon_0`	the electric constant (vacuum permittivity), ϵ_0
`h`	the Planck constant h
`hbar`	$\hbar = h/(2\pi)$
`G`	Newtonian constant of gravitation
`g`	standard acceleration of gravity
`e`	elementary charge
`R`	molar gas constant
`alpha`	fine-structure constant
`N_A`	Avogadro constant
`k`	Boltzmann constant
`sigma`	Stefan-Boltzmann constant σ
`Wien`	Wien displacement law constant
`Rydberg`	Rydberg constant
`m_e`	electron mass
`m_p`	proton mass
`m_n`	neutron mass

Constants database

In addition to the above variables, `scipy.constants` also contains the 2010 CODATA recommended values [CODATA2010] database containing more physical constants.

`value`(key)	Value in physical_constants indexed by key
`unit`(key)	Unit in physical_constants indexed by key
`precision`(key)	Relative precision in physical_constants indexed by key
`find`([sub, disp])	Return list of codata.physical_constant keys containing a given string.
`ConstantWarning`	Accessing a constant no longer in current CODATA data set

`scipy.constants.`**`value`**(*key*)

Value in physical_constants indexed by key

Parameters	**key** : Python string or unicode Key in dictionary `physical_constants`
Returns	**value** : float Value in `physical_constants` corresponding to *key*

See also:

`codata`	Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

Examples

```
>>> from scipy.constants import codata
>>> codata.value('elementary charge')
    1.602176487e-019
```

`scipy.constants.`**`unit`**(*key*)

Unit in physical_constants indexed by key

Parameters	**key** : Python string or unicode Key in dictionary `physical_constants`
Returns	**unit** : Python string Unit in `physical_constants` corresponding to *key*

See also:

`codata`	Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

Examples

```
>>> from scipy.constants import codata
>>> codata.unit(u'proton mass')
'kg'
```

`scipy.constants.`**`precision`**`(`*key*`)`

Relative precision in physical_constants indexed by key

Parameters	**key** : Python string or unicode Key in dictionary `physical_constants`
Returns	**prec** : float Relative precision in `physical_constants` corresponding to *key*

See also:

`codata`	Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

Examples

```
>>> from scipy.constants import codata
>>> codata.precision(u'proton mass')
4.96226989798e-08
```

`scipy.constants.`**`find`**`(`*sub=None*, *disp=False*`)`

Return list of codata.physical_constant keys containing a given string.

Parameters	**sub** : str, unicode Sub-string to search keys for. By default, return all keys. **disp** : bool If True, print the keys that are found, and return None. Otherwise, return the list of keys without printing anything.
Returns	**keys** : list or None If *disp* is False, the list of keys is returned. Otherwise, None is returned.

See also:

`codata`	Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

exception `scipy.constants.`**`ConstantWarning`**

Accessing a constant no longer in current CODATA data set

`scipy.constants.`**`physical_constants`**

Dictionary of physical constants, of the format `physical_constants[name] = (value, unit, uncertainty)`.

Available constants:

`alpha particle mass`	6.64465675e-27 kg
`alpha particle mass energy equivalent`	5.97191967e-10 J
`alpha particle mass energy equivalent in MeV`	3727.37924 MeV
`alpha particle mass in u`	4.00150617913 u
`alpha particle molar mass`	0.00400150617912 kg mol^-1
`alpha particle-electron mass ratio`	7294.2995361
`alpha particle-proton mass ratio`	3.97259968933
`Angstrom star`	1.00001495e-10 m
`atomic mass constant`	1.660538921e-27 kg
`atomic mass constant energy equivalent`	1.492417954e-10 J
`atomic mass constant energy equivalent in MeV`	931.494061 MeV
`atomic mass unit-electron volt relationship`	931494061.0 eV
`atomic mass unit-hartree relationship`	34231776.845 E_h
`atomic mass unit-hertz relationship`	2.2523427168e+23 Hz
`atomic mass unit-inverse meter relationship`	7.5130066042e+14 m^-1
`atomic mass unit-joule relationship`	1.492417954e-10 J
`atomic mass unit-kelvin relationship`	1.08095408e+13 K
`atomic mass unit-kilogram relationship`	1.660538921e-27 kg
`atomic unit of 1st hyperpolarizability`	3.206361449e-53 C^3 m^3 J^-2
`atomic unit of 2nd hyperpolarizability`	6.23538054e-65 C^4 m^4 J^-3
`atomic unit of action`	1.054571726e-34 J s
`atomic unit of charge`	1.602176565e-19 C
`atomic unit of charge density`	1.081202338e+12 C m^-3
`atomic unit of current`	0.00662361795 A
`atomic unit of electric dipole mom.`	8.47835326e-30 C m
`atomic unit of electric field`	5.14220652e+11 V m^-1
`atomic unit of electric field gradient`	9.717362e+21 V m^-2
`atomic unit of electric polarizability`	1.6487772754e-41 C^2 m^2 J^-1
`atomic unit of electric potential`	27.21138505 V
`atomic unit of electric quadrupole mom.`	4.486551331e-40 C m^2
`atomic unit of energy`	4.35974434e-18 J
`atomic unit of force`	8.23872278e-08 N
`atomic unit of length`	5.2917721092e-11 m
`atomic unit of mag.  dipole mom.`	1.854801936e-23 J T^-1
`atomic unit of mag.  flux density`	235051.7464 T
`atomic unit of magnetizability`	7.891036607e-29 J T^-2
`atomic unit of mass`	9.10938291e-31 kg
`atomic unit of mom.um`	1.99285174e-24 kg m s^-1
`atomic unit of permittivity`	1.11265005605e-10 F m^-1
`atomic unit of time`	2.4188843265e-17 s
`atomic unit of velocity`	2187691.26379 m s^-1
`Avogadro constant`	6.02214129e+23 mol^-1
`Bohr magneton`	9.27400968e-24 J T^-1
`Bohr magneton in eV/T`	5.7883818066e-05 eV T^-1
`Bohr magneton in Hz/T`	13996245550.0 Hz T^-1
`Bohr magneton in inverse meters per tesla`	46.6864498 m^-1 T^-1
`Bohr magneton in K/T`	0.67171388 K T^-1
`Bohr radius`	5.2917721092e-11 m
`Boltzmann constant`	1.3806488e-23 J K^-1
`Boltzmann constant in eV/K`	8.6173324e-05 eV K^-1

Continued on next page

Table 5.11 – continued from previous page

Boltzmann constant in Hz/K	20836618000.0 Hz K^-1
Boltzmann constant in inverse meters per kelvin	69.503476 m^-1 K^-1
characteristic impedance of vacuum	376.730313462 ohm
classical electron radius	2.8179403267e-15 m
Compton wavelength	2.4263102389e-12 m
Compton wavelength over 2 pi	3.86159268e-13 m
conductance quantum	7.7480917346e-05 S
conventional value of Josephson constant	4.835979e+14 Hz V^-1
conventional value of von Klitzing constant	25812.807 ohm
Cu x unit	1.00207697e-13 m
deuteron g factor	0.8574382308
deuteron mag. mom.	4.33073489e-27 J T^-1
deuteron mag. mom. to Bohr magneton ratio	0.0004669754556
deuteron mag. mom. to nuclear magneton ratio	0.8574382308
deuteron mass	3.34358348e-27 kg
deuteron mass energy equivalent	3.00506297e-10 J
deuteron mass energy equivalent in MeV	1875.612859 MeV
deuteron mass in u	2.01355321271 u
deuteron molar mass	0.00201355321271 kg mol^-1
deuteron rms charge radius	2.1424e-15 m
deuteron-electron mag. mom. ratio	-0.0004664345537
deuteron-electron mass ratio	3670.4829652
deuteron-neutron mag. mom. ratio	-0.44820652
deuteron-proton mag. mom. ratio	0.307012207
deuteron-proton mass ratio	1.99900750097
electric constant	8.85418781762e-12 F m^-1
electron charge to mass quotient	-1.758820088e+11 C kg^-1
electron g factor	-2.00231930436
electron gyromag. ratio	1.760859708e+11 s^-1 T^-1
electron gyromag. ratio over 2 pi	28024.95266 MHz T^-1
electron mag. mom.	-9.2847643e-24 J T^-1
electron mag. mom. anomaly	0.00115965218076
electron mag. mom. to Bohr magneton ratio	-1.00115965218
electron mag. mom. to nuclear magneton ratio	-1838.2819709
electron mass	9.10938291e-31 kg
electron mass energy equivalent	8.18710506e-14 J
electron mass energy equivalent in MeV	0.510998928 MeV
electron mass in u	0.00054857990946 u
electron molar mass	5.4857990946e-07 kg mol^-1
electron to alpha particle mass ratio	0.000137093355578
electron to shielded helion mag. mom. ratio	864.058257
electron to shielded proton mag. mom. ratio	-658.2275971
electron volt	1.602176565e-19 J
electron volt-atomic mass unit relationship	1.07354415e-09 u
electron volt-hartree relationship	0.03674932379 E_h
electron volt-hertz relationship	2.417989348e+14 Hz
electron volt-inverse meter relationship	806554.429 m^-1
electron volt-joule relationship	1.602176565e-19 J
electron volt-kelvin relationship	11604.519 K
electron volt-kilogram relationship	1.782661845e-36 kg

Continued on next page

Table 5.11 – continued from previous page

`electron-deuteron mag. mom. ratio`	-2143.923498
`electron-deuteron mass ratio`	0.00027244371095
`electron-helion mass ratio`	0.00018195430761
`electron-muon mag. mom. ratio`	206.7669896
`electron-muon mass ratio`	0.00483633166
`electron-neutron mag. mom. ratio`	960.9205
`electron-neutron mass ratio`	0.00054386734461
`electron-proton mag. mom. ratio`	-658.2106848
`electron-proton mass ratio`	0.00054461702178
`electron-tau mass ratio`	0.000287592
`electron-triton mass ratio`	0.00018192000653
`elementary charge`	1.602176565e-19 C
`elementary charge over h`	2.417989348e+14 A J^-1
`Faraday constant`	96485.3365 C mol^-1
`Faraday constant for conventional electric current`	96485.3321 C_90 mol^-1
`Fermi coupling constant`	1.166364e-05 GeV^-2
`fine-structure constant`	0.0072973525698
`first radiation constant`	3.74177153e-16 W m^2
`first radiation constant for spectral radiance`	1.191042869e-16 W m^2 sr^-1
`Hartree energy`	4.35974434e-18 J
`Hartree energy in eV`	27.21138505 eV
`hartree-atomic mass unit relationship`	2.9212623246e-08 u
`hartree-electron volt relationship`	27.21138505 eV
`hartree-hertz relationship`	6.57968392073e+15 Hz
`hartree-inverse meter relationship`	21947463.1371 m^-1
`hartree-joule relationship`	4.35974434e-18 J
`hartree-kelvin relationship`	315775.04 K
`hartree-kilogram relationship`	4.85086979e-35 kg
`helion g factor`	-4.255250613
`helion mag. mom.`	-1.074617486e-26 J T^-1
`helion mag. mom. to Bohr magneton ratio`	-0.001158740958
`helion mag. mom. to nuclear magneton ratio`	-2.127625306
`helion mass`	5.00641234e-27 kg
`helion mass energy equivalent`	4.49953902e-10 J
`helion mass energy equivalent in MeV`	2808.391482 MeV
`helion mass in u`	3.0149322468 u
`helion molar mass`	0.0030149322468 kg mol^-1
`helion-electron mass ratio`	5495.8852754
`helion-proton mass ratio`	2.9931526707
`hertz-atomic mass unit relationship`	4.4398216689e-24 u
`hertz-electron volt relationship`	4.135667516e-15 eV
`hertz-hartree relationship`	1.519829846e-16 E_h
`hertz-inverse meter relationship`	3.33564095198e-09 m^-1
`hertz-joule relationship`	6.62606957e-34 J
`hertz-kelvin relationship`	4.7992434e-11 K
`hertz-kilogram relationship`	7.37249668e-51 kg
`inverse fine-structure constant`	137.035999074
`inverse meter-atomic mass unit relationship`	1.3310250512e-15 u
`inverse meter-electron volt relationship`	1.23984193e-06 eV
`inverse meter-hartree relationship`	4.55633525276e-08 E_h

Continued on next page

Table 5.11 – continued from previous page

`inverse meter-hertz relationship`	299792458.0 Hz
`inverse meter-joule relationship`	1.986445684e-25 J
`inverse meter-kelvin relationship`	0.01438777 K
`inverse meter-kilogram relationship`	2.210218902e-42 kg
`inverse of conductance quantum`	12906.4037217 ohm
`Josephson constant`	4.8359787e+14 Hz V^-1
`joule-atomic mass unit relationship`	6700535850.0 u
`joule-electron volt relationship`	6.24150934e+18 eV
`joule-hartree relationship`	2.29371248e+17 E_h
`joule-hertz relationship`	1.509190311e+33 Hz
`joule-inverse meter relationship`	5.03411701e+24 m^-1
`joule-kelvin relationship`	7.2429716e+22 K
`joule-kilogram relationship`	1.11265005605e-17 kg
`kelvin-atomic mass unit relationship`	9.2510868e-14 u
`kelvin-electron volt relationship`	8.6173324e-05 eV
`kelvin-hartree relationship`	3.1668114e-06 E_h
`kelvin-hertz relationship`	20836618000.0 Hz
`kelvin-inverse meter relationship`	69.503476 m^-1
`kelvin-joule relationship`	1.3806488e-23 J
`kelvin-kilogram relationship`	1.536179e-40 kg
`kilogram-atomic mass unit relationship`	6.02214129e+26 u
`kilogram-electron volt relationship`	5.60958885e+35 eV
`kilogram-hartree relationship`	2.061485968e+34 E_h
`kilogram-hertz relationship`	1.356392608e+50 Hz
`kilogram-inverse meter relationship`	4.52443873e+41 m^-1
`kilogram-joule relationship`	8.98755178737e+16 J
`kilogram-kelvin relationship`	6.5096582e+39 K
`lattice parameter of silicon`	5.431020504e-10 m
`Loschmidt constant (273.15 K, 100 kPa)`	2.6516462e+25 m^-3
`Loschmidt constant (273.15 K, 101.325 kPa)`	2.6867805e+25 m^-3
`mag. constant`	1.25663706144e-06 N A^-2
`mag. flux quantum`	2.067833758e-15 Wb
`Mo x unit`	1.00209952e-13 m
`molar gas constant`	8.3144621 J mol^-1 K^-1
`molar mass constant`	0.001 kg mol^-1
`molar mass of carbon-12`	0.012 kg mol^-1
`molar Planck constant`	3.9903127176e-10 J s mol^-1
`molar Planck constant times c`	0.119626565779 J m mol^-1
`molar volume of ideal gas (273.15 K, 100 kPa)`	0.022710953 m^3 mol^-1
`molar volume of ideal gas (273.15 K, 101.325 kPa)`	0.022413968 m^3 mol^-1
`molar volume of silicon`	1.205883301e-05 m^3 mol^-1
`muon Compton wavelength`	1.173444103e-14 m
`muon Compton wavelength over 2 pi`	1.867594294e-15 m
`muon g factor`	-2.0023318418
`muon mag. mom.`	-4.49044807e-26 J T^-1
`muon mag. mom. anomaly`	0.00116592091
`muon mag. mom. to Bohr magneton ratio`	-0.00484197044
`muon mag. mom. to nuclear magneton ratio`	-8.89059697
`muon mass`	1.883531475e-28 kg
`muon mass energy equivalent`	1.692833667e-11 J

Continued on next page

Table 5.11 – continued from previous page

`muon mass energy equivalent in MeV`	105.6583715 MeV
`muon mass in u`	0.1134289267 u
`muon molar mass`	0.0001134289267 kg mol^-1
`muon-electron mass ratio`	206.7682843
`muon-neutron mass ratio`	0.1124545177
`muon-proton mag.  mom.  ratio`	-3.183345107
`muon-proton mass ratio`	0.1126095272
`muon-tau mass ratio`	0.0594649
`natural unit of action`	1.054571726e-34 J s
`natural unit of action in eV s`	6.58211928e-16 eV s
`natural unit of energy`	8.18710506e-14 J
`natural unit of energy in MeV`	0.510998928 MeV
`natural unit of length`	3.86159268e-13 m
`natural unit of mass`	9.10938291e-31 kg
`natural unit of mom.um`	2.73092429e-22 kg m s^-1
`natural unit of mom.um in MeV/c`	0.510998928 MeV/c
`natural unit of time`	1.28808866833e-21 s
`natural unit of velocity`	299792458.0 m s^-1
`neutron Compton wavelength`	1.3195909068e-15 m
`neutron Compton wavelength over 2 pi`	2.1001941568e-16 m
`neutron g factor`	-3.82608545
`neutron gyromag.  ratio`	183247179.0 s^-1 T^-1
`neutron gyromag.  ratio over 2 pi`	29.1646943 MHz T^-1
`neutron mag.  mom.`	-9.6623647e-27 J T^-1
`neutron mag.  mom.  to Bohr magneton ratio`	-0.00104187563
`neutron mag.  mom.  to nuclear magneton ratio`	-1.91304272
`neutron mass`	1.674927351e-27 kg
`neutron mass energy equivalent`	1.505349631e-10 J
`neutron mass energy equivalent in MeV`	939.565379 MeV
`neutron mass in u`	1.008664916 u
`neutron molar mass`	0.001008664916 kg mol^-1
`neutron to shielded proton mag.  mom.  ratio`	-0.68499694
`neutron-electron mag.  mom.  ratio`	0.00104066882
`neutron-electron mass ratio`	1838.6836605
`neutron-muon mass ratio`	8.892484
`neutron-proton mag.  mom.  ratio`	-0.68497934
`neutron-proton mass difference`	2.30557392e-30
`neutron-proton mass difference energy equivalent`	2.0721465e-13
`neutron-proton mass difference energy equivalent in MeV`	1.29333217
`neutron-proton mass difference in u`	0.00138844919
`neutron-proton mass ratio`	1.00137841917
`neutron-tau mass ratio`	0.52879
`Newtonian constant of gravitation`	6.67384e-11 m^3 kg^-1 s^-2
`Newtonian constant of gravitation over h-bar c`	6.70837e-39 (GeV/c^2)^-2
`nuclear magneton`	5.05078353e-27 J T^-1
`nuclear magneton in eV/T`	3.1524512605e-08 eV T^-1
`nuclear magneton in inverse meters per tesla`	0.02542623527 m^-1 T^-1
`nuclear magneton in K/T`	0.00036582682 K T^-1
`nuclear magneton in MHz/T`	7.62259357 MHz T^-1
`Planck constant`	6.62606957e-34 J s

Continued on next page

Table 5.11 – continued from previous page

Planck constant in eV s	4.135667516e-15 eV s
Planck constant over 2 pi	1.054571726e-34 J s
Planck constant over 2 pi in eV s	6.58211928e-16 eV s
Planck constant over 2 pi times c in MeV fm	197.3269718 MeV fm
Planck length	1.616199e-35 m
Planck mass	2.17651e-08 kg
Planck mass energy equivalent in GeV	1.220932e+19 GeV
Planck temperature	1.416833e+32 K
Planck time	5.39106e-44 s
proton charge to mass quotient	95788335.8 C kg^-1
proton Compton wavelength	1.32140985623e-15 m
proton Compton wavelength over 2 pi	2.1030891047e-16 m
proton g factor	5.585694713
proton gyromag. ratio	267522200.5 s^-1 T^-1
proton gyromag. ratio over 2 pi	42.5774806 MHz T^-1
proton mag. mom.	1.410606743e-26 J T^-1
proton mag. mom. to Bohr magneton ratio	0.00152103221
proton mag. mom. to nuclear magneton ratio	2.792847356
proton mag. shielding correction	2.5694e-05
proton mass	1.672621777e-27 kg
proton mass energy equivalent	1.503277484e-10 J
proton mass energy equivalent in MeV	938.272046 MeV
proton mass in u	1.00727646681 u
proton molar mass	0.00100727646681 kg mol^-1
proton rms charge radius	8.775e-16 m
proton-electron mass ratio	1836.15267245
proton-muon mass ratio	8.88024331
proton-neutron mag. mom. ratio	-1.45989806
proton-neutron mass ratio	0.99862347826
proton-tau mass ratio	0.528063
quantum of circulation	0.0003636947552 m^2 s^-1
quantum of circulation times 2	0.0007273895104 m^2 s^-1
Rydberg constant	10973731.5685 m^-1
Rydberg constant times c in Hz	3.28984196036e+15 Hz
Rydberg constant times hc in eV	13.60569253 eV
Rydberg constant times hc in J	2.179872171e-18 J
Sackur-Tetrode constant (1 K, 100 kPa)	-1.1517078
Sackur-Tetrode constant (1 K, 101.325 kPa)	-1.1648708
second radiation constant	0.01438777 m K
shielded helion gyromag. ratio	203789465.9 s^-1 T^-1
shielded helion gyromag. ratio over 2 pi	32.43410084 MHz T^-1
shielded helion mag. mom.	-1.074553044e-26 J T^-1
shielded helion mag. mom. to Bohr magneton ratio	-0.001158671471
shielded helion mag. mom. to nuclear magneton ratio	-2.127497718
shielded helion to proton mag. mom. ratio	-0.761766558
shielded helion to shielded proton mag. mom. ratio	-0.7617861313
shielded proton gyromag. ratio	267515326.8 s^-1 T^-1
shielded proton gyromag. ratio over 2 pi	42.5763866 MHz T^-1
shielded proton mag. mom.	1.410570499e-26 J T^-1
shielded proton mag. mom. to Bohr magneton ratio	0.001520993128

Continued on next page

Table 5.11 – continued from previous page

shielded proton mag. mom. to nuclear magneton ratio	2.792775598
speed of light in vacuum	299792458.0 m s^-1
standard acceleration of gravity	9.80665 m s^-2
standard atmosphere	101325.0 Pa
standard-state pressure	100000.0 Pa
Stefan-Boltzmann constant	5.670373e-08 W m^-2 K^-4
tau Compton wavelength	6.97787e-16 m
tau Compton wavelength over 2 pi	1.11056e-16 m
tau mass	3.16747e-27 kg
tau mass energy equivalent	2.84678e-10 J
tau mass energy equivalent in MeV	1776.82 MeV
tau mass in u	1.90749 u
tau molar mass	0.00190749 kg mol^-1
tau-electron mass ratio	3477.15
tau-muon mass ratio	16.8167
tau-neutron mass ratio	1.89111
tau-proton mass ratio	1.89372
Thomson cross section	6.652458734e-29 m^2
triton g factor	5.957924896
triton mag. mom.	1.504609447e-26 J T^-1
triton mag. mom. to Bohr magneton ratio	0.001622393657
triton mag. mom. to nuclear magneton ratio	2.978962448
triton mass	5.0073563e-27 kg
triton mass energy equivalent	4.50038741e-10 J
triton mass energy equivalent in MeV	2808.921005 MeV
triton mass in u	3.0155007134 u
triton molar mass	0.0030155007134 kg mol^-1
triton-electron mass ratio	5496.9215267
triton-proton mass ratio	2.9937170308
unified atomic mass unit	1.660538921e-27 kg
von Klitzing constant	25812.8074434 ohm
weak mixing angle	0.2223
Wien frequency displacement law constant	58789254000.0 Hz K^-1
Wien wavelength displacement law constant	0.0028977721 m K
{220} lattice spacing of silicon	1.920155714e-10 m

5.4.3 Units

SI prefixes

`yotta`	10^{24}
`zetta`	10^{21}
`exa`	10^{18}
`peta`	10^{15}
`tera`	10^{12}
`giga`	10^{9}
`mega`	10^{6}
`kilo`	10^{3}
`hecto`	10^{2}
`deka`	10^{1}
`deci`	10^{-1}
`centi`	10^{-2}
`milli`	10^{-3}
`micro`	10^{-6}
`nano`	10^{-9}
`pico`	10^{-12}
`femto`	10^{-15}
`atto`	10^{-18}
`zepto`	10^{-21}

Binary prefixes

`kibi`	2^{10}
`mebi`	2^{20}
`gibi`	2^{30}
`tebi`	2^{40}
`pebi`	2^{50}
`exbi`	2^{60}
`zebi`	2^{70}
`yobi`	2^{80}

Weight

`gram`	10^{-3} kg
`metric_ton`	10^{3} kg
`grain`	one grain in kg
`lb`	one pound (avoirdupous) in kg
`oz`	one ounce in kg
`stone`	one stone in kg
`grain`	one grain in kg
`long_ton`	one long ton in kg
`short_ton`	one short ton in kg
`troy_ounce`	one Troy ounce in kg
`troy_pound`	one Troy pound in kg
`carat`	one carat in kg
`m_u`	atomic mass constant (in kg)

Angle

`degree`	degree in radians
`arcmin`	arc minute in radians
`arcsec`	arc second in radians

Time

`minute`	one minute in seconds
`hour`	one hour in seconds
`day`	one day in seconds
`week`	one week in seconds
`year`	one year (365 days) in seconds
`Julian_year`	one Julian year (365.25 days) in seconds

Length

`inch`	one inch in meters
`foot`	one foot in meters
`yard`	one yard in meters
`mile`	one mile in meters
`mil`	one mil in meters
`pt`	one point in meters
`survey_foot`	one survey foot in meters
`survey_mile`	one survey mile in meters
`nautical_mile`	one nautical mile in meters
`fermi`	one Fermi in meters
`angstrom`	one Angstrom in meters
`micron`	one micron in meters
`au`	one astronomical unit in meters
`light_year`	one light year in meters
`parsec`	one parsec in meters

Pressure

`atm`	standard atmosphere in pascals
`bar`	one bar in pascals
`torr`	one torr (mmHg) in pascals
`psi`	one psi in pascals

Area

`hectare`	one hectare in square meters
`acre`	one acre in square meters

Volume

`liter`	one liter in cubic meters
`gallon`	one gallon (US) in cubic meters
`gallon_imp`	one gallon (UK) in cubic meters
`fluid_ounce`	one fluid ounce (US) in cubic meters
`fluid_ounce_imp`	one fluid ounce (UK) in cubic meters
`bbl`	one barrel in cubic meters

Speed

`kmh`	kilometers per hour in meters per second
`mph`	miles per hour in meters per second
`mach`	one Mach (approx., at 15 C, 1 atm) in meters per second
`knot`	one knot in meters per second

Temperature

`zero_Celsius`	zero of Celsius scale in Kelvin
`degree_Fahrenheit`	one Fahrenheit (only differences) in Kelvins

`C2K`(C)	Convert Celsius to Kelvin
`K2C`(K)	Convert Kelvin to Celsius
`F2C`(F)	Convert Fahrenheit to Celsius
`C2F`(C)	Convert Celsius to Fahrenheit
`F2K`(F)	Convert Fahrenheit to Kelvin
`K2F`(K)	Convert Kelvin to Fahrenheit

`scipy.constants.`**`C2K`**`(`*C*`)`

Convert Celsius to Kelvin

Parameters **C** : array_like

Celsius temperature(s) to be converted.

Returns **K** : float or array of floats

Equivalent Kelvin temperature(s).

Notes

Computes `K = C + zero_Celsius` where `zero_Celsius` = 273.15, i.e., (the absolute value of) temperature “absolute zero” as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import C2K
>>> C2K(_np.array([-40, 40.0]))
array([ 233.15,  313.15])
```

`scipy.constants.`**`K2C`**`(`*K*`)`

Convert Kelvin to Celsius

Parameters **K** : array_like

Kelvin temperature(s) to be converted.

Returns **C** : float or array of floats

Equivalent Celsius temperature(s).

Notes

Computes `C = K - zero_Celsius` where `zero_Celsius` = 273.15, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import K2C
>>> K2C(_np.array([233.15, 313.15]))
array([-40.,  40.])
```

`scipy.constants.`**`F2C`**`(F)`

Convert Fahrenheit to Celsius

Parameters	**F** : array_like Fahrenheit temperature(s) to be converted.
Returns	**C** : float or array of floats Equivalent Celsius temperature(s).

Notes

Computes `C = (F - 32) / 1.8`.

Examples

```
>>> from scipy.constants.constants import F2C
>>> F2C(_np.array([-40, 40.0]))
array([-40.        ,   4.44444444])
```

`scipy.constants.`**`C2F`**`(C)`

Convert Celsius to Fahrenheit

Parameters	**C** : array_like Celsius temperature(s) to be converted.
Returns	**F** : float or array of floats Equivalent Fahrenheit temperature(s).

Notes

Computes `F = 1.8 * C + 32`.

Examples

```
>>> from scipy.constants.constants import C2F
>>> C2F(_np.array([-40, 40.0]))
array([ -40.,  104.])
```

`scipy.constants.`**`F2K`**`(F)`

Convert Fahrenheit to Kelvin

Parameters	**F** : array_like Fahrenheit temperature(s) to be converted.
Returns	**K** : float or array of floats Equivalent Kelvin temperature(s).

Notes

Computes `K = (F - 32)/1.8 + zero_Celsius` where `zero_Celsius` = 273.15, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import F2K
>>> F2K(_np.array([-40, 104]))
array([ 233.15,  313.15])
```

`scipy.constants.`**`K2F`**`(`*K*`)`

Convert Kelvin to Fahrenheit

Parameters	**K** : array_like Kelvin temperature(s) to be converted.
Returns	**F** : float or array of floats Equivalent Fahrenheit temperature(s).

Notes

Computes `F = 1.8 * (K - zero_Celsius) + 32` where `zero_Celsius` = 273.15, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import K2F
>>> K2F(_np.array([233.15,  313.15]))
array([ -40.,  104.])
```

Energy

`eV`	one electron volt in Joules
`calorie`	one calorie (thermochemical) in Joules
`calorie_IT`	one calorie (International Steam Table calorie, 1956) in Joules
`erg`	one erg in Joules
`Btu`	one British thermal unit (International Steam Table) in Joules
`Btu_th`	one British thermal unit (thermochemical) in Joules
`ton_TNT`	one ton of TNT in Joules

Power

`hp`	one horsepower in watts

Force

`dyn`	one dyne in newtons
`lbf`	one pound force in newtons
`kgf`	one kilogram force in newtons

Optics

`lambda2nu`(**lambda_**)	Convert wavelength to optical frequency
`nu2lambda`(nu)	Convert optical frequency to wavelength.

`scipy.constants.`**`lambda2nu`**`(`*lambda_*`)`

Convert wavelength to optical frequency

Parameters	**lambda_** : array_like Wavelength(s) to be converted.
Returns	**nu** : float or array of floats Equivalent optical frequency.

Notes

Computes `nu = c / lambda` where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants.constants import lambda2nu
>>> lambda2nu(_np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

`scipy.constants.`**`nu2lambda`**`(`*nu*`)`

Convert optical frequency to wavelength.

Parameters	**nu** : array_like Optical frequency to be converted.
Returns	**lambda** : float or array of floats Equivalent wavelength(s).

Notes

Computes `lambda = c / nu` where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants.constants import nu2lambda
>>> nu2lambda(_np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

5.4.4 References

5.5 Discrete Fourier transforms (`scipy.fftpack`)

5.5.1 Fast Fourier Transforms (FFTs)

`fft`(x[, n, axis, overwrite_x])	Return discrete Fourier transform of real or complex sequence.
`ifft`(x[, n, axis, overwrite_x])	Return discrete inverse Fourier transform of real or complex sequence.
`fft2`(x[, shape, axes, overwrite_x])	2-D discrete Fourier transform.
`ifft2`(x[, shape, axes, overwrite_x])	2-D discrete inverse Fourier transform of real or complex sequence.
`fftn`(x[, shape, axes, overwrite_x])	Return multidimensional discrete Fourier transform.
`ifftn`(x[, shape, axes, overwrite_x])	Return inverse multi-dimensional discrete Fourier transform of arbitrary type sequence
`rfft`(x[, n, axis, overwrite_x])	Discrete Fourier transform of a real sequence.
`irfft`(x[, n, axis, overwrite_x])	Return inverse discrete Fourier transform of real sequence x.
`dct`(x[, type, n, axis, norm, overwrite_x])	Return the Discrete Cosine Transform of arbitrary type sequence x.
`idct`(x[, type, n, axis, norm, overwrite_x])	Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.
`dst`(x[, type, n, axis, norm, overwrite_x])	Return the Discrete Sine Transform of arbitrary type sequence x.

Continued on next pag

Table 5.14 – continued from previous page

`idst`(x[, type, n, axis, norm, overwrite_x])	Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

`scipy.fftpack.`**`fft`**(*x*, *n=None*, *axis=-1*, *overwrite_x=False*)

Return discrete Fourier transform of real or complex sequence.

The returned complex array contains `y(0), y(1),..., y(n-1)` where

`y(j) = (x * exp(-2*pi*sqrt(-1)*j*np.arange(n)/n)).sum()`.

Parameters

x : array_like
  Array to Fourier transform.

n : int, optional
  Length of the Fourier transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis : int, optional
  Axis along which the fft's are computed; the default is over the last axis (i.e., `axis=-1`).

overwrite_x : bool, optional
  If True, the contents of *x* can be destroyed; the default is False.

Returns

z : complex ndarray
  with the elements:

```
[y(0),y(1),..,y(n/2),y(1-n/2),...,y(-1)]        if n is even
[y(0),y(1),..,y((n-1)/2),y(-(n-1)/2),...,y(-1)]  if n is odd
```

  where:

```
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k* 2*pi/n), j = 0..n-1
```

  Note that `y(-j) = y(n-j).conjugate()`.

See also:

`ifft`	Inverse FFT
`rfft`	FFT of a real sequence

Notes

The packing of the result is "standard": If `A = fft(a, n)`, then `A[0]` contains the zero-frequency term, `A[1:n/2]` contains the positive-frequency terms, and `A[n/2:]` contains the negative-frequency terms, in order of decreasingly negative frequency. So for an 8-point transform, the frequencies of the result are [0, 1, 2, 3, -4, -3, -2, -1]. To rearrange the fft output so that the zero-frequency component is centered, like [-4, -3, -2, -1, 0, 1, 2, 3], use `fftshift`.

For *n* even, `A[n/2]` contains the sum of the positive and negative-frequency terms. For *n* even and *x* real, `A[n/2]` will always be real.

This function is most efficient when *n* is a power of two, and least efficient when *n* is prime.

If the data type of *x* is real, a "real FFT" algorithm is automatically used, which roughly halves the computation time. To increase efficiency a little further, use `rfft`, which does the same calculation, but only outputs half of the symmetrical spectrum. If the data is both real and symmetrical, the `dct` can again double the efficiency, by generating half of the spectrum from half of the signal.

Examples

```
>>> from scipy.fftpack import fft, ifft
>>> x = np.arange(5)
>>> np.allclose(fft(ifft(x)), x, atol=1e-15)  # within numerical accuracy.
True
```

`scipy.fftpack.`**`ifft`**`(`*x*, *n=None*, *axis=-1*, *overwrite_x=False*`)`

Return discrete inverse Fourier transform of real or complex sequence.

The returned complex array contains `y(0), y(1),..., y(n-1)` where

`y(j) = (x * exp(2*pi*sqrt(-1)*j*np.arange(n)/n)).mean().`

Parameters

x : array_like
  Transformed data to invert.

n : int, optional
  Length of the inverse Fourier transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis : int, optional
  Axis along which the ifft's are computed; the default is over the last axis (i.e., `axis=-1`).

overwrite_x : bool, optional
  If True, the contents of *x* can be destroyed; the default is False.

Returns

ifft : ndarray of floats
  The inverse discrete Fourier transform.

See also:

fft	Forward FFT

Notes

This function is most efficient when *n* is a power of two, and least efficient when *n* is prime.

If the data type of *x* is real, a "real IFFT" algorithm is automatically used, which roughly halves the computation time.

`scipy.fftpack.`**`fft2`**`(`*x*, *shape=None*, *axes=(-2, -1)*, *overwrite_x=False*`)`

2-D discrete Fourier transform.

Return the two-dimensional discrete Fourier transform of the 2-D argument *x*.

See also:

fftn	for detailed information.

`scipy.fftpack.`**`ifft2`**`(`*x*, *shape=None*, *axes=(-2, -1)*, *overwrite_x=False*`)`

2-D discrete inverse Fourier transform of real or complex sequence.

Return inverse two-dimensional discrete Fourier transform of arbitrary type sequence x.

See `ifft` for more information.

See also:

`fft2`, `ifft`

`scipy.fftpack.`**`fftn`**(*x*, *shape=None*, *axes=None*, *overwrite_x=False*)

Return multidimensional discrete Fourier transform.

The returned array contains:

```
y[j_1,..,j_d] = sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
   x[k_1,..,k_d] * prod[i=1..d] exp(-sqrt(-1)*2*pi/n_i * j_i * k_i)
```

where d = len(x.shape) and n = x.shape. Note that `y[..., -j_i, ...] = y[..., n_i-j_i, ...].conjugate()`.

Parameters

x : array_like
The (n-dimensional) array to transform.

shape : tuple of ints, optional
The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `scipy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the i-th dimension is padded with zeros. If `shape[i] < x.shape[i]`, the i-th dimension is truncated to length `shape[i]`.

axes : array_like of ints, optional
The axes of *x* (*y* if *shape* is not None) along which the transform is applied.

overwrite_x : bool, optional
If True, the contents of *x* can be destroyed. Default is False.

Returns

y : complex-valued n-dimensional numpy array
The (n-dimensional) DFT of the input array.

See also:

`ifftn`

Examples

```
>>> from scipy.fftpack import fftn, ifftn
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, fftn(ifftn(y)))
True
```

`scipy.fftpack.`**`ifftn`**(*x*, *shape=None*, *axes=None*, *overwrite_x=False*)

Return inverse multi-dimensional discrete Fourier transform of arbitrary type sequence x.

The returned array contains:

```
y[j_1,..,j_d] = 1/p * sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
   x[k_1,..,k_d] * prod[i=1..d] exp(sqrt(-1)*2*pi/n_i * j_i * k_i)
```

where `d = len(x.shape)`, `n = x.shape`, and `p = prod[i=1..d] n_i`.

For description of parameters see `fftn`.

See also:

`fftn`	for detailed information.

`scipy.fftpack.`**`rfft`**(*x*, *n=None*, *axis=-1*, *overwrite_x=False*)

Discrete Fourier transform of a real sequence.

Parameters

x : array_like, real-valued
The data to transform.

n : int, optional

Defines the length of the Fourier transform. If *n* is not specified (the default) then `n = x.shape[axis]`. If `n < x.shape[axis]`, *x* is truncated, if `n > x.shape[axis]`, *x* is zero-padded.

axis : int, optional

The axis along which the transform is applied. The default is the last axis.

overwrite_x : bool, optional

If set to true, the contents of *x* can be overwritten. Default is False.

Returns **z** : real ndarray

The returned real array contains:

```
[y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2))]              if n is even
[y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2)),Im(y(n/2))]   if n is odd
```

where:

```
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k*2*pi/n)
j = 0..n-1
```

Note that `y(-j) == y(n-j).conjugate()`.

See also:

`fft`, `irfft`, `scipy.fftpack.basic`

Notes

Within numerical accuracy, `y == rfft(irfft(y))`.

Examples

```
>>> from scipy.fftpack import fft, rfft
>>> a = [9, -9, 1, 3]
>>> fft(a)
array([  4. +0.j,   8.+12.j,  16. +0.j,   8.-12.j])
>>> rfft(a)
array([  4.,   8.,  12.,  16.])
```

`scipy.fftpack.`**`irfft`**(*x*, *n=None*, *axis=-1*, *overwrite_x=False*)

Return inverse discrete Fourier transform of real sequence x.

The contents of *x* are interpreted as the output of the `rfft` function.

Parameters **x** : array_like

Transformed data to invert.

n : int, optional

Length of the inverse Fourier transform. If n < x.shape[axis], x is truncated. If n > x.shape[axis], x is zero-padded. The default results in n = x.shape[axis].

axis : int, optional

Axis along which the ifft's are computed; the default is over the last axis (i.e., axis=-1).

overwrite_x : bool, optional

If True, the contents of *x* can be destroyed; the default is False.

Returns **irfft** : ndarray of floats

The inverse discrete Fourier transform.

See also:

`rfft`, `ifft`

Notes

The returned real array contains:

```
[y(0),y(1),...,y(n-1)]
```

where for n is even:

```
y(j) = 1/n (sum[k=1..n/2-1] (x[2*k-1]+sqrt(-1)*x[2*k])
                             * exp(sqrt(-1)*j*k* 2*pi/n)
            + c.c. + x[0] + (-1)**(j) x[n-1])
```

and for n is odd:

```
y(j) = 1/n (sum[k=1..(n-1)/2] (x[2*k-1]+sqrt(-1)*x[2*k])
                             * exp(sqrt(-1)*j*k* 2*pi/n)
            + c.c. + x[0])
```

c.c. denotes complex conjugate of preceding expression.

For details on input parameters, see `rfft`.

`scipy.fftpack.`**`dct`**(*x*, *type=2*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*)

Return the Discrete Cosine Transform of arbitrary type sequence x.

Parameters	**x** : array_like The input array. **type** : {1, 2, 3}, optional Type of the DCT (see Notes). Default type is 2. **n** : int, optional Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`. **axis** : int, optional Axis along which the dct is computed; the default is over the last axis (i.e., `axis=-1`). **norm** : {None, 'ortho'}, optional Normalization mode (see Notes). Default is None. **overwrite_x** : bool, optional If True, the contents of *x* can be destroyed; the default is False.
Returns	**y** : ndarray of real The transformed input array.

See also:

`idct`	Inverse DCT

Notes

For a single dimension array `x`, `dct(x, norm='ortho')` is equal to MATLAB `dct(x)`.

There are theoretically 8 types of the DCT, only the first 3 types are implemented in scipy. 'The' DCT generally refers to DCT type 2, and 'the' Inverse DCT generally refers to DCT type 3.

Type I

There are several definitions of the DCT-I; we use the following (for `norm=None`):

```
                                     N-2
y[k] = x[0] + (-1)**k x[N-1] + 2 * sum x[n]*cos(pi*k*n/(N-1))
                                     n=1
```

Only None is supported as normalization mode for DCT-I. Note also that the DCT-I is only supported for input size > 1

Type II

There are several definitions of the DCT-II; we use the following (for `norm=None`):

```
          N-1
y[k] = 2* sum x[n]*cos(pi*k*(2n+1)/(2*N)), 0 <= k < N.
          n=0
```

If `norm='ortho'`, `y[k]` is multiplied by a scaling factor *f*:

```
f = sqrt(1/(4*N)) if k = 0,
f = sqrt(1/(2*N)) otherwise.
```

Which makes the corresponding matrix of coefficients orthonormal (`OO' = Id`).

Type III

There are several definitions, we use the following (for `norm=None`):

```
                  N-1
y[k] = x[0] + 2 * sum x[n]*cos(pi*(k+0.5)*n/N), 0 <= k < N.
                  n=1
```

or, for `norm='ortho'` and 0 <= k < N:

```
                                        N-1
y[k] = x[0] / sqrt(N) + sqrt(2/N) * sum x[n]*cos(pi*(k+0.5)*n/N)
                                        n=1
```

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor *2N*. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT-II.

References

[R36], [R37]

Examples

The Type 1 DCT is equivalent to the FFT (though faster) for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the FFT input is used to generate half of the FFT output:

```
>>> from scipy.fftpack import fft, dct
>>> fft(np.array([4., 3., 5., 10., 5., 3.])).real
array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])
>>> dct(np.array([4., 3., 5., 10.]), 1)
array([ 30.,  -8.,   6.,  -2.])
```

`scipy.fftpack.`**`idct`**(*x*, *type=2*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*)

Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.

Parameters

x : array_like
  The input array.

type : {1, 2, 3}, optional
  Type of the DCT (see Notes). Default type is 2.

n : int, optional
  Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis : int, optional
  Axis along which the idct is computed; the default is over the last axis (i.e., `axis=-1`).

norm : {None, 'ortho'}, optional
  Normalization mode (see Notes). Default is None.

	overwrite_x : bool, optional If True, the contents of *x* can be destroyed; the default is False.
Returns	**idct** : ndarray of real The transformed input array.

See also:

dct	Forward DCT

Notes

For a single dimension array *x*, `idct(x, norm='ortho')` is equal to MATLAB `idct(x)`.

'The' IDCT is the IDCT of type 2, which is the same as DCT of type 3.

IDCT of type 1 is the DCT of type 1, IDCT of type 2 is the DCT of type 3, and IDCT of type 3 is the DCT of type 2. For the definition of these types, see `dct`.

Examples

The Type 1 DCT is equivalent to the DFT for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the IFFT input is used to generate half of the IFFT output:

```
>>> from scipy.fftpack import ifft, idct
>>> ifft(np.array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])).real
array([  4.,   3.,   5.,  10.,   5.,   3.])
>>> idct(np.array([ 30.,  -8.,   6.,  -2.]), 1) / 6
array([  4.,   3.,   5.,  10.])
```

`scipy.fftpack.`**`dst`**(*x*, *type=2*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*)

Return the Discrete Sine Transform of arbitrary type sequence x.

Parameters	**x** : array_like The input array. **type** : {1, 2, 3}, optional Type of the DST (see Notes). Default type is 2. **n** : int, optional Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`. **axis** : int, optional Axis along which the dst is computed; the default is over the last axis (i.e., `axis=-1`). **norm** : {None, 'ortho'}, optional Normalization mode (see Notes). Default is None. **overwrite_x** : bool, optional If True, the contents of *x* can be destroyed; the default is False.
Returns	**dst** : ndarray of reals The transformed input array.

See also:

idst	Inverse DST

Notes

For a single dimension array `x`.

There are theoretically 8 types of the DST for different combinations of even/odd boundary conditions and boundary off sets [R38], only the first 3 types are implemented in scipy.

Type I

There are several definitions of the DST-I; we use the following for `norm=None`. DST-I assumes the input is odd around n=-1 and n=N.

```
          N-1
y[k] = 2 * sum x[n]*sin(pi*(k+1)*(n+1)/(N+1))
          n=0
```

Only None is supported as normalization mode for DCT-I. Note also that the DCT-I is only supported for input size > 1 The (unnormalized) DCT-I is its own inverse, up to a factor *2(N+1)*.

Type II

There are several definitions of the DST-II; we use the following for `norm=None`. DST-II assumes the input is odd around n=-1/2 and n=N-1/2; the output is odd around k=-1 and even around k=N-1

```
         N-1
y[k] = 2* sum x[n]*sin(pi*(k+1)*(n+0.5)/N), 0 <= k < N.
         n=0
```

if `norm='ortho'`, `y[k]` is multiplied by a scaling factor *f*

```
f = sqrt(1/(4*N)) if k == 0
f = sqrt(1/(2*N)) otherwise.
```

Type III

There are several definitions of the DST-III, we use the following (for `norm=None`). DST-III assumes the input is odd around n=-1 and even around n=N-1

```
                             N-2
y[k] = x[N-1]*(-1)**k + 2* sum x[n]*sin(pi*(k+0.5)*(n+1)/N), 0 <= k < N.
                             n=0
```

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor *2N*. The orthonormalized DST-III is exactly the inverse of the orthonormalized DST-II.

New in version 0.11.0.

References

[R38]

`scipy.fftpack.`**`idst`**(*x*, *type=2*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*)

Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

Parameters

x : array_like
: The input array.

type : {1, 2, 3}, optional
: Type of the DST (see Notes). Default type is 2.

n : int, optional
: Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis : int, optional
: Axis along which the idst is computed; the default is over the last axis (i.e., `axis=-1`).

norm : {None, 'ortho'}, optional
: Normalization mode (see Notes). Default is None.

overwrite_x : bool, optional

If True, the contents of *x* can be destroyed; the default is False.

Returns **idst** : ndarray of real
The transformed input array.

See also:

dst	Forward DST

Notes

'The' IDST is the IDST of type 2, which is the same as DST of type 3.

IDST of type 1 is the DST of type 1, IDST of type 2 is the DST of type 3, and IDST of type 3 is the DST of type 2. For the definition of these types, see `dst`.

New in version 0.11.0.

5.5.2 Differential and pseudo-differential operators

`diff`(x[, order, period, _cache])	Return k-th derivative (or integral) of a periodic sequence x.
`tilbert`(x, h[, period, _cache])	Return h-Tilbert transform of a periodic sequence x.
`itilbert`(x, h[, period, _cache])	Return inverse h-Tilbert transform of a periodic sequence x.
`hilbert`(x[, _cache])	Return Hilbert transform of a periodic sequence x.
`ihilbert`(x)	Return inverse Hilbert transform of a periodic sequence x.
`cs_diff`(x, a, b[, period, _cache])	Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence.
`sc_diff`(x, a, b[, period, _cache])	Return (a,b)-sinh/cosh pseudo-derivative of a periodic sequence x.
`ss_diff`(x, a, b[, period, _cache])	Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x.
`cc_diff`(x, a, b[, period, _cache])	Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.
`shift`(x, a[, period, _cache])	Shift periodic sequence x by a: y(u) = x(u+a).

`scipy.fftpack.`**`diff`**(*x*, *order=1*, *period=None*, *_cache={}*)

Return k-th derivative (or integral) of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = pow(sqrt(-1)*j*2*pi/period, order) * x_j
y_0 = 0 if order is not 0.
```

Parameters **x** : array_like
Input array.
order : int, optional
The order of differentiation. Default order is 1. If order is negative, then integration is carried out under the assumption that `x_0 == 0`.
period : float, optional
The assumed period of the sequence. Default is `2*pi`.

Notes

If `sum(x, axis=0) = 0` then `diff(diff(x, k), -k) == x` (within numerical accuracy).

For odd order and even `len(x)`, the Nyquist mode is taken zero.

`scipy.fftpack.`**`tilbert`**(*x*, *h*, *period=None*, *_cache={}*)

Return h-Tilbert transform of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*coth(j*h*2*pi/period) * x_j
y_0 = 0
```

Parameters	**x** : array_like The input array to transform. **h** : float Defines the parameter of the Tilbert transform. **period** : float, optional The assumed period of the sequence. Default period is `2*pi`.
Returns	**tilbert** : ndarray The result of the transform.

Notes

If `sum(x, axis=0) == 0` and `n = len(x)` is odd then `tilbert(itilbert(x)) == x`.

If `2 * pi * h / period` is approximately 10 or larger, then numerically `tilbert == hilbert` (theoretically oo-Tilbert == Hilbert).

For even `len(x)`, the Nyquist mode of `x` is taken zero.

`scipy.fftpack.`**`itilbert`**(*x*, *h*, *period=None*, *_cache={}*)

Return inverse h-Tilbert transform of a periodic sequence x.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*tanh(j*h*2*pi/period) * x_j
y_0 = 0
```

For more details, see `tilbert`.

`scipy.fftpack.`**`hilbert`**(*x*, *_cache={}*)

Return Hilbert transform of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*sign(j) * x_j
y_0 = 0
```

Parameters	**x** : array_like The input array, should be periodic. **_cache** : dict, optional Dictionary that contains the kernel used to do a convolution with.
Returns	**y** : ndarray The transformed input.

Notes

If `sum(x, axis=0) == 0` then `hilbert(ihilbert(x)) == x`.

For even len(x), the Nyquist mode of x is taken zero.

The sign of the returned transform does not have a factor -1 that is more often than not found in the definition of the Hilbert transform. Note also that `scipy.signal.hilbert` does have an extra -1 factor compared to this function.

`scipy.fftpack.`**`ihilbert`**(*x*)

Return inverse Hilbert transform of a periodic sequence x.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*sign(j) * x_j
y_0 = 0
```

`scipy.fftpack.`**`cs_diff`**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*cosh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = 0
```

Parameters **x** : array_like
The array to take the pseudo-derivative from.
a, b : float
Defines the parameters of the cosh/sinh pseudo-differential operator.
period : float, optional
The period of the sequence. Default period is `2*pi`.

Returns **cs_diff** : ndarray
Pseudo-derivative of periodic sequence *x*.

Notes

For even len(*x*), the Nyquist mode of *x* is taken as zero.

`scipy.fftpack.`**`sc_diff`**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-sinh/cosh pseudo-derivative of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*sinh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j
y_0 = 0
```

Parameters **x** : array_like
Input array.
a,b : float
Defines the parameters of the sinh/cosh pseudo-differential operator.
period : float, optional
The period of the sequence x. Default is 2*pi.

Notes

`sc_diff(cs_diff(x,a,b),b,a) == x` For even `len(x)`, the Nyquist mode of x is taken as zero.

`scipy.fftpack.`**`ss_diff`**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sinh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = a/b * x_0
```

Parameters **x** : array_like
The array to take the pseudo-derivative from.
a,b
Defines the parameters of the sinh/sinh pseudo-differential operator.
period : float, optional
The period of the sequence x. Default is `2*pi`.

Notes

`ss_diff(ss_diff(x,a,b),b,a) == x`

`scipy.fftpack.`**`cc_diff`**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = cosh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j
```

Parameters **x** : array_like
The array to take the pseudo-derivative from.
a,b : float
Defines the parameters of the sinh/sinh pseudo-differential operator.
period : float, optional
The period of the sequence x. Default is `2*pi`.

Returns **cc_diff** : ndarray
Pseudo-derivative of periodic sequence *x*.

Notes

`cc_diff(cc_diff(x,a,b),b,a) == x`

`scipy.fftpack.`**`shift`**(*x*, *a*, *period=None*, *_cache={}*)

Shift periodic sequence x by a: y(u) = x(u+a).

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = exp(j*a*2*pi/period*sqrt(-1)) * x_f
```

Parameters **x** : array_like
The array to take the pseudo-derivative from.
a : float
Defines the parameters of the sinh/sinh pseudo-differential
period : float, optional
The period of the sequences x and y. Default period is `2*pi`.

5.5.3 Helper functions

`fftshift`(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
`ifftshift`(x[, axes])	The inverse of fftshift.
`fftfreq`(n[, d])	Return the Discrete Fourier Transform sample frequencies.
`rfftfreq`(n[, d])	DFT sample frequencies (for usage with rfft, irfft).

`scipy.fftpack.`**`fftshift`**(*x*, *axes=None*)

Shift the zero-frequency component to the center of the spectrum.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters **x** : array_like
Input array.
axes : int or shape tuple, optional
Axes over which to shift. Default is None, which shifts all axes.

Returns **y** : ndarray

The shifted array.

See also:

ifftshift	The inverse of `fftshift`.

Examples

```
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0.,  1.,  2.,  3.,  4., -5., -4., -3., -2., -1.])
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

`scipy.fftpack.`**`ifftshift`**`(`*x*, *axes=None*`)`

The inverse of fftshift.

Parameters	**x** : array_like Input array. **axes** : int or shape tuple, optional Axes over which to calculate. Defaults to None, which shifts all axes.
Returns	**y** : ndarray The shifted array.

See also:

fftshift	Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.ifftshift(np.fft.fftshift(freqs))
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

`scipy.fftpack.`**`fftfreq`**`(`*n*, *d=1.0*`)`

Return the Discrete Fourier Transform sample frequencies.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,   n/2-1,     -n/2, ..., -1] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n)   if n is odd
```

Parameters **n** : int
Window length.
d : scalar, optional
Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns **f** : ndarray
Array of length *n* containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> fourier = np.fft.fft(signal)
>>> n = signal.size
>>> timestep = 0.1
>>> freq = np.fft.fftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  2.5 ,  3.75, -5.  , -3.75, -2.5 , -1.25])
```

`scipy.fftpack.`**`rfftfreq`**`(`*n*, *d=1.0*`)`

DFT sample frequencies (for usage with rfft, irfft).

The returned float array contains the frequency bins in cycles/unit (with zero at the start) given a window length *n* and a sample spacing *d*:

```
f = [0,1,1,2,2,...,n/2-1,n/2-1,n/2]/(d*n)   if n is even
f = [0,1,1,2,2,...,n/2-1,n/2-1,n/2,n/2]/(d*n)   if n is odd
```

Parameters **n** : int
Window length.
d : scalar, optional
Sample spacing. Default is 1.

Returns **out** : ndarray
The array of length *n*, containing the sample frequencies.

Examples

```
>>> from scipy import fftpack
>>> sig = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> sig_fft = fftpack.rfft(sig)
>>> n = sig_fft.size
>>> timestep = 0.1
>>> freq = fftpack.rfftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  1.25,  2.5 ,  2.5 ,  3.75,  3.75,  5.  ])
```

Note that `fftshift`, `ifftshift` and `fftfreq` are numpy functions exposed by `fftpack`; importing them from `numpy` should be preferred.

5.5.4 Convolutions (`scipy.fftpack.convolve`)

`convolve`(x,omega,[swap_real_imag,overwrite_x])	Wrapper for `convolve`.
`convolve_z`(x,omega_real,omega_imag,[overwrite_x])	Wrapper for `convolve_z`.

Continued on next page

Table 5.17 – continued from previous page

`init_convolution_kernel`(...)	Wrapper for `init_convolution_kernel`.
`destroy_convolve_cache`()	Wrapper for `destroy_convolve_cache`.

`scipy.fftpack.convolve.`**`convolve`**(*x*, *omega*[, *swap_real_imag*, *overwrite_x*]) **= <fortran object>**

Wrapper for `convolve`.

Parameters **x** : input rank-1 array('d') with bounds (n)
omega : input rank-1 array('d') with bounds (n)

Returns **y** : rank-1 array('d') with bounds (n) and x storage

Other Parameters

overwrite_x : input int, optional
Default: 0

swap_real_imag : input int, optional
Default: 0

`scipy.fftpack.convolve.`**`convolve_z`**(*x*, *omega_real*, *omega_imag*[, *overwrite_x*]) **= <fortran object>**

Wrapper for `convolve_z`.

Parameters **x** : input rank-1 array('d') with bounds (n)
omega_real : input rank-1 array('d') with bounds (n)
omega_imag : input rank-1 array('d') with bounds (n)

Returns **y** : rank-1 array('d') with bounds (n) and x storage

Other Parameters

overwrite_x : input int, optional
Default: 0

`scipy.fftpack.convolve.`**`init_convolution_kernel`**(*n*, *kernel_func*[, *d*, *zero_nyquist*, *kernel_func_extra_args*]) **= <fortran object>**

Wrapper for `init_convolution_kernel`.

Parameters **n** : input int
kernel_func : call-back function

Returns **omega** : rank-1 array('d') with bounds (n)

Other Parameters

d : input int, optional
Default: 0

kernel_func_extra_args : input tuple, optional
Default: ()

zero_nyquist : input int, optional
Default: d%2

Notes

Call-back functions:

```
def kernel_func(k): return kernel_func
Required arguments:
  k : input int
Return objects:
  kernel_func : float
```

`scipy.fftpack.convolve.`**`destroy_convolve_cache`** **= <fortran object>**

Wrapper for `destroy_convolve_cache`.

5.6 Integration and ODEs (`scipy.integrate`)

5.6.1 Integrating functions, given function object

`quad`(func, a, b[, args, full_output, ...])	Compute a definite integral.
`dblquad`(func, a, b, gfun, hfun[, args, ...])	Compute a double integral.
`tplquad`(func, a, b, gfun, hfun, qfun, rfun)	Compute a triple (definite) integral.
`nquad`(func, ranges[, args, opts])	Integration over multiple variables.
`fixed_quad`(func, a, b[, args, n])	Compute a definite integral using fixed-order Gaussian quadrature.
`quadrature`(func, a, b[, args, tol, rtol, ...])	Compute a definite integral using fixed-tolerance Gaussian quadrature.
`romberg`(function, a, b[, args, tol, rtol, ...])	Romberg integration of a callable function or method.

`scipy.integrate.`**`quad`**(*func*, *a*, *b*, *args=()*, *full_output=0*, *epsabs=1.49e-08*, *epsrel=1.49e-08*, *limit=50*, *points=None*, *weight=None*, *wvar=None*, *wopts=None*, *maxp1=50*, *limlst=50*)

Compute a definite integral.

Integrate func from *a* to *b* (possibly infinite interval) using a technique from the Fortran library QUADPACK.

Parameters

func : function

A Python function or method to integrate. If *func* takes many arguments, it is integrated along the axis corresponding to the first argument. If the user desires improved integration performance, then f may instead be a `ctypes` function of the form:

f(int n, double args[n]),

where `args` is an array of function arguments and `n` is the length of `args`. `f.argtypes` should be set to `(c_int, c_double)`, and `f.restype` should be `(c_double,)`.

a : float

Lower limit of integration (use -numpy.inf for -infinity).

b : float

Upper limit of integration (use numpy.inf for +infinity).

args : tuple, optional

Extra arguments to pass to *func*.

full_output : int, optional

Non-zero to return a dictionary of integration information. If non-zero, warning messages are also suppressed and the message is appended to the output tuple.

Returns

y : float

The integral of func from *a* to *b*.

abserr : float

An estimate of the absolute error in the result.

infodict : dict

A dictionary containing additional information. Run scipy.integrate.quad_explain() for more information.

message :

A convergence message.

explain :

Appended only with ‘cos’ or ‘sin’ weighting and infinite integration limits, it contains an explanation of the codes in infodict[’ierlst’]

Other Parameters

epsabs : float or int, optional

Absolute error tolerance.

epsrel : float or int, optional

Relative error tolerance.

limit : float or int, optional
An upper bound on the number of subintervals used in the adaptive algorithm.

points : (sequence of floats,ints), optional
A sequence of break points in the bounded integration interval where local difficulties of the integrand may occur (e.g., singularities, discontinuities). The sequence does not have to be sorted.

weight : float or int, optional
String indicating weighting function. Full explanation for this and the remaining arguments can be found below.

wvar : optional
Variables for use with weighting functions.

wopts : optional
Optional input for reusing Chebyshev moments.

maxp1 : float or int, optional
An upper bound on the number of Chebyshev moments.

limlst : int, optional
Upper bound on the number of cycles (>=3) for use with a sinusoidal weighting and an infinite end-point.

See also:

`dblquad`	double integral
`tplquad`	triple integral
`nquad`	n-dimensional integrals (uses `quad` recursively)
`fixed_quad`	fixed-order Gaussian quadrature
`quadrature`	adaptive Gaussian quadrature
`odeint`	ODE integrator
`ode`	ODE integrator
`simps`	integrator for sampled data
`romb`	integrator for sampled data
`scipy.special`	for coefficients and roots of orthogonal polynomials

Notes

Extra information for quad() inputs and outputs

If full_output is non-zero, then the third output argument (infodict) is a dictionary with entries as tabulated below. For infinite limits, the range is transformed to (0,1) and the optional outputs are given with respect to this transformed range. Let M be the input argument limit and let K be infodict['last']. The entries are:

'neval'	The number of function evaluations.
'last'	The number, K, of subintervals produced in the subdivision process.
'alist'	A rank-1 array of length M, the first K elements of which are the left end points of the subintervals in the partition of the integration range.
'blist'	A rank-1 array of length M, the first K elements of which are the right end points of the subintervals.
'rlist'	A rank-1 array of length M, the first K elements of which are the integral approximations on the subintervals.

'elist' A rank-1 array of length M, the first K elements of which are the moduli of the absolute error estimates on the subintervals.

'iord' A rank-1 integer array of length M, the first L elements of which are pointers to the error estimates over the subintervals with `L=K` if `K<=M/2+2` or `L=M+1-K` otherwise. Let I be the sequence `infodict['iord']` and let E be the sequence `infodict['elist']`. Then `E[I[1]], ..., E[I[L]]` forms a decreasing sequence.

If the input argument points is provided (i.e. it is not None), the following additional outputs are placed in the output dictionary. Assume the points sequence is of length P.

'pts' A rank-1 array of length P+2 containing the integration limits and the break points of the intervals in ascending order. This is an array giving the subintervals over which integration will occur.

'level' A rank-1 integer array of length M (=limit), containing the subdivision levels of the subintervals, i.e., if (aa,bb) is a subinterval of `(pts[1], pts[2])` where `pts[0]` and `pts[2]` are adjacent elements of `infodict['pts']`, then (aa,bb) has level l if `|bb-aa| = |pts[2]-pts[1]| * 2**(-l)`.

'ndin' A rank-1 integer array of length P+2. After the first integration over the intervals (pts[1], pts[2]), the error estimates over some of the intervals may have been increased artificially in order to put their subdivision forward. This array has ones in slots corresponding to the subintervals for which this happens.

Weighting the integrand

The input variables, *weight* and *wvar*, are used to weight the integrand by a select list of functions. Different integration methods are used to compute the integral with these weighting functions. The possible values of weight and the corresponding weighting functions are.

`weight`	Weight function used	`wvar`
'cos'	cos(w*x)	wvar = w
'sin'	sin(w*x)	wvar = w
'alg'	g(x) = ((x-a)**alpha)*((b-x)**beta)	wvar = (alpha, beta)
'alg-loga'	g(x)*log(x-a)	wvar = (alpha, beta)
'alg-logb'	g(x)*log(b-x)	wvar = (alpha, beta)
'alg-log'	g(x)*log(x-a)*log(b-x)	wvar = (alpha, beta)
'cauchy'	1/(x-c)	wvar = c

wvar holds the parameter w, (alpha, beta), or c depending on the weight selected. In these expressions, a and b are the integration limits.

For the 'cos' and 'sin' weighting, additional inputs and outputs are available.

For finite integration limits, the integration is performed using a Clenshaw-Curtis method which uses Chebyshev moments. For repeated calculations, these moments are saved in the output dictionary:

'momcom' The maximum level of Chebyshev moments that have been computed, i.e., if `M_c` is `infodict['momcom']` then the moments have been computed for intervals of length `|b-a| * 2**(-l),l=0,1,...,M_c`.

'nnlog' A rank-1 integer array of length M(=limit), containing the subdivision levels of the subintervals, i.e., an element of this array is equal to l if the corresponding subinterval is `|b-a|* 2**(-l)`.

'chebmo' A rank-2 array of shape (25, maxp1) containing the computed Chebyshev moments. These can be passed on to an integration over the same interval by passing this array as the second element of the sequence wopts and passing infodict['momcom'] as the first element.

If one of the integration limits is infinite, then a Fourier integral is computed (assuming w neq 0). If full_output is 1 and a numerical error is encountered, besides the error message attached to the output tuple, a dictionary is also appended to the output tuple which translates the error codes in the array `info['ierlst']` to English messages. The output information dictionary contains the following entries instead of ‘last’, ‘alist’, ‘blist’, ‘rlist’, and ‘elist’:

‘lst’	The number of subintervals needed for the integration (call it `K_f`).
‘rslst’	A rank-1 array of length M_f=limlst, whose first `K_f` elements contain the integral contribution over the interval `(a+(k-1)c, a+kc)` where `c = (2*floor(|w|) + 1) * pi / |w|` and `k=1,2,...,K_f`.
‘erlst’	A rank-1 array of length `M_f` containing the error estimate corresponding to the interval in the same position in `infodict['rslist']`.
‘ierlst’	A rank-1 integer array of length `M_f` containing an error flag corresponding to the interval in the same position in `infodict['rslist']`. See the explanation dictionary (last entry in the output tuple) for the meaning of the codes.

Examples

Calculate $\int_0^4 x^2 dx$ and compare with an analytic result

```
>>> from scipy import integrate
>>> x2 = lambda x: x**2
>>> integrate.quad(x2, 0, 4)
(21.333333333333332, 2.3684757858670003e-13)
>>> print(4**3 / 3.)  # analytical result
21.3333333333
```

Calculate $\int_0^\infty e^{-x} dx$

```
>>> invexp = lambda x: np.exp(-x)
>>> integrate.quad(invexp, 0, np.inf)
(1.0, 5.842605999138044e-11)
```

```
>>> f = lambda x,a : a*x
>>> y, err = integrate.quad(f, 0, 1, args=(1,))
>>> y
0.5
>>> y, err = integrate.quad(f, 0, 1, args=(3,))
>>> y
1.5
```

Calculate $\int_0^1 x^2 + y^2 dx$ with ctypes, holding y parameter as 1:

```
testlib.c =>
    double func(int n, double args[n]){
        return args[0]*args[0] + args[1]*args[1];}
compile to library testlib.*
```

```
>>> from scipy import integrate
>>> import ctypes
>>> lib = ctypes.CDLL('/home/.../testlib.*') #use absolute path
>>> lib.func.restype = ctypes.c_double
>>> lib.func.argtypes = (ctypes.c_int,ctypes.c_double)
>>> integrate.quad(lib.func,0,1,(1))
(1.3333333333333333, 1.4802973661668752e-14)
>>> print((1.0**3/3.0 + 1.0) - (0.0**3/3.0 + 0.0)) #Analytic result
1.3333333333333333
```

`scipy.integrate.`**`dblquad`**(*func*, *a*, *b*, *gfun*, *hfun*, *args=()*, *epsabs=1.49e-08*, *epsrel=1.49e-08*)

Compute a double integral.

Return the double (definite) integral of `func(y, x)` from `x = a..b` and `y = gfun(x)..hfun(x)`.

Parameters

func : callable
A Python function or method of at least two variables: y must be the first argument and x the second argument.

a, b : float
The limits of integration in x: $a < b$

gfun : callable
The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result: a lambda function can be useful here.

hfun : callable
The upper boundary curve in y (same requirements as *gfun*).

args : sequence, optional
Extra arguments to pass to *func*.

epsabs : float, optional
Absolute tolerance passed directly to the inner 1-D quadrature integration. Default is 1.49e-8.

epsrel : float, optional
Relative tolerance of the inner 1-D integrals. Default is 1.49e-8.

Returns

y : float
The resultant integral.

abserr : float
An estimate of the error.

See also:

`quad`	single integral
`tplquad`	triple integral
`nquad`	N-dimensional integrals
`fixed_quad`	fixed-order Gaussian quadrature
`quadrature`	adaptive Gaussian quadrature
`odeint`	ODE integrator
`ode`	ODE integrator
`simps`	integrator for sampled data
`romb`	integrator for sampled data
`scipy.special`	for coefficients and roots of orthogonal polynomials

`scipy.integrate.`**`tplquad`**(*func*, *a*, *b*, *gfun*, *hfun*, *qfun*, *rfun*, *args=()*, *epsabs=1.49e-08*, *epsrel=1.49e-08*)

Compute a triple (definite) integral.

Return the triple integral of `func(z, y, x)` from `x = a..b`, `y = gfun(x)..hfun(x)`, and `z = qfun(x,y)..rfun(x,y)`.

Parameters

func : function
A Python function or method of at least three variables in the order (z, y, x).

a, b : float
The limits of integration in x: $a < b$

gfun : function
The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result: a lambda function can be useful here.

hfun : function

The upper boundary curve in y (same requirements as *gfun*).

qfun : function

The lower boundary surface in z. It must be a function that takes two floats in the order (x, y) and returns a float.

rfun : function

The upper boundary surface in z. (Same requirements as *qfun*.)

args : tuple, optional

Extra arguments to pass to *func*.

epsabs : float, optional

Absolute tolerance passed directly to the innermost 1-D quadrature integration. Default is 1.49e-8.

epsrel : float, optional

Relative tolerance of the innermost 1-D integrals. Default is 1.49e-8.

Returns **y** : float

The resultant integral.

abserr : float

An estimate of the error.

See also:

`quad`	Adaptive quadrature using QUADPACK
`quadrature`	Adaptive Gaussian quadrature
`fixed_quad`	Fixed-order Gaussian quadrature
`dblquad`	Double integrals
`nquad`	N-dimensional integrals
`romb`	Integrators for sampled data
`simps`	Integrators for sampled data
`ode`	ODE integrators
`odeint`	ODE integrators
`scipy.special`	For coefficients and roots of orthogonal polynomials

`scipy.integrate.`**`nquad`**(*func*, *ranges*, *args=None*, *opts=None*)

Integration over multiple variables.

Wraps `quad` to enable integration over multiple variables. Various options allow improved integration of discontinuous functions, as well as the use of weighted integration, and generally finer control of the integration process.

Parameters **func** : callable

The function to be integrated. Has arguments of `x0, ... xn`, `t0, tm`, where integration is carried out over `x0, ... xn`, which must be floats. Function signature should be `func(x0, x1, ..., xn, t0, t1, ..., tm)`. Integration is carried out in order. That is, integration over `x0` is the innermost integral, and `xn` is the outermost. If performance is a concern, this function may be a ctypes function of the form:

```
f(int n, double args[n])
```

where `n` is the number of extra parameters and args is an array of doubles of the additional parameters. This function may then be compiled to a dynamic/shared library then imported through `ctypes`, setting the function's argtypes to `(c_int, c_double)`, and the function's restype to `(c_double)`. Its pointer may then be passed into `nquad` normally. This allows the underlying Fortran library to evaluate the function in the innermost integration calls without callbacks to Python, and also speeds up the evaluation of the function itself.

ranges : iterable object

Each element of ranges may be either a sequence of 2 numbers, or else a callable that returns such a sequence. `ranges[0]` corresponds to integration over x0, and so on. If an element of ranges is a callable, then it will be called with all of the integration arguments available. e.g. if `func = f(x0, x1, x2)`, then `ranges[0]` may be defined as either `(a, b)` or else as `(a, b) = range0(x1, x2)`.

args : iterable object, optional

Additional arguments `t0, ..., tn`, required by *func*.

opts : iterable object or dict, optional

Options to be passed to `quad`. May be empty, a dict, or a sequence of dicts or functions that return a dict. If empty, the default options from scipy.integrate.quadare used. If a dict, the same options are used for all levels of integraion. If a sequence, then each element of the sequence corresponds to a particular integration. e.g. opts[0] corresponds to integration over x0, and so on. The available options together with their default values are:

- epsabs = 1.49e-08
- epsrel = 1.49e-08
- limit = 50
- points = None
- weight = None
- wvar = None
- wopts = None

The `full_output` option from `quad` is unavailable, due to the complexity of handling the large amount of data such an option would return for this kind of nested integration. For more information on these options, see `quad` and `quad_explain`.

Returns

result : float

The result of the integration.

abserr : float

The maximum of the estimates of the absolute error in the various integration results.

See also:

quad 1-dimensional numerical integration

`dblquad`, `tplquad`

fixed_quadfixed-order Gaussian quadrature

quadratureadaptive Gaussian quadrature

Examples

```
>>> from scipy import integrate
>>> func = lambda x0,x1,x2,x3 : x0**2 + x1*x2 - x3**3 + np.sin(x0) + (
...                                  1 if (x0-.2*x3-.5-.25*x1>0) else 0)
>>> points = [[lambda (x1,x2,x3) : 0.2*x3 + 0.5 + 0.25*x1], [], [], []]
>>> def opts0(*args, **kwargs):
...     return {'points':[0.2*args[2] + 0.5 + 0.25*args[0]]}
>>> integrate.nquad(func, [[0,1], [-1,1], [.13,.8], [-.15,1]],
```

```
...                    opts=[opts0,{},{},{}])
(1.5267454070738633, 2.9437360001402324e-14)

>>> scale = .1
>>> def func2(x0, x1, x2, x3, t0, t1):
...     return x0*x1*x3**2 + np.sin(x2) + 1 + (1 if x0+t1*x1-t0>0 else 0)
>>> def lim0(x1, x2, x3, t0, t1):
...     return [scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) - 1,
...             scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) + 1]
>>> def lim1(x2, x3, t0, t1):
...     return [scale * (t0*x2 + t1*x3) - 1,
...             scale * (t0*x2 + t1*x3) + 1]
>>> def lim2(x3, t0, t1):
...     return [scale * (x3 + t0**2*t1**3) - 1,
...             scale * (x3 + t0**2*t1**3) + 1]
>>> def lim3(t0, t1):
...     return [scale * (t0+t1) - 1, scale * (t0+t1) + 1]
>>> def opts0(x1, x2, x3, t0, t1):
...     return {'points' : [t0 - t1*x1]}
>>> def opts1(x2, x3, t0, t1):
...     return {}
>>> def opts2(x3, t0, t1):
...     return {}
>>> def opts3(t0, t1):
...     return {}
>>> integrate.nquad(func2, [lim0, lim1, lim2, lim3], args=(0,0),
...                    opts=[opts0, opts1, opts2, opts3])
(25.066666666666666, 2.7829590483937256e-13)
```

`scipy.integrate.`**`fixed_quad`**(*func*, *a*, *b*, *args=()*, *n=5*)

Compute a definite integral using fixed-order Gaussian quadrature.

Integrate *func* from *a* to *b* using Gaussian quadrature of order *n*.

Parameters

func : callable
  A Python function or method to integrate (must accept vector inputs).

a : float
  Lower limit of integration.

b : float
  Upper limit of integration.

args : tuple, optional
  Extra arguments to pass to function, if any.

n : int, optional
  Order of quadrature integration. Default is 5.

Returns

val : float
  Gaussian quadrature approximation to the integral

See also:

quad	adaptive quadrature using QUADPACK
dblquad	double integrals
tplquad	triple integrals
romberg	adaptive Romberg quadrature
quadrature	adaptive Gaussian quadrature
romb	integrators for sampled data

`simps`	integrators for sampled data
`cumtrapz`	cumulative integration for sampled data
`ode`	ODE integrator
`odeint`	ODE integrator

`scipy.integrate.quadrature(func, a, b, args=(), tol=1.49e-08, rtol=1.49e-08, maxiter=50, vec_func=True, miniter=1)`

Compute a definite integral using fixed-tolerance Gaussian quadrature.

Integrate *func* from *a* to *b* using Gaussian quadrature with absolute tolerance *tol*.

Parameters

func : function
A Python function or method to integrate.

a : float
Lower limit of integration.

b : float
Upper limit of integration.

args : tuple, optional
Extra arguments to pass to function.

tol, rtol : float, optional
Iteration stops when error between last two iterates is less than *tol* OR the relative change is less than *rtol*.

maxiter : int, optional
Maximum order of Gaussian quadrature.

vec_func : bool, optional
True or False if func handles arrays as arguments (is a "vector" function). Default is True.

miniter : int, optional
Minimum order of Gaussian quadrature.

Returns

val : float
Gaussian quadrature approximation (within tolerance) to integral.

err : float
Difference between last two estimates of the integral.

See also:

`romberg`	adaptive Romberg quadrature
`fixed_quad`	fixed-order Gaussian quadrature
`quad`	adaptive quadrature using QUADPACK
`dblquad`	double integrals
`tplquad`	triple integrals
`romb`	integrator for sampled data
`simps`	integrator for sampled data
`cumtrapz`	cumulative integration for sampled data
`ode`	ODE integrator
`odeint`	ODE integrator

`scipy.integrate.`**`romberg`**(*function*, *a*, *b*, *args=()*, *tol=1.48e-08*, *rtol=1.48e-08*, *show=False*, *divmax=10*, *vec_func=False*)

Romberg integration of a callable function or method.

Returns the integral of *function* (a function of one variable) over the interval (*a*, *b*).

If *show* is 1, the triangular array of the intermediate results will be printed. If *vec_func* is True (default is False), then *function* is assumed to support vector arguments.

Parameters

function : callable
  Function to be integrated.

a : float
  Lower limit of integration.

b : float
  Upper limit of integration.

Returns

results : float
  Result of the integration.

Other Parameters

args : tuple, optional
  Extra arguments to pass to function. Each element of *args* will be passed as a single argument to *func*. Default is to pass no extra arguments.

tol, rtol : float, optional
  The desired absolute and relative tolerances. Defaults are 1.48e-8.

show : bool, optional
  Whether to print the results. Default is False.

divmax : int, optional
  Maximum order of extrapolation. Default is 10.

vec_func : bool, optional
  Whether *func* handles arrays as arguments (i.e whether it is a “vector” function). Default is False.

See also:

`fixed_quad`	Fixed-order Gaussian quadrature.
`quad`	Adaptive quadrature using QUADPACK.
`dblquad`	Double integrals.
`tplquad`	Triple integrals.
`romb`	Integrators for sampled data.
`simps`	Integrators for sampled data.
`cumtrapz`	Cumulative integration for sampled data.
`ode`	ODE integrator.
`odeint`	ODE integrator.

References

[R39]

Examples

Integrate a gaussian from 0 to 1 and compare to the error function.

```
>>> from scipy import integrate
>>> from scipy.special import erf
>>> gaussian = lambda x: 1/np.sqrt(np.pi) * np.exp(-x**2)
>>> result = integrate.romberg(gaussian, 0, 1, show=True)
Romberg integration of <function vfunc at ...> from [0, 1]

Steps  StepSize  Results
    1  1.000000  0.385872
    2  0.500000  0.412631  0.421551
    4  0.250000  0.419184  0.421368  0.421356
    8  0.125000  0.420810  0.421352  0.421350  0.421350
   16  0.062500  0.421215  0.421350  0.421350  0.421350  0.421350
   32  0.031250  0.421317  0.421350  0.421350  0.421350  0.421350  0.421350
```

The final result is 0.421350396475 after 33 function evaluations.

```
>>> print("%g %g" % (2*result, erf(1)))
0.842701 0.842701
```

5.6.2 Integrating functions, given fixed samples

`cumtrapz`(y[, x, dx, axis, initial])	Cumulatively integrate y(x) using the composite trapezoidal rule.
`simps`(y[, x, dx, axis, even])	Integrate y(x) using samples along the given axis and the composite Simpson's rule.
`romb`(y[, dx, axis, show])	Romberg integration using samples of a function.

`scipy.integrate.`**`cumtrapz`**(*y*, *x=None*, *dx=1.0*, *axis=-1*, *initial=None*)

Cumulatively integrate y(x) using the composite trapezoidal rule.

Parameters

y : array_like
Values to integrate.

x : array_like, optional
The coordinate to integrate along. If None (default), use spacing *dx* between consecutive elements in *y*.

dx : int, optional
Spacing between elements of *y*. Only used if *x* is None.

axis : int, optional
Specifies the axis to cumulate. Default is -1 (last axis).

initial : scalar, optional
If given, uses this value as the first value in the returned result. Typically this value should be 0. Default is None, which means no value at `x[0]` is returned and *res* has one element less than *y* along the axis of integration.

Returns

res : ndarray
The result of cumulative integration of *y* along *axis*. If *initial* is None, the shape is such that the axis of integration has one less value than *y*. If *initial* is given, the shape is equal to that of *y*.

See also:

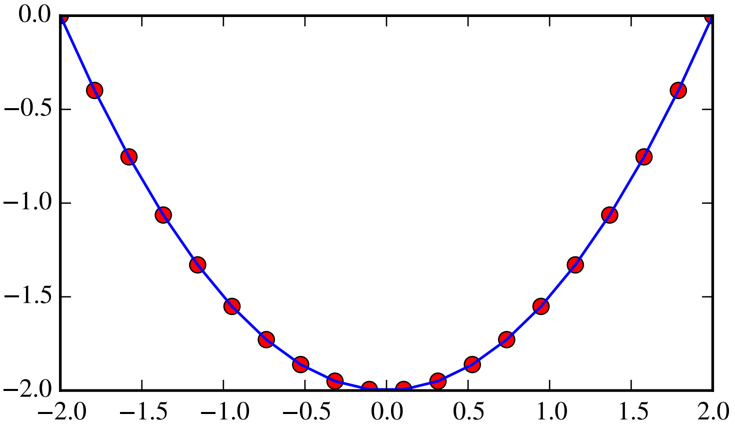
`numpy.cumsum`, `numpy.cumprod`

`quad`	adaptive quadrature using QUADPACK
`romberg`	adaptive Romberg quadrature
`quadrature`	adaptive Gaussian quadrature

`fixed_quad`	fixed-order Gaussian quadrature
`dblquad`	double integrals
`tplquad`	triple integrals
`romb`	integrators for sampled data
`ode`	ODE integrators
`odeint`	ODE integrators

Examples

```
>>> from scipy import integrate
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-2, 2, num=20)
>>> y = x
>>> y_int = integrate.cumtrapz(y, x, initial=0)
>>> plt.plot(x, y_int, 'ro', x, y[0] + 0.5 * x**2, 'b-')
>>> plt.show()
```



`scipy.integrate.`**`simps`**(*y*, *x=None*, *dx=1*, *axis=-1*, *even='avg'*)

Integrate y(x) using samples along the given axis and the composite Simpson's rule. If x is None, spacing of dx is assumed.

If there are an even number of samples, N, then there are an odd number of intervals (N-1), but Simpson's rule requires an even number of intervals. The parameter 'even' controls how this is handled.

Parameters

y : array_like
  Array to be integrated.

x : array_like, optional
  If given, the points at which *y* is sampled.

dx : int, optional
  Spacing of integration points along axis of *y*. Only used when *x* is None. Default is 1.

axis : int, optional
  Axis along which to integrate. Default is the last axis.

even : {'avg', 'first', 'str'}, optional

'avg'	[Average two results:1) use the first N-2 intervals with] a trapezoidal rule on the last interval and 2) use the last N-2 intervals with a trapezoidal rule on the first interval.
'first'	[Use Simpson's rule for the first N-2 intervals with] a trapezoidal rule on the last interval.
'last'	[Use Simpson's rule for the last N-2 intervals with a] trapezoidal rule on the first interval.

See also:

`quad`	adaptive quadrature using QUADPACK
`romberg`	adaptive Romberg quadrature
`quadrature`	adaptive Gaussian quadrature
`fixed_quad`	fixed-order Gaussian quadrature
`dblquad`	double integrals
`tplquad`	triple integrals
`romb`	integrators for sampled data
`cumtrapz`	cumulative integration for sampled data
`ode`	ODE integrators
`odeint`	ODE integrators

Notes

For an odd number of samples that are equally spaced the result is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

`scipy.integrate.`**`romb`**(*y*, *dx=1.0*, *axis=-1*, *show=False*)

Romberg integration using samples of a function.

Parameters **y** : array_like

A vector of `2**k + 1` equally-spaced samples of a function.

dx : float, optional

The sample spacing. Default is 1.

axis : int, optional

The axis along which to integrate. Default is -1 (last axis).

show : bool, optional

When *y* is a single 1-D array, then if this argument is True print the table showing Richardson extrapolation from the samples. Default is False.

Returns **romb** : ndarray

The integrated result for *axis*.

See also:

`quad`	adaptive quadrature using QUADPACK
`romberg`	adaptive Romberg quadrature
`quadrature`	adaptive Gaussian quadrature
`fixed_quad`	fixed-order Gaussian quadrature
`dblquad`	double integrals

`tplquad`	triple integrals
`simps`	integrators for sampled data
`cumtrapz`	cumulative integration for sampled data
`ode`	ODE integrators
`odeint`	ODE integrators

See also:

`scipy.special` for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

5.6.3 Integrators of ODE systems

`odeint`(func, y0, t[, args, Dfun, col_deriv, ...])	Integrate a system of ordinary differential equations.
`ode`(f[, jac])	A generic interface class to numeric integrators.
`complex_ode`(f[, jac])	A wrapper of ode for complex systems.

`scipy.integrate.`**`odeint`** (*func*, *y0*, *t*, *args=()*, *Dfun=None*, *col_deriv=0*, *full_output=0*, *ml=None*, *mu=None*, *rtol=None*, *atol=None*, *tcrit=None*, *h0=0.0*, *hmax=0.0*, *hmin=0.0*, *ixpr=0*, *mxstep=0*, *mxhnil=0*, *mxordn=12*, *mxords=5*, *printmessg=0*)

Integrate a system of ordinary differential equations.

Solve a system of ordinary differential equations using lsoda from the FORTRAN library odepack.

Solves the initial value problem for stiff or non-stiff systems of first order ode-s:

```
dy/dt = func(y,t0,...)
```

where y can be a vector.

Parameters

func : callable(y, t0, ...)
Computes the derivative of y at t0.

y0 : array
Initial condition on y (can be a vector).

t : array
A sequence of time points for which to solve for y. The initial value point should be the first element of this sequence.

args : tuple, optional
Extra arguments to pass to function.

Dfun : callable(y, t0, ...)
Gradient (Jacobian) of *func*.

col_deriv : bool, optional
True if *Dfun* defines derivatives down columns (faster), otherwise *Dfun* should define derivatives across rows.

full_output : bool, optional
True if to return a dictionary of optional outputs as the second output

printmessg : bool, optional
Whether to print the convergence message

Returns

y : array, shape (len(t), len(y0))
Array containing the value of y for each desired time in t, with the initial value *y0* in the first row.

infodict : dict, only returned if full_output == True

Dictionary containing additional output information

key	meaning
‘hu’	vector of step sizes successfully used for each time step.
‘tcur’	vector with the value of t reached for each time step. (will always be at least as large as the input times).
‘tolsf’	vector of tolerance scale factors, greater than 1.0, computed when a request for too much accuracy was detected.
‘tsw’	value of t at the time of the last method switch (given for each time step)
‘nst’	cumulative number of time steps
‘nfe’	cumulative number of function evaluations for each time step
‘nje’	cumulative number of jacobian evaluations for each time step
‘nqu’	a vector of method orders for each successful step.
‘imxer’	index of the component of largest magnitude in the weighted local error vector (e / ewt) on an error return, -1 otherwise.
‘lenrw’	the length of the double work array required.
‘leniw’	the length of integer work array required.
‘mused’	a vector of method indicators for each successful time step: 1: adams (nonstiff), 2: bdf (stiff)

Other Parameters

ml, mu : int, optional

If either of these are not None or non-negative, then the Jacobian is assumed to be banded. These give the number of lower and upper non-zero diagonals in this banded matrix. For the banded case, *Dfun* should return a matrix whose rows contain the non-zero bands (starting with the lowest diagonal). Thus, the return matrix *jac* from *Dfun* should have shape `(ml + mu + 1, len(y0))` when `ml >=0` or `mu >=0`. The data in *jac* must be stored such that `jac[i - j + mu, j]` holds the derivative of the *i‘th equation with respect to the ‘j‘th state variable. If ‘col_deriv* is True, the transpose of this *jac* must be returned.

rtol, atol : float, optional

The input parameters *rtol* and *atol* determine the error control performed by the solver. The solver will control the vector, e, of estimated local errors in y, according to an inequality of the form `max-norm of (e / ewt) <= 1`, where ewt is a vector of positive error weights computed as `ewt = rtol * abs(y) + atol`. rtol and atol can be either vectors the same length as y or scalars. Defaults to 1.49012e-8.

tcrit : ndarray, optional

Vector of critical points (e.g. singularities) where integration care should be taken.

h0 : float, (0: solver-determined), optional

The step size to be attempted on the first step.

hmax : float, (0: solver-determined), optional

The maximum absolute step size allowed.

hmin : float, (0: solver-determined), optional

The minimum absolute step size allowed.

ixpr : bool, optional

Whether to generate extra printing at method switches.

mxstep : int, (0: solver-determined), optional

Maximum number of (internally defined) steps allowed for each integration point in t.

mxhnil : int, (0: solver-determined), optional

Maximum number of messages printed.

mxordn : int, (0: solver-determined), optional

Maximum order to be allowed for the non-stiff (Adams) method.

mxords : int, (0: solver-determined), optional

Maximum order to be allowed for the stiff (BDF) method.

See also:

`ode`	a more object-oriented integrator based on VODE.
`quad`	for finding the area under a curve.

class `scipy.integrate.`**`ode`**(*f*, *jac=None*)

A generic interface class to numeric integrators.

Solve an equation system $y'(t) = f(t, y)$ with (optional) `jac = df/dy`.

Parameters **f** : callable `f(t, y, *f_args)`

Rhs of the equation. t is a scalar, `y.shape == (n,)`. `f_args` is set by calling `set_f_params(*args)`. *f* should return a scalar, array or list (not a tuple).

jac : callable `jac(t, y, *jac_args)`, optional

Jacobian of the rhs, `jac[i,j] = d f[i] / d y[j]`. `jac_args` is set by calling `set_f_params(*args)`.

See also:

`odeint`	an integrator with a simpler interface based on lsoda from ODEPACK
`quad`	for finding the area under a curve

Notes

Available integrators are listed below. They can be selected using the `set_integrator` method.

"vode"

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/ode/vode.f

> **Warning:** This integrator is not re-entrant. You cannot have two `ode` instances using the "vode" integrator at the same time.

This integrator accepts the following parameters in `set_integrator` method of the `ode` class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- lband : None or int
- uband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+uband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+uband, j] = jac[i,j]. The dimension of the matrix must be (lband+uband+1, len(y)).
- method: 'adams' or 'bdf' Which solver to use, Adams (non-stiff) or BDF (stiff)
- with_jacobian : bool This option is only considered when the user has not supplied a Jacobian function and has not indicated (by setting either band) that the Jacobian is banded. In this case, *with_jacobian* specifies whether the iteration method of the ODE solver's correction step is chord iteration with an internally generated full Jacobian or functional iteration with no Jacobian.
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- min_step : float
- max_step : float Limits for the step sizes used by the integrator.
- order : int Maximum order used by the integrator, order <= 12 for Adams, <= 5 for BDF.

"zvode"

Complex-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/ode/zvode.f

Warning: This integrator is not re-entrant. You cannot have two `ode` instances using the "zvode" integrator at the same time.

This integrator accepts the same parameters in `set_integrator` as the "vode" solver.

Note: When using ZVODE for a stiff system, it should only be used for the case in which the function f is analytic, that is, when each f(i) is an analytic function of each y(j). Analyticity means that the partial derivative df(i)/dy(j) is a unique complex number, and this fact is critical in the way ZVODE solves the dense or banded linear systems that arise in the stiff case. For a complex stiff ODE system in which f is not analytic, ZVODE is likely to have convergence failures, and for this problem one should instead use DVODE on the equivalent real system (in the real and imaginary parts of y).

"lsoda"

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides automatic method switching between implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/odepack

Warning: This integrator is not re-entrant. You cannot have two `ode` instances using the "lsoda" integrator at the same time.

This integrator accepts the following parameters in `set_integrator` method of the `ode` class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- lband : None or int
- uband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+uband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+uband, j] = jac[i,j].
- with_jacobian : bool *Not used.*
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- min_step : float
- max_step : float Limits for the step sizes used by the integrator.
- max_order_ns : int Maximum order used in the nonstiff case (default 12).
- max_order_s : int Maximum order used in the stiff case (default 5).
- max_hnil : int Maximum number of messages reporting too small step size (t + h = t) (default 0)
- ixpr : int Whether to generate extra printing at method switches (default False).

"dopri5"

This is an explicit runge-kutta method of order (4)5 due to Dormand & Prince (with stepsize control and dense output).
Authors:

E. Hairer and G. Wanner Universite de Geneve, Dept. de Mathematiques CH-1211 Geneve 24, Switzerland e-mail: ernst.hairer@math.unige.ch, gerhard.wanner@math.unige.ch

This code is described in [HNW93].
This integrator accepts the following parameters in set_integrator() method of the ode class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- max_step : float

- safety : float Safety factor on new step selection (default 0.9)
- ifactor : float
- dfactor : float Maximum factor to increase/decrease step size by in one step
- beta : float Beta parameter for stabilised step size control.
- verbosity : int Switch for printing messages (< 0 for no messages).

"dop853"

This is an explicit runge-kutta method of order 8(5,3) due to Dormand & Prince (with stepsize control and dense output).
Options and references the same as "dopri5".

References

[HNW93]

Examples

A problem to integrate and the corresponding jacobian:

```
>>> from scipy.integrate import ode
>>>
>>> y0, t0 = [1.0j, 2.0], 0
>>>
>>> def f(t, y, arg1):
...     return [1j*arg1*y[0] + y[1], -arg1*y[1]**2]
>>> def jac(t, y, arg1):
...     return [[1j*arg1, 1], [0, -arg1*2*y[1]]]
```

The integration:

```
>>> r = ode(f, jac).set_integrator('zvode', method='bdf')
>>> r.set_initial_value(y0, t0).set_f_params(2.0).set_jac_params(2.0)
>>> t1 = 10
>>> dt = 1
>>> while r.successful() and r.t < t1:
...     print(r.t, r.integrate(r.t+dt))
```

Attributes

t	(float) Current time.
y	(ndarray) Current variable values.

Methods

`integrate`(t[, step, relax])	Find y=y(t), set y as an initial condition, and return y.
`set_f_params`(*args)	Set extra parameters for user-supplied function f.
`set_initial_value`(y[, t])	Set initial conditions y(t) = y.
`set_integrator`(name, **integrator_params)	Set integrator by name.
`set_jac_params`(*args)	Set extra parameters for user-supplied function jac.
`set_solout`(solout)	Set callable to be called at every successful integration step.
`successful`()	Check if integration was successful.

`ode.`**`integrate`**(*t*, *step=0*, *relax=0*)

Find y=y(t), set y as an initial condition, and return y.

`ode.`**`set_f_params`**(**args*)

Set extra parameters for user-supplied function f.

`ode.`**`set_initial_value`**(*y*, *t=0.0*)

Set initial conditions y(t) = y.

`ode.`**`set_integrator`**(*name*, ***integrator_params*)

Set integrator by name.

Parameters **name** : str

Name of the integrator.

integrator_params :

Additional parameters for the integrator.

`ode.`**`set_jac_params`**(**args*)

Set extra parameters for user-supplied function jac.

`ode.`**`set_solout`**(*solout*)

Set callable to be called at every successful integration step.

Parameters **solout** : callable

`solout(t, y)` is called at each internal integrator step, t is a scalar providing the current independent position y is the current soloution `y.shape == (n,)` solout should return -1 to stop integration otherwise it should return None or 0

`ode.`**`successful`**()

Check if integration was successful.

class `scipy.integrate.`**`complex_ode`**(*f*, *jac=None*)

A wrapper of ode for complex systems.

This functions similarly as `ode`, but re-maps a complex-valued equation system to a real-valued one before using the integrators.

Parameters **f** : callable `f(t, y, *f_args)`

Rhs of the equation. t is a scalar, `y.shape == (n,)`. `f_args` is set by calling `set_f_params(*args)`.

jac : callable `jac(t, y, *jac_args)`

Jacobian of the rhs, `jac[i,j] = d f[i] / d y[j]`. `jac_args` is set by calling `set_f_params(*args)`.

Examples

For usage examples, see `ode`.

Attributes

t	(float) Current time.
y	(ndarray) Current variable values.

Methods

`integrate`(t[, step, relax])	Find y=y(t), set y as an initial condition, and return y.
`set_f_params`(*args)	Set extra parameters for user-supplied function f.
`set_initial_value`(y[, t])	Set initial conditions y(t) = y.
`set_integrator`(name, **integrator_params)	Set integrator by name.
`set_jac_params`(*args)	Set extra parameters for user-supplied function jac.
`set_solout`(solout)	Set callable to be called at every successful integration step.
`successful`()	Check if integration was successful.

`complex_ode.`**`integrate`**(*t*, *step=0*, *relax=0*)

Find y=y(t), set y as an initial condition, and return y.

`complex_ode.`**`set_f_params`**`(`**args*`)`

Set extra parameters for user-supplied function f.

`complex_ode.`**`set_initial_value`**`(`*y*, *t=0.0*`)`

Set initial conditions y(t) = y.

`complex_ode.`**`set_integrator`**`(`*name*, ***integrator_params*`)`

Set integrator by name.

Parameters **name** : str

Name of the integrator

integrator_params :

Additional parameters for the integrator.

`complex_ode.`**`set_jac_params`**`(`**args*`)`

Set extra parameters for user-supplied function jac.

`complex_ode.`**`set_solout`**`(`*solout*`)`

Set callable to be called at every successful integration step.

Parameters **solout** : callable

`solout(t, y)` is called at each internal integrator step, t is a scalar providing the current independent position y is the current soloution `y.shape == (n,)` solout should return -1 to stop integration otherwise it should return None or 0

`complex_ode.`**`successful`**`()`

Check if integration was successful.

5.7 Interpolation (`scipy.interpolate`)

Sub-package for objects used in interpolation.

As listed below, this sub-package contains spline functions and classes, one-dimensional and multi-dimensional (univariate and multivariate) interpolation classes, Lagrange and Taylor polynomial interpolators, and wrappers for FITPACK and DFITPACK functions.

5.7.1 Univariate interpolation

`interp1d`(x, y[, kind, axis, copy, ...])	Interpolate a 1-D function.
`BarycentricInterpolator`(xi[, yi, axis])	The interpolating polynomial for a set of points
`KroghInterpolator`(xi, yi[, axis])	Interpolating polynomial for a set of points.
`PiecewisePolynomial`(xi, yi[, orders, ...])	Piecewise polynomial curve specified by points and derivatives
`PchipInterpolator`(x, y[, axis, extrapolate])	PCHIP 1-d monotonic cubic interpolation
`barycentric_interpolate`(xi, yi, x[, axis])	Convenience function for polynomial interpolation.
`krogh_interpolate`(xi, yi, x[, der, axis])	Convenience function for polynomial interpolation.
`piecewise_polynomial_interpolate`(xi, yi, x)	Convenience function for piecewise polynomial interpolation.
`pchip_interpolate`(xi, yi, x[, der, axis])	Convenience function for pchip interpolation.
`Akima1DInterpolator`(x, y[, axis])	Akima interpolator
`PPoly`(c, x[, extrapolate, axis])	Piecewise polynomial in terms of coefficients and breakpoints
`BPoly`(c, x[, extrapolate, axis])	Piecewise polynomial in terms of coefficients and breakpoints

class `scipy.interpolate.`**`interp1d`**`(`*x*, *y*, *kind='linear'*, *axis=-1*, *copy=True*, *bounds_error=True*, *fill_value=nan*, *assume_sorted=False*`)`

Interpolate a 1-D function.

x and *y* are arrays of values used to approximate some function f: `y = f(x)`. This class returns a function whose call method uses interpolation to find the value of new points.

Parameters

x : (N,) array_like
  A 1-D array of real values.

y : (...,N,...) array_like
  A N-D array of real values. The length of *y* along the interpolation axis must be equal to the length of *x*.

kind : str or int, optional
  Specifies the kind of interpolation as a string ('linear', 'nearest', 'zero', 'slinear', 'quadratic, 'cubic' where 'slinear', 'quadratic' and 'cubic' refer to a spline interpolation of first, second or third order) or as an integer specifying the order of the spline interpolator to use. Default is 'linear'.

axis : int, optional
  Specifies the axis of *y* along which to interpolate. Interpolation defaults to the last axis of *y*.

copy : bool, optional
  If True, the class makes internal copies of x and y. If False, references to *x* and *y* are used. The default is to copy.

bounds_error : bool, optional
  If True, a ValueError is raised any time interpolation is attempted on a value outside of the range of x (where extrapolation is necessary). If False, out of bounds values are assigned *fill_value*. By default, an error is raised.

fill_value : float, optional
  If provided, then this value will be used to fill in for requested points outside of the data range. If not provided, then the default is NaN.

assume_sorted : bool, optional
  If False, values of *x* can be in any order and they are sorted first. If True, *x* has to be an array of monotonically increasing values.

See also:

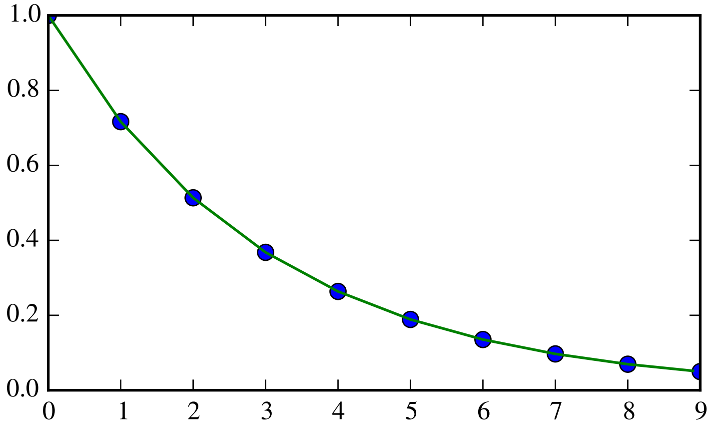
`splrep`, `splev`

`UnivariateSpline` An object-oriented wrapper of the FITPACK routines.

`interp2d` 2-D interpolation

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
>>> x = np.arange(0, 10)
>>> y = np.exp(-x/3.0)
>>> f = interpolate.interp1d(x, y)

>>> xnew = np.arange(0, 9, 0.1)
>>> ynew = f(xnew)   # use interpolation function returned by `interp1d`
>>> plt.plot(x, y, 'o', xnew, ynew, '-')
>>> plt.show()
```



Methods

`__call__`(x)	Evaluate the interpolant

`interp1d.`**`__call__`**(*x*)

Evaluate the interpolant

Parameters **x** : array_like

Points to evaluate the interpolant at.

Returns **y** : array_like

Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

class `scipy.interpolate.`**`BarycentricInterpolator`**(*xi*, *yi=None*, *axis=0*)

The interpolating polynomial for a set of points

Constructs a polynomial that passes through a given set of points. Allows evaluation of the polynomial, efficient changing of the y values to be interpolated, and updating by adding more x values. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

The values yi need to be provided before the function is evaluated, but none of the preprocessing depends on them, so rapid updates are possible.

Parameters **xi** : array_like

1-d array of x coordinates of the points the polynomial should pass through

yi : array_like, optional

The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later via the *set_y* method.

axis : int, optional

Axis in the yi array corresponding to the x-coordinate values.

Notes

This class uses a "barycentric interpolation" method that treats the problem as a special case of rational function interpolation. This algorithm is quite stable, numerically, but even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon.

Based on Berrut and Trefethen 2004, "Barycentric Lagrange Interpolation".

Methods

`__call__`(x)	Evaluate the interpolating polynomial at the points x
`add_xi`(xi[, yi])	Add more x values to the set to be interpolated
`set_yi`(yi[, axis])	Update the y values to be interpolated

`BarycentricInterpolator.`**`__call__`**(*x*)

Evaluate the interpolating polynomial at the points x

Parameters **x** : array_like

Points to evaluate the interpolant at.

Returns **y** : array_like

Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Currently the code computes an outer product between x and the weights, that is, it constructs an intermediate array of size N by len(x), where N is the degree of the polynomial.

`BarycentricInterpolator.`**`add_xi`**(*xi*, *yi=None*)

Add more x values to the set to be interpolated

The barycentric interpolation algorithm allows easy updating by adding more points for the polynomial to pass through.

Parameters **xi** : array_like

The x coordinates of the points that the polynomial should pass through.

yi : array_like, optional

The y coordinates of the points the polynomial should pass through. Should have shape `(xi.size, R)`; if R > 1 then the polynomial is vector-valued. If *yi* is not given, the y values will be supplied later. *yi* should be given if and only if the interpolator has y values specified.

`BarycentricInterpolator.`**`set_yi`**(*yi*, *axis=None*)

Update the y values to be interpolated

The barycentric interpolation algorithm requires the calculation of weights, but these depend only on the xi. The yi can be changed at any time.

Parameters **yi** : array_like

The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later.

axis : int, optional

Axis in the yi array corresponding to the x-coordinate values.

class `scipy.interpolate.`**`KroghInterpolator`**(*xi*, *yi*, *axis=0*)

Interpolating polynomial for a set of points.

The polynomial passes through all the pairs (xi,yi). One may additionally specify a number of derivatives at each point xi; this is done by repeating the value xi and specifying the derivatives as successive yi values.

Allows evaluation of the polynomial and all its derivatives. For reasons of numerical stability, this function does not compute the coefficients of the polynomial, although they can be obtained by evaluating all the derivatives.

Parameters **xi** : array_like, length N

Known x-coordinates. Must be sorted in increasing order.

yi : array_like
Known y-coordinates. When an xi occurs two or more times in a row, the corresponding yi's represent derivative values.

axis : int, optional
Axis in the yi array corresponding to the x-coordinate values.

Notes

Be aware that the algorithms implemented here are not necessarily the most numerically stable known. Moreover, even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon. In general, even with well-chosen x values, degrees higher than about thirty cause problems with numerical instability in this code.

Based on [R44].

References

[R44]

Examples

To produce a polynomial that is zero at 0 and 1 and has derivative 2 at 0, call

```
>>> KroghInterpolator([0,0,1],[0,2,0])
```

This constructs the quadratic 2*X**2-2*X. The derivative condition is indicated by the repeated zero in the xi array; the corresponding yi values are 0, the function value, and 2, the derivative value.

For another example, given xi, yi, and a derivative ypi for each point, appropriate arrays can be constructed as:

```
>>> xi_k, yi_k = np.repeat(xi, 2), np.ravel(np.dstack((yi,ypi)))
>>> KroghInterpolator(xi_k, yi_k)
```

To produce a vector-valued polynomial, supply a higher-dimensional array for yi:

```
>>> KroghInterpolator([0,1],[[2,3],[4,5]])
```

This constructs a linear polynomial giving (2,3) at 0 and (4,5) at 1.

Methods

`__call__`(x)	Evaluate the interpolant
`derivative`(x[, der])	Evaluate one derivative of the polynomial at the point x
`derivatives`(x[, der])	Evaluate many derivatives of the polynomial at the point x

`KroghInterpolator.`**`__call__`**(*x*)

Evaluate the interpolant

Parameters **x** : array_like
Points to evaluate the interpolant at.

Returns **y** : array_like
Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

`KroghInterpolator.`**`derivative`**(*x*, *der=1*)

Evaluate one derivative of the polynomial at the point x

Parameters **x** : array_like

Point or points at which to evaluate the derivatives

der : integer, optional

Which derivative to extract. This number includes the function value as 0th derivative.

Returns **d** : ndarray

Derivative interpolated at the x-points. Shape of d is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

This is computed by evaluating all derivatives up to the desired one (using self.derivatives()) and then discarding the rest.

`KroghInterpolator.`**`derivatives`**(*x*, *der=None*)

Evaluate many derivatives of the polynomial at the point x

Produce an array of all derivative values at the point x.

Parameters **x** : array_like

Point or points at which to evaluate the derivatives

der : int or None, optional

How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points). This number includes the function value as 0th derivative.

Returns **d** : ndarray

Array with derivatives; d[j] contains the j-th derivative. Shape of d[j] is determined by replacing the interpolation axis in the original array with the shape of x.

Examples

```
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives(0)
array([1.0,2.0,3.0])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])
array([[1.0,1.0],
       [2.0,2.0],
       [3.0,3.0]])
```

class `scipy.interpolate.`**`PiecewisePolynomial`**(*xi*, *yi*, *orders=None*, *direction=None*, *axis=0*)

Piecewise polynomial curve specified by points and derivatives

This class represents a curve that is a piecewise polynomial. It passes through a list of points and has specified derivatives at each point. The degree of the polynomial may vary from segment to segment, as may the number of derivatives available. The degree should not exceed about thirty.

Appending points to the end of the curve is efficient.

Parameters **xi** : array_like

A sorted 1-d array of x-coordinates.

yi : array_like or list of array_likes

`yi[i][j]` is the j-th derivative known at `xi[i]` (for `axis=0`).

orders : list of int, or int, optional

A list of polynomial orders, or a single universal order.

direction : {None, 1, -1}, optional

Indicates whether the *xi* are increasing or decreasing:

+1 : increasing values

-1 : decreasing values

None : direction will be deduced from the first two elements of *xi*

axis : int, optional

Axis in the *yi* array corresponding to the x-coordinate values.

Notes

If orders is None, or `orders[i]` is None, then the degree of the polynomial segment is exactly the degree required to match all `i` available derivatives at both endpoints. If `orders[i]` is not None, then some derivatives will be ignored. The code will try to use an equal number of derivatives from each end; if the total number of derivatives needed is odd, it will prefer the rightmost endpoint. If not enough derivatives are available, an exception is raised.

Methods

`__call__`(x)	Evaluate the interpolant
`append`(xi, yi[, order])	Append a single point with derivatives to the PiecewisePolynomial
`derivative`(x[, der])	Evaluate one derivative of the polynomial at the point x
`derivatives`(x[, der])	Evaluate many derivatives of the polynomial at the point x
`extend`(xi, yi[, orders])	Extend the PiecewisePolynomial by a list of points

`PiecewisePolynomial.`**`__call__`**(*x*)

Evaluate the interpolant

Parameters **x** : array_like

Points to evaluate the interpolant at.

Returns **y** : array_like

Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

`PiecewisePolynomial.`**`append`**(*xi*, *yi*, *order=None*)

Append a single point with derivatives to the PiecewisePolynomial

Parameters **xi** : float

Point to add.

yi : array_like

yi is the list of derivatives known at *xi*.

order : int or None, optional

A polynomial order, or instructions to use the highest possible order.

`PiecewisePolynomial.`**`derivative`**(*x*, *der=1*)

Evaluate one derivative of the polynomial at the point x

Parameters **x** : array_like

Point or points at which to evaluate the derivatives

der : integer, optional

Which derivative to extract. This number includes the function value as 0th derivative.

Returns **d** : ndarray

Derivative interpolated at the x-points. Shape of d is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

This is computed by evaluating all derivatives up to the desired one (using self.derivatives()) and then discarding the rest.

`PiecewisePolynomial.`**`derivatives`**(*x*, *der=None*)

Evaluate many derivatives of the polynomial at the point x

Produce an array of all derivative values at the point x.

Parameters **x** : array_like

Point or points at which to evaluate the derivatives

der : int or None, optional

How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points). This number includes the function value as 0th derivative.

Returns **d** : ndarray

Array with derivatives; d[j] contains the j-th derivative. Shape of d[j] is determined by replacing the interpolation axis in the original array with the shape of x.

Examples

```
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives(0)
array([1.0,2.0,3.0])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])
array([[1.0,1.0],
       [2.0,2.0],
       [3.0,3.0]])
```

`PiecewisePolynomial.`**`extend`**(*xi*, *yi*, *orders=None*)

Extend the PiecewisePolynomial by a list of points

Parameters **xi** : array_like

A sorted list of x-coordinates.

yi : list of lists of length N1

`yi[i]` (if `axis == 0`) is the list of derivatives known at `xi[i]`.

orders : int or list of ints, optional

A list of polynomial orders, or a single universal order.

class `scipy.interpolate.`**`PchipInterpolator`**(*x*, *y*, *axis=0*, *extrapolate=None*)

PCHIP 1-d monotonic cubic interpolation

x and y are arrays of values used to approximate some function f, with `y = f(x)`. The interpolant uses monotonic cubic splines to find the value of new points. (PCHIP stands for Piecewise Cubic Hermite Interpolating Polynomial).

Parameters **x** : ndarray

A 1-D array of monotonically increasing real values. `x` cannot include duplicate values (otherwise f is overspecified)

y : ndarray

A 1-D array of real values. *y*‘s length along the interpolation axis must be equal to the length of `x`. If N-D array, use axis parameter to select correct axis.

axis : int, optional

Axis in the y array corresponding to the x-coordinate values.

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.

See also:

`Akima1DInterpolator`

Notes

The first derivatives are guaranteed to be continuous, but the second derivatives may jump at x_k.

Preserves monotonicity in the interpolation data and does not overshoot if the data is not smooth.

Determines the derivatives at the points x_k, d_k, by using PCHIP algorithm:

Let m_k be the slope of the kth segment (between k and k+1) If m_k=0 or m_{k-1}=0 or sgn(m_k) != sgn(m_{k-1}) then d_k == 0 else use weighted harmonic mean:

> w_1 = 2h_k + h_{k-1}, w_2 = h_k + 2h_{k-1} 1/d_k = 1/(w_1 + w_2)*(w_1 / m_k + w_2 / m_{k-1})

where h_k is the spacing between x_k and x_{k+1}.

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.

`PchipInterpolator.`**`__call__`**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative

Parameters **x** : array_like
Points to evaluate the interpolant at.
nu : int, optional
Order of derivative to evaluate. Must be non-negative.
extrapolate : bool, optional
Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.

Returns **y** : array_like
Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`PchipInterpolator.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters **nu** : int, optional
Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.

Returns **bp** : BPoly
Piecewise polynomial of order k2 = k - nu representing the derivative of this polynomial.

`PchipInterpolator.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Parameters **nu** : int, optional
Order of derivative to evaluate. (Default: 1) If negative, the derivative is returned.

Returns **bp** : BPoly
Piecewise polynomial of order k2 = k + nu representing the antiderivative of this polynomial.

`scipy.interpolate.`**`barycentric_interpolate`**(*xi*, *yi*, *x*, *axis=0*)

Convenience function for polynomial interpolation.

Constructs a polynomial that passes through a given set of points, then evaluates the polynomial. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

This function uses a "barycentric interpolation" method that treats the problem as a special case of rational function interpolation. This algorithm is quite stable, numerically, but even in a world of exact computation, unless the *x* coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon.

Parameters

xi : array_like
  1-d array of x coordinates of the points the polynomial should pass through

yi : array_like
  The y coordinates of the points the polynomial should pass through.

x : scalar or array_like
  Points to evaluate the interpolator at.

axis : int, optional
  Axis in the yi array corresponding to the x-coordinate values.

Returns

y : scalar or array_like
  Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

See also:

`BarycentricInterpolator`

Notes

Construction of the interpolation weights is a relatively slow process. If you want to call this many times with the same xi (but possibly varying yi or x) you should use the class `BarycentricInterpolator`. This is what this function uses internally.

`scipy.interpolate.`**`krogh_interpolate`**(*xi*, *yi*, *x*, *der=0*, *axis=0*)

Convenience function for polynomial interpolation.

See `KroghInterpolator` for more details.

Parameters

xi : array_like
  Known x-coordinates.

yi : array_like
  Known y-coordinates, of shape `(xi.size, R)`. Interpreted as vectors of length R, or scalars if R=1.

x : array_like
  Point or points at which to evaluate the derivatives.

der : int or list, optional
  How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points), or a list of derivatives to extract. This number includes the function value as 0th derivative.

axis : int, optional
  Axis in the yi array corresponding to the x-coordinate values.

Returns

d : ndarray
  If the interpolator's values are R-dimensional then the returned array will be the number of derivatives by N by R. If *x* is a scalar, the middle dimension will be dropped; if the *yi* are scalars then the last dimension will be dropped.

See also:

`KroghInterpolator`

Notes

Construction of the interpolating polynomial is a relatively expensive process. If you want to evaluate it repeatedly consider using the class KroghInterpolator (which is what this function uses).

`scipy.interpolate.`**`piecewise_polynomial_interpolate`**(*xi*, *yi*, *x*, *orders=None*, *der=0*, *axis=0*)

Convenience function for piecewise polynomial interpolation.

Parameters	**xi** : array_like A sorted list of x-coordinates. **yi** : list of lists `yi[i]` is the list of derivatives known at `xi[i]`. **x** : scalar or array_like Coordinates at which to evalualte the polynomial. **orders** : int or list of ints, optional A list of polynomial orders, or a single universal order. **der** : int or list, optional How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points), or a list of derivatives to extract. This number includes the function value as 0th derivative. **axis** : int, optional Axis in the *yi* array corresponding to the x-coordinate values.
Returns	**y** : ndarray Interpolated values or derivatives. If multiple derivatives were requested, these are given along the first axis.

See also:

`PiecewisePolynomial`

Notes

If *orders* is None, or `orders[i]` is None, then the degree of the polynomial segment is exactly the degree required to match all i available derivatives at both endpoints. If `orders[i]` is not None, then some derivatives will be ignored. The code will try to use an equal number of derivatives from each end; if the total number of derivatives needed is odd, it will prefer the rightmost endpoint. If not enough derivatives are available, an exception is raised.

Construction of these piecewise polynomials can be an expensive process; if you repeatedly evaluate the same polynomial, consider using the class PiecewisePolynomial (which is what this function does).

`scipy.interpolate.`**`pchip_interpolate`**(*xi*, *yi*, *x*, *der=0*, *axis=0*)

Convenience function for pchip interpolation. xi and yi are arrays of values used to approximate some function f, with `yi = f(xi)`. The interpolant uses monotonic cubic splines to find the value of new points x and the derivatives there.

See `PchipInterpolator` for details.

Parameters	**xi** : array_like A sorted list of x-coordinates, of length N. **yi** : array_like A 1-D array of real values. *yi*'s length along the interpolation axis must be equal to the length of *xi*. If N-D array, use axis parameter to select correct axis. **x** : scalar or array_like Of length M. **der** : int or list, optional How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points), or a list of derivatives to extract. This number includes the function value as 0th derivative. **axis** : int, optional Axis in the yi array corresponding to the x-coordinate values.
Returns	**y** : scalar or array_like

The result, of length R or length M or M by R,

See also:

`PchipInterpolator`

class `scipy.interpolate.`**`Akima1DInterpolator`**(*x*, *y*, *axis=0*)

Akima interpolator

Fit piecewise cubic polynomials, given vectors x and y. The interpolation method by Akima uses a continuously differentiable sub-spline built from piecewise cubic polynomials. The resultant curve passes through the given data points and will appear smooth and natural.

Parameters

x : ndarray, shape (m,)
  1-D array of monotonically increasing real values.

y : ndarray, shape (m, ...)
  N-D array of real values. The length of *y* along the first axis must be equal to the length of `x`.

axis : int, optional
  Specifies the axis of *y* along which to interpolate. Interpolation defaults to the first axis of *y*.

See also:

`PchipInterpolator`

Notes

New in version 0.14.

Use only for precise data, as the fitted curve passes through the given points exactly. This routine is useful for plotting a pleasingly smooth curve through a few given points for purposes of plotting.

References

[1] A new method of interpolation and smooth curve fitting based
on local procedures. Hiroshi Akima, J. ACM, October 1970, 17(4), 589-602.

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.
`roots`([discontinuity, extrapolate])	Find real roots of the piecewise polynomial.

`Akima1DInterpolator.`**`__call__`**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative

Parameters

x : array_like
  Points to evaluate the interpolant at.

nu : int, optional
  Order of derivative to evaluate. Must be non-negative.

extrapolate : bool, optional
  Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.

Returns

y : array_like
  Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`Akima1DInterpolator.`**`derivative`**`(`*nu=1*`)`

Construct a new piecewise polynomial representing the derivative.

Parameters	**nu** : int, optional Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.
Returns	**pp** : PPoly Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`Akima1DInterpolator.`**`antiderivative`**`(`*nu=1*`)`

Construct a new piecewise polynomial representing the antiderivative.

Antiderivativative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters	**nu** : int, optional Order of antiderivative to evaluate. (Default: 1) If negative, the derivative is returned.
Returns	**pp** : PPoly Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

`Akima1DInterpolator.`**`roots`**`(`*discontinuity=True*, *extrapolate=None*`)`

Find real roots of the piecewise polynomial.

Parameters	**discontinuity** : bool, optional Whether to report sign changes across discontinuities at breakpoints as roots. **extrapolate** : bool, optional Whether to return roots from the polynomial extrapolated based on first and last intervals.
Returns	**roots** : ndarray Roots of the polynomial(s). If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

Notes

This routine works only on real-valued polynomials.

If the piecewise polynomial contains sections that are identically zero, the root list will contain the start point of the corresponding interval, followed by a `nan` value.

If the polynomial is discontinuous across a breakpoint, and there is a sign change across the breakpoint, this is reported if the *discont* parameter is True.

Examples

Finding roots of `[x**2 - 1, (x - 1)**2]` defined on intervals `[-2, 1], [1, 2]`:

```
>>> from scipy.interpolate import PPoly
>>> pp = PPoly(np.array([[1, 0, -1], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.roots()
array([-1.,  1.])
```

class `scipy.interpolate.`**`PPoly`**(*c*, *x*, *extrapolate=None*, *axis=0*)

Piecewise polynomial in terms of coefficients and breakpoints

The polynomial in the ith interval is `x[i] <= xp < x[i+1]`:

```
S = sum(c[m, i] * (xp - x[i])**(k-m) for m in range(k+1))
```

where `k` is the degree of the polynomial. This representation is the local power basis.

Parameters

c : ndarray, shape (k, m, ...)
  Polynomial coefficients, order *k* and *m* intervals

x : ndarray, shape (m+1,)
  Polynomial breakpoints. These must be sorted in increasing order.

extrapolate : bool, optional
  Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

axis : int, optional
  Interpolation axis. Default is zero.

See also:

BPoly	piecewise polynomials in the Bernstein basis

Notes

High-order polynomials in the power basis can be numerically unstable. Precision problems can start to appear for orders larger than 20-30.

Attributes

x	(ndarray) Breakpoints.
c	(ndarray) Coefficients of the polynomials. They are reshaped to a 3-dimensional array with the last dimension representing the trailing dimensions of the original coefficient array.
axis	(int) Interpolation axis.

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.
`integrate`(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.
`roots`([discontinuity, extrapolate])	Find real roots of the piecewise polynomial.
`extend`(c, x[, right])	Add additional breakpoints and coefficients to the polynomial.
`from_spline`(tck[, extrapolate])	Construct a piecewise polynomial from a spline
`from_bernstein_basis`(bp[, extrapolate])	Construct a piecewise polynomial in the power basis from a polynomial in Bernste
`construct_fast`(c, x[, extrapolate, axis])	Construct the piecewise polynomial without making checks.

`PPoly.`**`__call__`**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative

Parameters	**x** : array_like Points to evaluate the interpolant at. **nu** : int, optional Order of derivative to evaluate. Must be non-negative. **extrapolate** : bool, optional Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.
Returns	**y** : array_like Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`PPoly.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters	**nu** : int, optional Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.
Returns	**pp** : PPoly Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`PPoly.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivativative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters	**nu** : int, optional Order of antiderivative to evaluate. (Default: 1) If negative, the derivative is returned.
Returns	**pp** : PPoly Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

`PPoly.`**`integrate`**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters	**a** : float Lower integration bound **b** : float Upper integration bound

extrapolate : bool, optional
Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.

Returns **ig** : array_like
Definite integral of the piecewise polynomial over [a, b]

`PPoly.`**`roots`**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the piecewise polynomial.

Parameters **discontinuity** : bool, optional
Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate : bool, optional
Whether to return roots from the polynomial extrapolated based on first and last intervals.

Returns **roots** : ndarray
Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

Notes

This routine works only on real-valued polynomials.

If the piecewise polynomial contains sections that are identically zero, the root list will contain the start point of the corresponding interval, followed by a `nan` value.

If the polynomial is discontinuous across a breakpoint, and there is a sign change across the breakpoint, this is reported if the *discont* parameter is True.

Examples

Finding roots of `[x**2 - 1, (x - 1)**2]` defined on intervals `[-2, 1], [1, 2]`:

```
>>> from scipy.interpolate import PPoly
>>> pp = PPoly(np.array([[1, 0, -1], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.roots()
array([-1.,  1.])
```

`PPoly.`**`extend`**(*c*, *x*, *right=True*)

Add additional breakpoints and coefficients to the polynomial.

Parameters **c** : ndarray, size (k, m, ...)
Additional coefficients for polynomials in intervals `self.x[-1] <= x < x_right[0]`, `x_right[0] <= x < x_right[1]`, ..., `x_right[m-2] <= x < x_right[m-1]`

x : ndarray, size (m,)
Additional breakpoints. Must be sorted and either to the right or to the left of the current breakpoints.

right : bool, optional
Whether the new intervals are to the right or to the left of the current intervals.

classmethod `PPoly.`**`from_spline`**(*tck*, *extrapolate=None*)

Construct a piecewise polynomial from a spline

Parameters **tck**
A spline, as returned by `splrep`

extrapolate : bool, optional
Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

classmethod `PPoly.`**`from_bernstein_basis`**(*bp*, *extrapolate=None*)

Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.

Parameters **bp** : BPoly

A Bernstein basis polynomial, as created by BPoly

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

classmethod `PPoly.`**`construct_fast`**(*c*, *x*, *extrapolate=None*, *axis=0*)

Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.

class `scipy.interpolate.`**`BPoly`**(*c*, *x*, *extrapolate=None*, *axis=0*)

Piecewise polynomial in terms of coefficients and breakpoints

The polynomial in the `i`-th interval `x[i] <= xp < x[i+1]` is written in the Bernstein polynomial basis:

```
S = sum(c[a, i] * b(a, k; x) for a in range(k+1))
```

where `k` is the degree of the polynomial, and:

```
b(a, k; x) = comb(k, a) * t**k * (1 - t)**(k - a)
```

with `t = (x - x[i]) / (x[i+1] - x[i])`.

Parameters **c** : ndarray, shape (k, m, ...)

Polynomial coefficients, order *k* and *m* intervals

x : ndarray, shape (m+1,)

Polynomial breakpoints. These must be sorted in increasing order.

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

axis : int, optional

Interpolation axis. Default is zero.

See also:

`PPoly`	piecewise polynomials in the power basis

Notes

Properties of Bernstein polynomials are well documented in the literature. Here's a non-exhaustive list:

Examples

```
>>> x = [0, 1]
>>> c = [[1], [2], [3]]
>>> bp = BPoly(c, x)
```

This creates a 2nd order polynomial

$$\begin{aligned} B(x) &= 1 \times b_{0,2}(x) + 2 \times b_{1,2}(x) + 3 \times b_{2,2}(x) \\ &= 1 \times (1-x)^2 + 2 \times 2x(1-x) + 3 \times x^2 \end{aligned}$$

Attributes

x	(ndarray) Breakpoints.
c	(ndarray) Coefficients of the polynomials. They are reshaped to a 3-dimensional array with the last dimension representing the trailing dimensions of the original coefficient array.
axis	(int) Interpolation axis.

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative
`extend`(c, x[, right])	Add additional breakpoints and coefficients to the polynomial.
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.
`integrate`(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.
`construct_fast`(c, x[, extrapolate, axis])	Construct the piecewise polynomial without making checks.
`from_power_basis`(pp[, extrapolate])	Construct a piecewise polynomial in Bernstein basis from a power basis polyno
`from_derivatives`(xi, yi[, orders, extrapolate])	Construct a piecewise polynomial in the Bernstein basis, compatible with the s

`BPoly.`**`__call__`**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative

Parameters

x : array_like

Points to evaluate the interpolant at.

nu : int, optional

Order of derivative to evaluate. Must be non-negative.

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs.

Returns

y : array_like

Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

`BPoly.`**`extend`**(*c*, *x*, *right=True*)

Add additional breakpoints and coefficients to the polynomial.

Parameters

c : ndarray, size (k, m, ...)

Additional coefficients for polynomials in intervals `self.x[-1] <= x < x_right[0]`, `x_right[0] <= x < x_right[1]`, ..., `x_right[m-2] <= x < x_right[m-1]`

x : ndarray, size (m,)

Additional breakpoints. Must be sorted and either to the right or to the left of the current breakpoints.

right : bool, optional

Whether the new intervals are to the right or to the left of the current intervals.

`BPoly.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu : int, optional

Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.

Returns **bp** : BPoly

Piecewise polynomial of order k2 = k - nu representing the derivative of this polynomial.

`BPoly.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Parameters **nu** : int, optional

Order of derivative to evaluate. (Default: 1) If negative, the derivative is returned.

Returns **bp** : BPoly

Piecewise polynomial of order k2 = k + nu representing the antiderivative of this polynomial.

`BPoly.`**`integrate`**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters **a** : float

Lower integration bound

b : float

Upper integration bound

extrapolate : bool, optional

Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Defaults to `self.extrapolate`.

Returns array_like

Definite integral of the piecewise polynomial over [a, b]

classmethod `BPoly.`**`construct_fast`**(*c*, *x*, *extrapolate=None*, *axis=0*)

Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.

classmethod `BPoly.`**`from_power_basis`**(*pp*, *extrapolate=None*)

Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.

Parameters **pp** : PPoly

A piecewise polynomial in the power basis

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

classmethod `BPoly.`**`from_derivatives`**(*xi*, *yi*, *orders=None*, *extrapolate=None*)

Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.

Parameters **xi** : array_like

sorted 1D array of x-coordinates

yi : array_like or list of array_likes

`yi[i][j]` is the `j`-th derivative known at `xi[i]`

orders : None or int or array_like of ints. Default: None.

Specifies the degree of local polynomials. If not None, some derivatives are ignored.

extrapolate : bool, optional

Whether to extrapolate to ouf-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

Notes

If `k` derivatives are specified at a breakpoint `x`, the constructed polynomial is exactly `k` times continuously differentiable at `x`, unless the `order` is provided explicitly. In the latter case, the smoothness of the polynomial at the breakpoint is controlled by the `order`.

Deduces the number of derivatives to match at each end from `order` and the number of derivatives available. If possible it uses the same number of derivatives from each end; if the number is odd it tries to take the extra one from y2. In any case if not enough derivatives are available at one end or another it draws enough to make up the total from the other end.

If the order is too high and not enough derivatives are available, an exception is raised.

Examples

```
>>> BPoly.from_derivatives([0, 1], [[1, 2], [3, 4]])
```

Creates a polynomial $f(x)$ of degree 3, defined on $[0, 1]$ such that $f(0) = 1, df/dx(0) = 2, f(1) = 3, df/dx(1) = 4$

```
>>> BPoly.from_derivatives([0, 1, 2], [[0, 1], [0], [2]])
```

Creates a piecewise polynomial $f(x)$, such that $f(0) = f(1) = 0, f(2) = 2$, and $df/dx(0) = 1$. Based on the number of derivatives provided, the order of the local polynomials is 2 on $[0, 1]$ and 1 on $[1, 2]$. Notice that no restriction is imposed on the derivatives at $x = 1$ and $x = 2$.

Indeed, the explicit form of the polynomial is:

```
f(x) = | x * (1 - x),  0 <= x < 1
       | 2 * (x - 1),  1 <= x <= 2
```

So that f'(1-0) = -1 and f'(1+0) = 2

5.7.2 Multivariate interpolation

Unstructured data:

`griddata`(points, values, xi[, method, ...])	Interpolate unstructured D-dimensional data.
`LinearNDInterpolator`(points, values[, ...])	Piecewise linear interpolant in N dimensions.
`NearestNDInterpolator`(points, values)	Nearest-neighbour interpolation in N dimensions.
`CloughTocher2DInterpolator`(points, values[, tol])	Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.
`Rbf`(*args)	A class for radial basis function approximation/interpolation of n-dime
`interp2d`(x, y, z[, kind, copy, ...])	Interpolate over a 2-D grid.

`scipy.interpolate.`**`griddata`**(*points*, *values*, *xi*, *method='linear'*, *fill_value=nan*, *rescale=False*)

Interpolate unstructured D-dimensional data.

Parameters

points : ndarray of floats, shape (n, D)
Data point coordinates. Can either be an array of shape (n, D), or a tuple of *ndim* arrays.

values : ndarray of float or complex, shape (n,)
Data values.

xi : ndarray of float, shape (M, D)
Points at which to interpolate data.

method : {'linear', 'nearest', 'cubic'}, optional
Method of interpolation. One of

`nearest`	return the value at the data point closest to the point of interpolation. See `NearestNDInterpolator` for more details.
`linear`	tesselate the input point set to n-dimensional simplices, and interpolate linearly on each simplex. See `LinearNDInterpolator` for more details.
`cubic` (1-D)	return the value determined from a cubic spline.
`cubic` (2-D)	return the value determined from a piecewise cubic, continuously differentiable (C1), and approximately curvature-minimizing polynomial surface. See `CloughTocher2DInterpolator` for more details.

fill_value : float, optional

Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`. This option has no effect for the 'nearest' method.

rescale : bool, optional

Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

New in version 0.14.0.

Notes

New in version 0.9.

Examples

Suppose we want to interpolate the 2-D function

```
>>> def func(x, y):
...     return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```

on a grid in [0, 1]x[0, 1]

```
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

```
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```

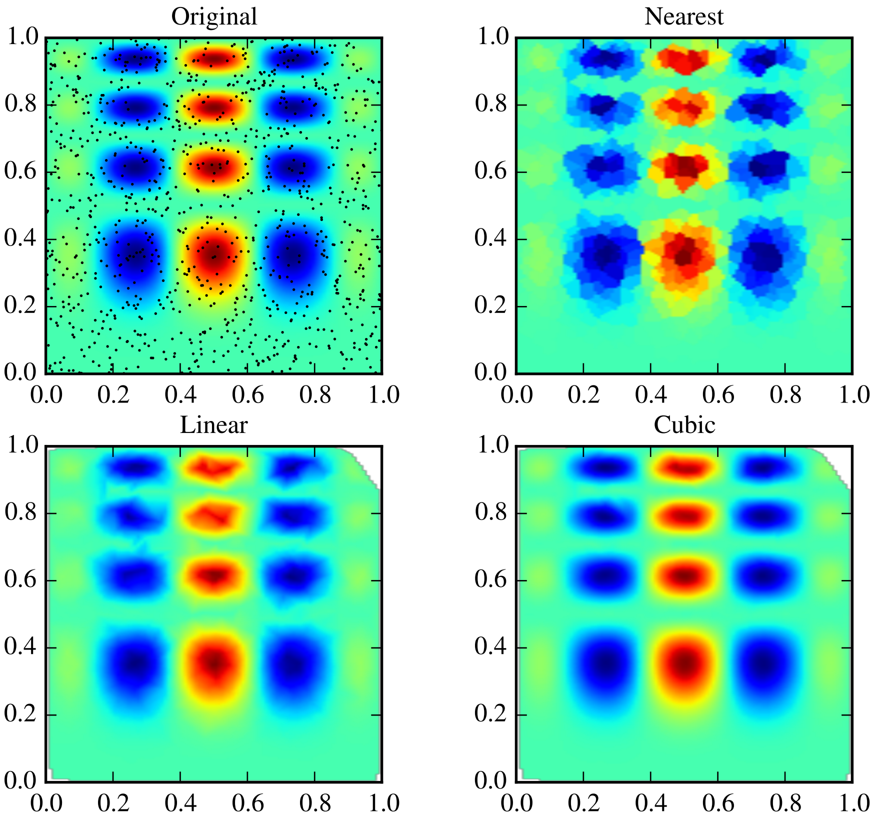
This can be done with `griddata` – below we try out all of the interpolation methods:

```
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(221)
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
```

```
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```



class `scipy.interpolate.`**`LinearNDInterpolator`**(*points*, *values*, *fill_value=np.nan*, *rescale=False*)

Piecewise linear interpolant in N dimensions.

New in version 0.9.

Parameters **points** : ndarray of floats, shape (npoints, ndims); or Delaunay

Data point coordinates, or a precomputed Delaunay triangulation.

values : ndarray of float or complex, shape (npoints, ...)

Data values.

fill_value : float, optional

Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`.

rescale : bool, optional
Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

Notes

The interpolant is constructed by triangulating the input data with Qhull [R45], and on each triangle performing linear barycentric interpolation.

References

[R45]

Methods

`__call__`(xi)	Evaluate interpolator at given points.

`LinearNDInterpolator.`**`__call__`**(*xi*)
Evaluate interpolator at given points.

Parameters **xi** : ndarray of float, shape (..., ndim)
Points where to interpolate data at.

class `scipy.interpolate.`**`NearestNDInterpolator`**(*points*, *values*)
Nearest-neighbour interpolation in N dimensions.

New in version 0.9.

Parameters **x** : (Npoints, Ndims) ndarray of floats
Data point coordinates.

y : (Npoints,) ndarray of float or complex
Data values.

rescale : boolean, optional
Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.
New in version 0.14.0.

Notes

Uses `scipy.spatial.cKDTree`

Methods

`__call__`(*args)	Evaluate interpolator at given points.

`NearestNDInterpolator.`**`__call__`**(**args*)
Evaluate interpolator at given points.

Parameters **xi** : ndarray of float, shape (..., ndim)
Points where to interpolate data at.

class `scipy.interpolate.`**`CloughTocher2DInterpolator`**(*points*, *values*, *tol=1e-6*)
Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.

New in version 0.9.

Parameters

points : ndarray of floats, shape (npoints, ndims); or Delaunay
Data point coordinates, or a precomputed Delaunay triangulation.

values : ndarray of float or complex, shape (npoints, ...)
Data values.

fill_value : float, optional
Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`.

tol : float, optional
Absolute/relative tolerance for gradient estimation.

maxiter : int, optional
Maximum number of iterations in gradient estimation.

rescale : bool, optional
Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

Notes

The interpolant is constructed by triangulating the input data with Qhull [R43], and constructing a piecewise cubic interpolating Bezier polynomial on each triangle, using a Clough-Tocher scheme [CT]. The interpolant is guaranteed to be continuously differentiable.

The gradients of the interpolant are chosen so that the curvature of the interpolating surface is approximatively minimized. The gradients necessary for this are estimated using the global algorithm described in [Nielson83,Renka84]_.

References

[R43], [CT], [Nielson83], [Renka84]

Methods

`__call__`(xi)	Evaluate interpolator at given points.

`CloughTocher2DInterpolator.`**`__call__`**(*xi*)
Evaluate interpolator at given points.

Parameters

xi : ndarray of float, shape (..., ndim)
Points where to interpolate data at.

class `scipy.interpolate.`**`Rbf`**(**args*)
A class for radial basis function approximation/interpolation of n-dimensional scattered data.

Parameters

***args** : arrays
x, y, z, ..., d, where x, y, z, ... are the coordinates of the nodes and d is the array of values at the nodes

function : str or callable, optional
The radial basis function, based on the radius, r, given by the norm (default is Euclidean distance); the default is 'multiquadric':

```
'multiquadric': sqrt((r/self.epsilon)**2 + 1)
'inverse': 1.0/sqrt((r/self.epsilon)**2 + 1)
'gaussian': exp(-(r/self.epsilon)**2)
'linear': r
'cubic': r**3
```

```
'quintic': r**5
'thin_plate': r**2 * log(r)
```

If callable, then it must take 2 arguments (self, r). The epsilon parameter will be available as self.epsilon. Other keyword arguments passed in will be available as well.

epsilon : float, optional
Adjustable constant for gaussian or multiquadrics functions - defaults to approximate average distance between nodes (which is a good start).

smooth : float, optional
Values greater than zero increase the smoothness of the approximation. 0 is for interpolation (default), the function will always go through the nodal points in this case.

norm : callable, optional
A function that returns the 'distance' between two points, with inputs as arrays of positions (x, y, z, ...), and an output as an array of distance. E.g, the default:

```
def euclidean_norm(x1, x2):
    return sqrt( ((x1 - x2)**2).sum(axis=0) )
```

which is called with x1=x1[ndims,newaxis,:] and x2=x2[ndims,:,newaxis] such that the result is a matrix of the distances from each point in x1 to each point in x2.

Examples

```
>>> rbfi = Rbf(x, y, z, d)  # radial basis function interpolator instance
>>> di = rbfi(xi, yi, zi)   # interpolated values
```

Methods

`__call__`(*args)	

`Rbf.`**`__call__`**`(`**args*`)`

class `scipy.interpolate.`**`interp2d`**`(`*x, y, z, kind='linear', copy=True, bounds_error=False, fill_value=nan*`)`

Interpolate over a 2-D grid.

x, *y* and *z* are arrays of values used to approximate some function f: `z = f(x, y)`. This class returns a function whose call method uses spline interpolation to find the value of new points.

If *x* and *y* represent a regular grid, consider using RectBivariateSpline.

Parameters

x, y : array_like
Arrays defining the data point coordinates.
If the points lie on a regular grid, *x* can specify the column coordinates and *y* the row coordinates, for example:

```
>>> x = [0,1,2];  y = [0,3]; z = [[1,2,3], [4,5,6]]
```

Otherwise, *x* and *y* must specify the full coordinates for each point, for example:

```
>>> x = [0,1,2,0,1,2];  y = [0,0,0,3,3,3]; z = [1,2,3,4,5,6]
```

If *x* and *y* are multi-dimensional, they are flattened before use.

z : array_like
The values of the function to interpolate at the data points. If *z* is a multi-dimensional array, it is flattened before use. The length of a flattened *z* array is either len(*x*)*len(*y*) if *x* and *y* specify the column and row coordinates or `len(z) == len(x) == len(y)` if *x* and *y* specify coordinates for each point.

kind : {‘linear’, ‘cubic’, ‘quintic’}, optional
The kind of spline interpolation to use. Default is ‘linear’.

copy : bool, optional
If True, the class makes internal copies of x, y and z. If False, references may be used. The default is to copy.

bounds_error : bool, optional
If True, when interpolated values are requested outside of the domain of the input data (x,y), a ValueError is raised. If False, then *fill_value* is used.

fill_value : number, optional
If provided, the value to use for points outside of the interpolation domain. If omitted (None), values outside the domain are extrapolated.

Returns **values_x** : ndarray, shape xi.shape[:-1] + values.shape[ndim:]
Interpolated values at input coordinates.

See also:

`RectBivariateSpline`
Much faster 2D interpolation if your input data is on a grid

`bisplrep`, `bisplev`

`BivariateSpline`
a more recent wrapper of the FITPACK routines

`interp1d` one dimension version of this function

Notes

The minimum number of data points required along the interpolation axis is `(k+1)**2`, with k=1 for linear, k=3 for cubic and k=5 for quintic interpolation.

The interpolator is constructed by `bisplrep`, with a smoothing factor of 0. If more control over smoothing is needed, `bisplrep` should be used directly.

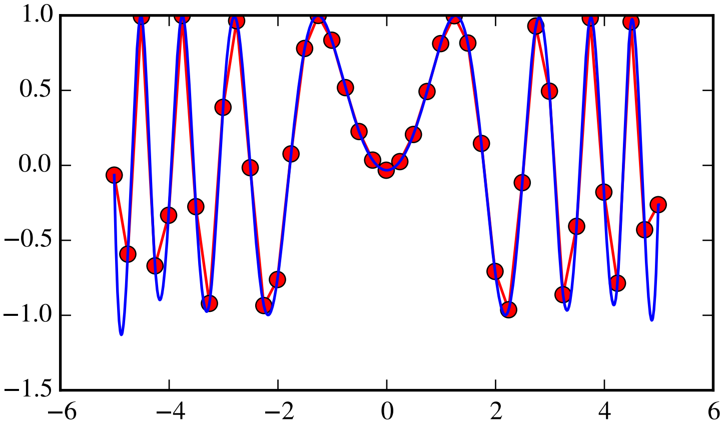
Examples

Construct a 2-D grid and interpolate on it:

```
>>> from scipy import interpolate
>>> x = np.arange(-5.01, 5.01, 0.25)
>>> y = np.arange(-5.01, 5.01, 0.25)
>>> xx, yy = np.meshgrid(x, y)
>>> z = np.sin(xx**2+yy**2)
>>> f = interpolate.interp2d(x, y, z, kind='cubic')
```

Now use the obtained interpolation function and plot the result:

```
>>> import matplotlib.pyplot as plt
>>> xnew = np.arange(-5.01, 5.01, 1e-2)
>>> ynew = np.arange(-5.01, 5.01, 1e-2)
>>> znew = f(xnew, ynew)
>>> plt.plot(x, z[0, :], 'ro-', xnew, znew[0, :], 'b-')
>>> plt.show()
```



Methods

`__call__`(x, y[, dx, dy, assume_sorted])	Interpolate the function.

`interp2d.`**`__call__`**(*x*, *y*, *dx=0*, *dy=0*, *assume_sorted=False*)

Interpolate the function.

Parameters **x** : 1D array
x-coordinates of the mesh on which to interpolate.

y : 1D array
y-coordinates of the mesh on which to interpolate.

dx : int >= 0, < kx
Order of partial derivatives in x.

dy : int >= 0, < ky
Order of partial derivatives in y.

assume_sorted : bool, optional
If False, values of *x* and *y* can be in any order and they are sorted first. If True, *x* and *y* have to be arrays of monotonically increasing values.

Returns **z** : 2D array with shape (len(y), len(x))
The interpolated values.

For data on a grid:

`interpn`(points, values, xi[, method, ...])	Multidimensional interpolation on regular grids.
`RegularGridInterpolator`(points, values[, ...])	Interpolation on a regular grid in arbitrary dimensions
`RectBivariateSpline`(x, y, z[, bbox, kx, ky, s])	Bivariate spline approximation over a rectangular mesh.

`scipy.interpolate.`**`interpn`**(*points*, *values*, *xi*, *method='linear'*, *bounds_error=True*, *fill_value=nan*)

Multidimensional interpolation on regular grids.

Parameters **points** : tuple of ndarray of float, with shapes (m1,), ..., (mn,)
The points defining the regular grid in n dimensions.

values : array_like, shape (m1, ..., mn, ...)
The data on the regular grid in n dimensions.

	xi : ndarray of shape (..., ndim) The coordinates to sample the gridded data at **method** : str, optional The method of interpolation to perform. Supported are “linear” and “nearest”, and “splinef2d”. “splinef2d” is only supported for 2-dimensional data. **bounds_error** : bool, optional If True, when interpolated values are requested outside of the domain of the input data, a ValueError is raised. If False, then *fill_value* is used. **fill_value** : number, optional If provided, the value to use for points outside of the interpolation domain. If None, values outside the domain are extrapolated. Extrapolation is not supported by method “splinef2d”.
Returns	**values_x** : ndarray, shape xi.shape[:-1] + values.shape[ndim:] Interpolated values at input coordinates.

See also:

`NearestNDInterpolator`
Nearest neighbour interpolation on unstructured data in N dimensions

`LinearNDInterpolator`
Piecewise linear interpolant on unstructured data in N dimensions

`RegularGridInterpolator`
Linear and nearest-neighbor Interpolation on a regular grid in arbitrary dimensions

`RectBivariateSpline`
Bivariate spline approximation over a rectangular mesh

Notes

New in version 0.14.

class `scipy.interpolate.`**`RegularGridInterpolator`**(*points*, *values*, *method='linear'*, *bounds_error=True*, *fill_value=nan*)

Interpolation on a regular grid in arbitrary dimensions

The data must be defined on a regular grid; the grid spacing however may be uneven. Linear and nearest-neighbour interpolation are supported. After setting up the interpolator object, the interpolation method (*linear* or *nearest*) may be chosen at each evaluation.

Parameters	**points** : tuple of ndarray of float, with shapes (m1,), ..., (mn,) The points defining the regular grid in n dimensions. **values** : array_like, shape (m1, ..., mn, ...) The data on the regular grid in n dimensions. **method** : str, optional The method of interpolation to perform. Supported are “linear” and “nearest”. This parameter will become the default for the object’s `__call__` method. Default is “linear”. **bounds_error** : bool, optional If True, when interpolated values are requested outside of the domain of the input data, a ValueError is raised. If False, then *fill_value* is used. **fill_value** : number, optional If provided, the value to use for points outside of the interpolation domain. If None, values outside the domain are extrapolated.

See also:

`NearestNDInterpolator`
Nearest neighbour interpolation on unstructured data in N dimensions

`LinearNDInterpolator`
Piecewise linear interpolant on unstructured data in N dimensions

Notes

Contrary to LinearNDInterpolator and NearestNDInterpolator, this class avoids expensive triangulation of the input data by taking advantage of the regular grid structure.

New in version 0.14.

References

[R46], [R47], [R48]

Examples

Evaluate a simple example function on the points of a 3D grid:

```
>>> from scipy.interpolate import RegularGridInterpolator
>>> def f(x,y,z):
...     return 2 * x**3 + 3 * y**2 - z
>>> x = np.linspace(1, 4, 11)
>>> y = np.linspace(4, 7, 22)
>>> z = np.linspace(7, 9, 33)
>>> data = f(*np.meshgrid(x, y, z, indexing='ij', sparse=True))
```

`data` is now a 3D array with `data[i,j,k] = f(x[i], y[j], z[k])`. Next, define an interpolating function from this data:

```
>>> my_interpolating_function = RegularGridInterpolator((x, y, z), data)
```

Evaluate the interpolating function at the two points `(x,y,z) = (2.1, 6.2, 8.3)` and `(3.3, 5.2, 7.1)`:

```
>>> pts = np.array([[2.1, 6.2, 8.3], [3.3, 5.2, 7.1]])
>>> my_interpolating_function(pts)
array([ 125.80469388,  146.30069388])
```

which is indeed a close approximation to `[f(2.1, 6.2, 8.3), f(3.3, 5.2, 7.1)]`.

Methods

`__call__`(xi[, method])	Interpolation at coordinates

`RegularGridInterpolator.`**`__call__`**(*xi, method=None*)
Interpolation at coordinates

Parameters **xi** : ndarray of shape (..., ndim)
The coordinates to sample the gridded data at
method : str
The method of interpolation to perform. Supported are “linear” and “nearest”.

class `scipy.interpolate.`**`RectBivariateSpline`**(*x, y, z, bbox=[None, None, None, None], kx=3, ky=3, s=0*)

Bivariate spline approximation over a rectangular mesh.

Can be used for both smoothing and interpolating data.

Parameters **x,y** : array_like

1-D arrays of coordinates in strictly ascending order.

z : array_like

2-D array of data with shape (x.size,y.size).

bbox : array_like, optional

Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x,tx),max(x,tx), min(y,ty),max(y,ty)]`.

kx, ky : ints, optional

Degrees of the bivariate spline. Default is 3.

s : float, optional

Positive smoothing factor defined for estimation condition: `sum((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) <= s` Default is `s=0`, which is for interpolation.

See also:

`SmoothBivariateSpline`
a smoothing bivariate spline for scattered data

`bisplrep` an older wrapping of FITPACK

`bisplev` an older wrapping of FITPACK

`UnivariateSpline`
a similar class for univariate spline interpolation

Methods

`__call__`(x, y[, mth, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(xi, yi[, dx, dy])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-var
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

`RectBivariateSpline.`**`__call__`**(*x*, *y*, *mth=None*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **x, y** : array_like

Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.

dx : int

Order of x-derivative
New in version 0.14.0.

dy : int

Order of y-derivative
New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

mth : str
Deprecated argument. Has no effect.

`RectBivariateSpline.`**`ev`**`(`*xi*, *yi*, *dx=0*, *dy=0*`)`
Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters **xi, yi** : array_like
Input coordinates. Standard Numpy broadcasting is obeyed.
dx : int, optional
Order of x-derivative
New in version 0.14.0.
dy : int, optional
Order of y-derivative
New in version 0.14.0.

`RectBivariateSpline.`**`get_coeffs`**`()`
Return spline coefficients.

`RectBivariateSpline.`**`get_knots`**`()`
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`RectBivariateSpline.`**`get_residual`**`()`
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

`RectBivariateSpline.`**`integral`**`(`*xa*, *xb*, *ya*, *yb*`)`
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters **xa, xb** : float
The end-points of the x integration interval.
ya, yb : float
The end-points of the y integration interval.
Returns **integ** : float
The value of the resulting integral.

See also:

`scipy.ndimage.interpolation.map_coordinates`

5.7.3 1-D Splines

`UnivariateSpline`(x, y[, w, bbox, k, s, ext, ...])	One-dimensional smoothing spline fit to a given set of data points.
`InterpolatedUnivariateSpline`(x, y[, w, ...])	One-dimensional interpolating spline for a given set of data points.
`LSQUnivariateSpline`(x, y, t[, w, bbox, k, ...])	One-dimensional spline with explicit internal knots.

class `scipy.interpolate.`**`UnivariateSpline`**`(`*x*, *y*, *w=None*, *bbox=[None, None]*, *k=3*, *s=None*, *ext=0*, *check_finite=False*`)`
One-dimensional smoothing spline fit to a given set of data points.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. `s` specifies the number of knots by specifying a smoothing condition.

Parameters **x** : (N,) array_like
1-D array of independent input data. Must be increasing.

y : (N,) array_like
: 1-D array of dependent input data, of the same length as *x*.

w : (N,) array_like, optional
: Weights for spline fitting. Must be positive. If None (default), weights are all equal.

bbox : (2,) array_like, optional
: 2-sequence specifying the boundary of the approximation interval. If None (default), `bbox=[x[0], x[-1]]`.

k : int, optional
: Degree of the smoothing spline. Must be <= 5. Default is k=3, a cubic spline.

s : float or None, optional
: Positive smoothing factor used to choose the number of knots. Number of knots will be increased until the smoothing condition is satisfied:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0) <= s
```

If None (default), `s = len(w)` which should be a good value if `1/w[i]` is an estimate of the standard deviation of `y[i]`. If 0, spline will interpolate through all data points.

ext : int or str, optional
: Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or ‘extrapolate’, return the extrapolated value.
- if ext=1 or ‘zeros’, return 0
- if ext=2 or ‘raise’, raise a ValueError
- if ext=3 of ‘const’, return the boundary value.

The default value is 0.

check_finite : bool, optional
: Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

`InterpolatedUnivariateSpline`	Subclass with smoothing forced to 0
`LSQUnivariateSpline`	Subclass in which knots are user-selected instead of being set by smoothing condition
`splrep`	An older, non object-oriented wrapping of FITPACK

`splev`, `sproot`, `splint`, `spalde`

`BivariateSpline`	A similar class for two-dimensional spline interpolation

Notes

The number of data points must be larger than the spline degree *k*.

NaN handling: If the input arrays contain `nan` values, the result is not useful, since the underlying spline fitting routines cannot deal with `nan` . A workaround is to use zero weights for not-a-number data points:

```
>>> w = np.isnan(y)
>>> y[w] = 0.
>>> spl = UnivariateSpline(x, y, w=~w)
```

Notice the need to replace a `nan` by a numerical value (precise value does not matter as long as the corresponding weight is zero.)

Examples

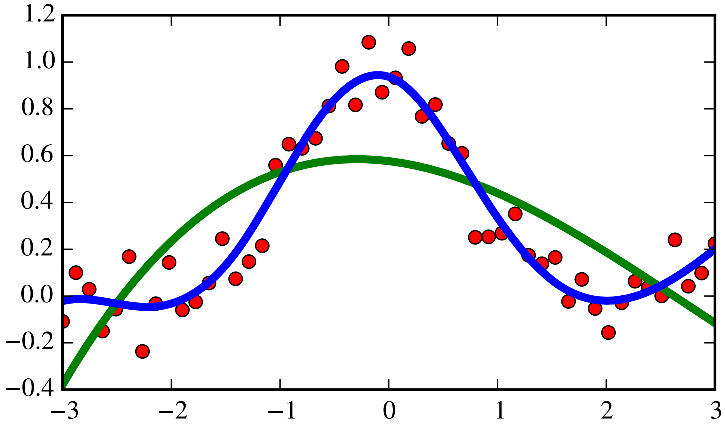
```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)
>>> plt.plot(x, y, 'ro', ms=5)
```

Use the default value for the smoothing parameter:

```
>>> spl = UnivariateSpline(x, y)
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(xs, spl(xs), 'g', lw=3)
```

Manually change the amount of smoothing:

```
>>> spl.set_smoothing_factor(0.5)
>>> plt.plot(xs, spl(xs), 'b', lw=3)
>>> plt.show()
```



Methods

`__call__`(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
`antiderivative`([n])	Construct a new spline representing the antiderivative of this spline.
`derivative`([n])	Construct a new spline representing the derivative of this spline.
`derivatives`(x)	Return all derivatives of the spline at the point x.
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return positions of interior knots of the spline.
`get_residual`()	Return weighted sum of squared residuals of the spline approximation.
`integral`(a, b)	Return definite integral of the spline between two given points.
`roots`()	Return the zeros of the spline.
`set_smoothing_factor`(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last

`UnivariateSpline.`**`__call__`**(*x*, *nu=0*, *ext=None*)

Evaluate spline (or its nu-th derivative) at positions x.

Parameters **x** : array_like

A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: `x` can be unordered but the evaluation is more efficient if `x` is (partially) ordered.

nu : int

The order of derivative of the spline to compute.

ext : int

Controls the value returned for elements of `x` not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 or 'const', return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

`UnivariateSpline.`**`antiderivative`**`(n=1)`

Construct a new spline representing the antiderivative of this spline.

Parameters **n** : int, optional

Order of antiderivative to evaluate. Default: 1

Returns **spline** : UnivariateSpline

Spline of order k2=k+n representing the antiderivative of this spline.

See also:

`splantider`, `derivative`

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

`UnivariateSpline.`**`derivative`**`(n=1)`

Construct a new spline representing the derivative of this spline.

Parameters **n** : int, optional

Order of derivative to evaluate. Default: 1

Returns **spline** : UnivariateSpline
Spline of order k2=k-n representing the derivative of this spline.

See also:

`splder`, `antiderivative`

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: `sproot` only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of *cos(x) = sin'(x)*.

`UnivariateSpline.`**`derivatives`**`(`*x*`)`

Return all derivatives of the spline at the point x.

Parameters **x** : float
The point to evaluate the derivatives at.

Returns **der** : ndarray, shape(k+1,)
Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

`UnivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`UnivariateSpline.`**`get_knots`**`()`

Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

`UnivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

`UnivariateSpline.`**`integral`**`(`*a*, *b*`)`

Return definite integral of the spline between two given points.

Parameters **a** : float
Lower limit of integration.
b : float
Upper limit of integration.

Returns **integral** : float
The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

`UnivariateSpline.`**`roots`**`()`

Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

`UnivariateSpline.`**`set_smoothing_factor`**`(`*s*`)`

Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

class `scipy.interpolate.`**`InterpolatedUnivariateSpline`**`(`*x, y, w=None, bbox=[None, None], k=3, ext=0, check_finite=False*`)`

One-dimensional interpolating spline for a given set of data points.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. Spline function passes through all provided points. Equivalent to `UnivariateSpline` with s=0.

Parameters **x** : (N,) array_like
Input dimension of data points – must be increasing
y : (N,) array_like
input dimension of data points
w : (N,) array_like, optional
Weights for spline fitting. Must be positive. If None (default), weights are all equal.
bbox : (2,) array_like, optional
2-sequence specifying the boundary of the approximation interval. If None (default), `bbox=[x[0], x[-1]]`.
k : int, optional
Degree of the smoothing spline. Must be 1 <= *k* <= 5.
ext : int or str, optional
Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 of 'const', return the boundary value.

The default value is 0.

check_finite : bool, optional

Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

`UnivariateSpline`	Superclass – allows knots to be selected by a smoothing condition
`LSQUnivariateSpline`	spline for which knots are user-selected
`splrep`	An older, non object-oriented wrapping of FITPACK

`splev`, `sproot`, `splint`, `spalde`

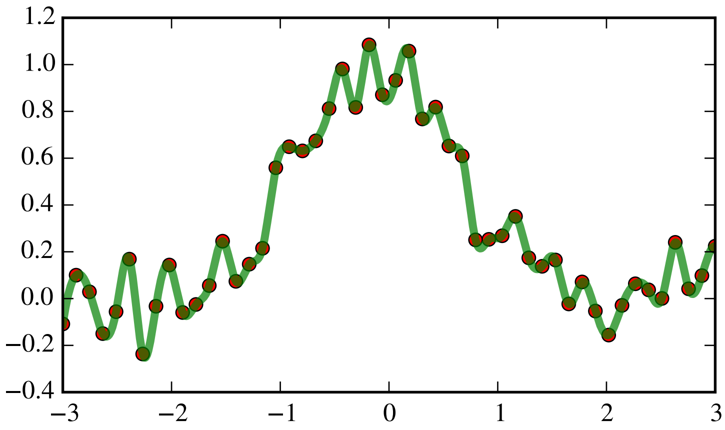
`BivariateSpline`	A similar class for two-dimensional spline interpolation

Notes

The number of data points must be larger than the spline degree *k*.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import InterpolatedUnivariateSpline
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)
>>> spl = InterpolatedUnivariateSpline(x, y)
>>> plt.plot(x, y, 'ro', ms=5)
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(xs, spl(xs), 'g', lw=3, alpha=0.7)
>>> plt.show()
```



Notice that the `spl(x)` interpolates *y*:

```
>>> spl.get_residual()
0.0
```

Methods

`__call__`(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
`antiderivative`([n])	Construct a new spline representing the antiderivative of this spline.
`derivative`([n])	Construct a new spline representing the derivative of this spline.
`derivatives`(x)	Return all derivatives of the spline at the point x.
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return positions of interior knots of the spline.
`get_residual`()	Return weighted sum of squared residuals of the spline approximation.
`integral`(a, b)	Return definite integral of the spline between two given points.
`roots`()	Return the zeros of the spline.
`set_smoothing_factor`(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last

`InterpolatedUnivariateSpline.`**`__call__`**(*x*, *nu=0*, *ext=None*)

Evaluate spline (or its nu-th derivative) at positions x.

Parameters **x** : array_like

A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

nu : int

The order of derivative of the spline to compute.

ext : int

Controls the value returned for elements of `x` not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 or 'const', return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

`InterpolatedUnivariateSpline.`**`antiderivative`**(*n=1*)

Construct a new spline representing the antiderivative of this spline.

Parameters **n** : int, optional

Order of antiderivative to evaluate. Default: 1

Returns **spline** : UnivariateSpline

Spline of order k2=k+n representing the antiderivative of this spline.

See also:

`splantider`, `derivative`

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

`InterpolatedUnivariateSpline.`**`derivative`**`(`*n=1*`)`

Construct a new spline representing the derivative of this spline.

Parameters **n** : int, optional

Order of derivative to evaluate. Default: 1

Returns **spline** : UnivariateSpline

Spline of order k2=k-n representing the derivative of this spline.

See also:

`splder`, `antiderivative`

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: `sproot` only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of *cos(x) = sin'(x)*.

`InterpolatedUnivariateSpline.`**`derivatives`**`(`*x*`)`

Return all derivatives of the spline at the point x.

Parameters **x** : float

The point to evaluate the derivatives at.

Returns **der** : ndarray, shape(k+1,)

Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

`InterpolatedUnivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`InterpolatedUnivariateSpline.`**`get_knots`**`()`

Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

`InterpolatedUnivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

`InterpolatedUnivariateSpline.`**`integral`**`(`*a*, *b*`)`

Return definite integral of the spline between two given points.

Parameters **a** : float

Lower limit of integration.

b : float

Upper limit of integration.

Returns **integral** : float

The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

`InterpolatedUnivariateSpline.`**`roots`**`()`

Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

`InterpolatedUnivariateSpline.`**`set_smoothing_factor`**`(`*s*`)`

Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

class `scipy.interpolate.`**`LSQUnivariateSpline`**(*x, y, t, w=None, bbox=[None, None], k=3, ext=0, check_finite=False*)

One-dimensional spline with explicit internal knots.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. *t* specifies the internal knots of the spline

Parameters

x : (N,) array_like
  Input dimension of data points – must be increasing

y : (N,) array_like
  Input dimension of data points

t : (M,) array_like
  interior knots of the spline. Must be in ascending order and:

```
bbox[0] < t[0] < ... < t[-1] < bbox[-1]
```

w : (N,) array_like, optional
  weights for spline fitting. Must be positive. If None (default), weights are all equal.

bbox : (2,) array_like, optional
  2-sequence specifying the boundary of the approximation interval. If None (default), `bbox = [x[0], x[-1]]`.

k : int, optional
  Degree of the smoothing spline. Must be 1 <= *k* <= 5. Default is k=3, a cubic spline.

ext : int or str, optional
  Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 of 'const', return the boundary value.

  The default value is 0.

check_finite : bool, optional
  Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

Raises

ValueError
  If the interior knots do not satisfy the Schoenberg-Whitney conditions

See also:

`UnivariateSpline`
  Superclass – knots are specified by setting a smoothing condition

`InterpolatedUnivariateSpline`
  spline passing through all points

`splrep` An older, non object-oriented wrapping of FITPACK

`splev`, `sproot`, `splint`, `spalde`

`BivariateSpline`
  A similar class for two-dimensional spline interpolation

Notes

The number of data points must be larger than the spline degree *k*.

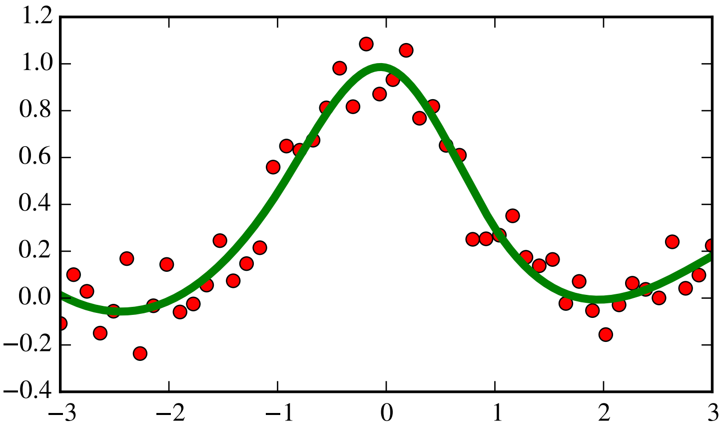
Knots *t* must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points `x[j]` such that `t[j] < x[j] < t[j+k+1]`, for `j=0, 1,...,n-k-2`.

Examples

```
>>> from scipy.interpolate import LSQUnivariateSpline
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)
```

Fit a smoothing spline with a pre-defined internal knots:

```
>>> t = [-1, 0, 1]
>>> spl = LSQUnivariateSpline(x, y, t)

>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(x, y, 'ro', ms=5)
>>> plt.plot(xs, spl(xs), 'g-', lw=3)
>>> plt.show()
```



Check the knot vector:

```
>>> spl.get_knots()
array([-3., -1., 0., 1., 3.])
```

Methods

`__call__`(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
`antiderivative`([n])	Construct a new spline representing the antiderivative of this spline.
`derivative`([n])	Construct a new spline representing the derivative of this spline.
`derivatives`(x)	Return all derivatives of the spline at the point x.
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return positions of interior knots of the spline.
`get_residual`()	Return weighted sum of squared residuals of the spline approximation.
`integral`(a, b)	Return definite integral of the spline between two given points.
`roots`()	Return the zeros of the spline.
`set_smoothing_factor`(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last

`LSQUnivariateSpline.`**`__call__`**`(`*x*, *nu=0*, *ext=None*`)`

Evaluate spline (or its nu-th derivative) at positions x.

Parameters **x** : array_like

A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

nu : int

The order of derivative of the spline to compute.

ext : int

Controls the value returned for elements of `x` not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 or 'const', return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

`LSQUnivariateSpline.`**`antiderivative`**`(`*n=1*`)`

Construct a new spline representing the antiderivative of this spline.

Parameters **n** : int, optional

Order of antiderivative to evaluate. Default: 1

Returns **spline** : UnivariateSpline

Spline of order k2=k+n representing the antiderivative of this spline.

See also:

`splantider`, `derivative`

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

`LSQUnivariateSpline.`**`derivative`**`(`*n=1*`)`

Construct a new spline representing the derivative of this spline.

Parameters	**n** : int, optional Order of derivative to evaluate. Default: 1
Returns	**spline** : UnivariateSpline Spline of order k2=k-n representing the derivative of this spline.

See also:

`splder`, `antiderivative`

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: `sproot` only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of *cos(x) = sin'(x)*.

`LSQUnivariateSpline.`**`derivatives`**`(x)`

Return all derivatives of the spline at the point x.

Parameters	**x** : float The point to evaluate the derivatives at.
Returns	**der** : ndarray, shape(k+1,) Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

`LSQUnivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`LSQUnivariateSpline.`**`get_knots`**`()`

Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

`LSQUnivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

`LSQUnivariateSpline.`**`integral`**`(`*a*, *b*`)`

Return definite integral of the spline between two given points.

Parameters	**a** : float Lower limit of integration. **b** : float Upper limit of integration.
Returns	**integral** : float The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

`LSQUnivariateSpline.`**`roots`**`()`

Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

`LSQUnivariateSpline.`**`set_smoothing_factor`**`(`*s*`)`

Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

Functional interface to FITPACK functions:

`splrep`(x, y[, w, xb, xe, k, task, s, t, ...])	Find the B-spline representation of 1-D curve.
`splprep`(x[, w, u, ub, ue, k, task, s, t, ...])	Find the B-spline representation of an N-dimensional curve.
`splev`(x, tck[, der, ext])	Evaluate a B-spline or its derivatives.
`splint`(a, b, tck[, full_output])	Evaluate the definite integral of a B-spline.
`sproot`(tck[, mest])	Find the roots of a cubic B-spline.
`spalde`(x, tck)	Evaluate all derivatives of a B-spline.
`splder`(tck[, n])	Compute the spline representation of the derivative of a given spline
`splantider`(tck[, n])	Compute the spline for the antiderivative (integral) of a given spline.

`scipy.interpolate.`**`splrep`**`(`*x*, *y*, *w=None*, *xb=None*, *xe=None*, *k=3*, *task=0*, *s=None*, *t=None*, *full_output=0*, *per=0*, *quiet=1*`)`

Find the B-spline representation of 1-D curve.

Given the set of data points `(x[i], y[i])` determine a smooth spline approximation of degree k on the interval `xb <= x <= xe`.

Parameters	**x, y** : array_like The data points defining a curve y = f(x). **w** : array_like, optional

Strictly positive rank-1 array of weights the same length as x and y. The weights are used in computing the weighted least-squares spline fit. If the errors in the y values have standard-deviation given by the vector d, then w should be 1/d. Default is ones(len(x)).

xb, xe : float, optional

The interval to fit. If None, these default to x[0] and x[-1] respectively.

k : int, optional

The order of the spline fit. It is recommended to use cubic splines. Even order splines should be avoided especially with small s values. 1 <= k <= 5

task : {1, 0, -1}, optional

If task==0 find t and c for a given smoothing factor, s.

If task==1 find t and c for another value of the smoothing factor, s. There must have been a previous call with task=0 or task=1 for the same set of data (t will be stored an used internally)

If task=-1 find the weighted least square spline for a given set of knots, t. These should be interior knots as knots on the ends will be added automatically.

s : float, optional

A smoothing condition. The amount of smoothness is determined by satisfying the conditions: sum((w * (y - g))**2,axis=0) <= s where g(x) is the smoothed interpolation of (x,y). The user can use s to control the tradeoff between closeness and smoothness of fit. Larger s means more smoothing while smaller values of s indicate less smoothing. Recommended values of s depend on the weights, w. If the weights represent the inverse of the standard-deviation of y, then a good s value should be found in the range (m-sqrt(2*m),m+sqrt(2*m)) where m is the number of datapoints in x, y, and w. default : s=m-sqrt(2*m) if weights are supplied. s = 0.0 (interpolating) if no weights are supplied.

t : array_like, optional

The knots needed for task=-1. If given then task is automatically set to -1.

full_output : bool, optional

If non-zero, then return optional outputs.

per : bool, optional

If non-zero, data points are considered periodic with period x[m-1] - x[0] and a smooth periodic spline approximation is returned. Values of y[m-1] and w[m-1] are not used.

quiet : bool, optional

Non-zero to suppress messages. This parameter is deprecated; use standard Python warning filters instead.

Returns **tck** : tuple

(t,c,k) a tuple containing the vector of knots, the B-spline coefficients, and the degree of the spline.

fp : array, optional

The weighted sum of squared residuals of the spline approximation.

ier : int, optional

An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

msg : str, optional

A message corresponding to the integer flag, ier.

See also:

`UnivariateSpline`, `BivariateSpline`, `splprep`, `splev`, `sproot`, `spalde`, `splint`, `bisplrep`, `bisplev`

Notes

See splev for evaluation of the spline and its derivatives. Uses the FORTRAN routine curfit from FITPACK.

If provided, knots *t* must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points `x[j]` such that `t[j] < x[j] < t[j+k+1]`, for `j=0, 1,...,n-k-2`.

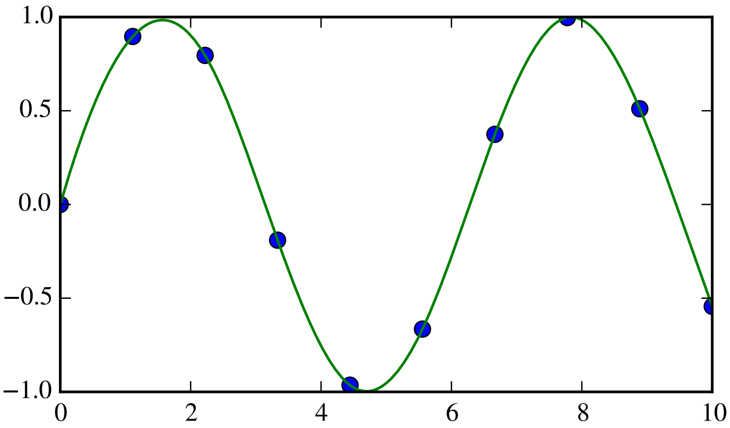
References

Based on algorithms described in [R66], [R67], [R68], and [R69]:

[R66], [R67], [R68], [R69]

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import splev, splrep
>>> x = np.linspace(0, 10, 10)
>>> y = np.sin(x)
>>> tck = splrep(x, y)
>>> x2 = np.linspace(0, 10, 200)
>>> y2 = splev(x2, tck)
>>> plt.plot(x, y, 'o', x2, y2)
>>> plt.show()
```



`scipy.interpolate.`**`splprep`**`(`*x*, *w=None*, *u=None*, *ub=None*, *ue=None*, *k=3*, *task=0*, *s=None*, *t=None*, *full_output=0*, *nest=None*, *per=0*, *quiet=1*`)`

Find the B-spline representation of an N-dimensional curve.

Given a list of N rank-1 arrays, *x*, which represent a curve in N-dimensional space parametrized by *u*, find a smooth approximating spline curve g(*u*). Uses the FORTRAN routine parcur from FITPACK.

Parameters

x : array_like

A list of sample vector arrays representing the curve.

w : array_like, optional

Strictly positive rank-1 array of weights the same length as *x[0]*. The weights are used in computing the weighted least-squares spline fit. If the errors in the *x* values have standard-deviation given by the vector d, then *w* should be 1/d. Default is `ones(len(x[0]))`.

u : array_like, optional

An array of parameter values. If not given, these values are calculated automatically as `M = len(x[0])`, where

v[0] = 0
v[i] = v[i-1] + distance(*x[i]*, *x[i-1]*)
u[i] = v[i] / v[M-1]

ub, ue : int, optional
The end-points of the parameters interval. Defaults to u[0] and u[-1].

k : int, optional
Degree of the spline. Cubic splines are recommended. Even values of *k* should be avoided especially with a small s-value. `1 <= k <= 5`, default is 3.

task : int, optional
If task==0 (default), find t and c for a given smoothing factor, s. If task==1, find t and c for another value of the smoothing factor, s. There must have been a previous call with task=0 or task=1 for the same set of data. If task=-1 find the weighted least square spline for a given set of knots, t.

s : float, optional
A smoothing condition. The amount of smoothness is determined by satisfying the conditions: `sum((w * (y - g))**2,axis=0) <= s`, where g(x) is the smoothed interpolation of (x,y). The user can use `s` to control the trade-off between closeness and smoothness of fit. Larger `s` means more smoothing while smaller values of `s` indicate less smoothing. Recommended values of `s` depend on the weights, w. If the weights represent the inverse of the standard-deviation of y, then a good `s` value should be found in the range `(m-sqrt(2*m),m+sqrt(2*m))`, where m is the number of data points in x, y, and w.

t : int, optional
The knots needed for task=-1.

full_output : int, optional
If non-zero, then return optional outputs.

nest : int, optional
An over-estimate of the total number of knots of the spline to help in determining the storage space. By default nest=m/2. Always large enough is nest=m+k+1.

per : int, optional
If non-zero, data points are considered periodic with period `x[m-1] - x[0]` and a smooth periodic spline approximation is returned. Values of `y[m-1]` and `w[m-1]` are not used.

quiet : int, optional
Non-zero to suppress messages. This parameter is deprecated; use standard Python warning filters instead.

Returns

tck : tuple
A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.

u : array
An array of the values of the parameter.

fp : float
The weighted sum of squared residuals of the spline approximation.

ier : int
An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

msg : str
A message corresponding to the integer flag, ier.

See also:

`splrep`, `splev`, `sproot`, `spalde`, `splint`, `bisplrep`, `bisplev`, `UnivariateSpline`, `BivariateSpline`

Notes

See `splev` for evaluation of the spline and its derivatives. The number of dimensions N must be smaller than 11.

References

[R63], [R64], [R65]

`scipy.interpolate.`**`splev`**(*x*, *tck*, *der=0*, *ext=0*)

Evaluate a B-spline or its derivatives.

Given the knots and coefficients of a B-spline representation, evaluate the value of the smoothing polynomial and its derivatives. This is a wrapper around the FORTRAN routines splev and splder of FITPACK.

Parameters **x** : array_like

An array of points at which to return the value of the smoothed spline or its derivatives. If *tck* was returned from `splprep`, then the parameter values, u should be given.

tck : tuple

A sequence of length 3 returned by `splrep` or `splprep` containing the knots, coefficients, and degree of the spline.

der : int, optional

The order of derivative of the spline to compute (must be less than or equal to k).

ext : int, optional

Controls the value returned for elements of `x` not in the interval defined by the knot sequence.

- if ext=0, return the extrapolated value.
- if ext=1, return 0
- if ext=2, raise a ValueError
- if ext=3, return the boundary value.

The default value is 0.

Returns **y** : ndarray or list of ndarrays

An array of values representing the spline function evaluated at the points in `x`. If *tck* was returned from `splprep`, then this is a list of arrays representing the curve in N-dimensional space.

See also:

`splprep`, `splrep`, `sproot`, `spalde`, `splint`, `bisplrep`, `bisplev`

References

[R58], [R59], [R60]

`scipy.interpolate.`**`splint`**(*a*, *b*, *tck*, *full_output=0*)

Evaluate the definite integral of a B-spline.

Given the knots and coefficients of a B-spline, evaluate the definite integral of the smoothing polynomial between two given points.

Parameters **a, b** : float

The end-points of the integration interval.

tck : tuple

A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline (see `splev`).

full_output : int, optional

Non-zero to return optional output.

Returns **integral** : float

The resulting integral.

wrk : ndarray

An array containing the integrals of the normalized B-splines defined on the set of knots.

See also:

`splprep`, `splrep`, `sproot`, `spalde`, `splev`, `bisplrep`, `bisplev`, `UnivariateSpline`, `BivariateSpline`

Notes

splint silently assumes that the spline function is zero outside the data interval (a, b).

References

[R61], [R62]

`scipy.interpolate.`**`sproot`**`(`*tck*, *mest=10*`)`

Find the roots of a cubic B-spline.

Given the knots (>=8) and coefficients of a cubic B-spline return the roots of the spline.

Parameters

tck : tuple

A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline. The number of knots must be >= 8, and the degree must be 3. The knots must be a montonically increasing sequence.

mest : int, optional

An estimate of the number of zeros (Default is 10).

Returns

zeros : ndarray

An array giving the roots of the spline.

See also:

`splprep`, `splrep`, `splint`, `spalde`, `splev`, `bisplrep`, `bisplev`, `UnivariateSpline`, `BivariateSpline`

References

[R70], [R71], [R72]

`scipy.interpolate.`**`spalde`**`(`*x*, *tck*`)`

Evaluate all derivatives of a B-spline.

Given the knots and coefficients of a cubic B-spline compute all derivatives up to order k at a point (or set of points).

Parameters

x : array_like

A point or a set of points at which to evaluate the derivatives. Note that `t(k) <= x <= t(n-k+1)` must hold for each *x*.

tck : tuple

A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.

Returns

results : {ndarray, list of ndarrays}

An array (or a list of arrays) containing all derivatives up to order k inclusive for each point *x*.

See also:

`splprep`, `splrep`, `splint`, `sproot`, `splev`, `bisplrep`, `bisplev`, `UnivariateSpline`, `BivariateSpline`

References

[R55], [R56], [R57]

`scipy.interpolate.`**`splder`**`(`*tck*, *n=1*`)`

Compute the spline representation of the derivative of a given spline

Parameters	**tck** : tuple of (t, c, k) Spline whose derivative to compute **n** : int, optional Order of derivative to evaluate. Default: 1
Returns	**tck_der** : tuple of (t2, c2, k2) Spline of order k2=k-n representing the derivative of the input spline.

See also:

`splantider`, `splev`, `spalde`

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import splrep, splder, sproot
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = splrep(x, y, k=4)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: `sproot` only works for order 3 splines, so we fit an order 4 spline):

```
>>> dspl = splder(spl)
>>> sproot(dspl) / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

`scipy.interpolate.`**`splantider`**`(`*tck*, *n=1*`)`

Compute the spline for the antiderivative (integral) of a given spline.

Parameters	**tck** : tuple of (t, c, k) Spline whose antiderivative to compute **n** : int, optional Order of antiderivative to evaluate. Default: 1
Returns	**tck_ader** : tuple of (t2, c2, k2) Spline of order k2=k+n representing the antiderivative of the input spline.

See also:

`splder`, `splev`, `spalde`

Notes

The `splder` function is the inverse operation of this function. Namely, `splder(splantider(tck))` is identical to *tck*, modulo rounding error.

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import splrep, splder, splantider, splev
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = splrep(x, y)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> splev(1.7, spl), splev(1.7, splder(splantider(spl)))
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = splantider(spl)
>>> splev(np.pi/2, ispl) - splev(0, ispl)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

5.7.4 2-D Splines

For data on a grid:

`RectBivariateSpline`(x, y, z[, bbox, kx, ky, s])	Bivariate spline approximation over a rectangular mesh.
`RectSphereBivariateSpline`(u, v, r[, s, ...])	Bivariate spline approximation over a rectangular mesh on a sphere.

class `scipy.interpolate.`**`RectBivariateSpline`**(*x, y, z, bbox=[None, None, None, None], kx=3, ky=3, s=0*)

Bivariate spline approximation over a rectangular mesh.

Can be used for both smoothing and interpolating data.

Parameters **x,y** : array_like

1-D arrays of coordinates in strictly ascending order.

z : array_like

2-D array of data with shape (x.size,y.size).

bbox : array_like, optional

Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x,tx),max(x,tx), min(y,ty),max(y,ty)]`.

kx, ky : ints, optional

Degrees of the bivariate spline. Default is 3.

s : float, optional

Positive smoothing factor defined for estimation condition: `sum((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) <= s` Default is `s=0`, which is for interpolation.

See also:

`SmoothBivariateSpline`
a smoothing bivariate spline for scattered data

bisplrep	an older wrapping of FITPACK
bisplev	an older wrapping of FITPACK
UnivariateSpline	a similar class for univariate spline interpolation

Methods

`__call__`(x, y[, mth, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(xi, yi[, dx, dy])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-var
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

`RectBivariateSpline.`**`__call__`**(*x*, *y*, *mth=None*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **x, y** : array_like

Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.

dx : int

Order of x-derivative
New in version 0.14.0.

dy : int

Order of y-derivative
New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

mth : str

Deprecated argument. Has no effect.

`RectBivariateSpline.`**`ev`**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters **xi, yi** : array_like

Input coordinates. Standard Numpy broadcasting is obeyed.

dx : int, optional

Order of x-derivative
New in version 0.14.0.

dy : int, optional

Order of y-derivative
New in version 0.14.0.

`RectBivariateSpline.`**`get_coeffs`**()

Return spline coefficients.

`RectBivariateSpline.`**`get_knots`**()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`RectBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

`RectBivariateSpline.`**`integral`**`(`*xa*, *xb*, *ya*, *yb*`)`

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb : float

The end-points of the x integration interval.

ya, yb : float

The end-points of the y integration interval.

Returns

integ : float

The value of the resulting integral.

class `scipy.interpolate.`**`RectSphereBivariateSpline`**`(`*u*, *v*, *r*, *s=0.0*, *pole_continuity=False*, *pole_values=None*, *pole_exact=False*, *pole_flat=False*`)`

Bivariate spline approximation over a rectangular mesh on a sphere.

Can be used for smoothing data.

New in version 0.11.0.

Parameters

u : array_like

1-D array of latitude coordinates in strictly ascending order. Coordinates must be given in radians and lie within the interval (0, pi).

v : array_like

1-D array of longitude coordinates in strictly ascending order. Coordinates must be given in radians, and must lie within (0, 2pi).

r : array_like

2-D array of data with shape `(u.size, v.size)`.

s : float, optional

Positive smoothing factor defined for estimation condition (`s=0` is for interpolation).

pole_continuity : bool or (bool, bool), optional

Order of continuity at the poles `u=0` (`pole_continuity[0]`) and `u=pi` (`pole_continuity[1]`). The order of continuity at the pole will be 1 or 0 when this is True or False, respectively. Defaults to False.

pole_values : float or (float, float), optional

Data values at the poles `u=0` and `u=pi`. Either the whole parameter or each individual element can be None. Defaults to None.

pole_exact : bool or (bool, bool), optional

Data value exactness at the poles `u=0` and `u=pi`. If True, the value is considered to be the right function value, and it will be fitted exactly. If False, the value will be considered to be a data value just like the other data values. Defaults to False.

pole_flat : bool or (bool, bool), optional

For the poles at `u=0` and `u=pi`, specify whether or not the approximation has vanishing derivatives. Defaults to False.

See also:

`RectBivariateSpline`

bivariate spline approximation over a rectangular mesh

Notes

Currently, only the smoothing spline approximation (`iopt[0] = 0` and `iopt[0] = 1` in the FITPACK routine) is supported. The exact least-squares spline approximation is not implemented yet.

When actually performing the interpolation, the requested *v* values must lie within the same length 2pi interval that the original *v* values were chosen from.

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid

```
>>> lats = np.linspace(10, 170, 9) * np.pi / 180.
>>> lons = np.linspace(0, 350, 18) * np.pi / 180.
>>> data = np.dot(np.atleast_2d(90. - np.linspace(-80., 80., 18)).T,
...               np.atleast_2d(180. - np.abs(np.linspace(0., 350., 9)))).T
```

We want to interpolate it to a global one-degree grid

```
>>> new_lats = np.linspace(1, 180, 180) * np.pi / 180
>>> new_lons = np.linspace(1, 360, 360) * np.pi / 180
>>> new_lats, new_lons = np.meshgrid(new_lats, new_lons)
```

We need to set up the interpolator object

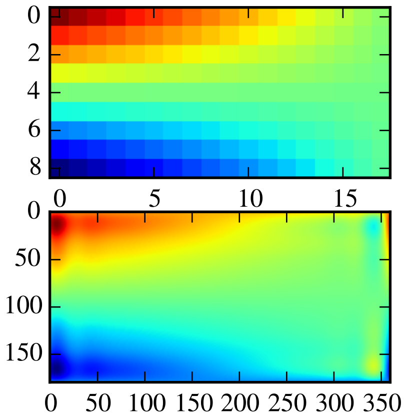
```
>>> from scipy.interpolate import RectSphereBivariateSpline
>>> lut = RectSphereBivariateSpline(lats, lons, data)
```

Finally we interpolate the data. The `RectSphereBivariateSpline` object only takes 1-D arrays as input, therefore we need to do some reshaping.

```
>>> data_interp = lut.ev(new_lats.ravel(),
...                      new_lons.ravel()).reshape((360, 180)).T
```

Looking at the original and the interpolated data, one can see that the interpolant reproduces the original data very well:

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(212)
>>> ax2.imshow(data_interp, interpolation='nearest')
>>> plt.show()
```

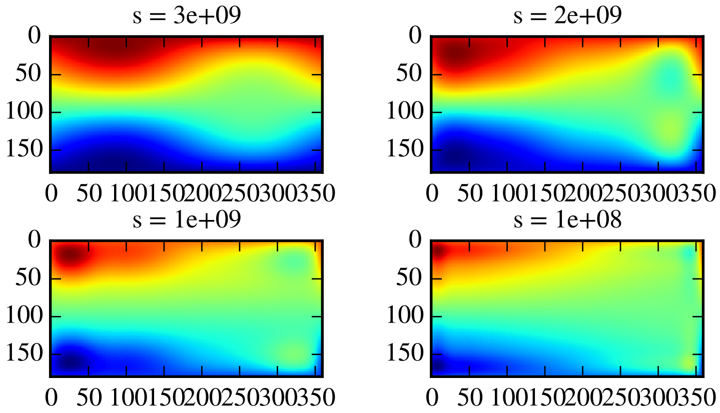


Chosing the optimal value of `s` can be a delicate task. Recommended values for `s` depend on the accuracy of the data values. If the user has an idea of the statistical errors on the data, she can also find a proper estimate for `s`. By assuming that, if she specifies the right `s`, the interpolator will use a spline `f(u,v)` which exactly reproduces the function underlying the data, she can evaluate `sum((r(i,j)-s(u(i),v(j)))**2)` to find a good estimate for this `s`. For example, if she knows that the statistical errors on her `r(i,j)`-values are not greater than 0.1, she may expect that a good `s` should have a value not larger than `u.size * v.size * (0.1)**2`.

If nothing is known about the statistical error in `r(i,j)`, `s` must be determined by trial and error. The best is then to start with a very large value of `s` (to determine the least-squares polynomial and the corresponding upper bound `fp0` for `s`) and then to progressively decrease the value of `s` (say by a factor 10 in the beginning, i.e. `s = fp0 / 10, fp0 / 100, ...` and more carefully as the approximation shows more detail) to obtain closer fits.

The interpolation results for different values of `s` give some insight into this process:

```
>>> fig2 = plt.figure()
>>> s = [3e9, 2e9, 1e9, 1e8]
>>> for ii in xrange(len(s)):
...     lut = RectSphereBivariateSpline(lats, lons, data, s=s[ii])
...     data_interp = lut.ev(new_lats.ravel(),
...                          new_lons.ravel()).reshape((360, 180)).T
...     ax = fig2.add_subplot(2, 2, ii+1)
...     ax.imshow(data_interp, interpolation='nearest')
...     ax.set_title("s = %g" % s[ii])
>>> plt.show()
```



Methods

`__call__`(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(theta, phi[, dtheta, dphi])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-,
`get_residual`()	Return weighted sum of squared residuals of the spline

`RectSphereBivariateSpline.`**`__call__`**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **theta, phi** : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta : int, optional

Order of theta-derivative

New in version 0.14.0.

dphi : int

Order of phi-derivative

New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.

New in version 0.14.0.

`RectSphereBivariateSpline.`**`ev`**(*theta*, *phi*, *dtheta=0*, *dphi=0*)

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters **theta, phi** : array_like

Input coordinates. Standard Numpy broadcasting is obeyed.

dtheta : int, optional

Order of theta-derivative

New in version 0.14.0.

dphi : int, optional

Order of phi-derivative

New in version 0.14.0.

`RectSphereBivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`RectSphereBivariateSpline.`**`get_knots`**`()`

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`RectSphereBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

For unstructured data:

`BivariateSpline`	Base class for bivariate splines.
`SmoothBivariateSpline`(x, y, z[, w, bbox, ...])	Smooth bivariate spline approximation.
`SmoothSphereBivariateSpline`(theta, phi, r[, ...])	Smooth bivariate spline approximation in spherical coordinates.
`LSQBivariateSpline`(x, y, z, tx, ty[, w, ...])	Weighted least-squares bivariate spline approximation.
`LSQSphereBivariateSpline`(theta, phi, r, tt, tp)	Weighted least-squares bivariate spline approximation in spherical coord

class `scipy.interpolate.`**`BivariateSpline`**

Base class for bivariate splines.

This describes a spline `s(x, y)` of degrees `kx` and `ky` on the rectangle `[xb, xe] * [yb, ye]` calculated from a given set of data points `(x, y, z)`.

This class is meant to be subclassed, not instantiated directly. To construct these splines, call either `SmoothBivariateSpline` or `LSQBivariateSpline`.

See also:

`UnivariateSpline`
a similar class for univariate spline interpolation

`SmoothBivariateSpline`
to create a BivariateSpline through the given points

`LSQBivariateSpline`
to create a BivariateSpline using weighted least-squares fitting

`SphereBivariateSpline`
bivariate spline interpolation in spherical cooridinates

`bisplrep` older wrapping of FITPACK

`bisplev` older wrapping of FITPACK

Methods

`__call__`(x, y[, mth, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(xi, yi[, dx, dy])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.

Continu

Table 5.50 – continued from previous page

`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-var
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

`BivariateSpline.`**`__call__`**(*x*, *y*, *mth=None*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **x, y** : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.

dx : int

Order of x-derivative

New in version 0.14.0.

dy : int

Order of y-derivative

New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.

New in version 0.14.0.

mth : str

Deprecated argument. Has no effect.

`BivariateSpline.`**`ev`**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters **xi, yi** : array_like

Input coordinates. Standard Numpy broadcasting is obeyed.

dx : int, optional

Order of x-derivative

New in version 0.14.0.

dy : int, optional

Order of y-derivative

New in version 0.14.0.

`BivariateSpline.`**`get_coeffs`**()

Return spline coefficients.

`BivariateSpline.`**`get_knots`**()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`BivariateSpline.`**`get_residual`**()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

`BivariateSpline.`**`integral`**(*xa*, *xb*, *ya*, *yb*)

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters **xa, xb** : float

The end-points of the x integration interval.

ya, yb : float
The end-points of the y integration interval.

Returns **integ** : float
The value of the resulting integral.

class `scipy.interpolate.`**`SmoothBivariateSpline`**(*x, y, z, w=None, bbox=[None, None, None, None], kx=3, ky=3, s=None, eps=None*)

Smooth bivariate spline approximation.

Parameters **x, y, z** : array_like
1-D sequences of data points (order is not important).

w : array_like, optional
Positive 1-D sequence of weights, of same length as *x*, *y* and *z*.

bbox : array_like, optional
Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x,tx),max(x,tx), min(y,ty),max(y,ty)]`.

kx, ky : ints, optional
Degrees of the bivariate spline. Default is 3.

s : float, optional
Positive smoothing factor defined for estimation condition: `sum((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) <= s` Default `s=len(w)` which should be a good value if `1/w[i]` is an estimate of the standard deviation of `z[i]`.

eps : float, optional
A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value between 0 and 1, the default is 1e-16.

See also:

`bisplrep`	an older wrapping of FITPACK
`bisplev`	an older wrapping of FITPACK
`UnivariateSpline`	a similar class for univariate spline interpolation
`LSQUnivariateSpline`	to create a BivariateSpline using weighted

Notes

The length of *x*, *y* and *z* should be at least `(kx+1) * (ky+1)`.

Methods

`__call__`(x, y[, mth, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(xi, yi[, dx, dy])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-var
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

`SmoothBivariateSpline.`**`__call__`**(*x*, *y*, *mth=None*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **x, y** : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.

dx : int

Order of x-derivative

New in version 0.14.0.

dy : int

Order of y-derivative

New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.

New in version 0.14.0.

mth : str

Deprecated argument. Has no effect.

`SmoothBivariateSpline.`**`ev`**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters **xi, yi** : array_like

Input coordinates. Standard Numpy broadcasting is obeyed.

dx : int, optional

Order of x-derivative

New in version 0.14.0.

dy : int, optional

Order of y-derivative

New in version 0.14.0.

`SmoothBivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`SmoothBivariateSpline.`**`get_knots`**`()`

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`SmoothBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

`SmoothBivariateSpline.`**`integral`**(*xa*, *xb*, *ya*, *yb*)

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters **xa, xb** : float

The end-points of the x integration interval.

ya, yb : float

The end-points of the y integration interval.

Returns **integ** : float

The value of the resulting integral.

class `scipy.interpolate.`**`SmoothSphereBivariateSpline`**(*theta*, *phi*, *r*, *w=None*, *s=0.0*, *eps=1e-16*)

Smooth bivariate spline approximation in spherical coordinates.

New in version 0.11.0.

Parameters **theta, phi, r** : array_like

1-D sequences of data points (order is not important). Coordinates must be given in radians. Theta must lie within the interval (0, pi), and phi must lie within the interval (0, 2pi).

w : array_like, optional

Positive 1-D sequence of weights.

s : float, optional

Positive smoothing factor defined for estimation condition: `sum((w(i)*(r(i) - s(theta(i), phi(i))))**2, axis=0) <= s` Default `s=len(w)` which should be a good value if 1/w[i] is an estimate of the standard deviation of r[i].

eps : float, optional

A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value between 0 and 1, the default is 1e-16.

Notes

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

```
>>> theta = np.linspace(0., np.pi, 7)
>>> phi = np.linspace(0., 2*np.pi, 9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
>>> data[1,1:-1], data[-2,1:-1] = 1., 1.
>>> data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[2,2:-2], data[-3,2:-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)
```

We need to set up the interpolator object

```
>>> lats, lons = np.meshgrid(theta, phi)
>>> from scipy.interpolate import SmoothSphereBivariateSpline
>>> lut = SmoothSphereBivariateSpline(lats.ravel(), lons.ravel(),
...                                   data.T.ravel(), s=3.5)
```

As a first test, we'll see what the algorithm returns when run on the input coordinates

```
>>> data_orig = lut(theta, phi)
```

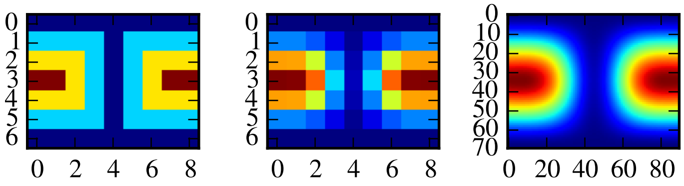
Finally we interpolate the data to a finer grid

```
>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2 * np.pi, 90)
```

```
>>> data_smth = lut(fine_lats, fine_lons)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(data_orig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)
```

```
>>> ax3.imshow(data_smth, interpolation='nearest')
>>> plt.show()
```



Methods

`__call__`(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(theta, phi[, dtheta, dphi])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-,
`get_residual`()	Return weighted sum of squared residuals of the spline

`SmoothSphereBivariateSpline.`**`__call__`**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

theta, phi : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta : int, optional

Order of theta-derivative

New in version 0.14.0.

dphi : int

Order of phi-derivative

New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.

New in version 0.14.0.

`SmoothSphereBivariateSpline.`**`ev`**(*theta*, *phi*, *dtheta=0*, *dphi=0*)

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters	**theta, phi** : array_like Input coordinates. Standard Numpy broadcasting is obeyed. **dtheta** : int, optional Order of theta-derivative New in version 0.14.0. **dphi** : int, optional Order of phi-derivative New in version 0.14.0.

`SmoothSphereBivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`SmoothSphereBivariateSpline.`**`get_knots`**`()`

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`SmoothSphereBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

class `scipy.interpolate.`**`LSQBivariateSpline`**(*x, y, z, tx, ty, w=None, bbox=[None, None, None, None], kx=3, ky=3, eps=None*)

Weighted least-squares bivariate spline approximation.

Parameters	**x, y, z** : array_like 1-D sequences of data points (order is not important). **tx, ty** : array_like Strictly ordered 1-D sequences of knots coordinates. **w** : array_like, optional Positive 1-D array of weights, of the same length as *x*, *y* and *z*. **bbox** : (4,) array_like, optional Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x,tx),max(x,tx), min(y,ty),max(y,ty)]`. **kx, ky** : ints, optional Degrees of the bivariate spline. Default is 3. **eps** : float, optional A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value between 0 and 1, the default is 1e-16.

See also:

`bisplrep`	an older wrapping of FITPACK
`bisplev`	an older wrapping of FITPACK
`UnivariateSpline`	a similar class for univariate spline interpolation
`SmoothBivariateSpline`	create a smoothing BivariateSpline

Notes

The length of *x*, *y* and *z* should be at least `(kx+1) * (ky+1)`.

Methods

`__call__`(x, y[, mth, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(xi, yi[, dx, dy])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-var
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

`LSQBivariateSpline.`**`__call__`**(*x*, *y*, *mth=None*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

x, y : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.

dx : int

Order of x-derivative

New in version 0.14.0.

dy : int

Order of y-derivative

New in version 0.14.0.

grid : bool

Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.

New in version 0.14.0.

mth : str

Deprecated argument. Has no effect.

`LSQBivariateSpline.`**`ev`**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters

xi, yi : array_like

Input coordinates. Standard Numpy broadcasting is obeyed.

dx : int, optional

Order of x-derivative

New in version 0.14.0.

dy : int, optional

Order of y-derivative

New in version 0.14.0.

`LSQBivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`LSQBivariateSpline.`**`get_knots`**`()`

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`LSQBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

`LSQBivariateSpline.`**`integral`**`(`*xa, xb, ya, yb*`)`

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters	**xa, xb** : float The end-points of the x integration interval. **ya, yb** : float The end-points of the y integration interval.
Returns	**integ** : float The value of the resulting integral.

class `scipy.interpolate.`**`LSQSphereBivariateSpline`**`(`*theta, phi, r, tt, tp, w=None, eps=1e-16*`)`

Weighted least-squares bivariate spline approximation in spherical coordinates.

New in version 0.11.0.

Parameters	**theta, phi, r** : array_like 1-D sequences of data points (order is not important). Coordinates must be given in radians. Theta must lie within the interval (0, pi), and phi must lie within the interval (0, 2pi). **tt, tp** : array_like Strictly ordered 1-D sequences of knots coordinates. Coordinates must satisfy `0 < tt[i] < pi`, `0 < tp[i] < 2*pi`. **w** : array_like, optional Positive 1-D sequence of weights, of the same length as *theta*, *phi* and *r*. **eps** : float, optional A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value between 0 and 1, the default is 1e-16.

Notes

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

```
>>> theta = np.linspace(0., np.pi, 7)
>>> phi = np.linspace(0., 2*np.pi, 9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
>>> data[1,1:-1], data[-2,1:-1] = 1., 1.
>>> data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[2,2:-2], data[-3,2:-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)
```

We need to set up the interpolator object. Here, we must also specify the coordinates of the knots to use.

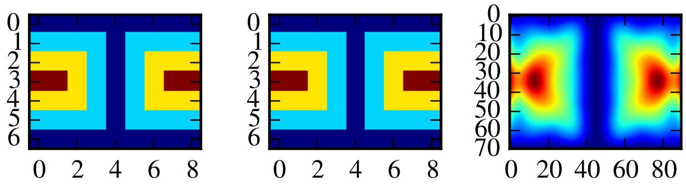
```
>>> lats, lons = np.meshgrid(theta, phi)
>>> knotst, knotsp = theta.copy(), phi.copy()
>>> knotst[0] += .0001
>>> knotst[-1] -= .0001
>>> knotsp[0] += .0001
>>> knotsp[-1] -= .0001
>>> from scipy.interpolate import LSQSphereBivariateSpline
>>> lut = LSQSphereBivariateSpline(lats.ravel(), lons.ravel(),
...                                 data.T.ravel(), knotst, knotsp)
```

As a first test, we'll see what the algorithm returns when run on the input coordinates

```
>>> data_orig = lut(theta, phi)
```

Finally we interpolate the data to a finer grid

```
>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2*np.pi, 90)

>>> data_lsq = lut(fine_lats, fine_lons)

>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(data_orig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)
>>> ax3.imshow(data_lsq, interpolation='nearest')
>>> plt.show()
```



Methods

`__call__`(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(theta, phi[, dtheta, dphi])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-,
`get_residual`()	Return weighted sum of squared residuals of the spline

`LSQSphereBivariateSpline.`**`__call__`**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters **theta, phi** : array_like

Input coordinates.

If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.

If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta : int, optional
Order of theta-derivative
New in version 0.14.0.

dphi : int
Order of phi-derivative
New in version 0.14.0.

grid : bool
Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

`LSQSphereBivariateSpline.`**`ev`**`(`*theta*, *phi*, *dtheta=0*, *dphi=0*`)`

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters

theta, phi : array_like
Input coordinates. Standard Numpy broadcasting is obeyed.

dtheta : int, optional
Order of theta-derivative
New in version 0.14.0.

dphi : int, optional
Order of phi-derivative
New in version 0.14.0.

`LSQSphereBivariateSpline.`**`get_coeffs`**`()`

Return spline coefficients.

`LSQSphereBivariateSpline.`**`get_knots`**`()`

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

`LSQSphereBivariateSpline.`**`get_residual`**`()`

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

Low-level interface to FITPACK functions:

`bisplrep`(x, y, z[, w, xb, xe, yb, ye, kx, ...])	Find a bivariate B-spline representation of a surface.
`bisplev`(x, y, tck[, dx, dy])	Evaluate a bivariate B-spline and its derivatives.

`scipy.interpolate.`**`bisplrep`**`(`*x*, *y*, *z*, *w=None*, *xb=None*, *xe=None*, *yb=None*, *ye=None*, *kx=3*, *ky=3*, *task=0*, *s=None*, *eps=1e-16*, *tx=None*, *ty=None*, *full_output=0*, *nxest=None*, *nyest=None*, *quiet=1*`)`

Find a bivariate B-spline representation of a surface.

Given a set of data points (x[i], y[i], z[i]) representing a surface z=f(x,y), compute a B-spline representation of the surface. Based on the routine SURFIT from FITPACK.

Parameters

x, y, z : ndarray
Rank-1 arrays of data points.

w : ndarray, optional
Rank-1 array of weights. By default `w=np.ones(len(x))`.

xb, xe : float, optional

End points of approximation interval in *x*. By default `xb = x.min()`, `xe=x.max()`.

yb, ye : float, optional

End points of approximation interval in *y*. By default `yb=y.min()`, `ye = y.max()`.

kx, ky : int, optional

The degrees of the spline (1 <= kx, ky <= 5). Third order (kx=ky=3) is recommended.

task : int, optional

If task=0, find knots in x and y and coefficients for a given smoothing factor, s. If task=1, find knots and coefficients for another value of the smoothing factor, s. bisplrep must have been previously called with task=0 or task=1. If task=-1, find coefficients for a given set of knots tx, ty.

s : float, optional

A non-negative smoothing factor. If weights correspond to the inverse of the standard-deviation of the errors in z, then a good s-value should be found in the range `(m-sqrt(2*m),m+sqrt(2*m))` where m=len(x).

eps : float, optional

A threshold for determining the effective rank of an over-determined linear system of equations (0 < eps < 1). *eps* is not likely to need changing.

tx, ty : ndarray, optional

Rank-1 arrays of the knots of the spline for task=-1

full_output : int, optional

Non-zero to return optional outputs.

nxest, nyest : int, optional

Over-estimates of the total number of knots. If None then `nxest = max(kx+sqrt(m/2),2*kx+3)`, `nyest = max(ky+sqrt(m/2),2*ky+3)`.

quiet : int, optional

Non-zero to suppress printing of messages. This parameter is deprecated; use standard Python warning filters instead.

Returns **tck** : array_like

A list [tx, ty, c, kx, ky] containing the knots (tx, ty) and coefficients (c) of the bivariate B-spline representation of the surface along with the degree of the spline.

fp : ndarray

The weighted sum of squared residuals of the spline approximation.

ier : int

An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

msg : str

A message corresponding to the integer flag, ier.

See also:

`splprep`, `splrep`, `splint`, `sproot`, `splev`, `UnivariateSpline`, `BivariateSpline`

Notes

See `bisplev` to evaluate the value of the B-spline given its tck representation.

References

[R52], [R53], [R54]

`scipy.interpolate.`**`bisplev`**(*x*, *y*, *tck*, *dx=0*, *dy=0*)

Evaluate a bivariate B-spline and its derivatives.

Return a rank-2 array of spline function values (or spline derivative values) at points given by the cross-product of the rank-1 arrays *x* and *y*. In special cases, return an array or just a float if either *x* or *y* or both are floats. Based on BISPEV from FITPACK.

Parameters

x, y : ndarray
Rank-1 arrays specifying the domain over which to evaluate the spline or its derivative.

tck : tuple
A sequence of length 5 returned by `bisplrep` containing the knot locations, the coefficients, and the degree of the spline: [tx, ty, c, kx, ky].

dx, dy : int, optional
The orders of the partial derivatives in *x* and *y* respectively.

Returns

vals : ndarray
The B-spline or its derivative evaluated over the set formed by the cross-product of *x* and *y*.

See also:

`splprep`, `splrep`, `splint`, `sproot`, `splev`, `UnivariateSpline`, `BivariateSpline`

Notes

See `bisplrep` to generate the *tck* representation.

References

[R49], [R50], [R51]

5.7.5 Additional tools

`lagrange`(x, w)	Return a Lagrange interpolating polynomial.
`approximate_taylor_polynomial`(f, x, degree, ...)	Estimate the Taylor polynomial of f at x by polynomial fitting.

`scipy.interpolate.`**`lagrange`**(*x*, *w*)

Return a Lagrange interpolating polynomial.

Given two 1-D arrays *x* and *w,* returns the Lagrange interpolating polynomial through the points `(x, w)`.

Warning: This implementation is numerically unstable. Do not expect to be able to use more than about 20 points even if they are chosen optimally.

Parameters

x : array_like
x represents the x-coordinates of a set of datapoints.

w : array_like
w represents the y-coordinates of a set of datapoints, i.e. f(*x*).

Returns

lagrange : numpy.poly1d instance
The Lagrange interpolating polynomial.

`scipy.interpolate.`**`approximate_taylor_polynomial`**(*f*, *x*, *degree*, *scale*, *order=None*)

Estimate the Taylor polynomial of f at x by polynomial fitting.

Parameters

f : callable
The function whose Taylor polynomial is sought. Should accept a vector of *x* values.

x : scalar
The point at which the polynomial is to be evaluated.

degree : int
The degree of the Taylor polynomial

scale : scalar

The width of the interval to use to evaluate the Taylor polynomial. Function values spread over a range this wide are used to fit the polynomial. Must be chosen carefully.

order : int or None, optional

The order of the polynomial to be used in the fitting; f will be evaluated `order+1` times. If None, use *degree*.

Returns **p** : poly1d instance

The Taylor polynomial (translated to the origin, so that for example p(0)=f(x)).

Notes

The appropriate choice of "scale" is a trade-off; too large and the function differs from its Taylor polynomial too much to get a good answer, too small and round-off errors overwhelm the higher-order terms. The algorithm used becomes numerically unstable around order 30 even under ideal circumstances.

Choosing order somewhat larger than degree may improve the higher-order terms.

See also:

`scipy.ndimage.interpolation.map_coordinates`, `scipy.ndimage.interpolation.spline_filter`, `scipy.signal.resample`, `scipy.signal.bspline`, `scipy.signal.gauss_spline`, `scipy.signal.qspline1d`, `scipy.signal.cspline1d`, `scipy.signal.qspline1d_eval`, `scipy.signal.cspline1d_eval`, `scipy.signal.qspline2d`, `scipy.signal.cspline2d`.

5.8 Input and output (`scipy.io`)

SciPy has many modules, classes, and functions available to read data from and write data to a variety of file formats.

See also:

numpy-reference.routines.io (in Numpy)

5.8.1 MATLAB® files

`loadmat`(file_name[, mdict, appendmat])	Load MATLAB file
`savemat`(file_name, mdict[, appendmat, ...])	Save a dictionary of names and arrays into a MATLAB-style .mat file.
`whosmat`(file_name[, appendmat])	List variables inside a MATLAB file

`scipy.io.`**`loadmat`** (*file_name*, *mdict=None*, *appendmat=True*, ***kwargs*)

Load MATLAB file

Parameters **file_name** : str

Name of the mat file (do not need .mat extension if appendmat==True) Can also pass open file-like object.

m_dict : dict, optional

Dictionary in which to insert matfile variables.

appendmat : bool, optional

True to append the .mat extension to the end of the given filename, if not already present.

byte_order : str or None, optional

None by default, implying byte order guessed from mat file. Otherwise can be one of ('native', '=', 'little', '<', 'BIG', '>').

mat_dtype : bool, optional

If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved).

squeeze_me : bool, optional
Whether to squeeze unit matrix dimensions or not.

chars_as_strings : bool, optional
Whether to convert char arrays to string arrays.

matlab_compatible : bool, optional
Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True).

struct_as_record : bool, optional
Whether to load MATLAB structs as numpy record arrays, or as old-style numpy arrays with dtype=object. Setting this flag to False replicates the behavior of scipy version 0.7.x (returning numpy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.

verify_compressed_data_integrity : bool, optional
Whether the length of compressed sequences in the MATLAB file should be checked, to ensure that they are not longer than we expect. It is advisable to enable this (the default) because overlong compressed sequences in MATLAB files generally indicate that the files have experienced some sort of corruption.

variable_names : None or sequence
If None (the default) - read all variables in file. Otherwise *variable_names* should be a sequence of strings, giving names of the matlab variables to read from the file. The reader will skip any variable with a name not in this sequence, possibly saving some read processing.

Returns **mat_dict** : dict
dictionary with variable names as keys, and loaded matrices as values

Notes

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 python library to read matlab 7.3 format mat files. Because scipy does not supply one, we do not implement the HDF5 / 7.3 interface here.

`scipy.io.`**`savemat`**(*file_name*, *mdict*, *appendmat=True*, *format='5'*, *long_field_names=False*, *do_compression=False*, *oned_as='row'*)

Save a dictionary of names and arrays into a MATLAB-style .mat file.

This saves the array objects in the given dictionary to a MATLAB- style .mat file.

Parameters **file_name** : str or file-like object
Name of the .mat file (.mat extension not needed if `appendmat == True`). Can also pass open file_like object.

mdict : dict
Dictionary from which to save matfile variables.

appendmat : bool, optional
True (the default) to append the .mat extension to the end of the given filename, if not already present.

format : {'5', '4'}, string, optional
'5' (the default) for MATLAB 5 and up (to 7.2), '4' for MATLAB 4 .mat files

long_field_names : bool, optional
False (the default) - maximum field name length in a structure is 31 characters which is the documented maximum length. True - maximum field name length in a structure is 63 characters which works for MATLAB 7.6+

do_compression : bool, optional
Whether or not to compress matrices on write. Default is False.

oned_as : {'row', 'column'}, optional
If 'column', write 1-D numpy arrays as column vectors. If 'row', write 1-D numpy arrays as row vectors.

See also:

`mio4.MatFile4Writer`, `mio5.MatFile5Writer`

`scipy.io.`**`whosmat`**(*file_name*, *appendmat=True*, ***kwargs*)

List variables inside a MATLAB file

Parameters	**file_name** : str Name of the mat file (do not need .mat extension if appendmat==True) Can also pass open file-like object. **appendmat** : bool, optional True to append the .mat extension to the end of the given filename, if not already present. **byte_order** : str or None, optional None by default, implying byte order guessed from mat file. Otherwise can be one of (‘native’, ‘=’, ‘little’, ‘<’, ‘BIG’, ‘>’). **mat_dtype** : bool, optional If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved). **squeeze_me** : bool, optional Whether to squeeze unit matrix dimensions or not. **chars_as_strings** : bool, optional Whether to convert char arrays to string arrays. **matlab_compatible** : bool, optional Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True). **struct_as_record** : bool, optional Whether to load MATLAB structs as numpy record arrays, or as old-style numpy arrays with dtype=object. Setting this flag to False replicates the behavior of scipy version 0.7.x (returning numpy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.
Returns	**variables** : list of tuples A list of tuples, where each tuple holds the matrix name (a string), its shape (tuple of ints), and its data class (a string). Possible data classes are: int8, uint8, int16, uint16, int32, uint32, int64, uint64, single, double, cell, struct, object, char, sparse, function, opaque, logical, unknown.

Notes

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 python library to read matlab 7.3 format mat files. Because scipy does not supply one, we do not implement the HDF5 / 7.3 interface here.

New in version 0.12.0.

5.8.2 IDL® files

`readsav`(file_name[, idict, python_dict, ...])	Read an IDL .sav file

`scipy.io.`**`readsav`**(*file_name*, *idict=None*, *python_dict=False*, *uncompressed_file_name=None*, *verbose=False*)

Read an IDL .sav file

Parameters	**file_name** : str Name of the IDL save file.

idict : dict, optional
Dictionary in which to insert .sav file variables

python_dict : bool, optional
By default, the object return is not a Python dictionary, but a case-insensitive dictionary with item, attribute, and call access to variables. To get a standard Python dictionary, set this option to True.

uncompressed_file_name : str, optional
This option only has an effect for .sav files written with the /compress option. If a file name is specified, compressed .sav files are uncompressed to this file. Otherwise, readsav will use the `tempfile` module to determine a temporary filename automatically, and will remove the temporary file upon successfully reading it in.

verbose : bool, optional
Whether to print out information about the save file, including the records read, and available variables.

Returns **idl_dict** : AttrDict or dict
If *python_dict* is set to False (default), this function returns a case-insensitive dictionary with item, attribute, and call access to variables. If *python_dict* is set to True, this function returns a Python dictionary with all variable names in lowercase. If *idict* was specified, then variables are written to the dictionary specified, and the updated dictionary is returned.

5.8.3 Matrix Market files

`mminfo`(source)	Queries the contents of the Matrix Market file ‘filename’ to extract size and storag
`mmread`(source)	Reads the contents of a Matrix Market file ‘filename’ into a matrix.
`mmwrite`(target, a[, comment, field, precision])	Writes the sparse or dense array *a* to a Matrix Market formatted file.

`scipy.io.`**`mminfo`**(*source*)

Queries the contents of the Matrix Market file ‘filename’ to extract size and storage information.

Parameters **source** : file
Matrix Market filename (extension .mtx) or open file object

Returns **rows,cols** : int
Number of matrix rows and columns

entries : int
Number of non-zero entries of a sparse matrix or rows*cols for a dense matrix

format : str
Either ‘coordinate’ or ‘array’.

field : str
Either ‘real’, ‘complex’, ‘pattern’, or ‘integer’.

symm : str
Either ‘general’, ‘symmetric’, ‘skew-symmetric’, or ‘hermitian’.

`scipy.io.`**`mmread`**(*source*)

Reads the contents of a Matrix Market file ‘filename’ into a matrix.

Parameters **source** : file
Matrix Market filename (extensions .mtx, .mtz.gz) or open file object.

Returns a:
Sparse or full matrix

`scipy.io.`**`mmwrite`**(*target*, *a*, *comment=’‘*, *field=None*, *precision=None*)

Writes the sparse or dense array *a* to a Matrix Market formatted file.

Parameters **target** : file
Matrix Market filename (extension .mtx) or open file object
a : array like
Sparse or dense 2D array
comment : str, optional
comments to be prepended to the Matrix Market file
field : None or str, optional
Either 'real', 'complex', 'pattern', or 'integer'.
precision : None or int, optional
Number of digits to display for real or complex values.

5.8.4 Unformatted Fortran files

`FortranFile`(filename[, mode, header_dtype])	A file object for unformatted sequential files from Fortran code.

class `scipy.io.`**`FortranFile`** (*filename*, *mode='r'*, *header_dtype=<type 'numpy.uint32'>*)
A file object for unformatted sequential files from Fortran code.

Parameters **filename** : file or str
Open file object or filename.
mode : {'r', 'w'}, optional
Read-write mode, default is 'r'.
header_dtype : dtype, optional
Data type of the header. Size and endiness must match the input/output file.

Notes

These files are broken up into records of unspecified types. The size of each record is given at the start (although the size of this header is not standard) and the data is written onto disk without any formatting. Fortran compilers supporting the BACKSPACE statement will write a second copy of the size to facilitate backwards seeking.

This class only supports files written with both sizes for the record. It also does not support the subrecords used in Intel and gfortran compilers for records which are greater than 2GB with a 4-byte header.

An example of an unformatted sequential file in Fortran would be written as:

```
OPEN(1, FILE=myfilename, FORM='unformatted')

WRITE(1) myvariable
```

Since this is a non-standard file format, whose contents depend on the compiler and the endianness of the machine, caution is advised. Files from gfortran 4.8.0 and gfortran 4.1.2 on x86_64 are known to work.

Consider using Fortran direct-access files or files from the newer Stream I/O, which can be easily read by `numpy.fromfile`.

Examples

To create an unformatted sequential Fortran file:

```
>>> from scipy.io import FortranFile
>>> f = FortranFile('test.unf', 'w')
>>> f.write_record(np.array([1,2,3,4,5],dtype=np.int32))
>>> f.write_record(np.linspace(0,1,20).reshape((5,-1)))
>>> f.close()
```

To read this file:

```
>>> from scipy.io import FortranFile
>>> f = FortranFile('test.unf', 'r')
>>> print(f.read_ints(dtype=np.int32))
[1 2 3 4 5]
>>> print(f.read_reals(dtype=np.float).reshape((5,-1)))
[[ 0.          0.05263158  0.10526316  0.15789474]
 [ 0.21052632  0.26315789  0.31578947  0.36842105]
 [ 0.42105263  0.47368421  0.52631579  0.57894737]
 [ 0.63157895  0.68421053  0.73684211  0.78947368]
 [ 0.84210526  0.89473684  0.94736842  1.        ]]
>>> f.close()
```

Methods

`close`()	Closes the file.
`read_ints`([dtype])	Reads a record of a given type from the file, defaulting to an integer
`read_reals`([dtype])	Reads a record of a given type from the file, defaulting to a floating
`read_record`([dtype])	Reads a record of a given type from the file.
`write_record`(s)	Write a record (including sizes) to the file.

`FortranFile.`**`close`**`()`

Closes the file. It is unsupported to call any other methods off this object after closing it. Note that this class supports the 'with' statement in modern versions of Python, to call this automatically

`FortranFile.`**`read_ints`**`(`*dtype='i4'*`)`

Reads a record of a given type from the file, defaulting to an integer type (INTEGER*4 in Fortran)

Parameters **dtype** : dtype, optional

Data type specifying the size and endiness of the data.

Returns **data** : ndarray

A one-dimensional array object.

See also:

`read_reals`, `read_record`

`FortranFile.`**`read_reals`**`(`*dtype='f8'*`)`

Reads a record of a given type from the file, defaulting to a floating point number (real*8 in Fortran)

Parameters **dtype** : dtype, optional

Data type specifying the size and endiness of the data.

Returns **data** : ndarray

A one-dimensional array object.

See also:

`read_ints`, `read_record`

`FortranFile.`**`read_record`**`(`*dtype=None*`)`

Reads a record of a given type from the file.

Parameters **dtype** : dtype, optional

Data type specifying the size and endiness of the data.

Returns **data** : ndarray

A one-dimensional array object.

See also:

`read_reals`, `read_ints`

Notes

If the record contains a multi-dimensional array, calling reshape or resize will restructure the array to the correct size. Since Fortran multidimensional arrays are stored in column-major format, this may have some non-intuitive consequences. If the variable was declared as 'INTEGER var(5,4)', for example, var could be read with 'read_record(dtype=np.integer).reshape((4,5))' since Python uses row-major ordering of indices.

One can transpose to obtain the indices in the same order as in Fortran.

For records that contain several variables or mixed types (as opposed to single scalar or array types), it is possible to specify a dtype with mixed types:

```
>>> record = f.read_record([('a', '<f4'), ('b', '<i4')])
>>> record['a']  # access the variable 'a'
5.6
```

and if any of the variables are arrays, the shape can be specified as the third item in the relevant tuple:

```
>>> record = f.read_record([('a', '<f4'), ('b', '<i4', (3,3))])
```

Numpy also supports a short syntax for this kind of type:

```
>>> record = f.read_record('<f4,(3,3)<i4')
>>> record['f0']  # variables are called f0, f1, ...
5.6
```

`FortranFile.`**`write_record`**(*s*)

Write a record (including sizes) to the file.

Parameters **s** : array_like

The data to write.

5.8.5 Wav sound files (`scipy.io.wavfile`)

`read`(filename[, mmap])	Return the sample rate (in samples/sec) and data from a WAV file
`write`(filename, rate, data)	Write a numpy array as a WAV file

`scipy.io.wavfile.`**`read`**(*filename*, *mmap=False*)

Return the sample rate (in samples/sec) and data from a WAV file

Parameters **filename** : string or open file handle

Input wav file.

mmap : bool, optional

Whether to read data as memory mapped. Only to be used on real files (Default: False)

New in version 0.12.0.

Returns **rate** : int

Sample rate of wav file

data : numpy array

Data read from wav file

Notes

- The file can be an open file or a filename.
- The returned sample rate is a Python integer.
- The data is returned as a numpy array with a data-type determined from the file.

- This function cannot read wav files with 24 bit data.

`scipy.io.wavfile.`**`write`**(*filename*, *rate*, *data*)

Write a numpy array as a WAV file

Parameters **filename** : string or open file handle

Output wav file

rate : int

The sample rate (in samples/sec).

data : ndarray

A 1-D or 2-D numpy array of either integer or float data-type.

Notes

- The file can be an open file or a filename.
- Writes a simple uncompressed WAV file.
- The bits-per-sample will be determined by the data-type.
- To write multiple-channels, use a 2-D array of shape (Nsamples, Nchannels).

5.8.6 Arff files (`scipy.io.arff`)

`loadarff`(f)	Read an arff file.

`scipy.io.arff.`**`loadarff`**(*f*)

Read an arff file.

The data is returned as a record array, which can be accessed much like a dictionary of numpy arrays. For example, if one of the attributes is called 'pressure', then its first 10 data points can be accessed from the `data` record array like so: `data['pressure'][0:10]`

Parameters **f** : file-like or str

File-like object to read from, or filename to open.

Returns **data** : record array

The data of the arff file, accessible by attribute names.

meta : `MetaData`

Contains information about the arff file such as name and type of attributes, the relation (name of the dataset), etc...

Raises **ParseArffError**

This is raised if the given file is not ARFF-formatted.

NotImplementedError

The ARFF file has an attribute which is not supported yet.

Notes

This function should be able to read most arff files. Not implemented functionality include:

- date type attributes
- string type attributes

It can read files with numeric and nominal attributes. It cannot read files with sparse data ({} in the file). However, this function can read files with missing data (? in the file), representing the data points as NaNs.

5.8.7 Netcdf (`scipy.io.netcdf`)

`netcdf_file`(filename[, mode, mmap, version])	A file object for NetCDF data.
`netcdf_variable`(data, typecode, size, shape, ...)	A data object for the *netcdf* module.

class `scipy.io.netcdf.`**`netcdf_file`**(*filename*, *mode='r'*, *mmap=None*, *version=1*)

A file object for NetCDF data.

A `netcdf_file` object has two standard attributes: *dimensions* and *variables*. The values of both are dictionaries, mapping dimension names to their associated lengths and variable names to variables, respectively. Application programs should never modify these dictionaries.

All other attributes correspond to global attributes defined in the NetCDF file. Global file attributes are created by assigning to an attribute of the `netcdf_file` object.

Parameters

filename : string or file-like
string -> filename

mode : {'r', 'w', 'a'}, optional
read-write-append mode, default is 'r'

mmap : None or bool, optional
Whether to mmap *filename* when reading. Default is True when *filename* is a file name, False when *filename* is a file-like object. Note that when mmap is in use, data arrays returned refer directly to the mmapped data on disk, and the file cannot be closed as long as references to it exist.

version : {1, 2}, optional
version of netcdf to read / write, where 1 means *Classic format* and 2 means *64-bit offset format*. Default is 1. See here for more info.

Notes

The major advantage of this module over other modules is that it doesn't require the code to be linked to the NetCDF libraries. This module is derived from pupynere.

NetCDF files are a self-describing binary data format. The file contains metadata that describes the dimensions and variables in the file. More details about NetCDF files can be found here. There are three main sections to a NetCDF data structure:

1. Dimensions
2. Variables
3. Attributes

The dimensions section records the name and length of each dimension used by the variables. The variables would then indicate which dimensions it uses and any attributes such as data units, along with containing the data values for the variable. It is good practice to include a variable that is the same name as a dimension to provide the values for that axes. Lastly, the attributes section would contain additional information such as the name of the file creator or the instrument used to collect the data.

When writing data to a NetCDF file, there is often the need to indicate the 'record dimension'. A record dimension is the unbounded dimension for a variable. For example, a temperature variable may have dimensions of latitude, longitude and time. If one wants to add more temperature data to the NetCDF file as time progresses, then the temperature variable should have the time dimension flagged as the record dimension.

In addition, the NetCDF file header contains the position of the data in the file, so access can be done in an efficient manner without loading unnecessary data into memory. It uses the `mmap` module to create Numpy arrays mapped to the data on disk, for the same purpose.

Note that when `netcdf_file` is used to open a file with mmap=True (default for read-only), arrays returned by it refer to data directly on the disk. The file should not be closed, and cannot be cleanly closed when asked, if such arrays are alive. You may want to copy data arrays obtained from mmapped Netcdf file if they are to be processed after the file is closed, see the example below.

Examples

To create a NetCDF file:

```
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'w')
>>> f.history = 'Created for a test'
>>> f.createDimension('time', 10)
>>> time = f.createVariable('time', 'i', ('time',))
>>> time[:] = np.arange(10)
>>> time.units = 'days since 2008-01-01'
>>> f.close()
```

Note the assignment of `range(10)` to `time[:]`. Exposing the slice of the time variable allows for the data to be set in the object, rather than letting `range(10)` overwrite the `time` variable.

To read the NetCDF file we just created:

```
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'r')
>>> print(f.history)
Created for a test
>>> time = f.variables['time']
>>> print(time.units)
days since 2008-01-01
>>> print(time.shape)
(10,)
>>> print(time[-1])
9
```

NetCDF files, when opened read-only, return arrays that refer directly to memory-mapped data on disk:

```
>>> data = time[:]
>>> data.base.base
<mmap.mmap object at 0x7fe753763180>
```

If the data is to be processed after the file is closed, it needs to be copied to main memory:

```
>>> data = time[:].copy()
>>> f.close()
>>> data.mean()
```

A NetCDF file can also be used as context manager:

```
>>> from scipy.io import netcdf
>>> with netcdf.netcdf_file('simple.nc', 'r') as f:
...     print(f.history)
Created for a test
```

Methods

`close`()	Closes the NetCDF file.
`createDimension`(name, length)	Adds a dimension to the Dimension section of the NetCDF data structure.
`createVariable`(name, type, dimensions)	Create an empty variable for the `netcdf_file` object, specifying its data type and
	Co

Table 5.65 – continued from previous page

`flush`()	Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.
`sync`()	Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

`netcdf_file.`**`close`**`()`

Closes the NetCDF file.

`netcdf_file.`**`createDimension`**`(`*name*, *length*`)`

Adds a dimension to the Dimension section of the NetCDF data structure.

Note that this function merely adds a new dimension that the variables can reference. The values for the dimension, if desired, should be added as a variable using `createVariable`, referring to this dimension.

Parameters **name** : str
Name of the dimension (Eg, 'lat' or 'time').
length : int
Length of the dimension.

See also:

`createVariable`

`netcdf_file.`**`createVariable`**`(`*name*, *type*, *dimensions*`)`

Create an empty variable for the `netcdf_file` object, specifying its data type and the dimensions it uses.

Parameters **name** : str
Name of the new variable.
type : dtype or str
Data type of the variable.
dimensions : sequence of str
List of the dimension names used by the variable, in the desired order.

Returns **variable** : netcdf_variable
The newly created `netcdf_variable` object. This object has also been added to the `netcdf_file` object as well.

See also:

`createDimension`

Notes

Any dimensions to be used by the variable should already exist in the NetCDF data structure or should be created by `createDimension` prior to creating the NetCDF variable.

`netcdf_file.`**`flush`**`()`

Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

See also:

`sync` Identical function

`netcdf_file.`**`sync`**`()`

Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

See also:

`sync` Identical function

class `scipy.io.netcdf.`**`netcdf_variable`**(*data*, *typecode*, *size*, *shape*, *dimensions*, *attributes=None*)

A data object for the *netcdf* module.

`netcdf_variable` objects are constructed by calling the method `netcdf_file.createVariable` on the `netcdf_file` object. `netcdf_variable` objects behave much like array objects defined in numpy, except that their data resides in a file. Data is read by indexing and written by assigning to an indexed subset; the entire array can be accessed by the index `[:]` or (for scalars) by using the methods `getValue` and `assignValue`. `netcdf_variable` objects also have attribute `shape` with the same meaning as for arrays, but the shape cannot be modified. There is another read-only attribute *dimensions*, whose value is the tuple of dimension names.

All other attributes correspond to variable attributes defined in the NetCDF file. Variable attributes are created by assigning to an attribute of the `netcdf_variable` object.

Parameters

data : array_like

The data array that holds the values for the variable. Typically, this is initialized as empty, but with the proper shape.

typecode : dtype character code

Desired data-type for the data array.

size : int

Desired element size for the data array.

shape : sequence of ints

The shape of the array. This should match the lengths of the variable's dimensions.

dimensions : sequence of strings

The names of the dimensions used by the variable. Must be in the same order of the dimension lengths given by `shape`.

attributes : dict, optional

Attribute values (any type) keyed by string names. These attributes become attributes for the netcdf_variable object.

See also:

`isrec`, `shape`

Attributes

dimensions	(list of str) List of names of dimensions used by the variable object.
isrec, shape	Properties

Methods

`assignValue`(value)	Assign a scalar value to a `netcdf_variable` of length one.
`getValue`()	Retrieve a scalar value from a `netcdf_variable` of length one.
`itemsize`()	Return the itemsize of the variable.
`typecode`()	Return the typecode of the variable.

`netcdf_variable.`**`assignValue`**(*value*)

Assign a scalar value to a `netcdf_variable` of length one.

Parameters

value : scalar

Scalar value (of compatible type) to assign to a length-one netcdf variable. This value will be written to file.

Raises

ValueError

If the input is not a scalar, or if the destination is not a length-one netcdf variable.

`netcdf_variable.`**`getValue`**()

Retrieve a scalar value from a `netcdf_variable` of length one.

Raises **ValueError**

If the netcdf variable is an array of length greater than one, this exception will be raised.

`netcdf_variable.`**`itemsize`**`()`

Return the itemsize of the variable.

Returns **itemsize** : int

The element size of the variable (eg, 8 for float64).

`netcdf_variable.`**`typecode`**`()`

Return the typecode of the variable.

Returns **typecode** : char

The character typecode of the variable (eg, 'i' for int).

5.9 Linear algebra (`scipy.linalg`)

Linear algebra functions.

See also:

`numpy.linalg` for more linear algebra functions. Note that although `scipy.linalg` imports most of them, identically named functions from `scipy.linalg` may offer more or slightly differing functionality.

5.9.1 Basics

`inv`(a[, overwrite_a, check_finite])	Compute the inverse of a matrix.
`solve`(a, b[, sym_pos, lower, overwrite_a, ...])	Solve the equation `a x = b` for `x`.
`solve_banded`(l_and_u, ab, b[, overwrite_ab, ...])	Solve the equation a x = b for x, assuming a is banded matrix.
`solveh_banded`(ab, b[, overwrite_ab, ...])	Solve equation a x = b.
`solve_circulant`(c, b[, singular, tol, ...])	Solve C x = b for x, where C is a circulant matrix.
`solve_triangular`(a, b[, trans, lower, ...])	Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.
`solve_toeplitz`(c_or_cr, b[, check_finite])	Solve a Toeplitz system using Levinson Recursion
`det`(a[, overwrite_a, check_finite])	Compute the determinant of a matrix
`norm`(a[, ord])	Matrix or vector norm.
`lstsq`(a, b[, cond, overwrite_a, ...])	Compute least-squares solution to equation Ax = b.
`pinv`(a[, cond, rcond, return_rank, check_finite])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.
`pinv2`(a[, cond, rcond, return_rank, ...])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.
`pinvh`(a[, cond, rcond, lower, return_rank, ...])	Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.
`kron`(a, b)	Kronecker product.
`tril`(m[, k])	Make a copy of a matrix with elements above the k-th diagonal zeroed.
`triu`(m[, k])	Make a copy of a matrix with elements below the k-th diagonal zeroed.
`orthogonal_procrustes`(A, B[, check_finite])	Compute the matrix solution of the orthogonal Procrustes problem.

`scipy.linalg.`**`inv`**`(`*a*, *overwrite_a=False*, *check_finite=True*`)`

Compute the inverse of a matrix.

Parameters **a** : array_like

Square matrix to be inverted.

overwrite_a : bool, optional

Discard data in *a* (may improve performance). Default is False.

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **ainv** : ndarray

Inverse of the matrix *a*.

Raises **LinAlgError :**

If *a* is singular.

ValueError :

If *a* is not square, or not 2-dimensional.

Examples

```
>>> from scipy import linalg
>>> a = np.array([[1., 2.], [3., 4.]])
>>> linalg.inv(a)
array([[-2. ,  1. ],
       [ 1.5, -0.5]])
>>> np.dot(a, linalg.inv(a))
array([[ 1.,  0.],
       [ 0.,  1.]])
```

`scipy.linalg.`**`solve`**(*a*, *b*, *sym_pos=False*, *lower=False*, *overwrite_a=False*, *overwrite_b=False*, *debug=False*, *check_finite=True*)

Solve the equation `a x = b` for `x`.

Parameters **a** : (M, M) array_like

A square matrix.

b : (M,) or (M, N) array_like

Right-hand side matrix in `a x = b`.

sym_pos : bool, optional

Assume *a* is symmetric and positive definite.

lower : bool, optional

Use only data contained in the lower triangle of *a*, if *sym_pos* is true. Default is to use upper triangle.

overwrite_a : bool, optional

Allow overwriting data in *a* (may enhance performance). Default is False.

overwrite_b : bool, optional

Allow overwriting data in *b* (may enhance performance). Default is False.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **x** : (M,) or (M, N) ndarray

Solution to the system `a x = b`. Shape of the return matches the shape of *b*.

Raises **LinAlgError**

If *a* is singular.

Examples

Given *a* and *b*, solve for *x*:

```
>>> a = np.array([[3, 2, 0], [1, -1, 0], [0, 5, 1]])
>>> b = np.array([2, 4, -1])
>>> from scipy import linalg
>>> x = linalg.solve(a, b)
```

```
>>> x
array([ 2., -2.,  9.])
>>> np.dot(a, x) == b
array([ True,  True,  True], dtype=bool)
```

`scipy.linalg.`**`solve_banded`**(*l_and_u*, *ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *debug=False*, *check_finite=True*)

Solve the equation a x = b for x, assuming a is banded matrix.

The matrix a is stored in *ab* using the matrix diagonal ordered form:

```
ab[u + i - j, j] == a[i,j]
```

Example of *ab* (shape of a is (6,6), *u* =1, *l* =2):

```
*    a01  a12  a23  a34  a45
a00  a11  a22  a33  a44  a55
a10  a21  a32  a43  a54   *
a20  a31  a42  a53   *    *
```

Parameters

(l, u) : (integer, integer)
Number of non-zero lower and upper diagonals

ab : ($l + u + 1$, M) array_like
Banded matrix

b : (M,) or (M, K) array_like
Right-hand side

overwrite_ab : bool, optional
Discard data in *ab* (may enhance performance)

overwrite_b : bool, optional
Discard data in *b* (may enhance performance)

check_finite : bool, optional
Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x : (M,) or (M, K) ndarray
The solution to the system a x = b. Returned shape depends on the shape of *b*.

`scipy.linalg.`**`solveh_banded`**(*ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *lower=False*, *check_finite=True*)

Solve equation a x = b. a is Hermitian positive-definite banded matrix.

The matrix a is stored in *ab* either in lower diagonal or upper diagonal ordered form:

> ab[u + i - j, j] == a[i,j] (if upper form; i <= j) ab[i - j, j] == a[i,j] (if lower form; i >= j)

Example of *ab* (shape of a is (6, 6), *u* =2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters **ab** : (u + 1, M) array_like
Banded matrix
b : (M,) or (M, K) array_like
Right-hand side
overwrite_ab : bool, optional
Discard data in *ab* (may enhance performance)
overwrite_b : bool, optional
Discard data in *b* (may enhance performance)
lower : bool, optional
Is the matrix in the lower form. (Default is upper form)
check_finite : bool, optional
Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **x** : (M,) or (M, K) ndarray
The solution to the system a x = b. Shape of return matches shape of *b*.

`scipy.linalg.`**`solve_circulant`**(*c*, *b*, *singular='raise'*, *tol=None*, *caxis=-1*, *baxis=0*, *outaxis=0*)

Solve C x = b for x, where C is a circulant matrix.

C is the circulant matrix associated with the vector *c*.

The system is solved by doing division in Fourier space. The calculation is:

```
x = ifft(fft(b) / fft(c))
```

where *fft* and *ifft* are the fast Fourier transform and its inverse, respectively. For a large vector *c*, this is *much* faster than solving the system with the full circulant matrix.

Parameters **c** : array_like
The coefficients of the circulant matrix.
b : array_like
Right-hand side matrix in `a x = b`.
singular : str, optional
This argument controls how a near singular circulant matrix is handled. If *singular* is “raise” and the circulant matrix is near singular, a `LinAlgError` is raised. If *singular* is “lstsq”, the least squares solution is returned. Default is “raise”.
tol : float, optional
If any eigenvalue of the circulant matrix has an absolute value that is less than or equal to *tol*, the matrix is considered to be near singular. If not given, *tol* is set to:

```
tol = abs_eigs.max() * abs_eigs.size * np.finfo(np.float64).eps
```

where *abs_eigs* is the array of absolute values of the eigenvalues of the circulant matrix.
caxis : int
When *c* has dimension greater than 1, it is viewed as a collection of circulant vectors. In this case, *caxis* is the axis of *c* that holds the vectors of circulant coefficients.
baxis : int
When *b* has dimension greater than 1, it is viewed as a collection of vectors. In this case, *baxis* is the axis of *b* that holds the right-hand side vectors.
outaxis : int
When *c* or *b* are multidimensional, the value returned by `solve_circulant` is multidimensional. In this case, *outaxis* is the axis of the result that holds the solution vectors.

Returns **x** : ndarray
Solution to the system `C x = b`.

Raises **LinAlgError**

If the circulant matrix associated with *c* is near singular.

See also:

`circulant`

Notes

For a one-dimensional vector *c* with length *m*, and an array *b* with shape `(m, ...)`,

solve_circulant(c, b)

returns the same result as

solve(circulant(c), b)

where `solve` and `circulant` are from `scipy.linalg`.

New in version 0.16.0.

Examples

```
>>> from scipy.linalg import solve_circulant, solve, circulant, lstsq

>>> c = np.array([2, 2, 4])
>>> b = np.array([1, 2, 3])
>>> solve_circulant(c, b)
array([ 0.75, -0.25,  0.25])
```

Compare that result to solving the system with `scipy.linalg.solve`:

```
>>> solve(circulant(c), b)
array([ 0.75, -0.25,  0.25])
```

A singular example:

```
>>> c = np.array([1, 1, 0, 0])
>>> b = np.array([1, 2, 3, 4])
```

Calling `solve_circulant(c, b)` will raise a `LinAlgError`. For the least square solution, use the option `singular='lstsq'`:

```
>>> solve_circulant(c, b, singular='lstsq')
array([ 0.25,  1.25,  2.25,  1.25])
```

Compare to `scipy.linalg.lstsq`:

```
>>> x, resid, rnk, s = lstsq(circulant(c), b)
>>> x
array([ 0.25,  1.25,  2.25,  1.25])
```

A broadcasting example:

Suppose we have the vectors of two circulant matrices stored in an array with shape (2, 5), and three *b* vectors stored in an array with shape (3, 5). For example,

```
>>> c = np.array([[1.5, 2, 3, 0, 0], [1, 1, 4, 3, 2]])
>>> b = np.arange(15).reshape(-1, 5)
```

We want to solve all combinations of circulant matrices and *b* vectors, with the result stored in an array with shape (2, 3, 5). When we disregard the axes of *c* and *b* that hold the vectors of coefficients, the shapes of the collections are (2,) and (3,), respectively, which are not compatible for broadcasting. To have a broadcast result with shape (2, 3), we add a trivial dimension to *c*: `c[:, np.newaxis, :]` has shape (2, 1, 5). The last dimension holds the coefficients of the circulant matrices, so when we call `solve_circulant`, we can use the default `caxis=-1`. The coefficients of the *b* vectors are in the last dimension of the array *b*, so we use `baxis=-1`. If we use the default *outaxis*, the result will have shape (5, 2, 3), so we'll use `outaxis=-1` to put the solution vectors in the last dimension.

```
>>> x = solve_circulant(c[:, np.newaxis, :], b, baxis=-1, outaxis=-1)
>>> x.shape
(2, 3, 5)
>>> np.set_printoptions(precision=3)  # For compact output of numbers.
>>> x
array([[[-0.118,  0.22 ,  1.277, -0.142,  0.302],
        [ 0.651,  0.989,  2.046,  0.627,  1.072],
        [ 1.42 ,  1.758,  2.816,  1.396,  1.841]],
       [[ 0.401,  0.304,  0.694, -0.867,  0.377],
        [ 0.856,  0.758,  1.149, -0.412,  0.831],
        [ 1.31 ,  1.213,  1.603,  0.042,  1.286]]])
```

Check by solving one pair of *c* and *b* vectors (cf. `x[1, 1, :]`):

```
>>> solve_circulant(c[1], b[1, :])
array([ 0.856,  0.758,  1.149, -0.412,  0.831])
```

`scipy.linalg.`**`solve_triangular`**`(`*a*, *b*, *trans=0*, *lower=False*, *unit_diagonal=False*, *overwrite_b=False*, *debug=False*, *check_finite=True*`)`

Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.

Parameters

a : (M, M) array_like

A triangular matrix

b : (M,) or (M, N) array_like

Right-hand side matrix in *a x = b*

lower : bool, optional

Use only data contained in the lower triangle of *a*. Default is to use upper triangle.

trans : {0, 1, 2, 'N', 'T', 'C'}, optional

Type of system to solve:

trans	system
0 or 'N'	a x = b
1 or 'T'	a^T x = b
2 or 'C'	a^H x = b

unit_diagonal : bool, optional

If True, diagonal elements of *a* are assumed to be 1 and will not be referenced.

overwrite_b : bool, optional

Allow overwriting data in *b* (may enhance performance)

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x : (M,) or (M, N) ndarray

Solution to the system *a x = b*. Shape of return matches *b*.

Raises

LinAlgError

If *a* is singular

Notes

New in version 0.9.0.

`scipy.linalg.`**`solve_toeplitz`**`(`*c_or_cr*, *b*, *check_finite=True*`)`

Solve a Toeplitz system using Levinson Recursion

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, `r == conjugate(c)` is assumed.

Parameters **c_or_cr** : array_like or tuple of (array_like, array_like)

The vector `c`, or a tuple of arrays (`c`, `r`). Whatever the actual shape of `c`, it will be converted to a 1-D array. If not supplied, `r = conjugate(c)` is assumed; in this case, if c[0] is real, the Toeplitz matrix is Hermitian. r[0] is ignored; the first row of the Toeplitz matrix is `[c[0], r[1:]]`. Whatever the actual shape of `r`, it will be converted to a 1-D array.

b : (M,) or (M, K) array_like

Right-hand side in `T x = b`.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (result entirely NaNs) if the inputs do contain infinities or NaNs.

Returns **x** : (M,) or (M, K) ndarray

The solution to the system `T x = b`. Shape of return matches shape of *b*.

Notes

The solution is computed using Levinson-Durbin recursion, which is faster than generic least-squares methods, but can be less numerically stable.

`scipy.linalg.`**`det`**`(`*a*, *overwrite_a=False*, *check_finite=True*`)`

Compute the determinant of a matrix

The determinant of a square matrix is a value derived arithmetically from the coefficients of the matrix.

The determinant for a 3x3 matrix, for example, is computed as follows:

```
a    b    c
d    e    f = A
g    h    i

det(A) = a*e*i + b*f*g + c*d*h - c*e*g - b*d*i - a*f*h
```

Parameters **a** : (M, M) array_like

A square matrix.

overwrite_a : bool, optional

Allow overwriting data in a (may enhance performance).

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **det** : float or complex

Determinant of *a*.

Notes

The determinant is computed via LU factorization, LAPACK routine z/dgetrf.

Examples

```
>>> from scipy import linalg
>>> a = np.array([[1,2,3], [4,5,6], [7,8,9]])
>>> linalg.det(a)
0.0
>>> a = np.array([[0,2,3], [4,5,6], [7,8,9]])
```

```
>>> linalg.det(a)
3.0
```

`scipy.linalg.`**`norm`**`(`*a*, *ord=None*`)`

Matrix or vector norm.

This function is able to return one of seven different matrix norms, or one of an infinite number of vector norms (described below), depending on the value of the `ord` parameter.

Parameters	**a** : (M,) or (M, N) array_like Input array. **ord** : {non-zero int, inf, -inf, 'fro'}, optional Order of the norm (see table under `Notes`). inf means numpy's *inf* object.
Returns	**norm** : float Norm of the matrix or vector.

Notes

For values of `ord <= 0`, the result is, strictly speaking, not a mathematical 'norm', but it may still be useful for various numerical purposes.

The following norms can be calculated:

ord	norm for matrices	norm for vectors
None	Frobenius norm	2-norm
'fro'	Frobenius norm	–
inf	max(sum(abs(x), axis=1))	max(abs(x))
-inf	min(sum(abs(x), axis=1))	min(abs(x))
0	–	sum(x != 0)
1	max(sum(abs(x), axis=0))	as below
-1	min(sum(abs(x), axis=0))	as below
2	2-norm (largest sing. value)	as below
-2	smallest singular value	as below
other	–	sum(abs(x)**ord)**(1./ord)

The Frobenius norm is given by [R86]:

$$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$$

References

[R86]

Examples

```
>>> from scipy.linalg import norm
>>> a = np.arange(9) - 4
>>> a
array([-4, -3, -2, -1,  0,  1,  2,  3,  4])
>>> b = a.reshape((3, 3))
>>> b
array([[-4, -3, -2],
       [-1,  0,  1],
       [ 2,  3,  4]])

>>> norm(a)
7.745966692414834
>>> norm(b)
7.745966692414834
```

```
>>> norm(b, 'fro')
7.745966692414834
>>> norm(a, np.inf)
4
>>> norm(b, np.inf)
9
>>> norm(a, -np.inf)
0
>>> norm(b, -np.inf)
2

>>> norm(a, 1)
20
>>> norm(b, 1)
7
>>> norm(a, -1)
-4.6566128774142013e-010
>>> norm(b, -1)
6
>>> norm(a, 2)
7.745966692414834
>>> norm(b, 2)
7.3484692283495345

>>> norm(a, -2)
nan
>>> norm(b, -2)
1.8570331885190563e-016
>>> norm(a, 3)
5.8480354764257312
>>> norm(a, -3)
nan
```

`scipy.linalg.`**`lstsq`**(*a*, *b*, *cond=None*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*)

Compute least-squares solution to equation Ax = b.

Compute a vector x such that the 2-norm `|b - A x|` is minimized.

Parameters **a** : (M, N) array_like

Left hand side matrix (2-D array).

b : (M,) or (M, K) array_like

Right hand side matrix or vector (1-D or 2-D array).

cond : float, optional

Cutoff for 'small' singular values; used to determine effective rank of a. Singular values smaller than `rcond * largest_singular_value` are considered zero.

overwrite_a : bool, optional

Discard data in *a* (may enhance performance). Default is False.

overwrite_b : bool, optional

Discard data in *b* (may enhance performance). Default is False.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **x** : (N,) or (N, K) ndarray

Least-squares solution. Return shape matches shape of *b*.

residues : () or (1,) or (K,) ndarray

Sums of residues, squared 2-norm for each column in `b - a x`. If rank of matrix a is < N or > M this is an empty array. If b was 1-D, this is an (1,) shape array, otherwise the shape is (K,).

rank : int

Effective rank of matrix *a*.

s : (min(M,N),) ndarray

Singular values of *a*. The condition number of a is `abs(s[0]/s[-1])`.

Raises **LinAlgError :**

If computation does not converge.

See also:

`optimize.nnls`
linear least squares with non-negativity constraint

`scipy.linalg.`**`pinv`**(*a*, *cond=None*, *rcond=None*, *return_rank=False*, *check_finite=True*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using a least-squares solver.

Parameters **a** : (M, N) array_like

Matrix to be pseudo-inverted.

cond, rcond : float, optional

Cutoff for 'small' singular values in the least-squares solver. Singular values smaller than `rcond * largest_singular_value` are considered zero.

return_rank : bool, optional

if True, return the effective rank of the matrix

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **B** : (N, M) ndarray

The pseudo-inverse of matrix *a*.

rank : int

The effective rank of the matrix. Returned if return_rank == True

Raises **LinAlgError**

If computation does not converge.

Examples

```
>>> from scipy import linalg
>>> a = np.random.randn(9, 6)
>>> B = linalg.pinv(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

`scipy.linalg.`**`pinv2`**(*a*, *cond=None*, *rcond=None*, *return_rank=False*, *check_finite=True*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using its singular-value decomposition and including all 'large' singular values.

Parameters **a** : (M, N) array_like

Matrix to be pseudo-inverted.

cond, rcond : float or None

Cutoff for ‘small’ singular values. Singular values smaller than `rcond*largest_singular_value` are considered zero. If None or -1, suitable machine precision is used.

return_rank : bool, optional

if True, return the effective rank of the matrix

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

B : (N, M) ndarray

The pseudo-inverse of matrix *a*.

rank : int

The effective rank of the matrix. Returned if return_rank == True

Raises

LinAlgError

If SVD computation does not converge.

Examples

```
>>> from scipy import linalg
>>> a = np.random.randn(9, 6)
>>> B = linalg.pinv2(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

`scipy.linalg.`**`pinvh`**(*a*, *cond=None*, *rcond=None*, *lower=True*, *return_rank=False*, *check_finite=True*)

Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.

Calculate a generalized inverse of a Hermitian or real symmetric matrix using its eigenvalue decomposition and including all eigenvalues with ‘large’ absolute value.

Parameters

a : (N, N) array_like

Real symmetric or complex hermetian matrix to be pseudo-inverted

cond, rcond : float or None

Cutoff for ‘small’ eigenvalues. Singular values smaller than rcond * largest_eigenvalue are considered zero.

If None or -1, suitable machine precision is used.

lower : bool, optional

Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

return_rank : bool, optional

if True, return the effective rank of the matrix

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

B : (N, N) ndarray

The pseudo-inverse of matrix *a*.

rank : int

The effective rank of the matrix. Returned if return_rank == True

Raises

LinAlgError

If eigenvalue does not converge

Examples

```
>>> from scipy.linalg import pinvh
>>> a = np.random.randn(9, 6)
>>> a = np.dot(a, a.T)
>>> B = pinvh(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

`scipy.linalg.`**`kron`**`(`*a*, *b*`)`

Kronecker product.

The result is the block matrix:

```
a[0,0]*b    a[0,1]*b  ... a[0,-1]*b
a[1,0]*b    a[1,1]*b  ... a[1,-1]*b
...
a[-1,0]*b   a[-1,1]*b ... a[-1,-1]*b
```

Parameters **a** : (M, N) ndarray

Input array

b : (P, Q) ndarray

Input array

Returns **A** : (M*P, N*Q) ndarray

Kronecker product of *a* and *b*.

Examples

```
>>> from numpy import array
>>> from scipy.linalg import kron
>>> kron(array([[1,2],[3,4]]), array([[1,1,1]]))
array([[1, 1, 1, 2, 2, 2],
       [3, 3, 3, 4, 4, 4]])
```

`scipy.linalg.`**`tril`**`(`*m*, *k=0*`)`

Make a copy of a matrix with elements above the k-th diagonal zeroed.

Parameters **m** : array_like

Matrix whose elements to return

k : int, optional

Diagonal above which to zero elements. $k == 0$ is the main diagonal, $k < 0$ subdiagonal and $k > 0$ superdiagonal.

Returns **tril** : ndarray

Return is the same shape and type as *m*.

Examples

```
>>> from scipy.linalg import tril
>>> tril([[1,2,3],[4,5,6],[7,8,9],[10,11,12]], -1)
array([[ 0,  0,  0],
       [ 4,  0,  0],
       [ 7,  8,  0],
       [10, 11, 12]])
```

`scipy.linalg.`**`triu`**`(`*m*, *k=0*`)`

Make a copy of a matrix with elements below the k-th diagonal zeroed.

Parameters **m** : array_like

Matrix whose elements to return

k : int, optional

Diagonal below which to zero elements. $k == 0$ is the main diagonal, $k < 0$ subdiagonal and $k > 0$ superdiagonal.

Returns **triu** : ndarray

Return matrix with zeroed elements below the k-th diagonal and has same shape and type as *m*.

Examples

```
>>> from scipy.linalg import triu
>>> triu([[1,2,3],[4,5,6],[7,8,9],[10,11,12]], -1)
array([[ 1,  2,  3],
       [ 4,  5,  6],
       [ 0,  8,  9],
       [ 0,  0, 12]])
```

`scipy.linalg.`**`orthogonal_procrustes`**(*A*, *B*, *check_finite=True*)

Compute the matrix solution of the orthogonal Procrustes problem.

Given matrices A and B of equal shape, find an orthogonal matrix R that most closely maps A to B [R87]. Note that unlike higher level Procrustes analyses of spatial data, this function only uses orthogonal transformations like rotations and reflections, and it does not use scaling or translation.

Parameters **A** : (M, N) array_like

Matrix to be mapped.

B : (M, N) array_like

Target matrix.

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **R** : (N, N) ndarray

The matrix solution of the orthogonal Procrustes problem. Minimizes the Frobenius norm of dot(A, R) - B, subject to dot(R.T, R) == I.

scale : float

Sum of the singular values of `dot(A.T, B)`.

Raises **ValueError**

If the input arrays are incompatibly shaped. This may also be raised if matrix A or B contains an inf or nan and check_finite is True, or if the matrix product AB contains an inf or nan.

Notes

New in version 0.15.0.

References

[R87]

5.9.2 Eigenvalue Problems

`eig`(a[, b, left, right, overwrite_a, ...])	Solve an ordinary or generalized eigenvalue problem of a square matrix.

Cor

Table 5.68 – continued from previous page

`eigvals`(a[, b, overwrite_a, check_finite])	Compute eigenvalues from an ordinary or generalized eigenvalue problem.
`eigh`(a[, b, lower, eigvals_only, ...])	Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or
`eigvalsh`(a[, b, lower, overwrite_a, ...])	Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or
`eig_banded`(a_band[, lower, eigvals_only, ...])	Solve real symmetric or complex hermitian band matrix eigenvalue problem.
`eigvals_banded`(a_band[, lower, ...])	Solve real symmetric or complex hermitian band matrix eigenvalue problem.

`scipy.linalg.`**`eig`**(*a*, *b=None*, *left=False*, *right=True*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*)

Solve an ordinary or generalized eigenvalue problem of a square matrix.

Find eigenvalues w and right or left eigenvectors of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
a.H vl[:,i] = w[i].conj() b.H vl[:,i]
```

where `.H` is the Hermitian conjugation.

Parameters

a : (M, M) array_like
A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b : (M, M) array_like, optional
Right-hand side matrix in a generalized eigenvalue problem. Default is None, identity matrix is assumed.

left : bool, optional
Whether to calculate and return left eigenvectors. Default is False.

right : bool, optional
Whether to calculate and return right eigenvectors. Default is True.

overwrite_a : bool, optional
Whether to overwrite *a*; may improve performance. Default is False.

overwrite_b : bool, optional
Whether to overwrite *b*; may improve performance. Default is False.

check_finite : bool, optional
Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

w : (M,) double or complex ndarray
The eigenvalues, each repeated according to its multiplicity.

vl : (M, M) double or complex ndarray
The normalized left eigenvector corresponding to the eigenvalue `w[i]` is the column vl[:,i]. Only returned if `left=True`.

vr : (M, M) double or complex ndarray
The normalized right eigenvector corresponding to the eigenvalue `w[i]` is the column `vr[:,i]`. Only returned if `right=True`.

Raises

LinAlgError
If eigenvalue computation does not converge.

See also:

`eigh`	Eigenvalues and right eigenvectors for symmetric/Hermitian arrays.

`scipy.linalg.`**`eigvals`**(*a*, *b=None*, *overwrite_a=False*, *check_finite=True*)

Compute eigenvalues from an ordinary or generalized eigenvalue problem.

Find eigenvalues of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
```

Parameters **a** : (M, M) array_like
A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b : (M, M) array_like, optional
Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

overwrite_a : bool, optional
Whether to overwrite data in a (may improve performance)

check_finite : bool, optional
Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **w** : (M,) double or complex ndarray
The eigenvalues, each repeated according to its multiplicity, but not in any specific order.

Raises **LinAlgError**
If eigenvalue computation does not converge

See also:

eigvalsh	eigenvalues of symmetric or Hermitian arrays,
eig	eigenvalues and right eigenvectors of general arrays.
eigh	eigenvalues and eigenvectors of symmetric/Hermitian arrays.

`scipy.linalg.`**`eigh`**(*a*, *b=None*, *lower=True*, *eigvals_only=False*, *overwrite_a=False*, *overwrite_b=False*, *turbo=True*, *eigvals=None*, *type=1*, *check_finite=True*)

Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues w and optionally eigenvectors v of matrix *a*, where *b* is positive definite:

```
                a v[:,i] = w[i] b v[:,i]
v[i,:].conj() a v[:,i] = w[i]
v[i,:].conj() b v[:,i] = 1
```

Parameters **a** : (M, M) array_like
A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

b : (M, M) array_like, optional
A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower : bool, optional
Whether the pertinent array data is taken from the lower or upper triangle of *a*. (Default: lower)

eigvals_only : bool, optional
Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)

turbo : bool, optional
Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

eigvals : tuple (lo, hi), optional

Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo <= hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

type : int, optional

Specifies the problem type to be solved:

type = 1: a v[:,i] = w[i] b v[:,i]
type = 2: a b v[:,i] = w[i] v[:,i]
type = 3: b a v[:,i] = w[i] v[:,i]

overwrite_a : bool, optional

Whether to overwrite data in *a* (may improve performance)

overwrite_b : bool, optional

Whether to overwrite data in *b* (may improve performance)

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

w : (N,) float ndarray

The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

v : (M, N) complex ndarray

(if eigvals_only == False)

The normalized selected eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

Normalization:

type 1 and 3: v.conj() a v = w
type 2: inv(v).conj() a inv(v) = w
type = 1 or 2: v.conj() b v = I
type = 3: v.conj() inv(b) v = I

Raises

LinAlgError :

If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or hermitian, no error is reported but results will be wrong.

See also:

`eig` eigenvalues and right eigenvectors for non-symmetric arrays

scipy.linalg.**eigvalsh**(*a*, *b=None*, *lower=True*, *overwrite_a=False*, *overwrite_b=False*, *turbo=True*, *eigvals=None*, *type=1*, *check_finite=True*)

Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues w of matrix a, where b is positive definite:

```
              a v[:,i] = w[i] b v[:,i]
v[i,:].conj() a v[:,i] = w[i]
v[i,:].conj() b v[:,i] = 1
```

Parameters

a : (M, M) array_like

A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

b : (M, M) array_like, optional

A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower : bool, optional

Whether the pertinent array data is taken from the lower or upper triangle of *a*. (Default: lower)

turbo : bool, optional

Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

eigvals : tuple (lo, hi), optional

Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo < hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

type : int, optional

Specifies the problem type to be solved:

type = 1: a v[:,i] = w[i] b v[:,i]
type = 2: a b v[:,i] = w[i] v[:,i]
type = 3: b a v[:,i] = w[i] v[:,i]

overwrite_a : bool, optional

Whether to overwrite data in *a* (may improve performance)

overwrite_b : bool, optional

Whether to overwrite data in *b* (may improve performance)

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **w** : (N,) float ndarray

The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises **LinAlgError :**

If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or hermitian, no error is reported but results will be wrong.

See also:

`eigvals`	eigenvalues of general arrays
`eigh`	eigenvalues and right eigenvectors for symmetric/Hermitian arrays
`eig`	eigenvalues and right eigenvectors for non-symmetric arrays

`scipy.linalg.`**`eig_banded`**(*a_band*, *lower=False*, *eigvals_only=False*, *overwrite_a_band=False*, *select='a'*, *select_range=None*, *max_ev=0*, *check_finite=True*)

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w and optionally right eigenvectors v of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

a_band[u + i - j, j] == a[i,j] (if upper form; i <= j) a_band[i - j, j] == a[i,j] (if lower form; i >= j)

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
```

```
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters

a_band : (u+1, M) array_like
The bands of the M by M matrix a.

lower : bool, optional
Is the matrix in the lower form. (Default is upper form)

eigvals_only : bool, optional
Compute only the eigenvalues and no eigenvectors. (Default: calculate also eigenvectors)

overwrite_a_band : bool, optional
Discard data in a_band (may enhance performance)

select : {'a', 'v', 'i'}, optional
Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range : (min, max), optional
Range of selected eigenvalues

max_ev : int, optional
For select=='v', maximum number of eigenvalues expected. For other values of select, has no meaning.
In doubt, leave this parameter untouched.

check_finite : bool, optional
Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

w : (M,) ndarray
The eigenvalues, in ascending order, each repeated according to its multiplicity.

v : (M, M) float or complex ndarray
The normalized eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

Raises LinAlgError if eigenvalue computation does not converge

`scipy.linalg.`**`eigvals_banded`**(*a_band*, *lower=False*, *overwrite_a_band=False*, *select='a'*, *select_range=None*, *check_finite=True*)

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

> a_band[u + i - j, j] == a[i,j] (if upper form; i <= j) a_band[i - j, j] == a[i,j] (if lower form; i >= j)

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters **a_band** : (u+1, M) array_like

The bands of the M by M matrix a.

lower : bool, optional

Is the matrix in the lower form. (Default is upper form)

overwrite_a_band : bool, optional

Discard data in a_band (may enhance performance)

select : {'a', 'v', 'i'}, optional

Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range : (min, max), optional

Range of selected eigenvalues

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns **w** : (M,) ndarray

The eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises LinAlgError if eigenvalue computation does not converge

See also:

eig_banded	eigenvalues and right eigenvectors for symmetric/Hermitian band matrices
eigvals	eigenvalues of general arrays
eigh	eigenvalues and right eigenvectors for symmetric/Hermitian arrays
eig	eigenvalues and right eigenvectors for non-symmetric arrays

5.9.3 Decompositions

`lu`(a[, permute_l, overwrite_a, check_finite])	Compute pivoted LU decomposition of a matrix.
`lu_factor`(a[, overwrite_a, check_finite])	Compute pivoted LU decomposition of a matrix.
`lu_solve`(lu_and_piv, b[, trans, ...])	Solve an equation system, a x = b, given the LU factorization of a
`svd`(a[, full_matrices, compute_uv, ...])	Singular Value Decomposition.
`svdvals`(a[, overwrite_a, check_finite])	Compute singular values of a matrix.
`diagsvd`(s, M, N)	Construct the sigma matrix in SVD from singular values and size M, N.
`orth`(A)	Construct an orthonormal basis for the range of A using SVD
`cholesky`(a[, lower, overwrite_a, check_finite])	Compute the Cholesky decomposition of a matrix.

Continued on next page

Table 5.69 – continued from previous page

`cholesky_banded`(ab[, overwrite_ab, lower, ...])	Cholesky decompose a banded Hermitian positive-definite matrix
`cho_factor`(a[, lower, overwrite_a, check_finite])	Compute the Cholesky decomposition of a matrix, to use in cho_solve
`cho_solve`(c_and_lower, b[, overwrite_b, ...])	Solve the linear equations A x = b, given the Cholesky factorization of A.
`cho_solve_banded`(cb_and_lower, b[, ...])	Solve the linear equations A x = b, given the Cholesky factorization of A.
`polar`(a[, side])	Compute the polar decomposition.
`qr`(a[, overwrite_a, lwork, mode, pivoting, ...])	Compute QR decomposition of a matrix.
`qr_multiply`(a, c[, mode, pivoting, ...])	Calculate the QR decomposition and multiply Q with a matrix.
`qr_update`(Q, R, u, v[, overwrite_qruv, ...])	Rank-k QR update
`qr_delete`(Q, R, k[, p, which, overwrite_qr, ...])	QR downdate on row or column deletions
`qr_insert`(Q, R, u, k[, which, rcond, ...])	QR update on row or column insertions
`rq`(a[, overwrite_a, lwork, mode, check_finite])	Compute RQ decomposition of a matrix.
`qz`(A, B[, output, lwork, sort, overwrite_a, ...])	QZ decomposition for generalized eigenvalues of a pair of matrices.
`schur`(a[, output, lwork, overwrite_a, sort, ...])	Compute Schur decomposition of a matrix.
`rsf2csf`(T, Z[, check_finite])	Convert real Schur form to complex Schur form.
`hessenberg`(a[, calc_q, overwrite_a, ...])	Compute Hessenberg form of a matrix.

`scipy.linalg.`**`lu`**(*a*, *permute_l=False*, *overwrite_a=False*, *check_finite=True*)

Compute pivoted LU decomposition of a matrix.

The decomposition is:

```
A = P L U
```

where P is a permutation matrix, L lower triangular with unit diagonal elements, and U upper triangular.

Parameters

a : (M, N) array_like
  Array to decompose

permute_l : bool, optional
  Perform the multiplication P*L (Default: do not permute)

overwrite_a : bool, optional
  Whether to overwrite data in a (may improve performance)

check_finite : bool, optional
  Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

(If permute_l == False)

p : (M, M) ndarray
  Permutation matrix

l : (M, K) ndarray
  Lower triangular or trapezoidal matrix with unit diagonal. K = min(M, N)

u : (K, N) ndarray
  Upper triangular or trapezoidal matrix

(If permute_l == True)

pl : (M, K) ndarray
  Permuted L matrix. K = min(M, N)

u : (K, N) ndarray
  Upper triangular or trapezoidal matrix

Notes

This is a LU factorization routine written for Scipy.

`scipy.linalg.`**`lu_factor`**(*a*, *overwrite_a=False*, *check_finite=True*)

Compute pivoted LU decomposition of a matrix.

The decomposition is:

```
A = P L U
```

where P is a permutation matrix, L lower triangular with unit diagonal elements, and U upper triangular.

Parameters

a : (M, M) array_like
  Matrix to decompose

overwrite_a : bool, optional
  Whether to overwrite data in A (may increase performance)

check_finite : bool, optional
  Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

lu : (N, N) ndarray
  Matrix containing U in its upper triangle, and L in its lower triangle. The unit diagonal elements of L are not stored.

piv : (N,) ndarray
  Pivot indices representing the permutation matrix P: row i of matrix was interchanged with row piv[i].

See also:

`lu_solve`	solve an equation system using the LU factorization of a matrix

Notes

This is a wrapper to the `*GETRF` routines from LAPACK.

`scipy.linalg.`**`lu_solve`**(*lu_and_piv*, *b*, *trans=0*, *overwrite_b=False*, *check_finite=True*)

Solve an equation system, a x = b, given the LU factorization of a

Parameters

(lu, piv)
  Factorization of the coefficient matrix a, as given by lu_factor

b : array
  Right-hand side

trans : {0, 1, 2}, optional
  Type of system to solve:

trans	system
0	a x = b
1	a^T x = b
2	a^H x = b

overwrite_b : bool, optional
  Whether to overwrite data in b (may increase performance)

check_finite : bool, optional
  Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x : array
  Solution to the system

See also:

`lu_factor`	LU factorize a matrix

`scipy.linalg.`**`svd`**(*a*, *full_matrices=True*, *compute_uv=True*, *overwrite_a=False*, *check_finite=True*)

Singular Value Decomposition.

Factorizes the matrix a into two unitary matrices U and Vh, and a 1-D array s of singular values (real, non-negative) such that `a == U*S*Vh`, where S is a suitably shaped matrix of zeros with main diagonal s.

Parameters

a : (M, N) array_like
Matrix to decompose.

full_matrices : bool, optional
If True, *U* and *Vh* are of shape `(M,M)`, `(N,N)`. If False, the shapes are `(M,K)` and `(K,N)`, where `K = min(M,N)`.

compute_uv : bool, optional
Whether to compute also *U* and *Vh* in addition to `s`. Default is True.

overwrite_a : bool, optional
Whether to overwrite *a*; may improve performance. Default is False.

check_finite : bool, optional
Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

U : ndarray
Unitary matrix having left singular vectors as columns. Of shape `(M,M)` or `(M,K)`, depending on *full_matrices*.

s : ndarray
The singular values, sorted in non-increasing order. Of shape (K,), with `K = min(M, N)`.

Vh : ndarray
Unitary matrix having right singular vectors as rows. Of shape `(N,N)` or `(K,N)` depending on *full_matrices*.

For `compute_uv = False`, only `s` is returned.

Raises

LinAlgError
If SVD computation does not converge.

See also:

`svdvals`	Compute singular values of a matrix.
`diagsvd`	Construct the Sigma matrix, given the vector s.

Examples

```
>>> from scipy import linalg
>>> a = np.random.randn(9, 6) + 1.j*np.random.randn(9, 6)
>>> U, s, Vh = linalg.svd(a)
>>> U.shape, Vh.shape, s.shape
((9, 9), (6, 6), (6,))

>>> U, s, Vh = linalg.svd(a, full_matrices=False)
>>> U.shape, Vh.shape, s.shape
((9, 6), (6, 6), (6,))
>>> S = linalg.diagsvd(s, 6, 6)
>>> np.allclose(a, np.dot(U, np.dot(S, Vh)))
True

>>> s2 = linalg.svd(a, compute_uv=False)
>>> np.allclose(s, s2)
True
```

`scipy.linalg.`**`svdvals`**`(`*a*, *overwrite_a=False*, *check_finite=True*`)`

Compute singular values of a matrix.

Parameters	**a** : (M, N) array_like Matrix to decompose. **overwrite_a** : bool, optional Whether to overwrite *a*; may improve performance. Default is False. **check_finite** : bool, optional Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
Returns	**s** : (min(M, N),) ndarray The singular values, sorted in decreasing order.
Raises	**LinAlgError** If SVD computation does not converge.

See also:

`svd`	Compute the full singular value decomposition of a matrix.
`diagsvd`	Construct the Sigma matrix, given the vector s.

Notes

`svdvals(a)` only differs from `svd(a, compute_uv=False)` by its handling of the edge case of empty `a`, where it returns an empty sequence:

```
>>> a = np.empty((0, 2))
>>> from scipy.linalg import svdvals
>>> svdvals(a)
array([], dtype=float64)
```

`scipy.linalg.`**`diagsvd`**`(`*s*, *M*, *N*`)`

Construct the sigma matrix in SVD from singular values and size M, N.

Parameters	**s** : (M,) or (N,) array_like Singular values **M** : int Size of the matrix whose singular values are `s`. **N** : int Size of the matrix whose singular values are `s`.
Returns	**S** : (M, N) ndarray The S-matrix in the singular value decomposition

`scipy.linalg.`**`orth`**`(`*A*`)`

Construct an orthonormal basis for the range of A using SVD

Parameters	**A** : (M, N) array_like Input array
Returns	**Q** : (M, K) ndarray Orthonormal basis for the range of A. K = effective rank of A, as determined by automatic cutoff

See also:

`svd`	Singular value decomposition of a matrix

`scipy.linalg.`**`cholesky`**(*a*, *lower=False*, *overwrite_a=False*, *check_finite=True*)

Compute the Cholesky decomposition of a matrix.

Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.

Parameters

a : (M, M) array_like
    Matrix to be decomposed

lower : bool, optional
    Whether to compute the upper or lower triangular Cholesky factorization. Default is upper-triangular.

overwrite_a : bool, optional
    Whether to overwrite data in *a* (may improve performance).

check_finite : bool, optional
    Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c : (M, M) ndarray
    Upper- or lower-triangular Cholesky factor of *a*.

Raises

LinAlgError : if decomposition fails.

Examples

```
>>> from scipy import array, linalg, dot
>>> a = array([[1,-2j],[2j,5]])
>>> L = linalg.cholesky(a, lower=True)
>>> L
array([[ 1.+0.j,  0.+0.j],
       [ 0.+2.j,  1.+0.j]])
>>> dot(L, L.T.conj())
array([[ 1.+0.j,  0.-2.j],
       [ 0.+2.j,  5.+0.j]])
```

`scipy.linalg.`**`cholesky_banded`**(*ab*, *overwrite_ab=False*, *lower=False*, *check_finite=True*)

Cholesky decompose a banded Hermitian positive-definite matrix

The matrix a is stored in ab either in lower diagonal or upper diagonal ordered form:

```
ab[u + i - j, j] == a[i,j]        (if upper form; i <= j)
ab[    i - j, j] == a[i,j]        (if lower form; i >= j)
```

Example of ab (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Parameters

ab : (u + 1, M) array_like
    Banded matrix

overwrite_ab : bool, optional
    Discard data in ab (may enhance performance)

lower : bool, optional
    Is the matrix in the lower form. (Default is upper form)

check_finite : bool, optional
Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c : (u + 1, M) ndarray
Cholesky factorization of a, in the same banded format as ab

`scipy.linalg.`**`cho_factor`**`(`*a*, *lower=False*, *overwrite_a=False*, *check_finite=True*`)`

Compute the Cholesky decomposition of a matrix, to use in cho_solve

Returns a matrix containing the Cholesky decomposition, `A = L L*` or `A = U* U` of a Hermitian positive-definite matrix *a*. The return value can be directly used as the first parameter to cho_solve.

Warning: The returned matrix also contains random data in the entries not used by the Cholesky decomposition. If you need to zero these entries, use the function `cholesky` instead.

Parameters

a : (M, M) array_like
Matrix to be decomposed

lower : bool, optional
Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

overwrite_a : bool, optional
Whether to overwrite data in a (may improve performance)

check_finite : bool, optional
Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c : (M, M) ndarray
Matrix whose upper or lower triangle contains the Cholesky factor of *a*. Other parts of the matrix contain random data.

lower : bool
Flag indicating whether the factor is in the lower or upper triangle

Raises

LinAlgError
Raised if decomposition fails.

See also:

`cho_solve`	Solve a linear set equations using the Cholesky factorization of a matrix.

`scipy.linalg.`**`cho_solve`**`(`*c_and_lower*, *b*, *overwrite_b=False*, *check_finite=True*`)`

Solve the linear equations A x = b, given the Cholesky factorization of A.

Parameters

(c, lower) : tuple, (array, bool)
Cholesky factorization of a, as given by cho_factor

b : array
Right-hand side

overwrite_b : bool, optional
Whether to overwrite data in b (may improve performance)

check_finite : bool, optional
Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x : array
The solution to the system A x = b

See also:

cho_factorCholesky factorization of a matrix

`scipy.linalg.`**`cho_solve_banded`**`(`*cb_and_lower*, *b*, *overwrite_b=False*, *check_finite=True*`)`

Solve the linear equations A x = b, given the Cholesky factorization of A.

Parameters	**(cb, lower)** : tuple, (array, bool) *cb* is the Cholesky factorization of A, as given by cholesky_banded. *lower* must be the same value that was given to cholesky_banded. **b** : array Right-hand side **overwrite_b** : bool, optional If True, the function will overwrite the values in *b*. **check_finite** : bool, optional Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
Returns	**x** : array The solution to the system A x = b

See also:

cholesky_banded
Cholesky factorization of a banded matrix

Notes

New in version 0.8.0.

`scipy.linalg.`**`polar`**`(`*a*, *side='right'*`)`

Compute the polar decomposition.

Returns the factors of the polar decomposition [R88] *u* and *p* such that `a = up` (if *side* is "right") or `a = pu` (if *side* is "left"), where *p* is positive semidefinite. Depending on the shape of *a*, either the rows or columns of *u* are orthonormal. When *a* is a square array, *u* is a square unitary array. When *a* is not square, the "canonical polar decomposition" [R89] is computed.

Parameters	**a** : (m, n) array_like The array to be factored. **side** : {'left', 'right'}, optional Determines whether a right or left polar decomposition is computed. If *side* is "right", then `a = up`. If *side* is "left", then `a = pu`. The default is "right".
Returns	**u** : (m, n) ndarray If *a* is square, then *u* is unitary. If m > n, then the columns of *a* are orthonormal, and if m < n, then the rows of *u* are orthonormal. **p** : ndarray *p* is Hermitian positive semidefinite. If *a* is nonsingular, *p* is positive definite. The shape of *p* is (n, n) or (m, m), depending on whether *side* is "right" or "left", respectively.

References

[R88], [R89]

Examples

```
>>> from scipy.linalg import polar
>>> a = np.array([[1, -1], [2, 4]])
>>> u, p = polar(a)
```

```
>>> u
array([[ 0.85749293, -0.51449576],
       [ 0.51449576,  0.85749293]])
>>> p
array([[ 1.88648444,  1.2004901 ],
       [ 1.2004901 ,  3.94446746]])
```

A non-square example, with m < n:

```
>>> b = np.array([[0.5, 1, 2], [1.5, 3, 4]])
>>> u, p = polar(b)
>>> u
array([[-0.21196618, -0.42393237,  0.88054056],
       [ 0.39378971,  0.78757942,  0.4739708 ]])
>>> p
array([[ 0.48470147,  0.96940295,  1.15122648],
       [ 0.96940295,  1.9388059 ,  2.30245295],
       [ 1.15122648,  2.30245295,  3.65696431]])
>>> u.dot(p)   # Verify the decomposition.
array([[ 0.5,  1. ,  2. ],
       [ 1.5,  3. ,  4. ]])
>>> u.dot(u.T)   # The rows of u are orthonormal.
array([[  1.00000000e+00,  -2.07353665e-17],
       [ -2.07353665e-17,   1.00000000e+00]])
```

Another non-square example, with m > n:

```
>>> c = b.T
>>> u, p = polar(c)
>>> u
array([[-0.21196618,  0.39378971],
       [-0.42393237,  0.78757942],
       [ 0.88054056,  0.4739708 ]])
>>> p
array([[ 1.23116567,  1.93241587],
       [ 1.93241587,  4.84930602]])
>>> u.dot(p)   # Verify the decomposition.
array([[ 0.5,  1.5],
       [ 1. ,  3. ],
       [ 2. ,  4. ]])
>>> u.T.dot(u)  # The columns of u are orthonormal.
array([[  1.00000000e+00,  -1.26363763e-16],
       [ -1.26363763e-16,   1.00000000e+00]])
```

`scipy.linalg.`**`qr`**(*a*, *overwrite_a=False*, *lwork=None*, *mode='full'*, *pivoting=False*, *check_finite=True*)

Compute QR decomposition of a matrix.

Calculate the decomposition `A = Q R` where Q is unitary/orthogonal and R upper triangular.

Parameters

a : (M, N) array_like
  Matrix to be decomposed

overwrite_a : bool, optional
  Whether data in a is overwritten (may improve performance)

lwork : int, optional
  Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.

mode : {'full', 'r', 'economic', 'raw'}, optional
  Determines what information is to be returned: either both Q and R ('full', default), only R ('r') or both Q and R but computed in economy-size ('economic', see Notes).

The final option 'raw' (added in Scipy 0.11) makes the function return two matrices (Q, TAU) in the internal format used by LAPACK.

pivoting : bool, optional

Whether or not factorization should include pivoting for rank-revealing qr decomposition. If pivoting, compute the decomposition `A P = Q R` as above, but where P is chosen such that the diagonal of R is non-increasing.

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

Q : float or complex ndarray

Of shape (M, M), or (M, K) for `mode='economic'`. Not returned if `mode='r'`.

R : float or complex ndarray

Of shape (M, N), or (K, N) for `mode='economic'`. `K = min(M, N)`.

P : int ndarray

Of shape (N,) for `pivoting=True`. Not returned if `pivoting=False`.

Raises

LinAlgError

Raised if decomposition fails

Notes

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dorgqr, zungqr, dgeqp3, and zgeqp3.

If `mode=economic`, the shapes of Q and R are (M, K) and (K, N) instead of (M,M) and (M,N), with `K=min(M,N)`.

Examples

```
>>> from scipy import random, linalg, dot, diag, all, allclose
>>> a = random.randn(9, 6)

>>> q, r = linalg.qr(a)
>>> allclose(a, np.dot(q, r))
True
>>> q.shape, r.shape
((9, 9), (9, 6))

>>> r2 = linalg.qr(a, mode='r')
>>> allclose(r, r2)
True

>>> q3, r3 = linalg.qr(a, mode='economic')
>>> q3.shape, r3.shape
((9, 6), (6, 6))

>>> q4, r4, p4 = linalg.qr(a, pivoting=True)
>>> d = abs(diag(r4))
>>> all(d[1:] <= d[:-1])
True
>>> allclose(a[:, p4], dot(q4, r4))
True
>>> q4.shape, r4.shape, p4.shape
((9, 9), (9, 6), (6,))

>>> q5, r5, p5 = linalg.qr(a, mode='economic', pivoting=True)
>>> q5.shape, r5.shape, p5.shape
((9, 6), (6, 6), (6,))
```

`scipy.linalg.`**`qr_multiply`**(*a*, *c*, *mode='right'*, *pivoting=False*, *conjugate=False*, *overwrite_a=False*, *overwrite_c=False*)

Calculate the QR decomposition and multiply Q with a matrix.

Calculate the decomposition `A = Q R` where Q is unitary/orthogonal and R upper triangular. Multiply Q with a vector or a matrix c.

Parameters

a : array_like, shape (M, N)
Matrix to be decomposed

c : array_like, one- or two-dimensional
calculate the product of c and q, depending on the mode:

mode : {'left', 'right'}, optional
`dot(Q, c)` is returned if mode is 'left', `dot(c, Q)` is returned if mode is 'right'. The shape of c must be appropriate for the matrix multiplications, if mode is 'left', `min(a.shape) == c.shape[0]`, if mode is 'right', `a.shape[0] == c.shape[1]`.

pivoting : bool, optional
Whether or not factorization should include pivoting for rank-revealing qr decomposition, see the documentation of qr.

conjugate : bool, optional
Whether Q should be complex-conjugated. This might be faster than explicit conjugation.

overwrite_a : bool, optional
Whether data in a is overwritten (may improve performance)

overwrite_c : bool, optional
Whether data in c is overwritten (may improve performance). If this is used, c must be big enough to keep the result, i.e. c.shape[0] = a.shape[0] if mode is 'left'.

Returns

CQ : float or complex ndarray
the product of Q and c, as defined in mode

R : float or complex ndarray
Of shape (K, N), `K = min(M, N)`.

P : ndarray of ints
Of shape (N,) for `pivoting=True`. Not returned if `pivoting=False`.

Raises

LinAlgError
Raised if decomposition fails

Notes

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dormqr, zunmqr, dgeqp3, and zgeqp3.

New in version 0.11.0.

`scipy.linalg.`**`qr_update`**(*Q*, *R*, *u*, *v*, *overwrite_qruv=False*, *check_finite=True*)

Rank-k QR update

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A + u v**T` for real `A` or `A + u v**H` for complex `A`.

Parameters

Q : (M, M) or (M, N) array_like
Unitary/orthogonal matrix from the qr decomposition of A.

R : (M, N) or (N, N) array_like
Upper triangular matrix from the qr decomposition of A.

u : (M,) or (M, k) array_like
Left update vector

v : (N,) or (N, k) array_like
Right update vector

overwrite_qruv : bool, optional

If True, consume Q, R, u, and v, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns **Q1** : ndarray

Updated unitary/orthogonal factor

R1 : ndarray

Updated upper triangular factor

See also:

`qr`, `qr_multiply`, `qr_delete`, `qr_insert`

Notes

This routine does not guarantee that the diagonal entries of *R1* are real or positive.

New in version 0.16.0.

References

[R96], [R97], [R98]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this q, r decomposition, perform a rank 1 update.

```
>>> u = np.array([7., -2., 4., 3., 5.])
>>> v = np.array([1., 3., -5.])
>>> q_up, r_up = linalg.qr_update(q, r, u, v, False)
>>> q_up
array([[ 0.54073807,  0.18645997,  0.81707661, -0.02136616,  0.06902409],
       [ 0.21629523, -0.63257324,  0.06567893,  0.34125904, -0.65749222],
       [ 0.05407381,  0.64757787, -0.12781284, -0.20031219, -0.72198188],
       [ 0.48666426, -0.30466718, -0.27487277, -0.77079214,  0.0256951 ],
       [ 0.64888568,  0.23001   , -0.4859845 ,  0.49883891,  0.20253783]])
>>> r_up
array([[ 18.49324201,  24.11691794, -44.98940746],
       [  0.        ,  31.95894662, -27.40998201],
       [  0.        ,   0.        ,  -9.25451794],
       [  0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

The update is equivalent, but faster than the following.

```
>>> a_up = a + np.outer(u, v)
>>> q_direct, r_direct = linalg.qr(a_up)
```

Check that we have equivalent results:

```
>>> np.allclose(np.dot(q_up, r_up), a_up)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q_up.T, q_up), np.eye(5))
True
```

Updating economic (reduced, thin) decompositions is also possible:

```
>>> qe, re = linalg.qr(a, mode='economic')
>>> qe_up, re_up = linalg.qr_update(qe, re, u, v, False)
>>> qe_up
array([[ 0.54073807,  0.18645997,  0.81707661],
       [ 0.21629523, -0.63257324,  0.06567893],
       [ 0.05407381,  0.64757787, -0.12781284],
       [ 0.48666426, -0.30466718, -0.27487277],
       [ 0.64888568,  0.23001   , -0.4859845 ]])
>>> re_up
array([[ 18.49324201,  24.11691794, -44.98940746],
       [  0.        ,  31.95894662, -27.40998201],
       [  0.        ,   0.        ,  -9.25451794]])
>>> np.allclose(np.dot(qe_up, re_up), a_up)
True
>>> np.allclose(np.dot(qe_up.T, qe_up), np.eye(3))
True
```

Similarly to the above, perform a rank 2 update.

```
>>> u2 = np.array([[ 7., -1,],
...                [-2.,  4.],
...                [ 4.,  2.],
...                [ 3., -6.],
...                [ 5.,  3.]])
>>> v2 = np.array([[ 1., 2.],
...                [ 3., 4.],
...                [-5., 2]])
>>> q_up2, r_up2 = linalg.qr_update(q, r, u, v, False)
>>> q_up2
array([[-0.33626508, -0.03477253,  0.61956287, -0.64352987, -0.29618884],
       [-0.50439762,  0.58319694, -0.43010077, -0.33395279,  0.33008064],
       [-0.21016568, -0.63123106,  0.0582249 , -0.13675572,  0.73163206],
       [ 0.12609941,  0.49694436,  0.64590024,  0.31191919,  0.47187344],
       [-0.75659643, -0.11517748,  0.10284903,  0.5986227 , -0.21299983]])
>>> r_up2
array([[-23.79075451, -41.1084062 ,  24.71548348],
       [  0.        , -33.83931057,  11.02226551],
       [  0.        ,   0.        , -48.91476811],
       [ -0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

This update is also a valid qr decomposition of `A + U V**T`.

```
>>> a_up2 = a + np.dot(u2, v2.T)
>>> np.allclose(a_up2, np.dot(q_up2, r_up2))
True
>>> np.allclose(np.dot(q_up2.T, q_up2), np.eye(5))
True
```

`scipy.linalg.`**`qr_delete`**(*Q*, *R*, *k*, *p=1*, *which='row'*, *overwrite_qr=False*, *check_finite=True*)

QR downdate on row or column deletions

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A` where `p` rows or columns have been removed starting at row or column `k`.

Parameters

Q : (M, M) or (M, N) array_like
  Unitary/orthogonal matrix from QR decomposition.

R : (M, N) or (N, N) array_like
  Upper triangular matrix from QR decomposition.

k : int
  Index of the first row or column to delete.

p : int, optional
  Number of rows or columns to delete, defaults to 1.

which: {'row', 'col'}, optional
  Determines if rows or columns will be deleted, defaults to 'row'

overwrite_qr : bool, optional
  If True, consume Q and R, overwriting their contents with their downdated versions, and returning approriately sized views. Defaults to False.

check_finite : bool, optional
  Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 : ndarray
  Updated unitary/orthogonal factor

R1 : ndarray
  Updated upper triangular factor

See also:

`qr`, `qr_multiply`, `qr_insert`, `qr_update`

Notes

This routine does not guarantee that the diagonal entries of `R1` are positive.

New in version 0.16.0.

References

[R90], [R91], [R92]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this QR decomposition, update q and r when 2 rows are removed.

```
>>> q1, r1 = linalg.qr_delete(q, r, 2, 2, 'row', False)
>>> q1
array([[ 0.30942637,  0.15347579,  0.93845645],
       [ 0.61885275,  0.71680171, -0.32127338],
       [ 0.72199487, -0.68017681, -0.12681844]])
>>> r1
array([[  9.69535971,  -0.4125685 ,  -6.80738023],
```

```
       [  0.        , -12.19958144,   1.62370412],
       [  0.        ,   0.        ,  -0.15218213]])
```

The update is equivalent, but faster than the following.

```
>>> a1 = np.delete(a, slice(2,4), 0)
>>> a1
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7.,  8., -6.]])
>>> q_direct, r_direct = linalg.qr(a1)
```

Check that we have equivalent results:

```
>>> np.dot(q1, r1)
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7.,  8., -6.]])
>>> np.allclose(np.dot(q1, r1), a1)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q1.T, q1), np.eye(3))
True
```

`scipy.linalg.`**`qr_insert`**`(`*Q*, *R*, *u*, *k*, *which='row'*, *rcond=None*, *overwrite_qru=False*, *check_finite=True*`)`

QR update on row or column insertions

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A` where rows or columns have been inserted starting at row or column `k`.

Parameters

Q : (M, M) array_like
  Unitary/orthogonal matrix from the QR decomposition of A.

R : (M, N) array_like
  Upper triangular matrix from the QR decomposition of A.

u : (N,), (p, N), (M,), or (M, p) array_like
  Rows or columns to insert

k : int
  Index before which *u* is to be inserted.

which: {'row', 'col'}, optional
  Determines if rows or columns will be inserted, defaults to 'row'

rcond : float
  Lower bound on the reciprocal condition number of `Q` augmented with `u/||u||` Only used when updating economic mode (thin, (M,N) (N,N)) decompositions. If None, machine precision is used. Defaults to None.

overwrite_qru : bool, optional
  If True, consume Q, R, and u, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.

check_finite : bool, optional
  Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 : ndarray
  Updated unitary/orthogonal factor

R1 : ndarray
  Updated upper triangular factor

Raises **LinAlgError :**

If updating a (M,N) (N,N) factorization and the reciprocal condition number of Q augmented with u/||u|| is smaller than rcond.

See also:

`qr`, `qr_multiply`, `qr_delete`, `qr_update`

Notes

This routine does not guarantee that the diagonal entries of `R1` are positive.

New in version 0.16.0.

References

[R93], [R94], [R95]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this QR decomposition, update q and r when 2 rows are inserted.

```
>>> u = np.array([[  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.]])
>>> q1, r1 = linalg.qr_insert(q, r, u, 2, 'row')
>>> q1
array([[-0.25445668,  0.02246245,  0.18146236, -0.72798806,  0.60979671],
       [-0.50891336,  0.23226178, -0.82836478, -0.02837033, -0.00828114],
       [-0.50891336,  0.35715302,  0.38937158,  0.58110733,  0.35235345],
       [ 0.25445668, -0.52202743, -0.32165498,  0.36263239,  0.65404509],
       [-0.59373225, -0.73856549,  0.16065817, -0.0063658 , -0.27595554]])
>>> r1
array([[-11.78982612,   6.44623587,   3.81685018],
       [  0.        , -16.01393278,   3.72202865],
       [  0.        ,   0.        ,  -6.13010256],
       [  0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

The update is equivalent, but faster than the following.

```
>>> a1 = np.insert(a, 2, u, 0)
>>> a1
array([[  3.,  -2.,  -2.],
       [  6.,  -7.,   4.],
       [  6.,  -9.,  -3.],
       [ -3.,  10.,   1.],
       [  7.,   8.,  -6.]])
>>> q_direct, r_direct = linalg.qr(a1)
```

Check that we have equivalent results:

```
>>> np.dot(q1, r1)
array([[  3.,  -2.,  -2.],
       [  6.,  -7.,   4.],
       [  6.,  -9.,  -3.],
```

```
       [ -3.,  10.,   1.],
       [  7.,   8.,  -6.]])
```

```
>>> np.allclose(np.dot(q1, r1), a1)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q1.T, q1), np.eye(5))
True
```

`scipy.linalg.`**`rq`**(*a*, *overwrite_a=False*, *lwork=None*, *mode='full'*, *check_finite=True*)

Compute RQ decomposition of a matrix.

Calculate the decomposition `A = R Q` where Q is unitary/orthogonal and R upper triangular.

Parameters

a : (M, N) array_like
  Matrix to be decomposed

overwrite_a : bool, optional
  Whether data in a is overwritten (may improve performance)

lwork : int, optional
  Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.

mode : {'full', 'r', 'economic'}, optional
  Determines what information is to be returned: either both Q and R ('full', default), only R ('r') or both Q and R but computed in economy-size ('economic', see Notes).

check_finite : bool, optional
  Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

R : float or complex ndarray
  Of shape (M, N) or (M, K) for `mode='economic'`. `K = min(M, N)`.

Q : float or complex ndarray
  Of shape (N, N) or (K, N) for `mode='economic'`. Not returned if `mode='r'`.

Raises

LinAlgError
  If decomposition fails.

Notes

This is an interface to the LAPACK routines sgerqf, dgerqf, cgerqf, zgerqf, sorgrq, dorgrq, cungrq and zungrq.

If `mode=economic`, the shapes of Q and R are (K, N) and (M, K) instead of (N,N) and (M,N), with `K=min(M,N)`.

Examples

```
>>> from scipy import linalg
>>> from numpy import random, dot, allclose
>>> a = random.randn(6, 9)
>>> r, q = linalg.rq(a)
>>> allclose(a, dot(r, q))
True
>>> r.shape, q.shape
((6, 9), (9, 9))
>>> r2 = linalg.rq(a, mode='r')
>>> allclose(r, r2)
True
>>> r3, q3 = linalg.rq(a, mode='economic')
>>> r3.shape, q3.shape
((6, 6), (6, 9))
```

`scipy.linalg.`**qz**(*A*, *B*, *output='real'*, *lwork=None*, *sort=None*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*)

QZ decomposition for generalized eigenvalues of a pair of matrices.

The QZ, or generalized Schur, decomposition for a pair of N x N nonsymmetric matrices (A,B) is:

```
(A,B) = (Q*AA*Z', Q*BB*Z')
```

where AA, BB is in generalized Schur form if BB is upper-triangular with non-negative diagonal and AA is upper-triangular, or for real QZ decomposition (`output='real'`) block upper triangular with 1x1 and 2x2 blocks. In this case, the 1x1 blocks correspond to real generalized eigenvalues and 2x2 blocks are 'standardized' by making the corresponding elements of BB have the form:

```
[ a 0 ]
[ 0 b ]
```

and the pair of corresponding 2x2 blocks in AA and BB will have a complex conjugate pair of generalized eigenvalues. If (`output='complex'`) or A and B are complex matrices, Z' denotes the conjugate-transpose of Z. Q and Z are unitary matrices.

Parameters

A : (N, N) array_like
  2d array to decompose

B : (N, N) array_like
  2d array to decompose

output : {'real', 'complex'}, optional
  Construct the real or complex QZ decomposition for real matrices. Default is 'real'.

lwork : int, optional
  Work array size. If None or -1, it is automatically computed.

sort : {None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional
  NOTE: THIS INPUT IS DISABLED FOR NOW, IT DOESN'T WORK WELL ON WINDOWS.
  Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). For real matrix pairs, the sort function takes three real arguments (alphar, alphai, beta). The eigenvalue x = (alphar + alphai*1j)/beta. For complex matrix pairs or output='complex', the sort function takes two complex arguments (alpha, beta). The eigenvalue x = (alpha/beta). Alternatively, string parameters may be used:

  - 'lhp' Left-hand plane (x.real < 0.0)
  - 'rhp' Right-hand plane (x.real > 0.0)
  - 'iuc' Inside the unit circle (x*x.conjugate() <= 1.0)
  - 'ouc' Outside the unit circle (x*x.conjugate() > 1.0)

  Defaults to None (no sorting).

overwrite_a : bool, optional
  Whether to overwrite data in a (may improve performance)

overwrite_b : bool, optional
  Whether to overwrite data in b (may improve performance)

check_finite : bool, optional
  If true checks the elements of *A* and *B* are finite numbers. If false does no checking and passes matrix through to underlying algorithm.

Returns

AA : (N, N) ndarray
  Generalized Schur form of A.

BB : (N, N) ndarray
  Generalized Schur form of B.

Q : (N, N) ndarray
  The left Schur vectors.

Z : (N, N) ndarray
The right Schur vectors.

sdim : int, optional
If sorting was requested, a fifth return value will contain the number of eigenvalues for which the sort condition was True.

Notes

Q is transposed versus the equivalent function in Matlab.

New in version 0.11.0.

Examples

```
>>> from scipy import linalg
>>> np.random.seed(1234)
>>> A = np.arange(9).reshape((3, 3))
>>> B = np.random.randn(3, 3)

>>> AA, BB, Q, Z = linalg.qz(A, B)
>>> AA
array([[-13.40928183,  -4.62471562,   1.09215523],
       [  0.        ,   0.        ,   1.22805978],
       [  0.        ,   0.        ,   0.31973817]])
>>> BB
array([[ 0.33362547, -1.37393632,  0.02179805],
       [ 0.        ,  1.68144922,  0.74683866],
       [ 0.        ,  0.        ,  0.9258294 ]])
>>> Q
array([[ 0.14134727, -0.97562773,  0.16784365],
       [ 0.49835904, -0.07636948, -0.86360059],
       [ 0.85537081,  0.20571399,  0.47541828]])
>>> Z
array([[-0.24900855, -0.51772687,  0.81850696],
       [-0.79813178,  0.58842606,  0.12938478],
       [-0.54861681, -0.6210585 , -0.55973739]])
```

`scipy.linalg.`**`schur`**(*a*, *output='real'*, *lwork=None*, *overwrite_a=False*, *sort=None*, *check_finite=True*)

Compute Schur decomposition of a matrix.

The Schur decomposition is:

```
A = Z T Z^H
```

where Z is unitary and T is either upper-triangular, or for real Schur decomposition (output='real'), quasi-upper triangular. In the quasi-triangular form, 2x2 blocks describing complex-valued eigenvalue pairs may extrude from the diagonal.

Parameters

a : (M, M) array_like
Matrix to decompose

output : {'real', 'complex'}, optional
Construct the real or complex Schur decomposition (for real matrices).

lwork : int, optional
Work array size. If None or -1, it is automatically computed.

overwrite_a : bool, optional
Whether to overwrite data in a (may improve performance).

sort : {None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional

Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). Alternatively, string parameters may be used:

```
'lhp'   Left-hand plane (x.real < 0.0)
'rhp'   Right-hand plane (x.real > 0.0)
'iuc'   Inside the unit circle (x*x.conjugate() <= 1.0)
'ouc'   Outside the unit circle (x*x.conjugate() > 1.0)
```

Defaults to None (no sorting).

check_finite : bool, optional

Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

T : (M, M) ndarray

Schur form of A. It is real-valued for the real Schur decomposition.

Z : (M, M) ndarray

An unitary Schur transformation matrix for A. It is real-valued for the real Schur decomposition.

sdim : int

If and only if sorting was requested, a third return value will contain the number of eigenvalues satisfying the sort condition.

Raises

LinAlgError

Error raised under three conditions:

1. The algorithm failed due to a failure of the QR algorithm to compute all eigenvalues
2. If eigenvalue sorting was requested, the eigenvalues could not be reordered due to a failure to separate eigenvalues, usually because of poor conditioning
3. If eigenvalue sorting was requested, roundoff errors caused the leading eigenvalues to no longer satisfy the sorting condition

See also:

`rsf2csf`	Convert real Schur form to complex Schur form

`scipy.linalg.`**`rsf2csf`**(*T*, *Z*, *check_finite=True*)

Convert real Schur form to complex Schur form.

Convert a quasi-diagonal real-valued Schur form to the upper triangular complex-valued Schur form.

Parameters

T : (M, M) array_like

Real Schur form of the original matrix

Z : (M, M) array_like

Schur transformation matrix

check_finite : bool, optional

Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

T : (M, M) ndarray

Complex Schur form of the original matrix

Z : (M, M) ndarray

Schur transformation matrix corresponding to the complex form

See also:

`schur`	Schur decompose a matrix

`scipy.linalg.`**`hessenberg`**(*a*, *calc_q=False*, *overwrite_a=False*, *check_finite=True*)

Compute Hessenberg form of a matrix.

The Hessenberg decomposition is:

```
A = Q H Q^H
```

where *Q* is unitary/orthogonal and *H* has only zero elements below the first sub-diagonal.

Parameters

a : (M, M) array_like
Matrix to bring into Hessenberg form.

calc_q : bool, optional
Whether to compute the transformation matrix. Default is False.

overwrite_a : bool, optional
Whether to overwrite *a*; may improve performance. Default is False.

check_finite : bool, optional
Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

H : (M, M) ndarray
Hessenberg form of *a*.

Q : (M, M) ndarray
Unitary/orthogonal similarity transformation matrix `A = Q H Q^H`. Only returned if `calc_q=True`.

See also:

`scipy.linalg.interpolative` – Interpolative matrix decompositions

5.9.4 Matrix Functions

`expm`(A[, q])	Compute the matrix exponential using Pade approximation.
`logm`(A[, disp])	Compute matrix logarithm.
`cosm`(A)	Compute the matrix cosine.
`sinm`(A)	Compute the matrix sine.
`tanm`(A)	Compute the matrix tangent.
`coshm`(A)	Compute the hyperbolic matrix cosine.
`sinhm`(A)	Compute the hyperbolic matrix sine.
`tanhm`(A)	Compute the hyperbolic matrix tangent.
`signm`(A[, disp])	Matrix sign function.
`sqrtm`(A[, disp, blocksize])	Matrix square root.
`funm`(A, func[, disp])	Evaluate a matrix function specified by a callable.
`expm_frechet`(A, E[, method, compute_expm, ...])	Frechet derivative of the matrix exponential of A in the direction E.
`expm_cond`(A[, check_finite])	Relative condition number of the matrix exponential in the Frobenius norm.
`fractional_matrix_power`(A, t)	Compute the fractional power of a matrix.

`scipy.linalg.`**`expm`**(*A*, *q=None*)

Compute the matrix exponential using Pade approximation.

Parameters

A : (N, N) array_like or sparse matrix
Matrix to be exponentiated.

Returns

expm : (N, N) ndarray
Matrix exponential of *A*.

References

[R75]

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Matrix version of the formula exp(0) = 1:

```
>>> expm(np.zeros((2,2)))
array([[ 1.,  0.],
       [ 0.,  1.]])
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

`scipy.linalg.`**`logm`**(*A*, *disp=True*)

Compute matrix logarithm.

The matrix logarithm is the inverse of expm: expm(logm(*A*)) == *A*

Parameters

A : (N, N) array_like
  Matrix whose logarithm to evaluate

disp : bool, optional
  Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

logm : (N, N) ndarray
  Matrix logarithm of *A*

errest : float
  (if disp == False)
  1-norm of the estimated error, ||err||_1 / ||A||_1

References

[R83], [R84], [R85]

Examples

```
>>> from scipy.linalg import logm, expm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = logm(a)
>>> b
array([[-1.02571087,  2.05142174],
       [ 0.68380725,  1.02571087]])
>>> expm(b)         # Verify expm(logm(a)) returns a
array([[ 1.,  3.],
       [ 1.,  4.]])
```

`scipy.linalg.`**`cosm`**(*A*)

Compute the matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like
Input array

Returns **cosm** : (N, N) ndarray
Matrix cosine of A

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

`scipy.linalg.`**`sinm`**`(`*A*`)`

Compute the matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like
Input array.

Returns **sinm** : (N, N) ndarray
Matrix cosine of *A*

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

`scipy.linalg.`**`tanm`**`(`*A*`)`

Compute the matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like
Input array.

Returns **tanm** : (N, N) ndarray
Matrix tangent of *A*

Examples

```
>>> from scipy.linalg import tanm, sinm, cosm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanm(a)
>>> t
```

```
array([[ -2.00876993,  -8.41880636],
       [ -2.80626879, -10.42757629]])
```

Verify tanm(a) = sinm(a).dot(inv(cosm(a)))

```
>>> s = sinm(a)
>>> c = cosm(a)
>>> s.dot(np.linalg.inv(c))
array([[ -2.00876993,  -8.41880636],
       [ -2.80626879, -10.42757629]])
```

`scipy.linalg.`**`coshm`**`(`*A*`)`

Compute the hyperbolic matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like
Input array.

Returns **coshm** : (N, N) ndarray
Hyperbolic matrix cosine of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> c = coshm(a)
>>> c
array([[ 11.24592233,  38.76236492],
       [ 12.92078831,  50.00828725]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> t = tanhm(a)
>>> s = sinhm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

`scipy.linalg.`**`sinhm`**`(`*A*`)`

Compute the hyperbolic matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like
Input array.

Returns **sinhm** : (N, N) ndarray
Hyperbolic matrix sine of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> s = sinhm(a)
>>> s
array([[ 10.57300653,  39.28826594],
       [ 13.09608865,  49.86127247]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> t = tanhm(a)
>>> c = coshm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

`scipy.linalg.`**`tanhm`**`(`*A*`)`

Compute the hyperbolic matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters **A** : (N, N) array_like

Input array

Returns **tanhm** : (N, N) ndarray

Hyperbolic matrix tangent of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanhm(a)
>>> t
array([[ 0.3428582 ,  0.51987926],
       [ 0.17329309,  0.86273746]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> s = sinhm(a)
>>> c = coshm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

`scipy.linalg.`**`signm`**`(`*A*, *disp=True*`)`

Matrix sign function.

Extension of the scalar sign(x) to matrices.

Parameters **A** : (N, N) array_like

Matrix at which to evaluate the sign function

disp : bool, optional

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns **signm** : (N, N) ndarray

Value of the sign function at *A*

errest : float

(if disp == False)

1-norm of the estimated error, ||err||_1 / ||A||_1

Examples

```
>>> from scipy.linalg import signm, eigvals
>>> a = [[1,2,3], [1,2,1], [1,1,1]]
>>> eigvals(a)
array([ 4.12488542+0.j, -0.76155718+0.j,  0.63667176+0.j])
>>> eigvals(signm(a))
array([-1.+0.j,  1.+0.j,  1.+0.j])
```

`scipy.linalg.`**`sqrtm`**`(`*A*, *disp=True*, *blocksize=64*`)`

Matrix square root.

Parameters **A** : (N, N) array_like

Matrix whose square root to evaluate

disp : bool, optional

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

blocksize : integer, optional

If the blocksize is not degenerate with respect to the size of the input array, then use a blocked algorithm. (Default: 64)

Returns **sqrtm** : (N, N) ndarray

Value of the sqrt function at *A*

errest : float

(if disp == False)

Frobenius norm of the estimated error, ||err||_F / ||A||_F

References

[R101]

Examples

```
>>> from scipy.linalg import sqrtm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> r = sqrtm(a)
>>> r
array([[ 0.75592895,  1.13389342],
       [ 0.37796447,  1.88982237]])
>>> r.dot(r)
array([[ 1.,  3.],
       [ 1.,  4.]])
```

`scipy.linalg.`**`funm`**`(`*A*, *func*, *disp=True*`)`

Evaluate a matrix function specified by a callable.

Returns the value of matrix-valued function `f` at *A*. The function `f` is an extension of the scalar-valued function *func* to matrices.

Parameters **A** : (N, N) array_like

Matrix at which to evaluate the function

func : callable

Callable object that evaluates a scalar function f. Must be vectorized (eg. using vectorize).

disp : bool, optional

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns **funm** : (N, N) ndarray

Value of the matrix function specified by func evaluated at *A*

errest : float

(if disp == False)

1-norm of the estimated error, ||err||_1 / ||A||_1

Notes

This function implements the general algorithm based on Schur decomposition (Algorithm 9.1.1. in [R78]).

If the input matrix is known to be diagonalizable, then relying on the eigendecomposition is likely to be faster. For example, if your matrix is Hermitian, you can do

```
>>> from scipy.linalg import eigh
>>> def funm_herm(a, func, check_finite=False):
...     w, v = eigh(a, check_finite=check_finite)
...     ## if you further know that your matrix is positive semidefinite,
...     ## you can optionally guard against precision errors by doing
...     # w = np.maximum(w, 0)
...     w = func(w)
...     return (v * w).dot(v.conj().T)
```

References

[R78]

Examples

```
>>> from scipy.linalg import funm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> funm(a, lambda x: x*x)
array([[  4.,  15.],
       [  5.,  19.]])
>>> a.dot(a)
array([[  4.,  15.],
       [  5.,  19.]])
```

`scipy.linalg.`**`expm_frechet`**(*A*, *E*, *method=None*, *compute_expm=True*, *check_finite=True*)

Frechet derivative of the matrix exponential of A in the direction E.

Parameters

A : (N, N) array_like
  Matrix of which to take the matrix exponential.

E : (N, N) array_like
  Matrix direction in which to take the Frechet derivative.

method : str, optional
  Choice of algorithm. Should be one of
  - *SPS* (default)
  - *blockEnlarge*

compute_expm : bool, optional
  Whether to compute also *expm_A* in addition to *expm_frechet_AE*. Default is True.

check_finite : bool, optional
  Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

expm_A : ndarray
  Matrix exponential of A.

expm_frechet_AE : ndarray
  Frechet derivative of the matrix exponential of A in the direction E.

For `compute_expm = False`, only *expm_frechet_AE* is returned.

See also:

`expm`	Compute the exponential of a matrix.

Notes

This section describes the available implementations that can be selected by the *method* parameter. The default method is *SPS*.

Method *blockEnlarge* is a naive algorithm.

Method *SPS* is Scaling-Pade-Squaring [R76]. It is a sophisticated implementation which should take only about 3/8 as much time as the naive implementation. The asymptotics are the same.

New in version 0.13.0.

References

[R76]

Examples

```
>>> import scipy.linalg
>>> A = np.random.randn(3, 3)
>>> E = np.random.randn(3, 3)
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> expm_A.shape, expm_frechet_AE.shape
((3, 3), (3, 3))
```

```
>>> import scipy.linalg
>>> A = np.random.randn(3, 3)
>>> E = np.random.randn(3, 3)
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> M = np.zeros((6, 6))
>>> M[:3, :3] = A; M[:3, 3:] = E; M[3:, 3:] = A
>>> expm_M = scipy.linalg.expm(M)
>>> np.allclose(expm_A, expm_M[:3, :3])
True
>>> np.allclose(expm_frechet_AE, expm_M[:3, 3:])
True
```

`scipy.linalg.`**`expm_cond`**`(`*A*, *check_finite=True*`)`

Relative condition number of the matrix exponential in the Frobenius norm.

Parameters	**A** : 2d array_like Square input matrix with shape (N, N). **check_finite** : bool, optional Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
Returns	**kappa** : float The relative condition number of the matrix exponential in the Frobenius norm

See also:

expm	Compute the exponential of a matrix.
expm_frechet	Compute the Frechet derivative of the matrix exponential.

Notes

A faster estimate for the condition number in the 1-norm has been published but is not yet implemented in scipy.

New in version 0.14.0.

`scipy.linalg.`**`fractional_matrix_power`**`(`*A*, *t*`)`

Compute the fractional power of a matrix.

Proceeds according to the discussion in section (6) of [R77].

Parameters	**A** : (N, N) array_like

Matrix whose fractional power to evaluate.

t : float

Fractional power.

Returns **X** : (N, N) array_like

The fractional power of the matrix.

References

[R77]

Examples

```
>>> from scipy.linalg import fractional_matrix_power
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = fractional_matrix_power(a, 0.5)
>>> b
array([[ 0.75592895,  1.13389342],
       [ 0.37796447,  1.88982237]])
>>> np.dot(b, b)      # Verify square root
array([[ 1.,  3.],
       [ 1.,  4.]])
```

5.9.5 Matrix Equation Solvers

`solve_sylvester`(a, b, q)	Computes a solution (X) to the Sylvester equation (AX + XB = Q).
`solve_continuous_are`(a, b, q, r)	Solves the continuous algebraic Riccati equation, or CARE, defined as (A'X + X
`solve_discrete_are`(a, b, q, r)	Solves the disctrete algebraic Riccati equation, or DARE, defined as (X = A'XA-
`solve_discrete_lyapunov`(a, q[, method])	Solves the discrete Lyapunov equation $(A'XA - X = -Q)$.
`solve_lyapunov`(a, q)	Solves the continuous Lyapunov equation (AX + XA^H = Q) given the values of

`scipy.linalg.`**`solve_sylvester`**(*a*, *b*, *q*)

Computes a solution (X) to the Sylvester equation (AX + XB = Q).

Parameters **a** : (M, M) array_like

Leading matrix of the Sylvester equation

b : (N, N) array_like

Trailing matrix of the Sylvester equation

q : (M, N) array_like

Right-hand side

Returns **x** : (M, N) ndarray

The solution to the Sylvester equation.

Raises **LinAlgError**

If solution was not found

Notes

Computes a solution to the Sylvester matrix equation via the Bartels- Stewart algorithm. The A and B matrices first undergo Schur decompositions. The resulting matrices are used to construct an alternative Sylvester equation (`RY + YS^T = F`) where the R and S matrices are in quasi-triangular form (or, when R, S or F are complex, triangular form). The simplified equation is then solved using `*TRSYL` from LAPACK directly.

New in version 0.11.0.

`scipy.linalg.`**`solve_continuous_are`**(*a*, *b*, *q*, *r*)

Solves the continuous algebraic Riccati equation, or CARE, defined as (A'X + XA - XBR^-1B'X+Q=0) directly using a Schur decomposition method.

Parameters	**a** : (M, M) array_like Input **b** : (M, N) array_like Input **q** : (M, M) array_like Input **r** : (N, N) array_like Non-singular, square matrix
Returns	**x** : (M, M) ndarray Solution to the continuous algebraic Riccati equation

See also:

`solve_discrete_are`
Solves the discrete algebraic Riccati equation

Notes

Method taken from: Laub, "A Schur Method for Solving Algebraic Riccati Equations." U.S. Energy Research and Development Agency under contract ERDA-E(49-18)-2087. http://dspace.mit.edu/bitstream/handle/1721.1/1301/R-0859-05666488.pdf

New in version 0.11.0.

`scipy.linalg.`**`solve_discrete_are`**(*a*, *b*, *q*, *r*)

Solves the disctrete algebraic Riccati equation, or DARE, defined as (X = A'XA-(A'XB)(R+B'XB)^-1(B'XA)+Q), directly using a Schur decomposition method.

Parameters	**a** : (M, M) array_like Non-singular, square matrix **b** : (M, N) array_like Input **q** : (M, M) array_like Input **r** : (N, N) array_like Non-singular, square matrix
Returns	**x** : ndarray Solution to the continuous Lyapunov equation

See also:

`solve_continuous_are`
Solves the continuous algebraic Riccati equation

Notes

Method taken from: Laub, "A Schur Method for Solving Algebraic Riccati Equations." U.S. Energy Research and Development Agency under contract ERDA-E(49-18)-2087. http://dspace.mit.edu/bitstream/handle/1721.1/1301/R-0859-05666488.pdf

New in version 0.11.0.

`scipy.linalg.`**`solve_discrete_lyapunov`**(*a*, *q*, *method=None*)

Solves the discrete Lyapunov equation $(A'XA - X = -Q)$.

Parameters	**a** : (M, M) array_like A square matrix

q : (M, M) array_like
Right-hand side square matrix

method : {'direct', 'bilinear'}, optional
Type of solver.
If not given, chosen to be `direct` if `M` is less than 10 and `bilinear` otherwise.

Returns

x : ndarray
Solution to the discrete Lyapunov equation

See also:

`solve_lyapunov`
computes the solution to the continuous Lyapunov equation

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *direct* if `M` is less than 10 and `bilinear` otherwise.

Method *direct* uses a direct analytical solution to the discrete Lyapunov equation. The algorithm is given in, for example, [R99]. However it requires the linear solution of a system with dimension M^2 so that performance degrades rapidly for even moderately sized matrices.

Method *bilinear* uses a bilinear transformation to convert the discrete Lyapunov equation to a continuous Lyapunov equation $(B'X + XB = -C)$ where $B = (A - I)(A + I)^{-1}$ and $C = 2(A' + I)^{-1}Q(A + I)^{-1}$. The continuous equation can be efficiently solved since it is a special case of a Sylvester equation. The transformation algorithm is from Popov (1964) as described in [R100].

New in version 0.11.0.

References

[R99], [R100]

`scipy.linalg.`**`solve_lyapunov`**(*a*, *q*)

Solves the continuous Lyapunov equation (AX + XA^H = Q) given the values of A and Q using the Bartels-Stewart algorithm.

Parameters

a : array_like
A square matrix

q : array_like
Right-hand side square matrix

Returns

x : array_like
Solution to the continuous Lyapunov equation

See also:

`solve_sylvester`
computes the solution to the Sylvester equation

Notes

Because the continuous Lyapunov equation is just a special form of the Sylvester equation, this solver relies entirely on solve_sylvester for a solution.

New in version 0.11.0.

5.9.6 Special Matrices

`block_diag`(*arrs)	Create a block diagonal matrix from provided arrays.
`circulant`(c)	Construct a circulant matrix.
`companion`(a)	Create a companion matrix.
`dft`(n[, scale])	Discrete Fourier transform matrix.
`hadamard`(n[, dtype])	Construct a Hadamard matrix.
`hankel`(c[, r])	Construct a Hankel matrix.
`helmert`(n[, full])	Create a Helmert matrix of order *n*.
`hilbert`(n)	Create a Hilbert matrix of order *n*.
`invhilbert`(n[, exact])	Compute the inverse of the Hilbert matrix of order *n*.
`leslie`(f, s)	Create a Leslie matrix.
`pascal`(n[, kind, exact])	Returns the n x n Pascal matrix.
`invpascal`(n[, kind, exact])	Returns the inverse of the n x n Pascal matrix.
`toeplitz`(c[, r])	Construct a Toeplitz matrix.
`tri`(N[, M, k, dtype])	Construct (N, M) matrix filled with ones at and below the k-th diagonal.

`scipy.linalg.`**`block_diag`**`(`*`*arrs`*`)`

Create a block diagonal matrix from provided arrays.

Given the inputs *A*, *B* and *C*, the output will have these arrays arranged on the diagonal:

```
[[A, 0, 0],
 [0, B, 0],
 [0, 0, C]]
```

Parameters **A, B, C, ...** : array_like, up to 2-D

Input arrays. A 1-D array or array_like sequence of length *n* is treated as a 2-D array with shape `(1,n)`.

Returns **D** : ndarray

Array with *A*, *B*, *C*, ... on the diagonal. *D* has the same dtype as *A*.

Notes

If all the input arrays are square, the output is known as a block diagonal matrix.

Empty sequences (i.e., array-likes of zero size) are ignored.

Examples

```
>>> from scipy.linalg import block_diag
>>> A = [[1, 0],
...      [0, 1]]
>>> B = [[3, 4, 5],
...      [6, 7, 8]]
>>> C = [[7]]
>>> block_diag(A, B, C)
[[1 0 0 0 0 0]
 [0 1 0 0 0 0]
 [0 0 3 4 5 0]
 [0 0 6 7 8 0]
 [0 0 0 0 0 7]]
>>> block_diag(1.0, [2, 3], [[4, 5], [6, 7]])
array([[ 1.,  0.,  0.,  0.,  0.],
       [ 0.,  2.,  3.,  0.,  0.],
       [ 0.,  0.,  0.,  4.,  5.],
       [ 0.,  0.,  0.,  6.,  7.]])
```

`scipy.linalg.`**`circulant`**`(`*c*`)`

Construct a circulant matrix.

Parameters	**c** : (N,) array_like 1-D array, the first column of the matrix.
Returns	**A** : (N, N) ndarray A circulant matrix whose first column is *c*.

See also:

`toeplitz`	Toeplitz matrix
`hankel`	Hankel matrix

Notes

New in version 0.8.0.

Examples

```
>>> from scipy.linalg import circulant
>>> circulant([1, 2, 3])
array([[1, 3, 2],
       [2, 1, 3],
       [3, 2, 1]])
```

`scipy.linalg.`**`companion`**`(`*a*`)`

Create a companion matrix.

Create the companion matrix [R73] associated with the polynomial whose coefficients are given in *a*.

Parameters	**a** : (N,) array_like 1-D array of polynomial coefficients. The length of *a* must be at least two, and `a[0]` must not be zero.
Returns	**c** : (N-1, N-1) ndarray The first row of *c* is `-a[1:]/a[0]`, and the first sub-diagonal is all ones. The data-type of the array is the same as the data-type of `1.0*a[0]`.
Raises	**ValueError** If any of the following are true: a) `a.ndim != 1`; b) `a.size < 2`; c) `a[0] == 0`.

Notes

New in version 0.8.0.

References

[R73]

Examples

```
>>> from scipy.linalg import companion
>>> companion([1, -10, 31, -30])
array([[ 10., -31.,  30.],
       [  1.,   0.,   0.],
       [  0.,   1.,   0.]])
```

`scipy.linalg.`**`dft`**`(`*n*, *scale=None*`)`

Discrete Fourier transform matrix.

Create the matrix that computes the discrete Fourier transform of a sequence [R74]. The n-th primitive root of unity used to generate the matrix is exp(-2*pi*i/n), where i = sqrt(-1).

Parameters	**n** : int Size the matrix to create. **scale** : str, optional Must be None, 'sqrtn', or 'n'. If *scale* is 'sqrtn', the matrix is divided by *sqrt(n)*. If *scale* is 'n', the matrix is divided by *n*. If *scale* is None (the default), the matrix is not normalized, and the return value is simply the Vandermonde matrix of the roots of unity.
Returns	**m** : (n, n) ndarray The DFT matrix.

Notes

When *scale* is None, multiplying a vector by the matrix returned by `dft` is mathematically equivalent to (but much less efficient than) the calculation performed by `scipy.fftpack.fft`.

New in version 0.14.0.

References

[R74]

Examples

```
>>> from scipy.linalg import dft
>>> np.set_printoptions(precision=5, suppress=True)
>>> x = np.array([1, 2, 3, 0, 3, 2, 1, 0])
>>> m = dft(8)
>>> m.dot(x)    # Compute the DFT of x
array([ 12.+0.j,  -2.-2.j,   0.-4.j,  -2.+2.j,   4.+0.j,  -2.-2.j,
        -0.+4.j,  -2.+2.j])
```

Verify that `m.dot(x)` is the same as `fft(x)`.

```
>>> from scipy.fftpack import fft
>>> fft(x)     # Same result as m.dot(x)
array([ 12.+0.j,  -2.-2.j,   0.-4.j,  -2.+2.j,   4.+0.j,  -2.-2.j,
         0.+4.j,  -2.+2.j])
```

`scipy.linalg.`**`hadamard`**`(`*n*, *dtype=<type 'int'>*`)`

Construct a Hadamard matrix.

Constructs an n-by-n Hadamard matrix, using Sylvester's construction. *n* must be a power of 2.

Parameters	**n** : int The order of the matrix. *n* must be a power of 2. **dtype** : dtype, optional The data type of the array to be constructed.
Returns	**H** : (n, n) ndarray The Hadamard matrix.

Notes

New in version 0.8.0.

Examples

```
>>> from scipy.linalg import hadamard
>>> hadamard(2, dtype=complex)
array([[ 1.+0.j,  1.+0.j],
       [ 1.+0.j, -1.-0.j]])
>>> hadamard(4)
array([[ 1,  1,  1,  1],
       [ 1, -1,  1, -1],
       [ 1,  1, -1, -1],
       [ 1, -1, -1,  1]])
```

`scipy.linalg.`**`hankel`**`(`*c*, *r=None*`)`

Construct a Hankel matrix.

The Hankel matrix has constant anti-diagonals, with *c* as its first column and *r* as its last row. If *r* is not given, then *r = zeros_like(c)* is assumed.

Parameters **c** : array_like

First column of the matrix. Whatever the actual shape of *c*, it will be converted to a 1-D array.

r : array_like, optional

Last row of the matrix. If None, `r = zeros_like(c)` is assumed. r[0] is ignored; the last row of the returned matrix is `[c[-1], r[1:]]`. Whatever the actual shape of *r*, it will be converted to a 1-D array.

Returns **A** : (len(c), len(r)) ndarray

The Hankel matrix. Dtype is the same as `(c[0] + r[0]).dtype`.

See also:

`toeplitz`	Toeplitz matrix
`circulant`	circulant matrix

Examples

```
>>> from scipy.linalg import hankel
>>> hankel([1, 17, 99])
array([[ 1, 17, 99],
       [17, 99,  0],
       [99,  0,  0]])
>>> hankel([1,2,3,4], [4,7,7,8,9])
array([[1, 2, 3, 4, 7],
       [2, 3, 4, 7, 7],
       [3, 4, 7, 7, 8],
       [4, 7, 7, 8, 9]])
```

`scipy.linalg.`**`helmert`**`(`*n*, *full=False*`)`

Create a Helmert matrix of order *n*.

This has applications in statistics, compositional or simplicial analysis, and in Aitchison geometry.

Parameters **n** : int

The size of the array to create.

full : bool, optional

If True the (n, n) ndarray will be returned. Otherwise the submatrix that does not include the first row will be returned. Default: False.

Returns **M** : ndarray

The Helmert matrix. The shape is (n, n) or (n-1, n) depending on the *full* argument.

Examples

```
>>> from scipy.linalg import helmert
>>> helmert(5, full=True)
array([[ 0.4472136 ,  0.4472136 ,  0.4472136 ,  0.4472136 ,  0.4472136 ],
       [ 0.70710678, -0.70710678,  0.        ,  0.        ,  0.        ],
       [ 0.40824829,  0.40824829, -0.81649658,  0.        ,  0.        ],
       [ 0.28867513,  0.28867513,  0.28867513, -0.8660254 ,  0.        ],
       [ 0.2236068 ,  0.2236068 ,  0.2236068 ,  0.2236068 , -0.89442719]])
```

`scipy.linalg.`**`hilbert`**`(`*n*`)`

Create a Hilbert matrix of order *n*.

Returns the *n* by *n* array with entries *h[i,j] = 1 / (i + j + 1)*.

Parameters **n** : int

The size of the array to create.

Returns **h** : (n, n) ndarray

The Hilbert matrix.

See also:

`invhilbert`	Compute the inverse of a Hilbert matrix.

Notes

New in version 0.10.0.

Examples

```
>>> from scipy.linalg import hilbert
>>> hilbert(3)
array([[ 1.        ,  0.5       ,  0.33333333],
       [ 0.5       ,  0.33333333,  0.25      ],
       [ 0.33333333,  0.25      ,  0.2       ]])
```

`scipy.linalg.`**`invhilbert`**`(`*n*, *exact=False*`)`

Compute the inverse of the Hilbert matrix of order *n*.

The entries in the inverse of a Hilbert matrix are integers. When *n* is greater than 14, some entries in the inverse exceed the upper limit of 64 bit integers. The *exact* argument provides two options for dealing with these large integers.

Parameters **n** : int

The order of the Hilbert matrix.

exact : bool, optional

If False, the data type of the array that is returned is np.float64, and the array is an approximation of the inverse. If True, the array is the exact integer inverse array. To represent the exact inverse when n > 14, the returned array is an object array of long integers. For n <= 14, the exact inverse is returned as an array with data type np.int64.

Returns **invh** : (n, n) ndarray

The data type of the array is np.float64 if *exact* is False. If *exact* is True, the data type is either np.int64 (for n <= 14) or object (for n > 14). In the latter case, the objects in the array will be long integers.

See also:

`hilbert`	Create a Hilbert matrix.

Notes

New in version 0.10.0.

Examples

```
>>> from scipy.linalg import invhilbert
>>> invhilbert(4)
array([[   16.,   -120.,    240.,   -140.],
       [ -120.,   1200., -2700.,   1680.],
       [  240.,  -2700.,  6480., -4200.],
       [ -140.,   1680., -4200.,   2800.]])
>>> invhilbert(4, exact=True)
array([[   16,   -120,    240,   -140],
       [ -120,   1200,  -2700,   1680],
       [  240,  -2700,   6480,  -4200],
       [ -140,   1680,  -4200,   2800]], dtype=int64)
>>> invhilbert(16)[7,7]
4.2475099528537506e+19
>>> invhilbert(16, exact=True)[7,7]
42475099528537378560L
```

`scipy.linalg.`**`leslie`**(*f*, *s*)

Create a Leslie matrix.

Given the length n array of fecundity coefficients *f* and the length n-1 array of survival coefficents `s`, return the associated Leslie matrix.

Parameters **f** : (N,) array_like

The "fecundity" coefficients.

s : (N-1,) array_like

The "survival" coefficients, has to be 1-D. The length of `s` must be one less than the length of *f*, and it must be at least 1.

Returns **L** : (N, N) ndarray

The array is zero except for the first row, which is *f*, and the first sub-diagonal, which is `s`. The data-type of the array will be the data-type of `f[0]+s[0]`.

Notes

New in version 0.8.0.

The Leslie matrix is used to model discrete-time, age-structured population growth [R81] [R82]. In a population with *n* age classes, two sets of parameters define a Leslie matrix: the *n* "fecundity coefficients", which give the number of offspring per-capita produced by each age class, and the *n* - 1 "survival coefficients", which give the per-capita survival rate of each age class.

References

[R81], [R82]

Examples

```
>>> from scipy.linalg import leslie
>>> leslie([0.1, 2.0, 1.0, 0.1], [0.2, 0.8, 0.7])
array([[ 0.1,  2. ,  1. ,  0.1],
       [ 0.2,  0. ,  0. ,  0. ],
       [ 0. ,  0.8,  0. ,  0. ],
       [ 0. ,  0. ,  0.7,  0. ]])
```

`scipy.linalg.`**`pascal`**`(`*n*, *kind='symmetric'*, *exact=True*`)`

Returns the n x n Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

Parameters **n** : int

The size of the matrix to create; that is, the result is an n x n matrix.

kind : str, optional

Must be one of 'symmetric', 'lower', or 'upper'. Default is 'symmetric'.

exact : bool, optional

If *exact* is True, the result is either an array of type numpy.uint64 (if n < 35) or an object array of Python long integers. If *exact* is False, the coefficients in the matrix are computed using `scipy.special.comb` with *exact=False*. The result will be a floating point array, and the values in the array will not be the exact coefficients, but this version is much faster than *exact=True*.

Returns **p** : (n, n) ndarray

The Pascal matrix.

See also:

`invpascal`

Notes

See http://en.wikipedia.org/wiki/Pascal_matrix for more information about Pascal matrices.

New in version 0.11.0.

Examples

```
>>> from scipy.linalg import pascal
>>> pascal(4)
array([[ 1,  1,  1,  1],
       [ 1,  2,  3,  4],
       [ 1,  3,  6, 10],
       [ 1,  4, 10, 20]], dtype=uint64)
>>> pascal(4, kind='lower')
array([[1, 0, 0, 0],
       [1, 1, 0, 0],
       [1, 2, 1, 0],
       [1, 3, 3, 1]], dtype=uint64)
>>> pascal(50)[-1, -1]
25477612258980856902730428600L
>>> from scipy.special import comb
>>> comb(98, 49, exact=True)
25477612258980856902730428600L
```

`scipy.linalg.`**`invpascal`**`(`*n*, *kind='symmetric'*, *exact=True*`)`

Returns the inverse of the n x n Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

Parameters **n** : int

The size of the matrix to create; that is, the result is an n x n matrix.

kind : str, optional

Must be one of 'symmetric', 'lower', or 'upper'. Default is 'symmetric'.

exact : bool, optional

If *exact* is True, the result is either an array of type `numpy.int64` (if *n* <= 35) or an object array of Python integers. If *exact* is False, the coefficients in the matrix are computed using `scipy.special.comb` with *exact=False*. The result will be a floating point array, and for large *n*, the values in the array will not be the exact coefficients.

Returns **invp** : (n, n) ndarray

The inverse of the Pascal matrix.

See also:

`pascal`

Notes

New in version 0.16.0.

References

[R79], [R80]

Examples

```
>>> from scipy.linalg import invpascal, pascal
>>> invp = invpascal(5)
>>> invp
array([[  5, -10,  10,  -5,   1],
       [-10,  30, -35,  19,  -4],
       [ 10, -35,  46, -27,   6],
       [ -5,  19, -27,  17,  -4],
       [  1,  -4,   6,  -4,   1]])
```

```
>>> p = pascal(5)
>>> p.dot(invp)
array([[ 1.,  0.,  0.,  0.,  0.],
       [ 0.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  1.]])
```

An example of the use of *kind* and *exact*:

```
>>> invpascal(5, kind='lower', exact=False)
array([[ 1., -0.,  0., -0.,  0.],
       [-1.,  1., -0.,  0., -0.],
       [ 1., -2.,  1., -0.,  0.],
       [-1.,  3., -3.,  1., -0.],
       [ 1., -4.,  6., -4.,  1.]])
```

`scipy.linalg.`**`toeplitz`**`(`*c*, *r=None*`)`

Construct a Toeplitz matrix.

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, `r == conjugate(c)` is assumed.

Parameters **c** : array_like

First column of the matrix. Whatever the actual shape of *c*, it will be converted to a 1-D array.

r : array_like, optional

First row of the matrix. If None, `r = conjugate(c)` is assumed; in this case, if c[0] is real, the result is a Hermitian matrix. r[0] is ignored; the first row of the returned matrix is `[c[0], r[1:]]`. Whatever the actual shape of *r*, it will be converted to a 1-D array.

Returns **A** : (len(c), len(r)) ndarray

The Toeplitz matrix. Dtype is the same as `(c[0] + r[0]).dtype`.

See also:

`circulant`	circulant matrix
`hankel`	Hankel matrix

Notes

The behavior when *c* or *r* is a scalar, or when *c* is complex and *r* is None, was changed in version 0.8.0. The behavior in previous versions was undocumented and is no longer supported.

Examples

```
>>> from scipy.linalg import toeplitz
>>> toeplitz([1,2,3], [1,4,5,6])
array([[1, 4, 5, 6],
       [2, 1, 4, 5],
       [3, 2, 1, 4]])
>>> toeplitz([1.0, 2+3j, 4-1j])
array([[ 1.+0.j,  2.-3.j,  4.+1.j],
       [ 2.+3.j,  1.+0.j,  2.-3.j],
       [ 4.-1.j,  2.+3.j,  1.+0.j]])
```

`scipy.linalg.`**`tri`**(*N*, *M=None*, *k=0*, *dtype=None*)

Construct (N, M) matrix filled with ones at and below the k-th diagonal.

The matrix has A[i,j] == 1 for i <= j + k

Parameters **N** : int

The size of the first dimension of the matrix.

M : int or None, optional

The size of the second dimension of the matrix. If M is None, $M = N$ is assumed.

k : int, optional

Number of subdiagonal below which matrix is filled with ones. $k = 0$ is the main diagonal, $k < 0$ subdiagonal and $k > 0$ superdiagonal.

dtype : dtype, optional

Data type of the matrix.

Returns **tri** : (N, M) ndarray

Tri matrix.

Examples

```
>>> from scipy.linalg import tri
>>> tri(3, 5, 2, dtype=int)
array([[1, 1, 1, 0, 0],
       [1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1]])
>>> tri(3, 5, -1, dtype=int)
array([[0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0],
       [1, 1, 0, 0, 0]])
```

5.9.7 Low-level routines

`get_blas_funcs`(names[, arrays, dtype])	Return available BLAS function objects from names.
`get_lapack_funcs`(names[, arrays, dtype])	Return available LAPACK function objects from names.
`find_best_blas_type`([arrays, dtype])	Find best-matching BLAS/LAPACK type.

`scipy.linalg.`**`get_blas_funcs`**(*names*, *arrays=()*, *dtype=None*)

Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters **names** : str or sequence of str

Name(s) of BLAS functions without type prefix.

arrays : sequence of ndarrays, optional

Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype : str or dtype, optional

Data-type specifier. Not used if *arrays* is non-empty.

Returns **funcs** : list

List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the numpy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes *typecode* and *dtype* of the returned functions.

`scipy.linalg.`**`get_lapack_funcs`**(*names*, *arrays=()*, *dtype=None*)

Return available LAPACK function objects from names.

Arrays are used to determine the optimal prefix of LAPACK routines.

Parameters **names** : str or sequence of str

Name(s) of LAPACK functions without type prefix.

arrays : sequence of ndarrays, optional

Arrays can be given to determine optimal prefix of LAPACK routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype : str or dtype, optional

Data-type specifier. Not used if *arrays* is non-empty.

Returns **funcs** : list

List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In LAPACK, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the numpy types {float32, float64, complex64, complex128} respectevely, and are stored in attribute *typecode* of the returned functions.

`scipy.linalg.`**`find_best_blas_type`**(*arrays=()*, *dtype=None*)

Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters
arrays : sequence of ndarrays, optional
Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.
dtype : str or dtype, optional
Data-type specifier. Not used if *arrays* is non-empty.

Returns
prefix : str
BLAS/LAPACK prefix character.
dtype : dtype
Inferred Numpy data type.
prefer_fortran : bool
Whether to prefer Fortran order routines over C order.

See also:

`scipy.linalg.blas` – Low-level BLAS functions

`scipy.linalg.lapack` – Low-level LAPACK functions

`scipy.linalg.cython_blas` – Low-level BLAS functions for Cython

`scipy.linalg.cython_lapack` – Low-level LAPACK functions for Cython

5.10 Low-level BLAS functions

This module contains low-level functions from the BLAS library.

New in version 0.12.0.

Warning: These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in `scipy.linalg`.

5.11 Finding functions

`get_blas_funcs`(names[, arrays, dtype])	Return available BLAS function objects from names.
`find_best_blas_type`([arrays, dtype])	Find best-matching BLAS/LAPACK type.

`scipy.linalg.blas.`**`get_blas_funcs`**(*names*, *arrays=()*, *dtype=None*)

Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters
names : str or sequence of str
Name(s) of BLAS functions without type prefix.
arrays : sequence of ndarrays, optional
Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.
dtype : str or dtype, optional
Data-type specifier. Not used if *arrays* is non-empty.

Returns
funcs : list

List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the numpy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes *typecode* and *dtype* of the returned functions.

`scipy.linalg.blas.`**`find_best_blas_type`**(*arrays=()*, *dtype=None*)

Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters **arrays** : sequence of ndarrays, optional

Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype : str or dtype, optional

Data-type specifier. Not used if *arrays* is non-empty.

Returns **prefix** : str

BLAS/LAPACK prefix character.

dtype : dtype

Inferred Numpy data type.

prefer_fortran : bool

Whether to prefer Fortran order routines over C order.

5.12 BLAS Level 1 functions

`caxpy`(x,y,[n,a,offx,incx,offy,incy])	Wrapper for `caxpy`.
`ccopy`(x,y,[n,offx,incx,offy,incy])	Wrapper for `ccopy`.
`cdotc`(x,y,[n,offx,incx,offy,incy])	Wrapper for `cdotc`.
`cdotu`(x,y,[n,offx,incx,offy,incy])	Wrapper for `cdotu`.
`crotg`(a,b)	Wrapper for `crotg`.
`cscal`(a,x,[n,offx,incx])	Wrapper for `cscal`.
`csrot`(...)	Wrapper for `csrot`.
`csscal`(a,x,[n,offx,incx,overwrite_x])	Wrapper for `csscal`.
`cswap`(x,y,[n,offx,incx,offy,incy])	Wrapper for `cswap`.
`dasum`(x,[n,offx,incx])	Wrapper for `dasum`.
`daxpy`(x,y,[n,a,offx,incx,offy,incy])	Wrapper for `daxpy`.
`dcopy`(x,y,[n,offx,incx,offy,incy])	Wrapper for `dcopy`.
`ddot`(x,y,[n,offx,incx,offy,incy])	Wrapper for `ddot`.
`dnrm2`(x,[n,offx,incx])	Wrapper for `dnrm2`.
`drot`(...)	Wrapper for `drot`.
`drotg`(a,b)	Wrapper for `drotg`.
`drotm`(...)	Wrapper for `drotm`.
`drotmg`(d1,d2,x1,y1)	Wrapper for `drotmg`.
`dscal`(a,x,[n,offx,incx])	Wrapper for `dscal`.
`dswap`(x,y,[n,offx,incx,offy,incy])	Wrapper for `dswap`.

Continued on next page

Table 5.75 – continued from previous page

`dzasum`(x,[n,offx,incx])	Wrapper for `dzasum`.
`dznrm2`(x,[n,offx,incx])	Wrapper for `dznrm2`.
`icamax`(x,[n,offx,incx])	Wrapper for `icamax`.
`idamax`(x,[n,offx,incx])	Wrapper for `idamax`.
`isamax`(x,[n,offx,incx])	Wrapper for `isamax`.
`izamax`(x,[n,offx,incx])	Wrapper for `izamax`.
`sasum`(x,[n,offx,incx])	Wrapper for `sasum`.
`saxpy`(x,y,[n,a,offx,incx,offy,incy])	Wrapper for `saxpy`.
`scasum`(x,[n,offx,incx])	Wrapper for `scasum`.
`scnrm2`(x,[n,offx,incx])	Wrapper for `scnrm2`.
`scopy`(x,y,[n,offx,incx,offy,incy])	Wrapper for `scopy`.
`sdot`(x,y,[n,offx,incx,offy,incy])	Wrapper for `sdot`.
`snrm2`(x,[n,offx,incx])	Wrapper for `snrm2`.
`srot`(...)	Wrapper for `srot`.
`srotg`(a,b)	Wrapper for `srotg`.
`srotm`(...)	Wrapper for `srotm`.
`srotmg`(d1,d2,x1,y1)	Wrapper for `srotmg`.
`sscal`(a,x,[n,offx,incx])	Wrapper for `sscal`.
`sswap`(x,y,[n,offx,incx,offy,incy])	Wrapper for `sswap`.
`zaxpy`(x,y,[n,a,offx,incx,offy,incy])	Wrapper for `zaxpy`.
`zcopy`(x,y,[n,offx,incx,offy,incy])	Wrapper for `zcopy`.
`zdotc`(x,y,[n,offx,incx,offy,incy])	Wrapper for `zdotc`.
`zdotu`(x,y,[n,offx,incx,offy,incy])	Wrapper for `zdotu`.
`zdrot`(...)	Wrapper for `zdrot`.
`zdscal`(a,x,[n,offx,incx,overwrite_x])	Wrapper for `zdscal`.
`zrotg`(a,b)	Wrapper for `zrotg`.
`zscal`(a,x,[n,offx,incx])	Wrapper for `zscal`.
`zswap`(x,y,[n,offx,incx,offy,incy])	Wrapper for `zswap`.

`scipy.linalg.blas.`**`caxpy`**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `caxpy`.

Parameters
x : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)

Returns
z : rank-1 array('F') with bounds (*) and y storage

Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
a : input complex, optional
Default: (1.0, 0.0)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`ccopy`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `ccopy`.

Parameters
x : input rank-1 array('F') with bounds (*)

y : input rank-1 array('F') with bounds (*)

Returns **y** : rank-1 array('F') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`cdotc`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran cdotc>**

Wrapper for `cdotc`.

Parameters **x** : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)

Returns **xy** : complex

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`cdotu`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran cdotu>**

Wrapper for `cdotu`.

Parameters **x** : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)

Returns **xy** : complex

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`crotg`**(*a*, *b*) **= <fortran object>**

Wrapper for `crotg`.

Parameters **a** : input complex
b : input complex

Returns **c** : complex
s : complex

`scipy.linalg.blas.`**`cscal`**(*a*, *x*[, *n*, *offx*, *incx*]) = **<fortran object>**

Wrapper for `cscal`.

Parameters **a** : input complex
x : input rank-1 array('F') with bounds (*)

Returns **x** : rank-1 array('F') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`csrot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) = **<fortran object>**

Wrapper for `csrot`.

Parameters **x** : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)
c : input float
s : input float

Returns **x** : rank-1 array('F') with bounds (*)
y : rank-1 array('F') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`csscal`**(*a*, *x*[, *n*, *offx*, *incx*, *overwrite_x*]) = **<fortran object>**

Wrapper for `csscal`.

Parameters **a** : input float
x : input rank-1 array('F') with bounds (*)

Returns **x** : rank-1 array('F') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`cswap`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `cswap`.

Parameters **x** : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)

Returns **x** : rank-1 array('F') with bounds (*)
y : rank-1 array('F') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`dasum`**(*x*[, *n*, *offx*, *incx*]) = **<fortran dasum>**

Wrapper for `dasum`.

Parameters **x** : input rank-1 array('d') with bounds (*)

Returns **s** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`daxpy`**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `daxpy`.

Parameters **x** : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)

Returns **z** : rank-1 array('d') with bounds (*) and y storage

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

a : input float, optional
Default: 1.0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`dcopy`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `dcopy`.

Parameters **x** : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)

Returns **y** : rank-1 array('d') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`ddot`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran ddot>**

Wrapper for `ddot`.

Parameters **x** : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)

Returns **xy** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`dnrm2`**(*x*[, *n*, *offx*, *incx*]) **= <fortran dnrm2>**

Wrapper for `dnrm2`.

Parameters **x** : input rank-1 array('d') with bounds (*)

Returns **n2** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`drot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for `drot`.

Parameters **x** : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)
c : input float
s : input float

Returns **x** : rank-1 array('d') with bounds (*)
y : rank-1 array('d') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1

overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`drotg`**(*a*, *b*) = **<fortran object>**

Wrapper for `drotg`.

Parameters
a : input float
b : input float

Returns
c : float
s : float

`scipy.linalg.blas.`**`drotm`**(*x*, *y*, *param*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) = **<fortran object>**

Wrapper for `drotm`.

Parameters
x : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)
param : input rank-1 array('d') with bounds (5)

Returns
x : rank-1 array('d') with bounds (*)
y : rank-1 array('d') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`drotmg`**(*d1*, *d2*, *x1*, *y1*) = **<fortran object>**

Wrapper for `drotmg`.

Parameters
d1 : input float
d2 : input float
x1 : input float
y1 : input float

Returns
param : rank-1 array('d') with bounds (5)

`scipy.linalg.blas.`**`dscal`**(*a*, *x*[, *n*, *offx*, *incx*]) = **<fortran object>**

Wrapper for `dscal`.

Parameters **a** : input float
x : input rank-1 array('d') with bounds (*)
Returns **x** : rank-1 array('d') with bounds (*)
Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`dswap`**`(`*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]`)` **= <fortran object>**

Wrapper for `dswap`.

Parameters **x** : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)
Returns **x** : rank-1 array('d') with bounds (*)
y : rank-1 array('d') with bounds (*)
Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`dzasum`**`(`*x*[, *n*, *offx*, *incx*]`)` **= <fortran dzasum>**

Wrapper for `dzasum`.

Parameters **x** : input rank-1 array('D') with bounds (*)
Returns **s** : float
Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`dznrm2`**`(`*x*[, *n*, *offx*, *incx*]`)` **= <fortran dznrm2>**

Wrapper for `dznrm2`.

Parameters **x** : input rank-1 array('D') with bounds (*)
Returns **n2** : float
Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`icamax`**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for `icamax`.

Parameters **x** : input rank-1 array('F') with bounds (*)

Returns **k** : int

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`idamax`**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for `idamax`.

Parameters **x** : input rank-1 array('d') with bounds (*)

Returns **k** : int

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`isamax`**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for `isamax`.

Parameters **x** : input rank-1 array('f') with bounds (*)

Returns **k** : int

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`izamax`**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for `izamax`.

Parameters **x** : input rank-1 array('D') with bounds (*)

Returns **k** : int

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`sasum`**(*x*[, *n*, *offx*, *incx*]) **= <fortran sasum>**

Wrapper for `sasum`.

Parameters **x** : input rank-1 array('f') with bounds (*)

Returns **s** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`saxpy`**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for `saxpy`.

Parameters **x** : input rank-1 array('f') with bounds (*)

y : input rank-1 array('f') with bounds (*)

Returns **z** : rank-1 array('f') with bounds (*) and y storage

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

a : input float, optional
Default: 1.0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`scasum`**(*x*[, *n*, *offx*, *incx*]) **= <fortran scasum>**

Wrapper for `scasum`.

Parameters **x** : input rank-1 array('F') with bounds (*)

Returns **s** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`scnrm2`**(*x*[, *n*, *offx*, *incx*]) **= <fortran scnrm2>**

Wrapper for `scnrm2`.

Parameters **x** : input rank-1 array('F') with bounds (*)

Returns **n2** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`scopy`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for `scopy`.

Parameters **x** : input rank-1 array('f') with bounds (*)
y : input rank-1 array('f') with bounds (*)

Returns **y** : rank-1 array('f') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`sdot`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran sdot>**

Wrapper for `sdot`.

Parameters **x** : input rank-1 array('f') with bounds (*)
y : input rank-1 array('f') with bounds (*)

Returns **xy** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`snrm2`**(*x*[, *n*, *offx*, *incx*]) **= <fortran snrm2>**

Wrapper for `snrm2`.

Parameters **x** : input rank-1 array('f') with bounds (*)

Returns **n2** : float

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`srot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for `srot`.

Parameters **x** : input rank-1 array('f') with bounds (*)
y : input rank-1 array('f') with bounds (*)
c : input float
s : input float

Returns **x** : rank-1 array('f') with bounds (*)
y : rank-1 array('f') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`srotg`**(*a*, *b*) **= <fortran object>**

Wrapper for `srotg`.

Parameters
a : input float
b : input float

Returns
c : float
s : float

`scipy.linalg.blas.`**`srotm`**(*x*, *y*, *param*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for `srotm`.

Parameters
x : input rank-1 array('f') with bounds (*)
y : input rank-1 array('f') with bounds (*)
param : input rank-1 array('f') with bounds (5)

Returns
x : rank-1 array('f') with bounds (*)
y : rank-1 array('f') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`srotmg`**(*d1*, *d2*, *x1*, *y1*) **= <fortran object>**

Wrapper for `srotmg`.

Parameters
d1 : input float
d2 : input float
x1 : input float
y1 : input float

Returns
param : rank-1 array('f') with bounds (5)

`scipy.linalg.blas.`**`sscal`**(*a*, *x*[, *n*, *offx*, *incx*]) = **<fortran object>**

Wrapper for `sscal`.

Parameters **a** : input float

x : input rank-1 array('f') with bounds (*)

Returns **x** : rank-1 array('f') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`sswap`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `sswap`.

Parameters **x** : input rank-1 array('f') with bounds (*)

y : input rank-1 array('f') with bounds (*)

Returns **x** : rank-1 array('f') with bounds (*)

y : rank-1 array('f') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zaxpy`**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `zaxpy`.

Parameters **x** : input rank-1 array('D') with bounds (*)

y : input rank-1 array('D') with bounds (*)

Returns **z** : rank-1 array('D') with bounds (*) and y storage

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)

a : input complex, optional
Default: (1.0, 0.0)

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zcopy`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**

Wrapper for `zcopy`.

Parameters **x** : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)

Returns **y** : rank-1 array('D') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zdotc`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran zdotc>**
Wrapper for `zdotc`.

Parameters **x** : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)

Returns **xy** : complex

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zdotu`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran zdotu>**
Wrapper for `zdotu`.

Parameters **x** : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)

Returns **xy** : complex

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zdrot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**
Wrapper for `zdrot`.

Parameters **x** : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)
c : input float
s : input float

Returns **x** : rank-1 array('D') with bounds (*)
y : rank-1 array('D') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.blas.`**`zdscal`**(*a*, *x*[, *n*, *offx*, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for `zdscal`.

Parameters **a** : input float
x : input rank-1 array('D') with bounds (*)

Returns **x** : rank-1 array('D') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`zrotg`**(*a*, *b*) **= <fortran object>**

Wrapper for `zrotg`.

Parameters **a** : input complex
b : input complex

Returns **c** : complex
s : complex

`scipy.linalg.blas.`**`zscal`**(*a*, *x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for `zscal`.

Parameters **a** : input complex
x : input rank-1 array('D') with bounds (*)

Returns **x** : rank-1 array('D') with bounds (*)

Other Parameters

n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.blas.`**`zswap`**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) = **<fortran object>**
Wrapper for `zswap`.

Parameters
x : input rank-1 array(‘D’) with bounds (*)
y : input rank-1 array(‘D’) with bounds (*)

Returns
x : rank-1 array(‘D’) with bounds (*)
y : rank-1 array(‘D’) with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-offx)/abs(incx)
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

5.13 BLAS Level 2 functions

`cgemv`(...)	Wrapper for `cgemv`.
`cgerc`(...)	Wrapper for `cgerc`.
`cgeru`(...)	Wrapper for `cgeru`.
`chemv`(...)	Wrapper for `chemv`.
`ctrmv`(...)	Wrapper for `ctrmv`.
`csyr`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `csyr`.
`cher`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `cher`.
`cher2`(...)	Wrapper for `cher2`.
`dgemv`(...)	Wrapper for `dgemv`.
`dger`(...)	Wrapper for `dger`.
`dsymv`(...)	Wrapper for `dsymv`.
`dtrmv`(...)	Wrapper for `dtrmv`.
`dsyr`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `dsyr`.
`dsyr2`(...)	Wrapper for `dsyr2`.
`sgemv`(...)	Wrapper for `sgemv`.
`sger`(...)	Wrapper for `sger`.
`ssymv`(...)	Wrapper for `ssymv`.
`strmv`(...)	Wrapper for `strmv`.
`ssyr`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `ssyr`.
`ssyr2`(...)	Wrapper for `ssyr2`.
`zgemv`(...)	Wrapper for `zgemv`.
`zgerc`(...)	Wrapper for `zgerc`.
`zgeru`(...)	Wrapper for `zgeru`.
`zhemv`(...)	Wrapper for `zhemv`.
`ztrmv`(...)	Wrapper for `ztrmv`.
`zsyr`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `zsyr`.

Continued on next page

Table 5.76 – continued from previous page

`zher`(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for `zher`.
`zher2`(...)	Wrapper for `zher2`.

`scipy.linalg.blas.`**`cgemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for `cgemv`.

Parameters **alpha** : input complex
a : input rank-2 array('F') with bounds (m,n)
x : input rank-1 array('F') with bounds (*)

Returns **y** : rank-1 array('F') with bounds (ly)

Other Parameters

beta : input complex, optional
Default: (0.0, 0.0)
y : input rank-1 array('F') with bounds (ly)
overwrite_y : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
trans : input int, optional
Default: 0

`scipy.linalg.blas.`**`cgerc`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgerc`.

Parameters **alpha** : input complex
x : input rank-1 array('F') with bounds (m)
y : input rank-1 array('F') with bounds (n)

Returns **a** : rank-2 array('F') with bounds (m,n)

Other Parameters

overwrite_x : input int, optional
Default: 1
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 1
incy : input int, optional
Default: 1
a : input rank-2 array('F') with bounds (m,n), optional
Default: (0.0,0.0)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`cgeru`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgeru`.

Parameters **alpha** : input complex
x : input rank-1 array('F') with bounds (m)
y : input rank-1 array('F') with bounds (n)

Returns **a** : rank-2 array('F') with bounds (m,n)

Other Parameters

overwrite_x : input int, optional
Default: 1

incx : input int, optional
Default: 1

overwrite_y : input int, optional
Default: 1

incy : input int, optional
Default: 1

a : input rank-2 array('F') with bounds (m,n), optional
Default: (0.0,0.0)

overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`chemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) **= <fortran object>**

Wrapper for `chemv`.

Parameters **alpha** : input complex
a : input rank-2 array('F') with bounds (n,n)
x : input rank-1 array('F') with bounds (*)

Returns **y** : rank-1 array('F') with bounds (ly)

Other Parameters

beta : input complex, optional
Default: (0.0, 0.0)

y : input rank-1 array('F') with bounds (ly)

overwrite_y : input int, optional
Default: 0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`ctrmv`**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *unitdiag*, *overwrite_x*]) **= <fortran object>**

Wrapper for `ctrmv`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
x : input rank-1 array('F') with bounds (*)

Returns **x** : rank-1 array('F') with bounds (*)

Other Parameters

overwrite_x : input int, optional
Default: 0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0

`scipy.linalg.blas.`**`csyr`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `csyr`.

Parameters **alpha** : input complex
x : input rank-1 array('F') with bounds (*)
Returns **a** : rank-2 array('F') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
a : input rank-2 array('F') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`cher`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cher`.

Parameters **alpha** : input complex
x : input rank-1 array('F') with bounds (*)
Returns **a** : rank-2 array('F') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
a : input rank-2 array('F') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`cher2`**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cher2`.

Parameters **alpha** : input complex
x : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)
Returns **a** : rank-2 array('F') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional

Default: 1
offx : input int, optional
Default: 0
incy : input int, optional
Default: 1
offy : input int, optional
Default: 0
n : input int, optional
Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
a : input rank-2 array('F') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`dgemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for `dgemv`.

Parameters **alpha** : input float
a : input rank-2 array('d') with bounds (m,n)
x : input rank-1 array('d') with bounds (*)

Returns **y** : rank-1 array('d') with bounds (ly)

Other Parameters
beta : input float, optional
Default: 0.0
y : input rank-1 array('d') with bounds (ly)
overwrite_y : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
trans : input int, optional
Default: 0

`scipy.linalg.blas.`**`dger`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dger`.

Parameters **alpha** : input float
x : input rank-1 array('d') with bounds (m)
y : input rank-1 array('d') with bounds (n)

Returns **a** : rank-2 array('d') with bounds (m,n)

Other Parameters
overwrite_x : input int, optional
Default: 1
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 1
incy : input int, optional
Default: 1

a : input rank-2 array('d') with bounds (m,n), optional
Default: 0.0
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsymv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) **= <fortran object>**

Wrapper for `dsymv`.

Parameters
alpha : input float
a : input rank-2 array('d') with bounds (n,n)
x : input rank-1 array('d') with bounds (*)

Returns
y : rank-1 array('d') with bounds (ly)

Other Parameters
beta : input float, optional
Default: 0.0
y : input rank-1 array('d') with bounds (ly)
overwrite_y : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`dtrmv`**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *unitdiag*, *overwrite_x*]) **= <fortran object>**

Wrapper for `dtrmv`.

Parameters
a : input rank-2 array('d') with bounds (n,n)
x : input rank-1 array('d') with bounds (*)

Returns
x : rank-1 array('d') with bounds (*)

Other Parameters
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsyr`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dsyr`.

Parameters
alpha : input float
x : input rank-1 array('d') with bounds (*)

Returns
a : rank-2 array('d') with bounds (n,n)

Other Parameters

lower : input int, optional
Default: 0

incx : input int, optional
Default: 1

offx : input int, optional
Default: 0

n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1

a : input rank-2 array('d') with bounds (n,n)

overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsyr2`**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dsyr2`.

Parameters **alpha** : input float
x : input rank-1 array('d') with bounds (*)
y : input rank-1 array('d') with bounds (*)

Returns **a** : rank-2 array('d') with bounds (n,n)

Other Parameters

lower : input int, optional
Default: 0

incx : input int, optional
Default: 1

offx : input int, optional
Default: 0

incy : input int, optional
Default: 1

offy : input int, optional
Default: 0

n : input int, optional
Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)

a : input rank-2 array('d') with bounds (n,n)

overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`sgemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for `sgemv`.

Parameters **alpha** : input float
a : input rank-2 array('f') with bounds (m,n)
x : input rank-1 array('f') with bounds (*)

Returns **y** : rank-1 array('f') with bounds (ly)

Other Parameters

beta : input float, optional
Default: 0.0

y : input rank-1 array('f') with bounds (ly)

overwrite_y : input int, optional
Default: 0

offx : input int, optional
Default: 0

incx : input int, optional

Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
trans : input int, optional
Default: 0

`scipy.linalg.blas.`**`sger`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for `sger`.

Parameters **alpha** : input float
x : input rank-1 array('f') with bounds (m)
y : input rank-1 array('f') with bounds (n)

Returns **a** : rank-2 array('f') with bounds (m,n)

Other Parameters
overwrite_x : input int, optional
Default: 1
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 1
incy : input int, optional
Default: 1
a : input rank-2 array('f') with bounds (m,n), optional
Default: 0.0
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssymv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for `ssymv`.

Parameters **alpha** : input float
a : input rank-2 array('f') with bounds (n,n)
x : input rank-1 array('f') with bounds (*)

Returns **y** : rank-1 array('f') with bounds (ly)

Other Parameters
beta : input float, optional
Default: 0.0
y : input rank-1 array('f') with bounds (ly)
overwrite_y : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`strmv`**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *unitdiag*, *overwrite_x*]) = **<fortran object>**

Wrapper for `strmv`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)
x : input rank-1 array('f') with bounds (*)

Returns **x** : rank-1 array('f') with bounds (*)

Other Parameters

overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssyr`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `ssyr`.

Parameters **alpha** : input float
x : input rank-1 array('f') with bounds (*)

Returns **a** : rank-2 array('f') with bounds (n,n)

Other Parameters

lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
a : input rank-2 array('f') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssyr2`**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `ssyr2`.

Parameters **alpha** : input float
x : input rank-1 array('f') with bounds (*)
y : input rank-1 array('f') with bounds (*)

Returns **a** : rank-2 array('f') with bounds (n,n)

Other Parameters

lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
incy : input int, optional
Default: 1
offy : input int, optional
Default: 0
n : input int, optional

Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)

a : input rank-2 array('f') with bounds (n,n)

overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`zgemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for `zgemv`.

Parameters
alpha : input complex
a : input rank-2 array('D') with bounds (m,n)
x : input rank-1 array('D') with bounds (*)

Returns
y : rank-1 array('D') with bounds (ly)

Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
y : input rank-1 array('D') with bounds (ly)
overwrite_y : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1
trans : input int, optional
Default: 0

`scipy.linalg.blas.`**`zgerc`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgerc`.

Parameters
alpha : input complex
x : input rank-1 array('D') with bounds (m)
y : input rank-1 array('D') with bounds (n)

Returns
a : rank-2 array('D') with bounds (m,n)

Other Parameters
overwrite_x : input int, optional
Default: 1
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 1
incy : input int, optional
Default: 1
a : input rank-2 array('D') with bounds (m,n), optional
Default: (0.0,0.0)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`zgeru`**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgeru`.

Parameters **alpha** : input complex
x : input rank-1 array('D') with bounds (m)
y : input rank-1 array('D') with bounds (n)

Returns **a** : rank-2 array('D') with bounds (m,n)

Other Parameters

overwrite_x : input int, optional
Default: 1

incx : input int, optional
Default: 1

overwrite_y : input int, optional
Default: 1

incy : input int, optional
Default: 1

a : input rank-2 array('D') with bounds (m,n), optional
Default: (0.0,0.0)

overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`zhemv`**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) **= <fortran object>**

Wrapper for `zhemv`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (n,n)
x : input rank-1 array('D') with bounds (*)

Returns **y** : rank-1 array('D') with bounds (ly)

Other Parameters

beta : input complex, optional
Default: (0.0, 0.0)

y : input rank-1 array('D') with bounds (ly)

overwrite_y : input int, optional
Default: 0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

offy : input int, optional
Default: 0

incy : input int, optional
Default: 1

lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`ztrmv`**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *unitdiag*, *overwrite_x*]) **= <fortran object>**

Wrapper for `ztrmv`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
x : input rank-1 array('D') with bounds (*)

Returns **x** : rank-1 array('D') with bounds (*)

Other Parameters

overwrite_x : input int, optional
Default: 0

offx : input int, optional
Default: 0

incx : input int, optional
Default: 1

lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0

`scipy.linalg.blas.`**`zsyr`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zsyr`.

Parameters **alpha** : input complex
x : input rank-1 array('D') with bounds (*)
Returns **a** : rank-2 array('D') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
a : input rank-2 array('D') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`zher`**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zher`.

Parameters **alpha** : input complex
x : input rank-1 array('D') with bounds (*)
Returns **a** : rank-2 array('D') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional
Default: 1
offx : input int, optional
Default: 0
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
a : input rank-2 array('D') with bounds (n,n)
overwrite_a : input int, optional
Default: 0

`scipy.linalg.blas.`**`zher2`**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zher2`.

Parameters **alpha** : input complex
x : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)
Returns **a** : rank-2 array('D') with bounds (n,n)
Other Parameters
lower : input int, optional
Default: 0
incx : input int, optional

Default: 1

offx : input int, optional
Default: 0

incy : input int, optional
Default: 1

offy : input int, optional
Default: 0

n : input int, optional
Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)

a : input rank-2 array('D') with bounds (n,n)

overwrite_a : input int, optional
Default: 0

5.14 BLAS Level 3 functions

`cgemm`(...)	Wrapper for `cgemm`.
`chemm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `chemm`.
`cherk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `cherk`.
`cher2k`(...)	Wrapper for `cher2k`.
`csymm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `csymm`.
`csyrk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `csyrk`.
`csyr2k`(...)	Wrapper for `csyr2k`.
`dgemm`(...)	Wrapper for `dgemm`.
`dsymm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `dsymm`.
`dsyrk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `dsyrk`.
`dsyr2k`(...)	Wrapper for `dsyr2k`.
`sgemm`(...)	Wrapper for `sgemm`.
`ssymm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `ssymm`.
`ssyrk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `ssyrk`.
`ssyr2k`(...)	Wrapper for `ssyr2k`.
`zgemm`(...)	Wrapper for `zgemm`.
`zhemm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `zhemm`.
`zherk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `zherk`.
`zher2k`(...)	Wrapper for `zher2k`.
`zsymm`(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for `zsymm`.
`zsyrk`(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for `zsyrk`.
`zsyr2k`(...)	Wrapper for `zsyr2k`.

`scipy.linalg.blas.`**`cgemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for `cgemm`.

Parameters
alpha : input complex
a : input rank-2 array('F') with bounds (lda,ka)
b : input rank-2 array('F') with bounds (ldb,kb)

Returns
c : rank-2 array('F') with bounds (m,n)

Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)

c : input rank-2 array('F') with bounds (m,n)

overwrite_c : input int, optional

Default: 0

trans_a : input int, optional

Default: 0

trans_b : input int, optional

Default: 0

`scipy.linalg.blas.`**`chemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `chemm`.

Parameters **alpha** : input complex

a : input rank-2 array('F') with bounds (lda,ka)

b : input rank-2 array('F') with bounds (ldb,kb)

Returns **c** : rank-2 array('F') with bounds (m,n)

Other Parameters

beta : input complex, optional

Default: (0.0, 0.0)

c : input rank-2 array('F') with bounds (m,n)

overwrite_c : input int, optional

Default: 0

side : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.blas.`**`cherk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `cherk`.

Parameters **alpha** : input complex

a : input rank-2 array('F') with bounds (lda,ka)

Returns **c** : rank-2 array('F') with bounds (n,n)

Other Parameters

beta : input complex, optional

Default: (0.0, 0.0)

c : input rank-2 array('F') with bounds (n,n)

overwrite_c : input int, optional

Default: 0

trans : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.blas.`**`cher2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `cher2k`.

Parameters **alpha** : input complex

a : input rank-2 array('F') with bounds (lda,ka)

b : input rank-2 array('F') with bounds (ldb,kb)

Returns **c** : rank-2 array('F') with bounds (n,n)

Other Parameters

beta : input complex, optional

Default: (0.0, 0.0)

c : input rank-2 array('F') with bounds (n,n)

overwrite_c : input int, optional

Default: 0

trans : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.blas.`**`csymm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `csymm`.

Parameters **alpha** : input complex
a : input rank-2 array('F') with bounds (lda,ka)
b : input rank-2 array('F') with bounds (ldb,kb)

Returns **c** : rank-2 array('F') with bounds (m,n)

Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('F') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
side : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`csyrk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `csyrk`.

Parameters **alpha** : input complex
a : input rank-2 array('F') with bounds (lda,ka)

Returns **c** : rank-2 array('F') with bounds (n,n)

Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('F') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`csyr2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `csyr2k`.

Parameters **alpha** : input complex
a : input rank-2 array('F') with bounds (lda,ka)
b : input rank-2 array('F') with bounds (ldb,kb)

Returns **c** : rank-2 array('F') with bounds (n,n)

Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('F') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`dgemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dgemm`.

Parameters **alpha** : input float
a : input rank-2 array('d') with bounds (lda,ka)
b : input rank-2 array('d') with bounds (ldb,kb)

Returns **c** : rank-2 array('d') with bounds (m,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('d') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
trans_a : input int, optional
Default: 0
trans_b : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsymm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dsymm`.

Parameters **alpha** : input float
a : input rank-2 array('d') with bounds (lda,ka)
b : input rank-2 array('d') with bounds (ldb,kb)

Returns **c** : rank-2 array('d') with bounds (m,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('d') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
side : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsyrk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dsyrk`.

Parameters **alpha** : input float
a : input rank-2 array('d') with bounds (lda,ka)

Returns **c** : rank-2 array('d') with bounds (n,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('d') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`dsyr2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dsyr2k`.

Parameters **alpha** : input float
a : input rank-2 array('d') with bounds (lda,ka)
b : input rank-2 array('d') with bounds (ldb,kb)

Returns **c** : rank-2 array('d') with bounds (n,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('d') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`sgemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for `sgemm`.

Parameters

alpha : input float
a : input rank-2 array('f') with bounds (lda,ka)
b : input rank-2 array('f') with bounds (ldb,kb)

Returns

c : rank-2 array('f') with bounds (m,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('f') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
trans_a : input int, optional
Default: 0
trans_b : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssymm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ssymm`.

Parameters

alpha : input float
a : input rank-2 array('f') with bounds (lda,ka)
b : input rank-2 array('f') with bounds (ldb,kb)

Returns

c : rank-2 array('f') with bounds (m,n)

Other Parameters

beta : input float, optional
Default: 0.0
c : input rank-2 array('f') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
side : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssyrk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ssyrk`.

Parameters

alpha : input float
a : input rank-2 array('f') with bounds (lda,ka)

Returns

c : rank-2 array('f') with bounds (n,n)

Other Parameters

beta : input float, optional
Default: 0.0

c : input rank-2 array('f') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`ssyr2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for `ssyr2k`.

Parameters **alpha** : input float
a : input rank-2 array('f') with bounds (lda,ka)
b : input rank-2 array('f') with bounds (ldb,kb)
Returns **c** : rank-2 array('f') with bounds (n,n)
Other Parameters
beta : input float, optional
Default: 0.0
c : input rank-2 array('f') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zgemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**
Wrapper for `zgemm`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (lda,ka)
b : input rank-2 array('D') with bounds (ldb,kb)
Returns **c** : rank-2 array('D') with bounds (m,n)
Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('D') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
trans_a : input int, optional
Default: 0
trans_b : input int, optional
Default: 0

`scipy.linalg.blas.`**`zhemm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for `zhemm`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (lda,ka)
b : input rank-2 array('D') with bounds (ldb,kb)
Returns **c** : rank-2 array('D') with bounds (m,n)
Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('D') with bounds (m,n)
overwrite_c : input int, optional
Default: 0

side : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zherk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for `zherk`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (lda,ka)
Returns **c** : rank-2 array('D') with bounds (n,n)
Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('D') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zher2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for `zher2k`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (lda,ka)
b : input rank-2 array('D') with bounds (ldb,kb)
Returns **c** : rank-2 array('D') with bounds (n,n)
Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('D') with bounds (n,n)
overwrite_c : input int, optional
Default: 0
trans : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zsymm`**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for `zsymm`.

Parameters **alpha** : input complex
a : input rank-2 array('D') with bounds (lda,ka)
b : input rank-2 array('D') with bounds (ldb,kb)
Returns **c** : rank-2 array('D') with bounds (m,n)
Other Parameters
beta : input complex, optional
Default: (0.0, 0.0)
c : input rank-2 array('D') with bounds (m,n)
overwrite_c : input int, optional
Default: 0
side : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zsyrk`**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `zsyrk`.

Parameters	**alpha** : input complex **a** : input rank-2 array('D') with bounds (lda,ka)
Returns	**c** : rank-2 array('D') with bounds (n,n)

Other Parameters

beta : input complex, optional
Default: (0.0, 0.0)

c : input rank-2 array('D') with bounds (n,n)

overwrite_c : input int, optional
Default: 0

trans : input int, optional
Default: 0

lower : input int, optional
Default: 0

`scipy.linalg.blas.`**`zsyr2k`**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `zsyr2k`.

Parameters	**alpha** : input complex **a** : input rank-2 array('D') with bounds (lda,ka) **b** : input rank-2 array('D') with bounds (ldb,kb)
Returns	**c** : rank-2 array('D') with bounds (n,n)

Other Parameters

beta : input complex, optional
Default: (0.0, 0.0)

c : input rank-2 array('D') with bounds (n,n)

overwrite_c : input int, optional
Default: 0

trans : input int, optional
Default: 0

lower : input int, optional
Default: 0

5.15 Low-level LAPACK functions

This module contains low-level functions from the LAPACK library.

New in version 0.12.0.

Warning: These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in `scipy.linalg`.

5.16 Finding functions

`get_lapack_funcs`(names[, arrays, dtype])	Return available LAPACK function objects from names.

5.17 All functions

`sgbsv`(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `sgbsv`.
`dgbsv`(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `dgbsv`.
`cgbsv`(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `cgbsv`.
`zgbsv`(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `zgbsv`.
`sgbtrf`(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `sgbtrf`.
`dgbtrf`(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `dgbtrf`.
`cgbtrf`(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `cgbtrf`.
`zgbtrf`(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `zgbtrf`.
`sgbtrs`(...)	Wrapper for `sgbtrs`.
`dgbtrs`(...)	Wrapper for `dgbtrs`.
`cgbtrs`(...)	Wrapper for `cgbtrs`.
`zgbtrs`(...)	Wrapper for `zgbtrs`.
`sgebal`(a,[scale,permute,overwrite_a])	Wrapper for `sgebal`.
`dgebal`(a,[scale,permute,overwrite_a])	Wrapper for `dgebal`.
`cgebal`(a,[scale,permute,overwrite_a])	Wrapper for `cgebal`.
`zgebal`(a,[scale,permute,overwrite_a])	Wrapper for `zgebal`.
`sgees`(...)	Wrapper for `sgees`.
`dgees`(...)	Wrapper for `dgees`.
`cgees`(...)	Wrapper for `cgees`.
`zgees`(...)	Wrapper for `zgees`.
`sgeev`(...)	Wrapper for `sgeev`.
`dgeev`(...)	Wrapper for `dgeev`.
`cgeev`(...)	Wrapper for `cgeev`.
`zgeev`(...)	Wrapper for `zgeev`.
`sgeev_lwork`(n,[compute_vl,compute_vr])	Wrapper for `sgeev_lwork`.
`dgeev_lwork`(n,[compute_vl,compute_vr])	Wrapper for `dgeev_lwork`.
`cgeev_lwork`(n,[compute_vl,compute_vr])	Wrapper for `cgeev_lwork`.
`zgeev_lwork`(n,[compute_vl,compute_vr])	Wrapper for `zgeev_lwork`.
`sgegv`(...)	Wrapper for `sgegv`.
`dgegv`(...)	Wrapper for `dgegv`.
`cgegv`(...)	Wrapper for `cgegv`.
`zgegv`(...)	Wrapper for `zgegv`.
`sgehrd`(a,[lo,hi,lwork,overwrite_a])	Wrapper for `sgehrd`.
`dgehrd`(a,[lo,hi,lwork,overwrite_a])	Wrapper for `dgehrd`.
`cgehrd`(a,[lo,hi,lwork,overwrite_a])	Wrapper for `cgehrd`.
`zgehrd`(a,[lo,hi,lwork,overwrite_a])	Wrapper for `zgehrd`.
`sgehrd_lwork`(n,[lo,hi])	Wrapper for `sgehrd_lwork`.
`dgehrd_lwork`(n,[lo,hi])	Wrapper for `dgehrd_lwork`.
`cgehrd_lwork`(n,[lo,hi])	Wrapper for `cgehrd_lwork`.
`zgehrd_lwork`(n,[lo,hi])	Wrapper for `zgehrd_lwork`.
`sgelss`(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for `sgelss`.
`dgelss`(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for `dgelss`.
`cgelss`(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for `cgelss`.
`zgelss`(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for `zgelss`.
`sgelss_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `sgelss_lwork`.
`dgelss_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `dgelss_lwork`.
`cgelss_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `cgelss_lwork`.
`zgelss_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `zgelss_lwork`.
`sgelsd`(...)	Wrapper for `sgelsd`.
`dgelsd`(...)	Wrapper for `dgelsd`.

Continued on next page

Table 5.79 – continued from previous page

`cgelsd`(...)	Wrapper for `cgelsd`.
`zgelsd`(...)	Wrapper for `zgelsd`.
`sgelsd_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `sgelsd_lwork`.
`dgelsd_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `dgelsd_lwork`.
`cgelsd_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `cgelsd_lwork`.
`zgelsd_lwork`(m,n,nrhs,[cond,lwork])	Wrapper for `zgelsd_lwork`.
`sgelsy`(...)	Wrapper for `sgelsy`.
`dgelsy`(...)	Wrapper for `dgelsy`.
`cgelsy`(...)	Wrapper for `cgelsy`.
`zgelsy`(...)	Wrapper for `zgelsy`.
`sgelsy_lwork`(m,n,nrhs,cond,[lwork])	Wrapper for `sgelsy_lwork`.
`dgelsy_lwork`(m,n,nrhs,cond,[lwork])	Wrapper for `dgelsy_lwork`.
`cgelsy_lwork`(m,n,nrhs,cond,[lwork])	Wrapper for `cgelsy_lwork`.
`zgelsy_lwork`(m,n,nrhs,cond,[lwork])	Wrapper for `zgelsy_lwork`.
`sgeqp3`(a,[lwork,overwrite_a])	Wrapper for `sgeqp3`.
`dgeqp3`(a,[lwork,overwrite_a])	Wrapper for `dgeqp3`.
`cgeqp3`(a,[lwork,overwrite_a])	Wrapper for `cgeqp3`.
`zgeqp3`(a,[lwork,overwrite_a])	Wrapper for `zgeqp3`.
`sgeqrf`(a,[lwork,overwrite_a])	Wrapper for `sgeqrf`.
`dgeqrf`(a,[lwork,overwrite_a])	Wrapper for `dgeqrf`.
`cgeqrf`(a,[lwork,overwrite_a])	Wrapper for `cgeqrf`.
`zgeqrf`(a,[lwork,overwrite_a])	Wrapper for `zgeqrf`.
`sgerqf`(a,[lwork,overwrite_a])	Wrapper for `sgerqf`.
`dgerqf`(a,[lwork,overwrite_a])	Wrapper for `dgerqf`.
`cgerqf`(a,[lwork,overwrite_a])	Wrapper for `cgerqf`.
`zgerqf`(a,[lwork,overwrite_a])	Wrapper for `zgerqf`.
`sgesdd`(...)	Wrapper for `sgesdd`.
`dgesdd`(...)	Wrapper for `dgesdd`.
`cgesdd`(...)	Wrapper for `cgesdd`.
`zgesdd`(...)	Wrapper for `zgesdd`.
`sgesdd_lwork`(m,n,[compute_uv,full_matrices])	Wrapper for `sgesdd_lwork`.
`dgesdd_lwork`(m,n,[compute_uv,full_matrices])	Wrapper for `dgesdd_lwork`.
`cgesdd_lwork`(m,n,[compute_uv,full_matrices])	Wrapper for `cgesdd_lwork`.
`zgesdd_lwork`(m,n,[compute_uv,full_matrices])	Wrapper for `zgesdd_lwork`.
`sgesv`(a,b,[overwrite_a,overwrite_b])	Wrapper for `sgesv`.
`dgesv`(a,b,[overwrite_a,overwrite_b])	Wrapper for `dgesv`.
`cgesv`(a,b,[overwrite_a,overwrite_b])	Wrapper for `cgesv`.
`zgesv`(a,b,[overwrite_a,overwrite_b])	Wrapper for `zgesv`.
`sgetrf`(a,[overwrite_a])	Wrapper for `sgetrf`.
`dgetrf`(a,[overwrite_a])	Wrapper for `dgetrf`.
`cgetrf`(a,[overwrite_a])	Wrapper for `cgetrf`.
`zgetrf`(a,[overwrite_a])	Wrapper for `zgetrf`.
`sgetri`(lu,piv,[lwork,overwrite_lu])	Wrapper for `sgetri`.
`dgetri`(lu,piv,[lwork,overwrite_lu])	Wrapper for `dgetri`.
`cgetri`(lu,piv,[lwork,overwrite_lu])	Wrapper for `cgetri`.
`zgetri`(lu,piv,[lwork,overwrite_lu])	Wrapper for `zgetri`.
`sgetri_lwork`(n)	Wrapper for `sgetri_lwork`.
`dgetri_lwork`(n)	Wrapper for `dgetri_lwork`.
`cgetri_lwork`(n)	Wrapper for `cgetri_lwork`.
`zgetri_lwork`(n)	Wrapper for `zgetri_lwork`.

Continued on next page

Table 5.79 – continued from previous page

`sgetrs`(lu,piv,b,[trans,overwrite_b])	Wrapper for `sgetrs`.
`dgetrs`(lu,piv,b,[trans,overwrite_b])	Wrapper for `dgetrs`.
`cgetrs`(lu,piv,b,[trans,overwrite_b])	Wrapper for `cgetrs`.
`zgetrs`(lu,piv,b,[trans,overwrite_b])	Wrapper for `zgetrs`.
`sgges`(...)	Wrapper for `sgges`.
`dgges`(...)	Wrapper for `dgges`.
`cgges`(...)	Wrapper for `cgges`.
`zgges`(...)	Wrapper for `zgges`.
`sggev`(...)	Wrapper for `sggev`.
`dggev`(...)	Wrapper for `dggev`.
`cggev`(...)	Wrapper for `cggev`.
`zggev`(...)	Wrapper for `zggev`.
`chbevd`(...)	Wrapper for `chbevd`.
`zhbevd`(...)	Wrapper for `zhbevd`.
`chbevx`(...)	Wrapper for `chbevx`.
`zhbevx`(...)	Wrapper for `zhbevx`.
`cheev`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `cheev`.
`zheev`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `zheev`.
`cheevd`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `cheevd`.
`zheevd`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `zheevd`.
`cheevr`(...)	Wrapper for `cheevr`.
`zheevr`(...)	Wrapper for `zheevr`.
`chegv`(...)	Wrapper for `chegv`.
`zhegv`(...)	Wrapper for `zhegv`.
`chegvd`(...)	Wrapper for `chegvd`.
`zhegvd`(...)	Wrapper for `zhegvd`.
`chegvx`(...)	Wrapper for `chegvx`.
`zhegvx`(...)	Wrapper for `zhegvx`.
`slarf`(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for `slarf`.
`dlarf`(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for `dlarf`.
`clarf`(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for `clarf`.
`zlarf`(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for `zlarf`.
`slarfg`(n,alpha,x,[incx,overwrite_x])	Wrapper for `slarfg`.
`dlarfg`(n,alpha,x,[incx,overwrite_x])	Wrapper for `dlarfg`.
`clarfg`(n,alpha,x,[incx,overwrite_x])	Wrapper for `clarfg`.
`zlarfg`(n,alpha,x,[incx,overwrite_x])	Wrapper for `zlarfg`.
`slartg`(f,g)	Wrapper for `slartg`.
`dlartg`(f,g)	Wrapper for `dlartg`.
`clartg`(f,g)	Wrapper for `clartg`.
`zlartg`(f,g)	Wrapper for `zlartg`.
`dlasd4`(i,d,z,[rho])	Wrapper for `dlasd4`.
`slasd4`(i,d,z,[rho])	Wrapper for `slasd4`.
`slaswp`(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for `slaswp`.
`dlaswp`(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for `dlaswp`.
`claswp`(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for `claswp`.
`zlaswp`(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for `zlaswp`.
`slauum`(c,[lower,overwrite_c])	Wrapper for `slauum`.
`dlauum`(c,[lower,overwrite_c])	Wrapper for `dlauum`.
`clauum`(c,[lower,overwrite_c])	Wrapper for `clauum`.
`zlauum`(c,[lower,overwrite_c])	Wrapper for `zlauum`.

Continued on next page

Table 5.79 – continued from previous page

`spbsv`(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for `spbsv`.
`dpbsv`(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for `dpbsv`.
`cpbsv`(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for `cpbsv`.
`zpbsv`(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for `zpbsv`.
`spbtrf`(ab,[lower,ldab,overwrite_ab])	Wrapper for `spbtrf`.
`dpbtrf`(ab,[lower,ldab,overwrite_ab])	Wrapper for `dpbtrf`.
`cpbtrf`(ab,[lower,ldab,overwrite_ab])	Wrapper for `cpbtrf`.
`zpbtrf`(ab,[lower,ldab,overwrite_ab])	Wrapper for `zpbtrf`.
`spbtrs`(ab,b,[lower,ldab,overwrite_b])	Wrapper for `spbtrs`.
`dpbtrs`(ab,b,[lower,ldab,overwrite_b])	Wrapper for `dpbtrs`.
`cpbtrs`(ab,b,[lower,ldab,overwrite_b])	Wrapper for `cpbtrs`.
`zpbtrs`(ab,b,[lower,ldab,overwrite_b])	Wrapper for `zpbtrs`.
`sposv`(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for `sposv`.
`dposv`(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for `dposv`.
`cposv`(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for `cposv`.
`zposv`(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for `zposv`.
`spotrf`(a,[lower,clean,overwrite_a])	Wrapper for `spotrf`.
`dpotrf`(a,[lower,clean,overwrite_a])	Wrapper for `dpotrf`.
`cpotrf`(a,[lower,clean,overwrite_a])	Wrapper for `cpotrf`.
`zpotrf`(a,[lower,clean,overwrite_a])	Wrapper for `zpotrf`.
`spotri`(c,[lower,overwrite_c])	Wrapper for `spotri`.
`dpotri`(c,[lower,overwrite_c])	Wrapper for `dpotri`.
`cpotri`(c,[lower,overwrite_c])	Wrapper for `cpotri`.
`zpotri`(c,[lower,overwrite_c])	Wrapper for `zpotri`.
`spotrs`(c,b,[lower,overwrite_b])	Wrapper for `spotrs`.
`dpotrs`(c,b,[lower,overwrite_b])	Wrapper for `dpotrs`.
`cpotrs`(c,b,[lower,overwrite_b])	Wrapper for `cpotrs`.
`zpotrs`(c,b,[lower,overwrite_b])	Wrapper for `zpotrs`.
`crot`(...)	Wrapper for `crot`.
`zrot`(...)	Wrapper for `zrot`.
`strsyl`(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for `strsyl`.
`dtrsyl`(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for `dtrsyl`.
`ctrsyl`(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for `ctrsyl`.
`ztrsyl`(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for `ztrsyl`.
`strtri`(c,[lower,unitdiag,overwrite_c])	Wrapper for `strtri`.
`dtrtri`(c,[lower,unitdiag,overwrite_c])	Wrapper for `dtrtri`.
`ctrtri`(c,[lower,unitdiag,overwrite_c])	Wrapper for `ctrtri`.
`ztrtri`(c,[lower,unitdiag,overwrite_c])	Wrapper for `ztrtri`.
`strtrs`(...)	Wrapper for `strtrs`.
`dtrtrs`(...)	Wrapper for `dtrtrs`.
`ctrtrs`(...)	Wrapper for `ctrtrs`.
`ztrtrs`(...)	Wrapper for `ztrtrs`.
`cunghr`(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for `cunghr`.
`zunghr`(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for `zunghr`.
`cungqr`(a,tau,[lwork,overwrite_a])	Wrapper for `cungqr`.
`zungqr`(a,tau,[lwork,overwrite_a])	Wrapper for `zungqr`.
`cungrq`(a,tau,[lwork,overwrite_a])	Wrapper for `cungrq`.
`zungrq`(a,tau,[lwork,overwrite_a])	Wrapper for `zungrq`.
`cunmqr`(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for `cunmqr`.
`zunmqr`(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for `zunmqr`.

Continued on next page

Table 5.79 – continued from previous page

`sgtsv`(...)	Wrapper for `sgtsv`.
`dgtsv`(...)	Wrapper for `dgtsv`.
`cgtsv`(...)	Wrapper for `cgtsv`.
`zgtsv`(...)	Wrapper for `zgtsv`.
`sptsv`(...)	Wrapper for `sptsv`.
`dptsv`(...)	Wrapper for `dptsv`.
`cptsv`(...)	Wrapper for `cptsv`.
`zptsv`(...)	Wrapper for `zptsv`.
`slamch`(cmach)	Wrapper for `slamch`.
`dlamch`(cmach)	Wrapper for `dlamch`.
`sorghr`(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for `sorghr`.
`dorghr`(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for `dorghr`.
`sorgqr`(a,tau,[lwork,overwrite_a])	Wrapper for `sorgqr`.
`dorgqr`(a,tau,[lwork,overwrite_a])	Wrapper for `dorgqr`.
`sorgrq`(a,tau,[lwork,overwrite_a])	Wrapper for `sorgrq`.
`dorgrq`(a,tau,[lwork,overwrite_a])	Wrapper for `dorgrq`.
`sormqr`(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for `sormqr`.
`dormqr`(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for `dormqr`.
`ssbev`(ab,[compute_v,lower,ldab,overwrite_ab])	Wrapper for `ssbev`.
`dsbev`(ab,[compute_v,lower,ldab,overwrite_ab])	Wrapper for `dsbev`.
`ssbevd`(...)	Wrapper for `ssbevd`.
`dsbevd`(...)	Wrapper for `dsbevd`.
`ssbevx`(...)	Wrapper for `ssbevx`.
`dsbevx`(...)	Wrapper for `dsbevx`.
`ssyev`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `ssyev`.
`dsyev`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `dsyev`.
`ssyevd`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `ssyevd`.
`dsyevd`(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for `dsyevd`.
`ssyevr`(...)	Wrapper for `ssyevr`.
`dsyevr`(...)	Wrapper for `dsyevr`.
`ssygv`(...)	Wrapper for `ssygv`.
`dsygv`(...)	Wrapper for `dsygv`.
`ssygvd`(...)	Wrapper for `ssygvd`.
`dsygvd`(...)	Wrapper for `dsygvd`.
`ssygvx`(...)	Wrapper for `ssygvx`.
`dsygvx`(...)	Wrapper for `dsygvx`.
`slange`(norm,a)	Wrapper for `slange`.
`dlange`(norm,a)	Wrapper for `dlange`.
`clange`(norm,a)	Wrapper for `clange`.
`zlange`(norm,a)	Wrapper for `zlange`.

`scipy.linalg.lapack.`**`sgbsv`**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgbsv`.

Parameters

kl : input int
ku : input int
ab : input rank-2 array(‘f’) with bounds (2*kl+ku+1,n)
b : input rank-2 array(‘f’) with bounds (n,nrhs)

Returns

lub : rank-2 array(‘f’) with bounds (2*kl+ku+1,n) and ab storage
piv : rank-1 array(‘i’) with bounds (n)
x : rank-2 array(‘f’) with bounds (n,nrhs) and b storage
info : int

Other Parameters

overwrite_ab : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgbsv`**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgbsv`.

Parameters

kl : input int
ku : input int
ab : input rank-2 array('d') with bounds (2*kl+ku+1,n)
b : input rank-2 array('d') with bounds (n,nrhs)

Returns

lub : rank-2 array('d') with bounds (2*kl+ku+1,n) and ab storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('d') with bounds (n,nrhs) and b storage
info : int

Other Parameters

overwrite_ab : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgbsv`**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgbsv`.

Parameters

kl : input int
ku : input int
ab : input rank-2 array('F') with bounds (2*kl+ku+1,n)
b : input rank-2 array('F') with bounds (n,nrhs)

Returns

lub : rank-2 array('F') with bounds (2*kl+ku+1,n) and ab storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('F') with bounds (n,nrhs) and b storage
info : int

Other Parameters

overwrite_ab : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgbsv`**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgbsv`.

Parameters

kl : input int
ku : input int
ab : input rank-2 array('D') with bounds (2*kl+ku+1,n)
b : input rank-2 array('D') with bounds (n,nrhs)

Returns

lub : rank-2 array('D') with bounds (2*kl+ku+1,n) and ab storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('D') with bounds (n,nrhs) and b storage
info : int

Other Parameters

overwrite_ab : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgbtrf`**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `sgbtrf`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,*)
kl : input int
ku : input int

Returns **lu** : rank-2 array('f') with bounds (ldab,*) and ab storage
ipiv : rank-1 array('i') with bounds (MIN(m,n))
info : int

Other Parameters

m : input int, optional
Default: shape(ab,1)

n : input int, optional
Default: shape(ab,1)

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`dgbtrf`**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `dgbtrf`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,*)
kl : input int
ku : input int

Returns **lu** : rank-2 array('d') with bounds (ldab,*) and ab storage
ipiv : rank-1 array('i') with bounds (MIN(m,n))
info : int

Other Parameters

m : input int, optional
Default: shape(ab,1)

n : input int, optional
Default: shape(ab,1)

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`cgbtrf`**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `cgbtrf`.

Parameters **ab** : input rank-2 array('F') with bounds (ldab,*)
kl : input int
ku : input int

Returns **lu** : rank-2 array('F') with bounds (ldab,*) and ab storage
ipiv : rank-1 array('i') with bounds (MIN(m,n))
info : int

Other Parameters

m : input int, optional
Default: shape(ab,1)

n : input int, optional
Default: shape(ab,1)

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`zgbtrf`**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `zgbtrf`.

Parameters
ab : input rank-2 array('D') with bounds (ldab,*)
kl : input int
ku : input int

Returns
lu : rank-2 array('D') with bounds (ldab,*) and ab storage
ipiv : rank-1 array('i') with bounds (MIN(m,n))
info : int

Other Parameters
m : input int, optional
Default: shape(ab,1)
n : input int, optional
Default: shape(ab,1)
overwrite_ab : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`sgbtrs`**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgbtrs`.

Parameters
ab : input rank-2 array('f') with bounds (ldab,*)
kl : input int
ku : input int
b : input rank-2 array('f') with bounds (ldb,*)
ipiv : input rank-1 array('i') with bounds (n)

Returns
x : rank-2 array('f') with bounds (ldb,*) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
trans : input int, optional
Default: 0
n : input int, optional
Default: shape(ab,1)
ldab : input int, optional
Default: shape(ab,0)
ldb : input int, optional
Default: shape(b,0)

`scipy.linalg.lapack.`**`dgbtrs`**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgbtrs`.

Parameters
ab : input rank-2 array('d') with bounds (ldab,*)
kl : input int
ku : input int
b : input rank-2 array('d') with bounds (ldb,*)
ipiv : input rank-1 array('i') with bounds (n)

Returns
x : rank-2 array('d') with bounds (ldb,*) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
trans : input int, optional

Default: 0
n : input int, optional
Default: shape(ab,1)
ldab : input int, optional
Default: shape(ab,0)
ldb : input int, optional
Default: shape(b,0)

`scipy.linalg.lapack.`**`cgbtrs`**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgbtrs`.

Parameters
ab : input rank-2 array(‘F’) with bounds (ldab,*)
kl : input int
ku : input int
b : input rank-2 array(‘F’) with bounds (ldb,*)
ipiv : input rank-1 array(‘i’) with bounds (n)

Returns
x : rank-2 array(‘F’) with bounds (ldb,*) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
trans : input int, optional
Default: 0
n : input int, optional
Default: shape(ab,1)
ldab : input int, optional
Default: shape(ab,0)
ldb : input int, optional
Default: shape(b,0)

`scipy.linalg.lapack.`**`zgbtrs`**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgbtrs`.

Parameters
ab : input rank-2 array(‘D’) with bounds (ldab,*)
kl : input int
ku : input int
b : input rank-2 array(‘D’) with bounds (ldb,*)
ipiv : input rank-1 array(‘i’) with bounds (n)

Returns
x : rank-2 array(‘D’) with bounds (ldb,*) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
trans : input int, optional
Default: 0
n : input int, optional
Default: shape(ab,1)
ldab : input int, optional
Default: shape(ab,0)
ldb : input int, optional
Default: shape(b,0)

`scipy.linalg.lapack.`**`sgebal`**(*a*[, *scale*, *permute*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgebal`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

Returns **ba** : rank-2 array('f') with bounds (m,n) and a storage
lo : int
hi : int
pivscale : rank-1 array('f') with bounds (n)
info : int

Other Parameters
scale : input int, optional
Default: 0
permute : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgebal`**`(`*a*[, *scale*, *permute*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `dgebal`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

Returns **ba** : rank-2 array('d') with bounds (m,n) and a storage
lo : int
hi : int
pivscale : rank-1 array('d') with bounds (n)
info : int

Other Parameters
scale : input int, optional
Default: 0
permute : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgebal`**`(`*a*[, *scale*, *permute*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `cgebal`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)

Returns **ba** : rank-2 array('F') with bounds (m,n) and a storage
lo : int
hi : int
pivscale : rank-1 array('f') with bounds (n)
info : int

Other Parameters
scale : input int, optional
Default: 0
permute : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgebal`**`(`*a*[, *scale*, *permute*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `zgebal`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)

Returns **ba** : rank-2 array('D') with bounds (m,n) and a storage
lo : int
hi : int
pivscale : rank-1 array('d') with bounds (n)
info : int

Other Parameters

scale : input int, optional
Default: 0

permute : input int, optional
Default: 0

overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgees`**(*sselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *sselect_extra_args*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgees`.

Parameters

sselect : call-back function

a : input rank-2 array('f') with bounds (n,n)

Returns

t : rank-2 array('f') with bounds (n,n) and a storage

sdim : int

wr : rank-1 array('f') with bounds (n)

wi : rank-1 array('f') with bounds (n)

vs : rank-2 array('f') with bounds (ldvs,n)

work : rank-1 array('f') with bounds (MAX(lwork,1))

info : int

Other Parameters

compute_v : input int, optional
Default: 1

sort_t : input int, optional
Default: 0

sselect_extra_args : input tuple, optional
Default: ()

overwrite_a : input int, optional
Default: 0

lwork : input int, optional
Default: 3*n

Notes

Call-back functions:

```
def sselect(arg1,arg2): return sselect
Required arguments:
  arg1 : input float
  arg2 : input float
Return objects:
  sselect : int
```

`scipy.linalg.lapack.`**`dgees`**(*dselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *dselect_extra_args*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dgees`.

Parameters

dselect : call-back function

a : input rank-2 array('d') with bounds (n,n)

Returns

t : rank-2 array('d') with bounds (n,n) and a storage

sdim : int

wr : rank-1 array('d') with bounds (n)

wi : rank-1 array('d') with bounds (n)

vs : rank-2 array('d') with bounds (ldvs,n)

work : rank-1 array('d') with bounds (MAX(lwork,1))

info : int

Other Parameters

compute_v : input int, optional
  Default: 1

sort_t : input int, optional
  Default: 0

dselect_extra_args : input tuple, optional
  Default: ()

overwrite_a : input int, optional
  Default: 0

lwork : input int, optional
  Default: 3*n

Notes

Call-back functions:

```
def dselect(arg1,arg2): return dselect
Required arguments:
  arg1 : input float
  arg2 : input float
Return objects:
  dselect : int
```

`scipy.linalg.lapack.`**`cgees`**(*cselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *cselect_extra_args*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgees`.

Parameters

cselect : call-back function

a : input rank-2 array('F') with bounds (n,n)

Returns

t : rank-2 array('F') with bounds (n,n) and a storage

sdim : int

w : rank-1 array('F') with bounds (n)

vs : rank-2 array('F') with bounds (ldvs,n)

work : rank-1 array('F') with bounds (MAX(lwork,1))

info : int

Other Parameters

compute_v : input int, optional
  Default: 1

sort_t : input int, optional
  Default: 0

cselect_extra_args : input tuple, optional
  Default: ()

overwrite_a : input int, optional
  Default: 0

lwork : input int, optional
  Default: 3*n

Notes

Call-back functions:

```
def cselect(arg): return cselect
Required arguments:
  arg : input complex
Return objects:
  cselect : int
```

`scipy.linalg.lapack.`**`zgees`**(*zselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *zselect_extra_args*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgees`.

Parameters **zselect** : call-back function
a : input rank-2 array('D') with bounds (n,n)

Returns **t** : rank-2 array('D') with bounds (n,n) and a storage
sdim : int
w : rank-1 array('D') with bounds (n)
vs : rank-2 array('D') with bounds (ldvs,n)
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters

compute_v : input int, optional
Default: 1
sort_t : input int, optional
Default: 0
zselect_extra_args : input tuple, optional
Default: ()
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

Notes

Call-back functions:

```
def zselect(arg): return zselect
Required arguments:
  arg : input complex
Return objects:
  zselect : int
```

`scipy.linalg.lapack.`**`sgeev`**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgeev`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

Returns **wr** : rank-1 array('f') with bounds (n)
wi : rank-1 array('f') with bounds (n)
vl : rank-2 array('f') with bounds (ldvl,n)
vr : rank-2 array('f') with bounds (ldvr,n)
info : int

Other Parameters

compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 4*n

`scipy.linalg.lapack.`**`dgeev`**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dgeev`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

Returns **wr** : rank-1 array('d') with bounds (n)
wi : rank-1 array('d') with bounds (n)
vl : rank-2 array('d') with bounds (ldvl,n)
vr : rank-2 array('d') with bounds (ldvr,n)
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 4*n

`scipy.linalg.lapack.`**`cgeev`**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `cgeev`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
Returns **w** : rank-1 array('F') with bounds (n)
vl : rank-2 array('F') with bounds (ldvl,n)
vr : rank-2 array('F') with bounds (ldvr,n)
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n

`scipy.linalg.lapack.`**`zgeev`**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `zgeev`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
Returns **w** : rank-1 array('D') with bounds (n)
vl : rank-2 array('D') with bounds (ldvl,n)
vr : rank-2 array('D') with bounds (ldvr,n)
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n

`scipy.linalg.lapack.`**`sgeev_lwork`**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**
Wrapper for `sgeev_lwork`.

Parameters **n** : input int
Returns **work** : float
info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional
Default: 1

`scipy.linalg.lapack.`**`dgeev_lwork`**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for `dgeev_lwork`.

Parameters **n** : input int

Returns **work** : float

info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional
Default: 1

`scipy.linalg.lapack.`**`cgeev_lwork`**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for `cgeev_lwork`.

Parameters **n** : input int

Returns **work** : complex

info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional
Default: 1

`scipy.linalg.lapack.`**`zgeev_lwork`**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for `zgeev_lwork`.

Parameters **n** : input int

Returns **work** : complex

info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional
Default: 1

`scipy.linalg.lapack.`**`sgegv`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgegv`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

b : input rank-2 array('f') with bounds (n,n)

Returns **alphar** : rank-1 array('f') with bounds (n)

alphai : rank-1 array('f') with bounds (n)

beta : rank-1 array('f') with bounds (n)

vl : rank-2 array('f') with bounds (ldvl,n)

vr : rank-2 array('f') with bounds (ldvr,n)

info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional

Default: 1

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

lwork : input int, optional

Default: 8*n

`scipy.linalg.lapack.`**`dgegv`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dgegv`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

b : input rank-2 array('d') with bounds (n,n)

Returns **alphar** : rank-1 array('d') with bounds (n)

alphai : rank-1 array('d') with bounds (n)

beta : rank-1 array('d') with bounds (n)

vl : rank-2 array('d') with bounds (ldvl,n)

vr : rank-2 array('d') with bounds (ldvr,n)

info : int

Other Parameters

compute_vl : input int, optional

Default: 1

compute_vr : input int, optional

Default: 1

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

lwork : input int, optional

Default: 8*n

`scipy.linalg.lapack.`**`cgegv`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `cgegv`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

b : input rank-2 array('F') with bounds (n,n)

Returns **alpha** : rank-1 array('F') with bounds (n)

beta : rank-1 array('F') with bounds (n)

vl : rank-2 array('F') with bounds (ldvl,n)

vr : rank-2 array('F') with bounds (ldvr,n)

info : int

Other Parameters

compute_vl : input int, optional

Default: 1

compute_vr : input int, optional

Default: 1

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

lwork : input int, optional

Default: 2*n

`scipy.linalg.lapack.`**`zgegv`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zgegv`.

Parameters
a : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,n)

Returns
alpha : rank-1 array('D') with bounds (n)
beta : rank-1 array('D') with bounds (n)
vl : rank-2 array('D') with bounds (ldvl,n)
vr : rank-2 array('D') with bounds (ldvr,n)
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n

`scipy.linalg.lapack.`**`sgehrd`**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for `sgehrd`.

Parameters
a : input rank-2 array('f') with bounds (n,n)

Returns
ht : rank-2 array('f') with bounds (n,n) and a storage
tau : rank-1 array('f') with bounds (n - 1)
info : int

Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: MAX(n,1)

`scipy.linalg.lapack.`**`dgehrd`**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for `dgehrd`.

Parameters
a : input rank-2 array('d') with bounds (n,n)

Returns
ht : rank-2 array('d') with bounds (n,n) and a storage
tau : rank-1 array('d') with bounds (n - 1)
info : int

Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: MAX(n,1)

`scipy.linalg.lapack.`**`cgehrd`**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgehrd`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

Returns **ht** : rank-2 array('F') with bounds (n,n) and a storage

tau : rank-1 array('F') with bounds (n - 1)

info : int

Other Parameters

lo : input int, optional
Default: 0

hi : input int, optional
Default: n-1

overwrite_a : input int, optional
Default: 0

lwork : input int, optional
Default: MAX(n,1)

`scipy.linalg.lapack.`**`zgehrd`**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgehrd`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)

Returns **ht** : rank-2 array('D') with bounds (n,n) and a storage

tau : rank-1 array('D') with bounds (n - 1)

info : int

Other Parameters

lo : input int, optional
Default: 0

hi : input int, optional
Default: n-1

overwrite_a : input int, optional
Default: 0

lwork : input int, optional
Default: MAX(n,1)

`scipy.linalg.lapack.`**`sgehrd_lwork`**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for `sgehrd_lwork`.

Parameters **n** : input int

Returns **work** : float

info : int

Other Parameters

lo : input int, optional
Default: 0

hi : input int, optional
Default: n-1

`scipy.linalg.lapack.`**`dgehrd_lwork`**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for `dgehrd_lwork`.

Parameters **n** : input int

Returns **work** : float

info : int

Other Parameters

lo : input int, optional
Default: 0

hi : input int, optional
Default: n-1

`scipy.linalg.lapack.`**`cgehrd_lwork`**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for `cgehrd_lwork`.

Parameters **n** : input int

Returns **work** : complex

info : int

Other Parameters

lo : input int, optional

Default: 0

hi : input int, optional

Default: n-1

`scipy.linalg.lapack.`**`zgehrd_lwork`**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for `zgehrd_lwork`.

Parameters **n** : input int

Returns **work** : complex

info : int

Other Parameters

lo : input int, optional

Default: 0

hi : input int, optional

Default: n-1

`scipy.linalg.lapack.`**`sgelss`**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgelss`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

b : input rank-2 array('f') with bounds (maxmn,nrhs)

Returns **v** : rank-2 array('f') with bounds (m,n) and a storage

x : rank-2 array('f') with bounds (maxmn,nrhs) and b storage

s : rank-1 array('f') with bounds (minmn)

rank : int

work : rank-1 array('f') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

cond : input float, optional

Default: -1.0

lwork : input int, optional

Default: 3*minmn+MAX(2*minmn,MAX(maxmn,nrhs))

`scipy.linalg.lapack.`**`dgelss`**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgelss`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

b : input rank-2 array('d') with bounds (maxmn,nrhs)

Returns **v** : rank-2 array('d') with bounds (m,n) and a storage

x : rank-2 array('d') with bounds (maxmn,nrhs) and b storage

s : rank-1 array('d') with bounds (minmn)

rank : int

work : rank-1 array('d') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

cond : input float, optional
Default: -1.0

lwork : input int, optional
Default: 3*minmn+MAX(2*minmn,MAX(maxmn,nrhs))

`scipy.linalg.lapack.`**`cgelss`**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgelss`.

Parameters

a : input rank-2 array('F') with bounds (m,n)

b : input rank-2 array('F') with bounds (maxmn,nrhs)

Returns

v : rank-2 array('F') with bounds (m,n) and a storage

x : rank-2 array('F') with bounds (maxmn,nrhs) and b storage

s : rank-1 array('f') with bounds (minmn)

rank : int

work : rank-1 array('F') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

cond : input float, optional
Default: -1.0

lwork : input int, optional
Default: 2*minmn+MAX(maxmn,nrhs)

`scipy.linalg.lapack.`**`zgelss`**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgelss`.

Parameters

a : input rank-2 array('D') with bounds (m,n)

b : input rank-2 array('D') with bounds (maxmn,nrhs)

Returns

v : rank-2 array('D') with bounds (m,n) and a storage

x : rank-2 array('D') with bounds (maxmn,nrhs) and b storage

s : rank-1 array('d') with bounds (minmn)

rank : int

work : rank-1 array('D') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

cond : input float, optional
Default: -1.0

lwork : input int, optional
Default: 2*minmn+MAX(maxmn,nrhs)

`scipy.linalg.lapack.`**`sgelss_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `sgelss_lwork`.

Parameters **m** : input int
n : input int
nrhs : input int
Returns **work** : float
info : int
Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`dgelss_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `dgelss_lwork`.

Parameters **m** : input int
n : input int
nrhs : input int
Returns **work** : float
info : int
Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`cgelss_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `cgelss_lwork`.

Parameters **m** : input int
n : input int
nrhs : input int
Returns **work** : complex
info : int
Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`zgelss_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `zgelss_lwork`.

Parameters **m** : input int
n : input int
nrhs : input int
Returns **work** : complex
info : int
Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`sgelsd`**(*a*, *b*, *lwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgelsd`.

Parameters
a : input rank-2 array('f') with bounds (m,n)
b : input rank-2 array('f') with bounds (maxmn,nrhs)
lwork : input int
size_iwork : input int

Returns
x : rank-2 array('f') with bounds (maxmn,nrhs) and b storage
s : rank-1 array('f') with bounds (minmn)
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
cond : input float, optional
Default: -1.0

`scipy.linalg.lapack.`**`dgelsd`**(*a*, *b*, *lwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgelsd`.

Parameters
a : input rank-2 array('d') with bounds (m,n)
b : input rank-2 array('d') with bounds (maxmn,nrhs)
lwork : input int
size_iwork : input int

Returns
x : rank-2 array('d') with bounds (maxmn,nrhs) and b storage
s : rank-1 array('d') with bounds (minmn)
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
cond : input float, optional
Default: -1.0

`scipy.linalg.lapack.`**`cgelsd`**(*a*, *b*, *lwork*, *size_rwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgelsd`.

Parameters
a : input rank-2 array('F') with bounds (m,n)
b : input rank-2 array('F') with bounds (maxmn,nrhs)
lwork : input int
size_rwork : input int
size_iwork : input int

Returns
x : rank-2 array('F') with bounds (maxmn,nrhs) and b storage
s : rank-1 array('f') with bounds (minmn)
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
cond : input float, optional
Default: -1.0

`scipy.linalg.lapack.`**`zgelsd`**(*a*, *b*, *lwork*, *size_rwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgelsd`.

Parameters
a : input rank-2 array('D') with bounds (m,n)
b : input rank-2 array('D') with bounds (maxmn,nrhs)
lwork : input int
size_rwork : input int
size_iwork : input int

Returns
x : rank-2 array('D') with bounds (maxmn,nrhs) and b storage
s : rank-1 array('d') with bounds (minmn)
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
cond : input float, optional
Default: -1.0

`scipy.linalg.lapack.`**`sgelsd_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `sgelsd_lwork`.

Parameters
m : input int
n : input int
nrhs : input int

Returns
work : float
iwork : int
info : int

Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`dgelsd_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `dgelsd_lwork`.

Parameters
m : input int
n : input int
nrhs : input int

Returns
work : float
iwork : int
info : int

Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`cgelsd_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `cgelsd_lwork`.

Parameters
m : input int
n : input int
nrhs : input int

Returns **work** : complex
rwork : float
iwork : int
info : int

Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`zgelsd_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) = **<fortran object>**

Wrapper for `zgelsd_lwork`.

Parameters **m** : input int
n : input int
nrhs : input int

Returns **work** : complex
rwork : float
iwork : int
info : int

Other Parameters
cond : input float, optional
Default: -1.0
lwork : input int, optional
Default: -1

`scipy.linalg.lapack.`**`sgelsy`**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `sgelsy`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)
b : input rank-2 array('f') with bounds (maxmn,nrhs)
jptv : input rank-1 array('i') with bounds (n)
cond : input float
lwork : input int

Returns **v** : rank-2 array('f') with bounds (m,n) and a storage
x : rank-2 array('f') with bounds (maxmn,nrhs) and b storage
j : rank-1 array('i') with bounds (n) and jptv storage
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgelsy`**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dgelsy`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)
b : input rank-2 array('d') with bounds (maxmn,nrhs)
jptv : input rank-1 array('i') with bounds (n)
cond : input float
lwork : input int

Returns
v : rank-2 array('d') with bounds (m,n) and a storage
x : rank-2 array('d') with bounds (maxmn,nrhs) and b storage
j : rank-1 array('i') with bounds (n) and jptv storage
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgelsy`**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgelsy`.

Parameters
a : input rank-2 array('F') with bounds (m,n)
b : input rank-2 array('F') with bounds (maxmn,nrhs)
jptv : input rank-1 array('i') with bounds (n)
cond : input float
lwork : input int

Returns
v : rank-2 array('F') with bounds (m,n) and a storage
x : rank-2 array('F') with bounds (maxmn,nrhs) and b storage
j : rank-1 array('i') with bounds (n) and jptv storage
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgelsy`**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgelsy`.

Parameters
a : input rank-2 array('D') with bounds (m,n)
b : input rank-2 array('D') with bounds (maxmn,nrhs)
jptv : input rank-1 array('i') with bounds (n)
cond : input float
lwork : input int

Returns
v : rank-2 array('D') with bounds (m,n) and a storage
x : rank-2 array('D') with bounds (maxmn,nrhs) and b storage
j : rank-1 array('i') with bounds (n) and jptv storage
rank : int
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgelsy_lwork`**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for `sgelsy_lwork`.

Parameters
m : input int
n : input int
nrhs : input int

cond : input float

Returns **work** : float

info : int

Other Parameters

lwork : input int, optional

Default: -1

`scipy.linalg.lapack.`**`dgelsy_lwork`**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for `dgelsy_lwork`.

Parameters **m** : input int

n : input int

nrhs : input int

cond : input float

Returns **work** : float

info : int

Other Parameters

lwork : input int, optional

Default: -1

`scipy.linalg.lapack.`**`cgelsy_lwork`**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for `cgelsy_lwork`.

Parameters **m** : input int

n : input int

nrhs : input int

cond : input float

Returns **work** : complex

info : int

Other Parameters

lwork : input int, optional

Default: -1

`scipy.linalg.lapack.`**`zgelsy_lwork`**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for `zgelsy_lwork`.

Parameters **m** : input int

n : input int

nrhs : input int

cond : input float

Returns **work** : complex

info : int

Other Parameters

lwork : input int, optional

Default: -1

`scipy.linalg.lapack.`**`sgeqp3`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgeqp3`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

Returns **qr** : rank-2 array('f') with bounds (m,n) and a storage

jpvt : rank-1 array('i') with bounds (n)

tau : rank-1 array('f') with bounds (MIN(m,n))

work : rank-1 array('f') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional
Default: 3*(n+1)

`scipy.linalg.lapack.`**`dgeqp3`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `dgeqp3`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

Returns **qr** : rank-2 array('d') with bounds (m,n) and a storage
jpvt : rank-1 array('i') with bounds (n)
tau : rank-1 array('d') with bounds (MIN(m,n))
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*(n+1)

`scipy.linalg.lapack.`**`cgeqp3`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `cgeqp3`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)

Returns **qr** : rank-2 array('F') with bounds (m,n) and a storage
jpvt : rank-1 array('i') with bounds (n)
tau : rank-1 array('F') with bounds (MIN(m,n))
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*(n+1)

`scipy.linalg.lapack.`**`zgeqp3`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `zgeqp3`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)

Returns **qr** : rank-2 array('D') with bounds (m,n) and a storage
jpvt : rank-1 array('i') with bounds (n)
tau : rank-1 array('D') with bounds (MIN(m,n))
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*(n+1)

`scipy.linalg.lapack.`**`sgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `sgeqrf`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

Returns **qr** : rank-2 array('f') with bounds (m,n) and a storage
tau : rank-1 array('f') with bounds (MIN(m,n))
work : rank-1 array('f') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*n

`scipy.linalg.lapack.`**`dgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dgeqrf`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

Returns **qr** : rank-2 array('d') with bounds (m,n) and a storage

tau : rank-1 array('d') with bounds (MIN(m,n))

work : rank-1 array('d') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*n

`scipy.linalg.lapack.`**`cgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgeqrf`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)

Returns **qr** : rank-2 array('F') with bounds (m,n) and a storage

tau : rank-1 array('F') with bounds (MIN(m,n))

work : rank-1 array('F') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*n

`scipy.linalg.lapack.`**`zgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgeqrf`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)

Returns **qr** : rank-2 array('D') with bounds (m,n) and a storage

tau : rank-1 array('D') with bounds (MIN(m,n))

work : rank-1 array('D') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*n

`scipy.linalg.lapack.`**`sgerqf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgerqf`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

Returns **qr** : rank-2 array('f') with bounds (m,n) and a storage

tau : rank-1 array('f') with bounds (MIN(m,n))

work : rank-1 array('f') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*m

`scipy.linalg.lapack.`**`dgerqf`**`(`*a*[, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `dgerqf`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

Returns **qr** : rank-2 array('d') with bounds (m,n) and a storage

tau : rank-1 array('d') with bounds (MIN(m,n))

work : rank-1 array('d') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*m

`scipy.linalg.lapack.`**`cgerqf`**`(`*a*[, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `cgerqf`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)

Returns **qr** : rank-2 array('F') with bounds (m,n) and a storage

tau : rank-1 array('F') with bounds (MIN(m,n))

work : rank-1 array('F') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*m

`scipy.linalg.lapack.`**`zgerqf`**`(`*a*[, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `zgerqf`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)

Returns **qr** : rank-2 array('D') with bounds (m,n) and a storage

tau : rank-1 array('D') with bounds (MIN(m,n))

work : rank-1 array('D') with bounds (MAX(lwork,1))

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 3*m

`scipy.linalg.lapack.`**`sgesdd`**`(`*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `sgesdd`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)

Returns **u** : rank-2 array('f') with bounds (u0,u1)

s : rank-1 array('f') with bounds (minmn)

vt : rank-2 array('f') with bounds (vt0,vt1)

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

compute_uv : input int, optional

Default: 1

full_matrices : input int, optional
Default: 1

lwork : input int, optional
Default: (compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn:MAX(14*minmn+4,10*minmn+2+25

`scipy.linalg.lapack.`**`dgesdd`**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dgesdd`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)

Returns

u : rank-2 array('d') with bounds (u0,u1)
s : rank-1 array('d') with bounds (minmn)
vt : rank-2 array('d') with bounds (vt0,vt1)
info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

compute_uv : input int, optional
Default: 1

full_matrices : input int, optional
Default: 1

lwork : input int, optional
Default: (compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn:MAX(14*minmn+4,10*minmn+2+25

`scipy.linalg.lapack.`**`cgesdd`**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgesdd`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)

Returns

u : rank-2 array('F') with bounds (u0,u1)
s : rank-1 array('f') with bounds (minmn)
vt : rank-2 array('F') with bounds (vt0,vt1)
info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

compute_uv : input int, optional
Default: 1

full_matrices : input int, optional
Default: 1

lwork : input int, optional
Default: (compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(m,n))

`scipy.linalg.lapack.`**`zgesdd`**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zgesdd`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)

Returns

u : rank-2 array('D') with bounds (u0,u1)
s : rank-1 array('d') with bounds (minmn)
vt : rank-2 array('D') with bounds (vt0,vt1)
info : int

Other Parameters

overwrite_a : input int, optional
Default: 0

compute_uv : input int, optional
Default: 1

full_matrices : input int, optional
Default: 1
lwork : input int, optional
Default: (compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(m,n))

`scipy.linalg.lapack.`**`sgesdd_lwork`**(*m*, *n*[, *compute_uv*, *full_matrices*]) **= <fortran object>**
Wrapper for `sgesdd_lwork`.

Parameters **m** : input int
n : input int
Returns **work** : float
info : int
Other Parameters
compute_uv : input int, optional
Default: 1
full_matrices : input int, optional
Default: 1

`scipy.linalg.lapack.`**`dgesdd_lwork`**(*m*, *n*[, *compute_uv*, *full_matrices*]) **= <fortran object>**
Wrapper for `dgesdd_lwork`.

Parameters **m** : input int
n : input int
Returns **work** : float
info : int
Other Parameters
compute_uv : input int, optional
Default: 1
full_matrices : input int, optional
Default: 1

`scipy.linalg.lapack.`**`cgesdd_lwork`**(*m*, *n*[, *compute_uv*, *full_matrices*]) **= <fortran object>**
Wrapper for `cgesdd_lwork`.

Parameters **m** : input int
n : input int
Returns **work** : complex
info : int
Other Parameters
compute_uv : input int, optional
Default: 1
full_matrices : input int, optional
Default: 1

`scipy.linalg.lapack.`**`zgesdd_lwork`**(*m*, *n*[, *compute_uv*, *full_matrices*]) **= <fortran object>**
Wrapper for `zgesdd_lwork`.

Parameters **m** : input int
n : input int
Returns **work** : complex
info : int
Other Parameters
compute_uv : input int, optional
Default: 1
full_matrices : input int, optional
Default: 1

`scipy.linalg.lapack.`**`sgesv`**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgesv`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)
b : input rank-2 array('f') with bounds (n,nrhs)

Returns **lu** : rank-2 array('f') with bounds (n,n) and a storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('f') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgesv`**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgesv`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)
b : input rank-2 array('d') with bounds (n,nrhs)

Returns **lu** : rank-2 array('d') with bounds (n,n) and a storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('d') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgesv`**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgesv`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,nrhs)

Returns **lu** : rank-2 array('F') with bounds (n,n) and a storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('F') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgesv`**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgesv`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,nrhs)

Returns **lu** : rank-2 array('D') with bounds (n,n) and a storage
piv : rank-1 array('i') with bounds (n)
x : rank-2 array('D') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `sgetrf`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)
Returns **lu** : rank-2 array('f') with bounds (m,n) and a storage
piv : rank-1 array('i') with bounds (MIN(m,n))
info : int
Other Parameters
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `dgetrf`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)
Returns **lu** : rank-2 array('d') with bounds (m,n) and a storage
piv : rank-1 array('i') with bounds (MIN(m,n))
info : int
Other Parameters
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `cgetrf`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)
Returns **lu** : rank-2 array('F') with bounds (m,n) and a storage
piv : rank-1 array('i') with bounds (MIN(m,n))
info : int
Other Parameters
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `zgetrf`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)
Returns **lu** : rank-2 array('D') with bounds (m,n) and a storage
piv : rank-1 array('i') with bounds (MIN(m,n))
info : int
Other Parameters
overwrite_a : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgetri`**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**
Wrapper for `sgetri`.

Parameters **lu** : input rank-2 array('f') with bounds (n,n)
piv : input rank-1 array('i') with bounds (n)
Returns **inv_a** : rank-2 array('f') with bounds (n,n) and lu storage
info : int
Other Parameters
overwrite_lu : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`dgetri`**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for `dgetri`.

Parameters **lu** : input rank-2 array('d') with bounds (n,n)
piv : input rank-1 array('i') with bounds (n)

Returns **inv_a** : rank-2 array('d') with bounds (n,n) and lu storage
info : int

Other Parameters
overwrite_lu : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`cgetri`**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for `cgetri`.

Parameters **lu** : input rank-2 array('F') with bounds (n,n)
piv : input rank-1 array('i') with bounds (n)

Returns **inv_a** : rank-2 array('F') with bounds (n,n) and lu storage
info : int

Other Parameters
overwrite_lu : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`zgetri`**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for `zgetri`.

Parameters **lu** : input rank-2 array('D') with bounds (n,n)
piv : input rank-1 array('i') with bounds (n)

Returns **inv_a** : rank-2 array('D') with bounds (n,n) and lu storage
info : int

Other Parameters
overwrite_lu : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`sgetri_lwork`**(*n*) **= <fortran object>**

Wrapper for `sgetri_lwork`.

Parameters **n** : input int

Returns **work** : float
info : int

`scipy.linalg.lapack.`**`dgetri_lwork`**(*n*) **= <fortran object>**

Wrapper for `dgetri_lwork`.

Parameters **n** : input int

Returns **work** : float
info : int

`scipy.linalg.lapack.`**`cgetri_lwork`**(*n*) **= <fortran object>**

Wrapper for `cgetri_lwork`.

Parameters **n** : input int

Returns **work** : complex
info : int

`scipy.linalg.lapack.`**`zgetri_lwork`**(*n*) **= <fortran object>**

Wrapper for `zgetri_lwork`.

Parameters **n** : input int

Returns **work** : complex

info : int

`scipy.linalg.lapack.`**`sgetrs`**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgetrs`.

Parameters **lu** : input rank-2 array('f') with bounds (n,n)

piv : input rank-1 array('i') with bounds (n)

b : input rank-2 array('f') with bounds (n,nrhs)

Returns **x** : rank-2 array('f') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_b : input int, optional

Default: 0

trans : input int, optional

Default: 0

`scipy.linalg.lapack.`**`dgetrs`**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgetrs`.

Parameters **lu** : input rank-2 array('d') with bounds (n,n)

piv : input rank-1 array('i') with bounds (n)

b : input rank-2 array('d') with bounds (n,nrhs)

Returns **x** : rank-2 array('d') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_b : input int, optional

Default: 0

trans : input int, optional

Default: 0

`scipy.linalg.lapack.`**`cgetrs`**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgetrs`.

Parameters **lu** : input rank-2 array('F') with bounds (n,n)

piv : input rank-1 array('i') with bounds (n)

b : input rank-2 array('F') with bounds (n,nrhs)

Returns **x** : rank-2 array('F') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_b : input int, optional

Default: 0

trans : input int, optional

Default: 0

`scipy.linalg.lapack.`**`zgetrs`**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgetrs`.

Parameters **lu** : input rank-2 array('D') with bounds (n,n)

piv : input rank-1 array('i') with bounds (n)

b : input rank-2 array('D') with bounds (n,nrhs)

Returns **x** : rank-2 array('D') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_b : input int, optional
Default: 0

trans : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgges`**(*sselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *sselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sgges`.

Parameters

sselect : call-back function
a : input rank-2 array('f') with bounds (lda,*)
b : input rank-2 array('f') with bounds (ldb,*)

Returns

a : rank-2 array('f') with bounds (lda,*)
b : rank-2 array('f') with bounds (ldb,*)
sdim : int
alphar : rank-1 array('f') with bounds (n)
alphai : rank-1 array('f') with bounds (n)
beta : rank-1 array('f') with bounds (n)
vsl : rank-2 array('f') with bounds (ldvsl,n)
vsr : rank-2 array('f') with bounds (ldvsr,n)
work : rank-1 array('f') with bounds (MAX(lwork,1))
info : int

Other Parameters

jobvsl : input int, optional
Default: 1

jobvsr : input int, optional
Default: 1

sort_t : input int, optional
Default: 0

sselect_extra_args : input tuple, optional
Default: ()

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

ldvsl : input int, optional
Default: ((jobvsl==1)?n:1)

ldvsr : input int, optional
Default: ((jobvsr==1)?n:1)

lwork : input int, optional
Default: 8*n+16

Notes

Call-back functions:

```
def sselect(alphar,alphai,beta): return sselect
Required arguments:
  alphar : input float
  alphai : input float
  beta : input float
Return objects:
  sselect : int
```

`scipy.linalg.lapack.`**`dgges`**(*dselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *dselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dgges`.

Parameters

dselect : call-back function
a : input rank-2 array('d') with bounds (lda,*)
b : input rank-2 array('d') with bounds (ldb,*)

Returns

a : rank-2 array('d') with bounds (lda,*)
b : rank-2 array('d') with bounds (ldb,*)
sdim : int
alphar : rank-1 array('d') with bounds (n)
alphai : rank-1 array('d') with bounds (n)
beta : rank-1 array('d') with bounds (n)
vsl : rank-2 array('d') with bounds (ldvsl,n)
vsr : rank-2 array('d') with bounds (ldvsr,n)
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters

jobvsl : input int, optional
Default: 1
jobvsr : input int, optional
Default: 1
sort_t : input int, optional
Default: 0
dselect_extra_args : input tuple, optional
Default: ()
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
ldvsl : input int, optional
Default: ((jobvsl==1)?n:1)
ldvsr : input int, optional
Default: ((jobvsr==1)?n:1)
lwork : input int, optional
Default: 8*n+16

Notes

Call-back functions:

```
def dselect(alphar,alphai,beta): return dselect
Required arguments:
  alphar : input float
  alphai : input float
  beta : input float
Return objects:
  dselect : int
```

`scipy.linalg.lapack.`**`cgges`**(*cselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *cselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cgges`.

Parameters

cselect : call-back function
a : input rank-2 array('F') with bounds (lda,*)
b : input rank-2 array('F') with bounds (ldb,*)

Returns

a : rank-2 array('F') with bounds (lda,*)
b : rank-2 array('F') with bounds (ldb,*)
sdim : int
alpha : rank-1 array('F') with bounds (n)
beta : rank-1 array('F') with bounds (n)
vsl : rank-2 array('F') with bounds (ldvsl,n)
vsr : rank-2 array('F') with bounds (ldvsr,n)
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters

jobvsl : input int, optional
  Default: 1
jobvsr : input int, optional
  Default: 1
sort_t : input int, optional
  Default: 0
cselect_extra_args : input tuple, optional
  Default: ()
overwrite_a : input int, optional
  Default: 0
overwrite_b : input int, optional
  Default: 0
ldvsl : input int, optional
  Default: ((jobvsl==1)?n:1)
ldvsr : input int, optional
  Default: ((jobvsr==1)?n:1)
lwork : input int, optional
  Default: 2*n

Notes

Call-back functions:

```
def cselect(alpha,beta): return cselect
Required arguments:
  alpha : input complex
  beta : input complex
Return objects:
  cselect : int
```

`scipy.linalg.lapack.`**`zgges`**(*zselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *zselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgges`.

Parameters

zselect : call-back function
a : input rank-2 array('D') with bounds (lda,*)
b : input rank-2 array('D') with bounds (ldb,*)

Returns

a : rank-2 array('D') with bounds (lda,*)
b : rank-2 array('D') with bounds (ldb,*)
sdim : int
alpha : rank-1 array('D') with bounds (n)
beta : rank-1 array('D') with bounds (n)
vsl : rank-2 array('D') with bounds (ldvsl,n)
vsr : rank-2 array('D') with bounds (ldvsr,n)
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters

jobvsl : input int, optional
Default: 1

jobvsr : input int, optional
Default: 1

sort_t : input int, optional
Default: 0

zselect_extra_args : input tuple, optional
Default: ()

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

ldvsl : input int, optional
Default: ((jobvsl==1)?n:1)

ldvsr : input int, optional
Default: ((jobvsr==1)?n:1)

lwork : input int, optional
Default: 2*n

Notes

Call-back functions:

```
def zselect(alpha,beta): return zselect
Required arguments:
  alpha : input complex
  beta : input complex
Return objects:
  zselect : int
```

`scipy.linalg.lapack.`**`sggev`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `sggev`.

Parameters

a : input rank-2 array('f') with bounds (n,n)

b : input rank-2 array('f') with bounds (n,n)

Returns

alphar : rank-1 array('f') with bounds (n)

alphai : rank-1 array('f') with bounds (n)

beta : rank-1 array('f') with bounds (n)

vl : rank-2 array('f') with bounds (ldvl,n)

vr : rank-2 array('f') with bounds (ldvr,n)

work : rank-1 array('f') with bounds (MAX(lwork,1))

info : int

Other Parameters

compute_vl : input int, optional
Default: 1

compute_vr : input int, optional
Default: 1

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

lwork : input int, optional
Default: 8*n

`scipy.linalg.lapack.`**`dggev`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dggev`.

Parameters
a : input rank-2 array('d') with bounds (n,n)
b : input rank-2 array('d') with bounds (n,n)

Returns
alphar : rank-1 array('d') with bounds (n)
alphai : rank-1 array('d') with bounds (n)
beta : rank-1 array('d') with bounds (n)
vl : rank-2 array('d') with bounds (ldvl,n)
vr : rank-2 array('d') with bounds (ldvr,n)
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 8*n

`scipy.linalg.lapack.`**`cggev`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `cggev`.

Parameters
a : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,n)

Returns
alpha : rank-1 array('F') with bounds (n)
beta : rank-1 array('F') with bounds (n)
vl : rank-2 array('F') with bounds (ldvl,n)
vr : rank-2 array('F') with bounds (ldvr,n)
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n

`scipy.linalg.lapack.`**`zggev`**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zggev`.

Parameters
a : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,n)

Returns
alpha : rank-1 array('D') with bounds (n)
beta : rank-1 array('D') with bounds (n)
vl : rank-2 array('D') with bounds (ldvl,n)
vr : rank-2 array('D') with bounds (ldvr,n)
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters
compute_vl : input int, optional
Default: 1
compute_vr : input int, optional
Default: 1
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n

`scipy.linalg.lapack.`**`chbevd`**(*ab*[, *compute_v*, *lower*, *ldab*, *lrwork*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `chbevd`.

Parameters
ab : input rank-2 array('F') with bounds (ldab,*)

Returns
w : rank-1 array('f') with bounds (n)
z : rank-2 array('F') with bounds (ldz,ldz)
info : int

Other Parameters
overwrite_ab : input int, optional
Default: 1
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
lrwork : input int, optional
Default: (compute_v?1+5*n+2*n*n:n)
liwork : input int, optional
Default: (compute_v?3+5*n:1)

`scipy.linalg.lapack.`**`zhbevd`**(*ab*[, *compute_v*, *lower*, *ldab*, *lrwork*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `zhbevd`.

Parameters
ab : input rank-2 array('D') with bounds (ldab,*)

Returns
w : rank-1 array('d') with bounds (n)
z : rank-2 array('D') with bounds (ldz,ldz)
info : int

Other Parameters
overwrite_ab : input int, optional
Default: 1
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
ldab : input int, optional

Default: shape(ab,0)
lrwork : input int, optional
Default: (compute_v?1+5*n+2*n*n:n)
liwork : input int, optional
Default: (compute_v?3+5*n:1)

`scipy.linalg.lapack.`**`chbevx`**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `chbevx`.

Parameters
ab : input rank-2 array('F') with bounds (ldab,*)
vl : input float
vu : input float
il : input int
iu : input int

Returns
w : rank-1 array('f') with bounds (n)
z : rank-2 array('F') with bounds (ldz,mmax)
m : int
ifail : rank-1 array('i') with bounds ((compute_v?n:1))
info : int

Other Parameters
overwrite_ab : input int, optional
Default: 1
ldab : input int, optional
Default: shape(ab,0)
compute_v : input int, optional
Default: 1
range : input int, optional
Default: 0
lower : input int, optional
Default: 0
abstol : input float, optional
Default: 0.0
mmax : input int, optional
Default: (compute_v?(range==2?(iu-il+1):n):1)

`scipy.linalg.lapack.`**`zhbevx`**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `zhbevx`.

Parameters
ab : input rank-2 array('D') with bounds (ldab,*)
vl : input float
vu : input float
il : input int
iu : input int

Returns
w : rank-1 array('d') with bounds (n)
z : rank-2 array('D') with bounds (ldz,mmax)
m : int
ifail : rank-1 array('i') with bounds ((compute_v?n:1))
info : int

Other Parameters
overwrite_ab : input int, optional
Default: 1
ldab : input int, optional
Default: shape(ab,0)
compute_v : input int, optional

Default: 1

range : input int, optional

Default: 0

lower : input int, optional

Default: 0

abstol : input float, optional

Default: 0.0

mmax : input int, optional

Default: (compute_v?(range==2?(iu-il+1):n):1)

`scipy.linalg.lapack.`**`cheev`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cheev`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

Returns **w** : rank-1 array('f') with bounds (n)

v : rank-2 array('F') with bounds (n,n) and a storage

info : int

Other Parameters

compute_v : input int, optional

Default: 1

lower : input int, optional

Default: 0

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 2*n-1

`scipy.linalg.lapack.`**`zheev`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zheev`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)

Returns **w** : rank-1 array('d') with bounds (n)

v : rank-2 array('D') with bounds (n,n) and a storage

info : int

Other Parameters

compute_v : input int, optional

Default: 1

lower : input int, optional

Default: 0

overwrite_a : input int, optional

Default: 0

lwork : input int, optional

Default: 2*n-1

`scipy.linalg.lapack.`**`cheevd`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cheevd`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

Returns **w** : rank-1 array('f') with bounds (n)

v : rank-2 array('F') with bounds (n,n) and a storage

info : int

Other Parameters

compute_v : input int, optional

Default: 1

lower : input int, optional

Default: 0

overwrite_a : input int, optional

Default: 0
lwork : input int, optional
Default: (compute_v?2*n+n*n:n+1)

`scipy.linalg.lapack.`**`zheevd`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zheevd`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)

Returns **w** : rank-1 array('d') with bounds (n)
v : rank-2 array('D') with bounds (n,n) and a storage
info : int

Other Parameters
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: (compute_v?2*n+n*n:n+1)

`scipy.linalg.lapack.`**`cheevr`**(*a*[, *jobz*, *range*, *uplo*, *il*, *iu*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cheevr`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

Returns **w** : rank-1 array('f') with bounds (n)
z : rank-2 array('F') with bounds (n,m)
info : int

Other Parameters
jobz : input string(len=1), optional
Default: 'V'
range : input string(len=1), optional
Default: 'A'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
il : input int, optional
Default: 1
iu : input int, optional
Default: n
lwork : input int, optional
Default: 18*n

`scipy.linalg.lapack.`**`zheevr`**(*a*[, *jobz*, *range*, *uplo*, *il*, *iu*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zheevr`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)

Returns **w** : rank-1 array('d') with bounds (n)
z : rank-2 array('D') with bounds (n,m)
info : int

Other Parameters
jobz : input string(len=1), optional
Default: 'V'
range : input string(len=1), optional
Default: 'A'
uplo : input string(len=1), optional

Default: 'L'
overwrite_a : input int, optional
Default: 0
il : input int, optional
Default: 1
iu : input int, optional
Default: n
lwork : input int, optional
Default: 18*n

`scipy.linalg.lapack.`**`chegv`**(*a*, *b*[, *itype*, *jobz*, *uplo*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `chegv`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,n)
Returns **a** : rank-2 array('F') with bounds (n,n)
w : rank-1 array('f') with bounds (n)
info : int
Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zhegv`**(*a*, *b*[, *itype*, *jobz*, *uplo*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zhegv`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,n)
Returns **a** : rank-2 array('D') with bounds (n,n)
w : rank-1 array('d') with bounds (n)
info : int
Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`chegvd`**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `chegvd`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,n)

Returns
a : rank-2 array('F') with bounds (n,n)
w : rank-1 array('f') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n+n*n

`scipy.linalg.lapack.`**`zhegvd`**`(`*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]`)` **= <fortran object>**

Wrapper for `zhegvd`.

Parameters
a : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,n)

Returns
a : rank-2 array('D') with bounds (n,n)
w : rank-1 array('d') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 2*n+n*n

`scipy.linalg.lapack.`**`chegvx`**`(`*a*, *b*, *iu*[, *itype*, *jobz*, *uplo*, *il*, *lwork*, *overwrite_a*, *overwrite_b*]`)` **= <fortran object>**

Wrapper for `chegvx`.

Parameters
a : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,n)
iu : input int

Returns
w : rank-1 array('f') with bounds (n)
z : rank-2 array('F') with bounds (n,m)
ifail : rank-1 array('i') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'

uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
il : input int, optional
Default: 1
lwork : input int, optional
Default: 18*n-1

`scipy.linalg.lapack.`**`zhegvx`**(*a*, *b*, *iu*[, *itype*, *jobz*, *uplo*, *il*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zhegvx`.

Parameters
a : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,n)
iu : input int

Returns
w : rank-1 array('d') with bounds (n)
z : rank-2 array('D') with bounds (n,m)
ifail : rank-1 array('i') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
il : input int, optional
Default: 1
lwork : input int, optional
Default: 18*n-1

`scipy.linalg.lapack.`**`slarf`**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) = **<fortran object>**

Wrapper for `slarf`.

Parameters
v : input rank-1 array('f') with bounds (*)
tau : input float
c : input rank-2 array('f') with bounds (m,n)
work : input rank-1 array('f') with bounds (*)

Returns
c : rank-2 array('f') with bounds (m,n)

Other Parameters
side : input string(len=1), optional
Default: 'L'
incv : input int, optional
Default: 1
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dlarf`**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) = **<fortran object>**

Wrapper for `dlarf`.

Parameters **v** : input rank-1 array('d') with bounds (*)
tau : input float
c : input rank-2 array('d') with bounds (m,n)
work : input rank-1 array('d') with bounds (*)

Returns **c** : rank-2 array('d') with bounds (m,n)

Other Parameters
side : input string(len=1), optional
Default: 'L'
incv : input int, optional
Default: 1
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`clarf`**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**

Wrapper for `clarf`.

Parameters **v** : input rank-1 array('F') with bounds (*)
tau : input complex
c : input rank-2 array('F') with bounds (m,n)
work : input rank-1 array('F') with bounds (*)

Returns **c** : rank-2 array('F') with bounds (m,n)

Other Parameters
side : input string(len=1), optional
Default: 'L'
incv : input int, optional
Default: 1
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zlarf`**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**

Wrapper for `zlarf`.

Parameters **v** : input rank-1 array('D') with bounds (*)
tau : input complex
c : input rank-2 array('D') with bounds (m,n)
work : input rank-1 array('D') with bounds (*)

Returns **c** : rank-2 array('D') with bounds (m,n)

Other Parameters
side : input string(len=1), optional
Default: 'L'
incv : input int, optional
Default: 1
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`slarfg`**(*n*, *alpha*, *x*[, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for `slarfg`.

Parameters **n** : input int
alpha : input float
x : input rank-1 array('f') with bounds (*)

Returns **alpha** : float
x : rank-1 array('f') with bounds (*)
tau : float

Other Parameters
overwrite_x : input int, optional
Default: 0

incx : input int, optional
Default: 1

`scipy.linalg.lapack.`**`dlarfg`**`(`*n*, *alpha*, *x*[, *incx*, *overwrite_x*]`)` **= <fortran object>**

Wrapper for `dlarfg`.

Parameters
n : input int
alpha : input float
x : input rank-1 array('d') with bounds (*)

Returns
alpha : float
x : rank-1 array('d') with bounds (*)
tau : float

Other Parameters
overwrite_x : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.lapack.`**`clarfg`**`(`*n*, *alpha*, *x*[, *incx*, *overwrite_x*]`)` **= <fortran object>**

Wrapper for `clarfg`.

Parameters
n : input int
alpha : input complex
x : input rank-1 array('F') with bounds (*)

Returns
alpha : complex
x : rank-1 array('F') with bounds (*)
tau : complex

Other Parameters
overwrite_x : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.lapack.`**`zlarfg`**`(`*n*, *alpha*, *x*[, *incx*, *overwrite_x*]`)` **= <fortran object>**

Wrapper for `zlarfg`.

Parameters
n : input int
alpha : input complex
x : input rank-1 array('D') with bounds (*)

Returns
alpha : complex
x : rank-1 array('D') with bounds (*)
tau : complex

Other Parameters
overwrite_x : input int, optional
Default: 0
incx : input int, optional
Default: 1

`scipy.linalg.lapack.`**`slartg`**`(`*f*, *g*`)` **= <fortran object>**

Wrapper for `slartg`.

Parameters
f : input float
g : input float

Returns
cs : float
sn : float
r : float

`scipy.linalg.lapack.`**`dlartg`**(*f*, *g*) **= <fortran object>**

Wrapper for `dlartg`.

Parameters **f** : input float
g : input float

Returns **cs** : float
sn : float
r : float

`scipy.linalg.lapack.`**`clartg`**(*f*, *g*) **= <fortran object>**

Wrapper for `clartg`.

Parameters **f** : input complex
g : input complex

Returns **cs** : float
sn : complex
r : complex

`scipy.linalg.lapack.`**`zlartg`**(*f*, *g*) **= <fortran object>**

Wrapper for `zlartg`.

Parameters **f** : input complex
g : input complex

Returns **cs** : float
sn : complex
r : complex

`scipy.linalg.lapack.`**`dlasd4`**(*i*, *d*, *z*[, *rho*]) **= <fortran object>**

Wrapper for `dlasd4`.

Parameters **i** : input int
d : input rank-1 array(‘d’) with bounds (n)
z : input rank-1 array(‘d’) with bounds (n)

Returns **delta** : rank-1 array(‘d’) with bounds (n)
sigma : float
work : rank-1 array(‘d’) with bounds (n)
info : int

Other Parameters

rho : input float, optional
Default: 1.0

`scipy.linalg.lapack.`**`slasd4`**(*i*, *d*, *z*[, *rho*]) **= <fortran object>**

Wrapper for `slasd4`.

Parameters **i** : input int
d : input rank-1 array(‘f’) with bounds (n)
z : input rank-1 array(‘f’) with bounds (n)

Returns **delta** : rank-1 array(‘f’) with bounds (n)
sigma : float
work : rank-1 array(‘f’) with bounds (n)
info : int

Other Parameters

rho : input float, optional
Default: 1.0

`scipy.linalg.lapack.`**`slaswp`**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**

Wrapper for `slaswp`.

Parameters **a** : input rank-2 array('f') with bounds (nrows,n)
piv : input rank-1 array('i') with bounds (*)

Returns **a** : rank-2 array('f') with bounds (nrows,n)

Other Parameters

overwrite_a : input int, optional
Default: 0

k1 : input int, optional
Default: 0

k2 : input int, optional
Default: len(piv)-1

off : input int, optional
Default: 0

inc : input int, optional
Default: 1

`scipy.linalg.lapack.`**`dlaswp`**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**
Wrapper for `dlaswp`.

Parameters **a** : input rank-2 array('d') with bounds (nrows,n)
piv : input rank-1 array('i') with bounds (*)

Returns **a** : rank-2 array('d') with bounds (nrows,n)

Other Parameters

overwrite_a : input int, optional
Default: 0

k1 : input int, optional
Default: 0

k2 : input int, optional
Default: len(piv)-1

off : input int, optional
Default: 0

inc : input int, optional
Default: 1

`scipy.linalg.lapack.`**`claswp`**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**
Wrapper for `claswp`.

Parameters **a** : input rank-2 array('F') with bounds (nrows,n)
piv : input rank-1 array('i') with bounds (*)

Returns **a** : rank-2 array('F') with bounds (nrows,n)

Other Parameters

overwrite_a : input int, optional
Default: 0

k1 : input int, optional
Default: 0

k2 : input int, optional
Default: len(piv)-1

off : input int, optional
Default: 0

inc : input int, optional
Default: 1

`scipy.linalg.lapack.`**`zlaswp`**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**
Wrapper for `zlaswp`.

Parameters **a** : input rank-2 array('D') with bounds (nrows,n)
piv : input rank-1 array('i') with bounds (*)

Returns **a** : rank-2 array('D') with bounds (nrows,n)

Other Parameters

overwrite_a : input int, optional
Default: 0

k1 : input int, optional
Default: 0

k2 : input int, optional
Default: len(piv)-1

off : input int, optional
Default: 0

inc : input int, optional
Default: 1

`scipy.linalg.lapack.`**`slauum`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `slauum`.

Parameters **c** : input rank-2 array(‘f’) with bounds (n,n)

Returns **a** : rank-2 array(‘f’) with bounds (n,n) and c storage
info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dlauum`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dlauum`.

Parameters **c** : input rank-2 array(‘d’) with bounds (n,n)

Returns **a** : rank-2 array(‘d’) with bounds (n,n) and c storage
info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`clauum`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `clauum`.

Parameters **c** : input rank-2 array(‘F’) with bounds (n,n)

Returns **a** : rank-2 array(‘F’) with bounds (n,n) and c storage
info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zlauum`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `zlauum`.

Parameters **c** : input rank-2 array(‘D’) with bounds (n,n)

Returns **a** : rank-2 array(‘D’) with bounds (n,n) and c storage
info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.lapack.`**`spbsv`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `spbsv`.

Parameters
ab : input rank-2 array('f') with bounds (ldab,n)
b : input rank-2 array('f') with bounds (ldb,nrhs)

Returns
c : rank-2 array('f') with bounds (ldab,n) and ab storage
x : rank-2 array('f') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
overwrite_ab : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dpbsv`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dpbsv`.

Parameters
ab : input rank-2 array('d') with bounds (ldab,n)
b : input rank-2 array('d') with bounds (ldb,nrhs)

Returns
c : rank-2 array('d') with bounds (ldab,n) and ab storage
x : rank-2 array('d') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
overwrite_ab : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cpbsv`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cpbsv`.

Parameters
ab : input rank-2 array('F') with bounds (ldab,n)
b : input rank-2 array('F') with bounds (ldb,nrhs)

Returns
c : rank-2 array('F') with bounds (ldab,n) and ab storage
x : rank-2 array('F') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
overwrite_ab : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zpbsv`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zpbsv`.

Parameters **ab** : input rank-2 array('D') with bounds (ldab,n)
b : input rank-2 array('D') with bounds (ldb,nrhs)

Returns **c** : rank-2 array('D') with bounds (ldab,n) and ab storage
x : rank-2 array('D') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters

lower : input int, optional
Default: 0

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`spbtrf`**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `spbtrf`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,n)

Returns **c** : rank-2 array('f') with bounds (ldab,n) and ab storage
info : int

Other Parameters

lower : input int, optional
Default: 0

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`dpbtrf`**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `dpbtrf`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,n)

Returns **c** : rank-2 array('d') with bounds (ldab,n) and ab storage
info : int

Other Parameters

lower : input int, optional
Default: 0

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`cpbtrf`**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `cpbtrf`.

Parameters **ab** : input rank-2 array('F') with bounds (ldab,n)

Returns **c** : rank-2 array('F') with bounds (ldab,n) and ab storage
info : int

Other Parameters

lower : input int, optional
Default: 0

overwrite_ab : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`zpbtrf`**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `zpbtrf`.

Parameters **ab** : input rank-2 array('D') with bounds (ldab,n)

Returns **c** : rank-2 array('D') with bounds (ldab,n) and ab storage
info : int

Other Parameters
lower : input int, optional
Default: 0
overwrite_ab : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`spbtrs`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `spbtrs`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,n)
b : input rank-2 array('f') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('f') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dpbtrs`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dpbtrs`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,n)
b : input rank-2 array('d') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('d') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cpbtrs`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cpbtrs`.

Parameters **ab** : input rank-2 array('F') with bounds (ldab,n)
b : input rank-2 array('F') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('F') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters
lower : input int, optional
Default: 0
ldab : input int, optional

Default: shape(ab,0)

overwrite_b : input int, optional

Default: 0

`scipy.linalg.lapack.`**`zpbtrs`**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zpbtrs`.

Parameters **ab** : input rank-2 array('D') with bounds (ldab,n)

b : input rank-2 array('D') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('D') with bounds (ldb,nrhs) and b storage

info : int

Other Parameters

lower : input int, optional

Default: 0

ldab : input int, optional

Default: shape(ab,0)

overwrite_b : input int, optional

Default: 0

`scipy.linalg.lapack.`**`sposv`**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `sposv`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

b : input rank-2 array('f') with bounds (n,nrhs)

Returns **c** : rank-2 array('f') with bounds (n,n) and a storage

x : rank-2 array('f') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.lapack.`**`dposv`**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dposv`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

b : input rank-2 array('d') with bounds (n,nrhs)

Returns **c** : rank-2 array('d') with bounds (n,n) and a storage

x : rank-2 array('d') with bounds (n,nrhs) and b storage

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

overwrite_b : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.lapack.`**`cposv`**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cposv`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

b : input rank-2 array('F') with bounds (n,nrhs)

Returns **c** : rank-2 array('F') with bounds (n,n) and a storage
x : rank-2 array('F') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zposv`**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for `zposv`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,nrhs)

Returns **c** : rank-2 array('D') with bounds (n,n) and a storage
x : rank-2 array('D') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`spotrf`**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**
Wrapper for `spotrf`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

Returns **c** : rank-2 array('f') with bounds (n,n) and a storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lower : input int, optional
Default: 0
clean : input int, optional
Default: 1

`scipy.linalg.lapack.`**`dpotrf`**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**
Wrapper for `dpotrf`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

Returns **c** : rank-2 array('d') with bounds (n,n) and a storage
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lower : input int, optional
Default: 0
clean : input int, optional
Default: 1

`scipy.linalg.lapack.`**`cpotrf`**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**
Wrapper for `cpotrf`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)

Returns **c** : rank-2 array('F') with bounds (n,n) and a storage

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lower : input int, optional

Default: 0

clean : input int, optional

Default: 1

`scipy.linalg.lapack.`**`zpotrf`**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zpotrf`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)

Returns **c** : rank-2 array('D') with bounds (n,n) and a storage

info : int

Other Parameters

overwrite_a : input int, optional

Default: 0

lower : input int, optional

Default: 0

clean : input int, optional

Default: 1

`scipy.linalg.lapack.`**`spotri`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `spotri`.

Parameters **c** : input rank-2 array('f') with bounds (n,n)

Returns **inv_a** : rank-2 array('f') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.lapack.`**`dpotri`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dpotri`.

Parameters **c** : input rank-2 array('d') with bounds (n,n)

Returns **inv_a** : rank-2 array('d') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional

Default: 0

lower : input int, optional

Default: 0

`scipy.linalg.lapack.`**`cpotri`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `cpotri`.

Parameters **c** : input rank-2 array('F') with bounds (n,n)

Returns **inv_a** : rank-2 array('F') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional

Default: 0

lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zpotri`**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for `zpotri`.

Parameters **c** : input rank-2 array('D') with bounds (n,n)

Returns **inv_a** : rank-2 array('D') with bounds (n,n) and c storage
info : int

Other Parameters
overwrite_c : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`spotrs`**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for `spotrs`.

Parameters **c** : input rank-2 array('f') with bounds (n,n)
b : input rank-2 array('f') with bounds (n,nrhs)

Returns **x** : rank-2 array('f') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dpotrs`**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dpotrs`.

Parameters **c** : input rank-2 array('d') with bounds (n,n)
b : input rank-2 array('d') with bounds (n,nrhs)

Returns **x** : rank-2 array('d') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cpotrs`**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cpotrs`.

Parameters **c** : input rank-2 array('F') with bounds (n,n)
b : input rank-2 array('F') with bounds (n,nrhs)

Returns **x** : rank-2 array('F') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zpotrs`**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zpotrs`.

Parameters **c** : input rank-2 array('D') with bounds (n,n)
b : input rank-2 array('D') with bounds (n,nrhs)

Returns **x** : rank-2 array('D') with bounds (n,nrhs) and b storage
info : int

Other Parameters
overwrite_b : input int, optional
Default: 0
lower : input int, optional
Default: 0

`scipy.linalg.lapack.`**`crot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for `crot`.

Parameters **x** : input rank-1 array('F') with bounds (*)
y : input rank-1 array('F') with bounds (*)
c : input float
s : input complex

Returns **x** : rank-1 array('F') with bounds (*)
y : rank-1 array('F') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional
Default: 0
incy : input int, optional
Default: 1

`scipy.linalg.lapack.`**`zrot`**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for `zrot`.

Parameters **x** : input rank-1 array('D') with bounds (*)
y : input rank-1 array('D') with bounds (*)
c : input float
s : input complex

Returns **x** : rank-1 array('D') with bounds (*)
y : rank-1 array('D') with bounds (*)

Other Parameters
n : input int, optional
Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x : input int, optional
Default: 0
offx : input int, optional
Default: 0
incx : input int, optional
Default: 1
overwrite_y : input int, optional
Default: 0
offy : input int, optional

Default: 0

incy : input int, optional

Default: 1

`scipy.linalg.lapack.`**`strsyl`**`(`*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]`)` **= <fortran object>**

Wrapper for `strsyl`.

Parameters

a : input rank-2 array('f') with bounds (m,m)

b : input rank-2 array('f') with bounds (n,n)

c : input rank-2 array('f') with bounds (m,n)

Returns

x : rank-2 array('f') with bounds (m,n) and c storage

scale : float

info : int

Other Parameters

trana : input string(len=1), optional

Default: 'N'

tranb : input string(len=1), optional

Default: 'N'

isgn : input int, optional

Default: 1

overwrite_c : input int, optional

Default: 0

`scipy.linalg.lapack.`**`dtrsyl`**`(`*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]`)` **= <fortran object>**

Wrapper for `dtrsyl`.

Parameters

a : input rank-2 array('d') with bounds (m,m)

b : input rank-2 array('d') with bounds (n,n)

c : input rank-2 array('d') with bounds (m,n)

Returns

x : rank-2 array('d') with bounds (m,n) and c storage

scale : float

info : int

Other Parameters

trana : input string(len=1), optional

Default: 'N'

tranb : input string(len=1), optional

Default: 'N'

isgn : input int, optional

Default: 1

overwrite_c : input int, optional

Default: 0

`scipy.linalg.lapack.`**`ctrsyl`**`(`*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]`)` **= <fortran object>**

Wrapper for `ctrsyl`.

Parameters

a : input rank-2 array('F') with bounds (m,m)

b : input rank-2 array('F') with bounds (n,n)

c : input rank-2 array('F') with bounds (m,n)

Returns

x : rank-2 array('F') with bounds (m,n) and c storage

scale : float

info : int

Other Parameters

trana : input string(len=1), optional

Default: 'N'

tranb : input string(len=1), optional

Default: 'N'

isgn : input int, optional

Default: 1

overwrite_c : input int, optional

Default: 0

scipy.linalg.lapack.**ztrsyl**(*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ztrsyl`.

Parameters **a** : input rank-2 array('D') with bounds (m,m)

b : input rank-2 array('D') with bounds (n,n)

c : input rank-2 array('D') with bounds (m,n)

Returns **x** : rank-2 array('D') with bounds (m,n) and c storage

scale : float

info : int

Other Parameters

trana : input string(len=1), optional

Default: 'N'

tranb : input string(len=1), optional

Default: 'N'

isgn : input int, optional

Default: 1

overwrite_c : input int, optional

Default: 0

scipy.linalg.lapack.**strtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for `strtri`.

Parameters **c** : input rank-2 array('f') with bounds (n,n)

Returns **inv_c** : rank-2 array('f') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional

Default: 0

lower : input int, optional

Default: 0

unitdiag : input int, optional

Default: 0

scipy.linalg.lapack.**dtrtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dtrtri`.

Parameters **c** : input rank-2 array('d') with bounds (n,n)

Returns **inv_c** : rank-2 array('d') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional

Default: 0

lower : input int, optional

Default: 0

unitdiag : input int, optional

Default: 0

scipy.linalg.lapack.**ctrtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ctrtri`.

Parameters **c** : input rank-2 array('F') with bounds (n,n)

Returns **inv_c** : rank-2 array('F') with bounds (n,n) and c storage

info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional
Default: 0

unitdiag : input int, optional
Default: 0

`scipy.linalg.lapack.`**`ztrtri`**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ztrtri`.

Parameters **c** : input rank-2 array('D') with bounds (n,n)

Returns **inv_c** : rank-2 array('D') with bounds (n,n) and c storage
info : int

Other Parameters

overwrite_c : input int, optional
Default: 0

lower : input int, optional
Default: 0

unitdiag : input int, optional
Default: 0

`scipy.linalg.lapack.`**`strtrs`**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for `strtrs`.

Parameters **a** : input rank-2 array('f') with bounds (lda,n)
b : input rank-2 array('f') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('f') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters

lower : input int, optional
Default: 0

trans : input int, optional
Default: 0

unitdiag : input int, optional
Default: 0

lda : input int, optional
Default: shape(a,0)

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dtrtrs`**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for `dtrtrs`.

Parameters **a** : input rank-2 array('d') with bounds (lda,n)
b : input rank-2 array('d') with bounds (ldb,nrhs)

Returns **x** : rank-2 array('d') with bounds (ldb,nrhs) and b storage
info : int

Other Parameters

lower : input int, optional
Default: 0

trans : input int, optional
Default: 0

unitdiag : input int, optional
Default: 0

lda : input int, optional
Default: shape(a,0)

overwrite_b : input int, optional
Default: 0

scipy.linalg.lapack.**ctrtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) = **<fortran object>**
Wrapper for `ctrtrs`.

Parameters **a** : input rank-2 array('F') with bounds (lda,n)
b : input rank-2 array('F') with bounds (ldb,nrhs)
Returns **x** : rank-2 array('F') with bounds (ldb,nrhs) and b storage
info : int
Other Parameters
lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0
lda : input int, optional
Default: shape(a,0)
overwrite_b : input int, optional
Default: 0

scipy.linalg.lapack.**ztrtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) = **<fortran object>**
Wrapper for `ztrtrs`.

Parameters **a** : input rank-2 array('D') with bounds (lda,n)
b : input rank-2 array('D') with bounds (ldb,nrhs)
Returns **x** : rank-2 array('D') with bounds (ldb,nrhs) and b storage
info : int
Other Parameters
lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0
lda : input int, optional
Default: shape(a,0)
overwrite_b : input int, optional
Default: 0

scipy.linalg.lapack.**cunghr**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) = **<fortran object>**
Wrapper for `cunghr`.

Parameters **a** : input rank-2 array('F') with bounds (n,n)
tau : input rank-1 array('F') with bounds (n - 1)
Returns **ht** : rank-2 array('F') with bounds (n,n) and a storage
info : int
Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: hi-lo

`scipy.linalg.lapack.`**`zunghr`**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zunghr`.

Parameters **a** : input rank-2 array('D') with bounds (n,n)
tau : input rank-1 array('D') with bounds (n - 1)

Returns **ht** : rank-2 array('D') with bounds (n,n) and a storage
info : int

Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: hi-lo

`scipy.linalg.lapack.`**`cungqr`**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cungqr`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)
tau : input rank-1 array('F') with bounds (k)

Returns **q** : rank-2 array('F') with bounds (m,n) and a storage
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`zungqr`**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zungqr`.

Parameters **a** : input rank-2 array('D') with bounds (m,n)
tau : input rank-1 array('D') with bounds (k)

Returns **q** : rank-2 array('D') with bounds (m,n) and a storage
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`cungrq`**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cungrq`.

Parameters **a** : input rank-2 array('F') with bounds (m,n)
tau : input rank-1 array('F') with bounds (k)

Returns **q** : rank-2 array('F') with bounds (m,n) and a storage
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional

Default: 3*m

`scipy.linalg.lapack.`**`zungrq`**(*a*, *tau*[, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for `zungrq`.

Parameters
a : input rank-2 array('D') with bounds (m,n)
tau : input rank-1 array('D') with bounds (k)

Returns
q : rank-2 array('D') with bounds (m,n) and a storage
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*m

`scipy.linalg.lapack.`**`cunmqr`**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) = **<fortran object>**

Wrapper for `cunmqr`.

Parameters
side : input string(len=1)
trans : input string(len=1)
a : input rank-2 array('F') with bounds (lda,k)
tau : input rank-1 array('F') with bounds (k)
c : input rank-2 array('F') with bounds (ldc,n)
lwork : input int

Returns
cq : rank-2 array('F') with bounds (ldc,n) and c storage
work : rank-1 array('F') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zunmqr`**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) = **<fortran object>**

Wrapper for `zunmqr`.

Parameters
side : input string(len=1)
trans : input string(len=1)
a : input rank-2 array('D') with bounds (lda,k)
tau : input rank-1 array('D') with bounds (k)
c : input rank-2 array('D') with bounds (ldc,n)
lwork : input int

Returns
cq : rank-2 array('D') with bounds (ldc,n) and c storage
work : rank-1 array('D') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sgtsv`**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for `sgtsv`.

Parameters
dl : input rank-1 array('f') with bounds (n - 1)
d : input rank-1 array('f') with bounds (*)
du : input rank-1 array('f') with bounds (n - 1)
b : input rank-2 array('f') with bounds (,)

Returns **du2** : rank-1 array('f') with bounds (n - 1) and dl storage
d : rank-1 array('f') with bounds (*)
du : rank-1 array('f') with bounds (n - 1)
x : rank-2 array('f') with bounds (,) and b storage
info : int

Other Parameters
overwrite_dl : input int, optional
Default: 0
overwrite_d : input int, optional
Default: 0
overwrite_du : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dgtsv`**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dgtsv`.

Parameters **dl** : input rank-1 array('d') with bounds (n - 1)
d : input rank-1 array('d') with bounds (*)
du : input rank-1 array('d') with bounds (n - 1)
b : input rank-2 array('d') with bounds (,)

Returns **du2** : rank-1 array('d') with bounds (n - 1) and dl storage
d : rank-1 array('d') with bounds (*)
du : rank-1 array('d') with bounds (n - 1)
x : rank-2 array('d') with bounds (,) and b storage
info : int

Other Parameters
overwrite_dl : input int, optional
Default: 0
overwrite_d : input int, optional
Default: 0
overwrite_du : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cgtsv`**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for `cgtsv`.

Parameters **dl** : input rank-1 array('F') with bounds (n - 1)
d : input rank-1 array('F') with bounds (*)
du : input rank-1 array('F') with bounds (n - 1)
b : input rank-2 array('F') with bounds (,)

Returns **du2** : rank-1 array('F') with bounds (n - 1) and dl storage
d : rank-1 array('F') with bounds (*)
du : rank-1 array('F') with bounds (n - 1)
x : rank-2 array('F') with bounds (,) and b storage
info : int

Other Parameters
overwrite_dl : input int, optional
Default: 0
overwrite_d : input int, optional
Default: 0

overwrite_du : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zgtsv`**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zgtsv`.

Parameters **dl** : input rank-1 array('D') with bounds (n - 1)
d : input rank-1 array('D') with bounds (*)
du : input rank-1 array('D') with bounds (n - 1)
b : input rank-2 array('D') with bounds (,)

Returns **du2** : rank-1 array('D') with bounds (n - 1) and dl storage
d : rank-1 array('D') with bounds (*)
du : rank-1 array('D') with bounds (n - 1)
x : rank-2 array('D') with bounds (,) and b storage
info : int

Other Parameters
overwrite_dl : input int, optional
Default: 0
overwrite_d : input int, optional
Default: 0
overwrite_du : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`sptsv`**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) = **<fortran object>**

Wrapper for `sptsv`.

Parameters **d** : input rank-1 array('f') with bounds (*)
e : input rank-1 array('f') with bounds (n - 1)
b : input rank-2 array('f') with bounds (,)

Returns **d** : rank-1 array('f') with bounds (*)
du : rank-1 array('f') with bounds (n - 1) and e storage
x : rank-2 array('f') with bounds (,) and b storage
info : int

Other Parameters
overwrite_d : input int, optional
Default: 0
overwrite_e : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dptsv`**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dptsv`.

Parameters **d** : input rank-1 array('d') with bounds (*)
e : input rank-1 array('d') with bounds (n - 1)
b : input rank-2 array('d') with bounds (,)

Returns **d** : rank-1 array('d') with bounds (*)
du : rank-1 array('d') with bounds (n - 1) and e storage
x : rank-2 array('d') with bounds (,) and b storage
info : int

Other Parameters

overwrite_d : input int, optional
Default: 0
overwrite_e : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`cptsv`**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**

Wrapper for `cptsv`.

Parameters
d : input rank-1 array('f') with bounds (*)
e : input rank-1 array('F') with bounds (n - 1)
b : input rank-2 array('F') with bounds (,)

Returns
d : rank-1 array('f') with bounds (*)
du : rank-1 array('F') with bounds (n - 1) and e storage
x : rank-2 array('F') with bounds (,) and b storage
info : int

Other Parameters

overwrite_d : input int, optional
Default: 0
overwrite_e : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`zptsv`**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zptsv`.

Parameters
d : input rank-1 array('d') with bounds (*)
e : input rank-1 array('D') with bounds (n - 1)
b : input rank-2 array('D') with bounds (,)

Returns
d : rank-1 array('d') with bounds (*)
du : rank-1 array('D') with bounds (n - 1) and e storage
x : rank-2 array('D') with bounds (,) and b storage
info : int

Other Parameters

overwrite_d : input int, optional
Default: 0
overwrite_e : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`slamch`**(*cmach*) **= <fortran slamch>**

Wrapper for `slamch`.

Parameters
cmach : input string(len=1)

Returns
slamch : float

`scipy.linalg.lapack.`**`dlamch`**(*cmach*) **= <fortran dlamch>**

Wrapper for `dlamch`.

Parameters
cmach : input string(len=1)

Returns
dlamch : float

`scipy.linalg.lapack.`**`sorghr`**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sorghr`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)
tau : input rank-1 array('f') with bounds (n - 1)

Returns **ht** : rank-2 array('f') with bounds (n,n) and a storage
info : int

Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: hi-lo

`scipy.linalg.lapack.`**`dorghr`**`(`*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]`)` **= <fortran object>**
Wrapper for `dorghr`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)
tau : input rank-1 array('d') with bounds (n - 1)

Returns **ht** : rank-2 array('d') with bounds (n,n) and a storage
info : int

Other Parameters
lo : input int, optional
Default: 0
hi : input int, optional
Default: n-1
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: hi-lo

`scipy.linalg.lapack.`**`sorgqr`**`(`*a*, *tau*[, *lwork*, *overwrite_a*]`)` **= <fortran object>**
Wrapper for `sorgqr`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)
tau : input rank-1 array('f') with bounds (k)

Returns **q** : rank-2 array('f') with bounds (m,n) and a storage
work : rank-1 array('f') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n

`scipy.linalg.lapack.`**`dorgqr`**`(`*a*, *tau*[, *lwork*, *overwrite_a*]`)` **= <fortran object>**
Wrapper for `dorgqr`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)
tau : input rank-1 array('d') with bounds (k)

Returns **q** : rank-2 array('d') with bounds (m,n) and a storage
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional

Default: 3*n

`scipy.linalg.lapack.`**`sorgrq`**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sorgrq`.

Parameters **a** : input rank-2 array('f') with bounds (m,n)
tau : input rank-1 array('f') with bounds (k)

Returns **q** : rank-2 array('f') with bounds (m,n) and a storage
work : rank-1 array('f') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*m

`scipy.linalg.lapack.`**`dorgrq`**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dorgrq`.

Parameters **a** : input rank-2 array('d') with bounds (m,n)
tau : input rank-1 array('d') with bounds (k)

Returns **q** : rank-2 array('d') with bounds (m,n) and a storage
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*m

`scipy.linalg.lapack.`**`sormqr`**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for `sormqr`.

Parameters **side** : input string(len=1)
trans : input string(len=1)
a : input rank-2 array('f') with bounds (lda,k)
tau : input rank-1 array('f') with bounds (k)
c : input rank-2 array('f') with bounds (ldc,n)
lwork : input int

Returns **cq** : rank-2 array('f') with bounds (ldc,n) and c storage
work : rank-1 array('f') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dormqr`**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for `dormqr`.

Parameters **side** : input string(len=1)
trans : input string(len=1)
a : input rank-2 array('d') with bounds (lda,k)
tau : input rank-1 array('d') with bounds (k)
c : input rank-2 array('d') with bounds (ldc,n)
lwork : input int

Returns **cq** : rank-2 array('d') with bounds (ldc,n) and c storage
work : rank-1 array('d') with bounds (MAX(lwork,1))
info : int

Other Parameters
overwrite_c : input int, optional
Default: 0

`scipy.linalg.lapack.`**`ssbev`**(*ab*[, *compute_v*, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**
Wrapper for `ssbev`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,*)
Returns **w** : rank-1 array('f') with bounds (n)
z : rank-2 array('f') with bounds (ldz,ldz)
info : int
Other Parameters
overwrite_ab : input int, optional
Default: 1
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`dsbev`**(*ab*[, *compute_v*, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**
Wrapper for `dsbev`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,*)
Returns **w** : rank-1 array('d') with bounds (n)
z : rank-2 array('d') with bounds (ldz,ldz)
info : int
Other Parameters
overwrite_ab : input int, optional
Default: 1
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)

`scipy.linalg.lapack.`**`ssbevd`**(*ab*[, *compute_v*, *lower*, *ldab*, *liwork*, *overwrite_ab*]) **= <fortran object>**
Wrapper for `ssbevd`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,*)
Returns **w** : rank-1 array('f') with bounds (n)
z : rank-2 array('f') with bounds (ldz,ldz)
info : int
Other Parameters
overwrite_ab : input int, optional
Default: 1
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
ldab : input int, optional
Default: shape(ab,0)
liwork : input int, optional
Default: (compute_v?3+5*n:1)

`scipy.linalg.lapack.`**`dsbevd`**(*ab*[, *compute_v*, *lower*, *ldab*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `dsbevd`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,*)

Returns **w** : rank-1 array('d') with bounds (n)

z : rank-2 array('d') with bounds (ldz,ldz)

info : int

Other Parameters

overwrite_ab : input int, optional
Default: 1

compute_v : input int, optional
Default: 1

lower : input int, optional
Default: 0

ldab : input int, optional
Default: shape(ab,0)

liwork : input int, optional
Default: (compute_v?3+5*n:1)

`scipy.linalg.lapack.`**`ssbevx`**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `ssbevx`.

Parameters **ab** : input rank-2 array('f') with bounds (ldab,*)

vl : input float

vu : input float

il : input int

iu : input int

Returns **w** : rank-1 array('f') with bounds (n)

z : rank-2 array('f') with bounds (ldz,mmax)

m : int

ifail : rank-1 array('i') with bounds ((compute_v?n:1))

info : int

Other Parameters

overwrite_ab : input int, optional
Default: 1

ldab : input int, optional
Default: shape(ab,0)

compute_v : input int, optional
Default: 1

range : input int, optional
Default: 0

lower : input int, optional
Default: 0

abstol : input float, optional
Default: 0.0

mmax : input int, optional
Default: (compute_v?(range==2?(iu-il+1):n):1)

`scipy.linalg.lapack.`**`dsbevx`**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for `dsbevx`.

Parameters **ab** : input rank-2 array('d') with bounds (ldab,*)

vl : input float

vu : input float

il : input int
iu : input int

Returns
w : rank-1 array('d') with bounds (n)
z : rank-2 array('d') with bounds (ldz,mmax)
m : int
ifail : rank-1 array('i') with bounds ((compute_v?n:1))
info : int

Other Parameters
overwrite_ab : input int, optional
Default: 1
ldab : input int, optional
Default: shape(ab,0)
compute_v : input int, optional
Default: 1
range : input int, optional
Default: 0
lower : input int, optional
Default: 0
abstol : input float, optional
Default: 0.0
mmax : input int, optional
Default: (compute_v?(range==2?(iu-il+1):n):1)

`scipy.linalg.lapack.`**`ssyev`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `ssyev`.

Parameters
a : input rank-2 array('f') with bounds (n,n)

Returns
w : rank-1 array('f') with bounds (n)
v : rank-2 array('f') with bounds (n,n) and a storage
info : int

Other Parameters
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n-1

`scipy.linalg.lapack.`**`dsyev`**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dsyev`.

Parameters
a : input rank-2 array('d') with bounds (n,n)

Returns
w : rank-1 array('d') with bounds (n)
v : rank-2 array('d') with bounds (n,n) and a storage
info : int

Other Parameters
compute_v : input int, optional
Default: 1
lower : input int, optional
Default: 0
overwrite_a : input int, optional
Default: 0
lwork : input int, optional
Default: 3*n-1

`scipy.linalg.lapack.`**`ssyevd`**`(`*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `ssyevd`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

Returns **w** : rank-1 array('f') with bounds (n)

v : rank-2 array('f') with bounds (n,n) and a storage

info : int

Other Parameters

compute_v : input int, optional
Default: 1

lower : input int, optional
Default: 0

overwrite_a : input int, optional
Default: 0

lwork : input int, optional
Default: (compute_v?1+6*n+2*n*n:2*n+1)

`scipy.linalg.lapack.`**`dsyevd`**`(`*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `dsyevd`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

Returns **w** : rank-1 array('d') with bounds (n)

v : rank-2 array('d') with bounds (n,n) and a storage

info : int

Other Parameters

compute_v : input int, optional
Default: 1

lower : input int, optional
Default: 0

overwrite_a : input int, optional
Default: 0

lwork : input int, optional
Default: (compute_v?1+6*n+2*n*n:2*n+1)

`scipy.linalg.lapack.`**`ssyevr`**`(`*a*[, *jobz*, *range*, *uplo*, *il*, *iu*, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `ssyevr`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

Returns **w** : rank-1 array('f') with bounds (n)

z : rank-2 array('f') with bounds (n,m)

info : int

Other Parameters

jobz : input string(len=1), optional
Default: 'V'

range : input string(len=1), optional
Default: 'A'

uplo : input string(len=1), optional
Default: 'L'

overwrite_a : input int, optional
Default: 0

il : input int, optional
Default: 1

iu : input int, optional
Default: n

lwork : input int, optional
Default: 26*n

`scipy.linalg.lapack.`**`dsyevr`**`(`*a*[, *jobz*, *range*, *uplo*, *il*, *iu*, *lwork*, *overwrite_a*]`)` **= <fortran object>**

Wrapper for `dsyevr`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

Returns **w** : rank-1 array('d') with bounds (n)

z : rank-2 array('d') with bounds (n,m)

info : int

Other Parameters

jobz : input string(len=1), optional
Default: 'V'

range : input string(len=1), optional
Default: 'A'

uplo : input string(len=1), optional
Default: 'L'

overwrite_a : input int, optional
Default: 0

il : input int, optional
Default: 1

iu : input int, optional
Default: n

lwork : input int, optional
Default: 26*n

`scipy.linalg.lapack.`**`ssygv`**`(`*a*, *b*[, *itype*, *jobz*, *uplo*, *overwrite_a*, *overwrite_b*]`)` **= <fortran object>**

Wrapper for `ssygv`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)

b : input rank-2 array('f') with bounds (n,n)

Returns **a** : rank-2 array('f') with bounds (n,n)

w : rank-1 array('f') with bounds (n)

info : int

Other Parameters

itype : input int, optional
Default: 1

jobz : input string(len=1), optional
Default: 'V'

uplo : input string(len=1), optional
Default: 'L'

overwrite_a : input int, optional
Default: 0

overwrite_b : input int, optional
Default: 0

`scipy.linalg.lapack.`**`dsygv`**`(`*a*, *b*[, *itype*, *jobz*, *uplo*, *overwrite_a*, *overwrite_b*]`)` **= <fortran object>**

Wrapper for `dsygv`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)

b : input rank-2 array('d') with bounds (n,n)

Returns **a** : rank-2 array('d') with bounds (n,n)

w : rank-1 array('d') with bounds (n)

info : int

Other Parameters

itype : input int, optional
Default: 1

jobz : input string(len=1), optional
Default: 'V'

uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0

scipy.linalg.lapack.**ssygvd**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `ssygvd`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)
b : input rank-2 array('f') with bounds (n,n)
Returns **a** : rank-2 array('f') with bounds (n,n)
w : rank-1 array('f') with bounds (n)
info : int
Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 1+6*n+2*n*n

scipy.linalg.lapack.**dsygvd**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dsygvd`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)
b : input rank-2 array('d') with bounds (n,n)
Returns **a** : rank-2 array('d') with bounds (n,n)
w : rank-1 array('d') with bounds (n)
info : int
Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
lwork : input int, optional
Default: 1+6*n+2*n*n

scipy.linalg.lapack.**ssygvx**(*a*, *b*, *iu*[, *itype*, *jobz*, *uplo*, *il*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `ssygvx`.

Parameters **a** : input rank-2 array('f') with bounds (n,n)
b : input rank-2 array('f') with bounds (n,n)
iu : input int

Returns **w** : rank-1 array('f') with bounds (n)
z : rank-2 array('f') with bounds (n,m)
ifail : rank-1 array('i') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
il : input int, optional
Default: 1
lwork : input int, optional
Default: 8*n

`scipy.linalg.lapack.`**`dsygvx`**(*a*, *b*, *iu*[, *itype*, *jobz*, *uplo*, *il*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `dsygvx`.

Parameters **a** : input rank-2 array('d') with bounds (n,n)
b : input rank-2 array('d') with bounds (n,n)
iu : input int

Returns **w** : rank-1 array('d') with bounds (n)
z : rank-2 array('d') with bounds (n,m)
ifail : rank-1 array('i') with bounds (n)
info : int

Other Parameters
itype : input int, optional
Default: 1
jobz : input string(len=1), optional
Default: 'V'
uplo : input string(len=1), optional
Default: 'L'
overwrite_a : input int, optional
Default: 0
overwrite_b : input int, optional
Default: 0
il : input int, optional
Default: 1
lwork : input int, optional
Default: 8*n

`scipy.linalg.lapack.`**`slange`**(*norm*, *a*) = **<fortran slange>**

Wrapper for `slange`.

Parameters **norm** : input string(len=1)
a : input rank-2 array('f') with bounds (m,n)

Returns **n2** : float

`scipy.linalg.lapack.`**`dlange`**(*norm*, *a*) **= <fortran dlange>**

Wrapper for `dlange`.

Parameters	**norm** : input string(len=1) **a** : input rank-2 array('d') with bounds (m,n)
Returns	**n2** : float

`scipy.linalg.lapack.`**`clange`**(*norm*, *a*) **= <fortran clange>**

Wrapper for `clange`.

Parameters	**norm** : input string(len=1) **a** : input rank-2 array('F') with bounds (m,n)
Returns	**n2** : float

`scipy.linalg.lapack.`**`zlange`**(*norm*, *a*) **= <fortran zlange>**

Wrapper for `zlange`.

Parameters	**norm** : input string(len=1) **a** : input rank-2 array('D') with bounds (m,n)
Returns	**n2** : float

5.18 BLAS Functions for Cython

Usable from Cython via:

```
cimport scipy.linalg.cython_blas
```

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):

- caxpy
- ccopy
- cdotc
- cdotu
- cgbmv
- cgemm
- cgemv
- cgerc
- cgeru
- chbmv
- chemm
- chemv
- cher
- cher2
- cher2k
- cherk

- chpmv
- chpr
- chpr2
- crotg
- cscal
- csrot
- csscal
- cswap
- csymm
- csyr2k
- csyrk
- ctbmv
- ctbsv
- ctpmv
- ctpsv
- ctrmm
- ctrmv
- ctrsm
- ctrsv
- dasum
- daxpy
- dcabs1
- dcopy
- ddot
- dgbmv
- dgemm
- dgemv
- dger
- dnrm2
- drot
- drotg
- drotm
- drotmg
- dsbmv
- dscal
- dsdot

- dspmv
- dspr
- dspr2
- dswap
- dsymm
- dsymv
- dsyr
- dsyr2
- dsyr2k
- dsyrk
- dtbmv
- dtbsv
- dtpmv
- dtpsv
- dtrmm
- dtrmv
- dtrsm
- dtrsv
- dzasum
- dznrm2
- icamax
- idamax
- isamax
- izamax
- lsame
- sasum
- saxpy
- scasum
- scnrm2
- scopy
- sdot
- sdsdot
- sgbmv
- sgemm
- sgemv
- sger

- snrm2
- srot
- srotg
- srotm
- srotmg
- ssbmv
- sscal
- sspmv
- sspr
- sspr2
- sswap
- ssymm
- ssymv
- ssyr
- ssyr2
- ssyr2k
- ssyrk
- stbmv
- stbsv
- stpmv
- stpsv
- strmm
- strmv
- strsm
- strsv
- zaxpy
- zcopy
- zdotc
- zdotu
- zdrot
- zdscal
- zgbmv
- zgemm
- zgemv
- zgerc
- zgeru

- zhbmv
- zhemm
- zhemv
- zher
- zher2
- zher2k
- zherk
- zhpmv
- zhpr
- zhpr2
- zrotg
- zscal
- zswap
- zsymm
- zsyr2k
- zsyrk
- ztbmv
- ztbsv
- ztpmv
- ztpsv
- ztrmm
- ztrmv
- ztrsm
- ztrsv

5.19 LAPACK functions for Cython

Usable from Cython via:

```
cimport scipy.linalg.cython_lapack
```

This module provides Cython-level wrappers for all primary routines included in LAPACK 3.1.0 except for `zcgesv` since its interface is not consistent from LAPACK 3.1.0 to 3.5.0. It also provides some of the fixed-api auxiliary routines.

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):

- cbdsqr
- cgbbrd

- cgbcon
- cgbequ
- cgbrfs
- cgbsv
- cgbsvx
- cgbtf2
- cgbtrf
- cgbtrs
- cgebak
- cgebal
- cgebd2
- cgebrd
- cgecon
- cgeequ
- cgees
- cgeesx
- cgeev
- cgeevx
- cgegs
- cgegv
- cgehd2
- cgehrd
- cgelq2
- cgelqf
- cgels
- cgelsd
- cgelss
- cgelsx
- cgelsy
- cgeql2
- cgeqlf
- cgeqp3
- cgeqpf
- cgeqr2
- cgeqrf
- cgerfs

- cgerq2
- cgerqf
- cgesc2
- cgesdd
- cgesv
- cgesvd
- cgesvx
- cgetc2
- cgetf2
- cgetrf
- cgetri
- cgetrs
- cggbak
- cggbal
- cgges
- cggesx
- cggev
- cggevx
- cggglm
- cgghrd
- cgglse
- cggqrf
- cggrqf
- cggsvd
- cggsvp
- cgtcon
- cgtrfs
- cgtsv
- cgtsvx
- cgttrf
- cgttrs
- cgtts2
- chbev
- chbevd
- chbevx
- chbgst

- chbgv
- chbgvd
- chbgvx
- chbtrd
- checon
- cheev
- cheevd
- cheevr
- cheevx
- chegs2
- chegst
- chegv
- chegvd
- chegvx
- cherfs
- chesv
- chesvx
- chetd2
- chetf2
- chetrd
- chetrf
- chetri
- chetrs
- chgeqz
- chpcon
- chpev
- chpevd
- chpevx
- chpgst
- chpgv
- chpgvd
- chpgvx
- chprfs
- chpsv
- chpsvx
- chptrd

- chptrf
- chptri
- chptrs
- chsein
- chseqr
- clabrd
- clacgv
- clacn2
- clacon
- clacp2
- clacpy
- clacrm
- clacrt
- cladiv
- claed0
- claed7
- claed8
- claein
- claesy
- claev2
- clag2z
- clags2
- clagtm
- clahef
- clahqr
- clahr2
- clahrd
- claic1
- clals0
- clalsa
- clalsd
- clangb
- clange
- clangt
- clanhb
- clanhe

- clanhp
- clanhs
- clanht
- clansb
- clansp
- clansy
- clantb
- clantp
- clantr
- clapll
- clapmt
- claqgb
- claqge
- claqhb
- claqhe
- claqhp
- claqp2
- claqps
- claqr0
- claqr1
- claqr2
- claqr3
- claqr4
- claqr5
- claqsb
- claqsp
- claqsy
- clar1v
- clar2v
- clarcm
- clarf
- clarfb
- clarfg
- clarft
- clarfx
- clargv

- clarnv
- clarrv
- clartg
- clartv
- clarz
- clarzb
- clarzt
- clascl
- claset
- clasr
- classq
- claswp
- clasyf
- clatbs
- clatdf
- clatps
- clatrd
- clatrs
- clatrz
- clatzm
- clauu2
- clauum
- cpbcon
- cpbequ
- cpbrfs
- cpbstf
- cpbsv
- cpbsvx
- cpbtf2
- cpbtrf
- cpbtrs
- cpocon
- cpoequ
- cporfs
- cposv
- cposvx

- cpotf2
- cpotrf
- cpotri
- cpotrs
- cppcon
- cppequ
- cpprfs
- cppsv
- cppsvx
- cpptrf
- cpptri
- cpptrs
- cptcon
- cpteqr
- cptrfs
- cptsv
- cptsvx
- cpttrf
- cpttrs
- cptts2
- crot
- cspcon
- cspmv
- cspr
- csprfs
- cspsv
- cspsvx
- csptrf
- csptri
- csptrs
- csrscl
- cstedc
- cstegr
- cstein
- cstemr
- csteqr

- csycon
- csymv
- csyr
- csyrfs
- csysv
- csysvx
- csytf2
- csytrf
- csytri
- csytrs
- ctbcon
- ctbrfs
- ctbtrs
- ctgevc
- ctgex2
- ctgexc
- ctgsen
- ctgsja
- ctgsna
- ctgsy2
- ctgsyl
- ctpcon
- ctprfs
- ctptri
- ctptrs
- ctrcon
- ctrevc
- ctrexc
- ctrrfs
- ctrsen
- ctrsna
- ctrsyl
- ctrti2
- ctrtri
- ctrtrs
- ctzrqf

- ctzrzf
- cung2l
- cung2r
- cungbr
- cunghr
- cungl2
- cunglq
- cungql
- cungqr
- cungr2
- cungrq
- cungtr
- cunm2l
- cunm2r
- cunmbr
- cunmhr
- cunml2
- cunmlq
- cunmql
- cunmqr
- cunmr2
- cunmr3
- cunmrq
- cunmrz
- cunmtr
- cupgtr
- cupmtr
- dbdsdc
- dbdsqr
- ddisna
- dgbbrd
- dgbcon
- dgbequ
- dgbrfs
- dgbsv
- dgbsvx

- dgbtf2
- dgbtrf
- dgbtrs
- dgebak
- dgebal
- dgebd2
- dgebrd
- dgecon
- dgeequ
- dgees
- dgeesx
- dgeev
- dgeevx
- dgegs
- dgegv
- dgehd2
- dgehrd
- dgelq2
- dgelqf
- dgels
- dgelsd
- dgelss
- dgelsx
- dgelsy
- dgeql2
- dgeqlf
- dgeqp3
- dgeqpf
- dgeqr2
- dgeqrf
- dgerfs
- dgerq2
- dgerqf
- dgesc2
- dgesdd
- dgesv

- dgesvd
- dgesvx
- dgetc2
- dgetf2
- dgetrf
- dgetri
- dgetrs
- dggbak
- dggbal
- dgges
- dggesx
- dggev
- dggevx
- dggglm
- dgghrd
- dgglse
- dggqrf
- dggrqf
- dggsvd
- dggsvp
- dgtcon
- dgtrfs
- dgtsv
- dgtsvx
- dgttrf
- dgttrs
- dgtts2
- dhgeqz
- dhsein
- dhseqr
- disnan
- dlabad
- dlabrd
- dlacn2
- dlacon
- dlacpy

- dladiv
- dlae2
- dlaebz
- dlaed0
- dlaed1
- dlaed2
- dlaed3
- dlaed4
- dlaed5
- dlaed6
- dlaed7
- dlaed8
- dlaed9
- dlaeda
- dlaein
- dlaev2
- dlaexc
- dlag2
- dlag2s
- dlags2
- dlagtf
- dlagtm
- dlagts
- dlagv2
- dlahqr
- dlahr2
- dlahrd
- dlaic1
- dlaln2
- dlals0
- dlalsa
- dlalsd
- dlamch
- dlamrg
- dlaneg
- dlangb

- dlange
- dlangt
- dlanhs
- dlansb
- dlansp
- dlanst
- dlansy
- dlantb
- dlantp
- dlantr
- dlanv2
- dlapll
- dlapmt
- dlapy2
- dlapy3
- dlaqgb
- dlaqge
- dlaqp2
- dlaqps
- dlaqr0
- dlaqr1
- dlaqr2
- dlaqr3
- dlaqr4
- dlaqr5
- dlaqsb
- dlaqsp
- dlaqsy
- dlaqtr
- dlar1v
- dlar2v
- dlarf
- dlarfb
- dlarfg
- dlarft
- dlarfx

- dlargv
- dlarnv
- dlarra
- dlarrb
- dlarrc
- dlarrd
- dlarre
- dlarrf
- dlarrj
- dlarrk
- dlarrr
- dlarrv
- dlartg
- dlartv
- dlaruv
- dlarz
- dlarzb
- dlarzt
- dlas2
- dlascl
- dlasd0
- dlasd1
- dlasd2
- dlasd3
- dlasd4
- dlasd5
- dlasd6
- dlasd7
- dlasd8
- dlasda
- dlasdq
- dlasdt
- dlaset
- dlasq1
- dlasq2
- dlasq6

- dlasr
- dlasrt
- dlassq
- dlasv2
- dlaswp
- dlasy2
- dlasyf
- dlatbs
- dlatdf
- dlatps
- dlatrd
- dlatrs
- dlatrz
- dlatzm
- dlauu2
- dlauum
- dopgtr
- dopmtr
- dorg2l
- dorg2r
- dorgbr
- dorghr
- dorgl2
- dorglq
- dorgql
- dorgqr
- dorgr2
- dorgrq
- dorgtr
- dorm2l
- dorm2r
- dormbr
- dormhr
- dorml2
- dormlq
- dormql

- dormqr
- dormr2
- dormr3
- dormrq
- dormrz
- dormtr
- dpbcon
- dpbequ
- dpbrfs
- dpbstf
- dpbsv
- dpbsvx
- dpbtf2
- dpbtrf
- dpbtrs
- dpocon
- dpoequ
- dporfs
- dposv
- dposvx
- dpotf2
- dpotrf
- dpotri
- dpotrs
- dppcon
- dppequ
- dpprfs
- dppsv
- dppsvx
- dpptrf
- dpptri
- dpptrs
- dptcon
- dpteqr
- dptrfs
- dptsv

- dptsvx
- dpttrf
- dpttrs
- dptts2
- drscl
- dsbev
- dsbevd
- dsbevx
- dsbgst
- dsbgv
- dsbgvd
- dsbgvx
- dsbtrd
- dsgesv
- dspcon
- dspev
- dspevd
- dspevx
- dspgst
- dspgv
- dspgvd
- dspgvx
- dsprfs
- dspsv
- dspsvx
- dsptrd
- dsptrf
- dsptri
- dsptrs
- dstebz
- dstedc
- dstegr
- dstein
- dstemr
- dsteqr
- dsterf

- dstev
- dstevd
- dstevr
- dstevx
- dsycon
- dsyev
- dsyevd
- dsyevr
- dsyevx
- dsygs2
- dsygst
- dsygv
- dsygvd
- dsygvx
- dsyrfs
- dsysv
- dsysvx
- dsytd2
- dsytf2
- dsytrd
- dsytrf
- dsytri
- dsytrs
- dtbcon
- dtbrfs
- dtbtrs
- dtgevc
- dtgex2
- dtgexc
- dtgsen
- dtgsja
- dtgsna
- dtgsy2
- dtgsyl
- dtpcon
- dtprfs

- dtptri
- dtptrs
- dtrcon
- dtrevc
- dtrexc
- dtrrfs
- dtrsen
- dtrsna
- dtrsyl
- dtrti2
- dtrtri
- dtrtrs
- dtzrqf
- dtzrzf
- dzsum1
- icmax1
- ieeeck
- ilaver
- izmax1
- sbdsdc
- sbdsqr
- scsum1
- sdisna
- sgbbrd
- sgbcon
- sgbequ
- sgbrfs
- sgbsv
- sgbsvx
- sgbtf2
- sgbtrf
- sgbtrs
- sgebak
- sgebal
- sgebd2
- sgebrd

- sgecon
- sgeequ
- sgees
- sgeesx
- sgeev
- sgeevx
- sgegs
- sgegv
- sgehd2
- sgehrd
- sgelq2
- sgelqf
- sgels
- sgelsd
- sgelss
- sgelsx
- sgelsy
- sgeql2
- sgeqlf
- sgeqp3
- sgeqpf
- sgeqr2
- sgeqrf
- sgerfs
- sgerq2
- sgerqf
- sgesc2
- sgesdd
- sgesv
- sgesvd
- sgesvx
- sgetc2
- sgetf2
- sgetrf
- sgetri
- sgetrs

- sggbak
- sggbal
- sgges
- sggesx
- sggev
- sggevx
- sggglm
- sgghrd
- sgglse
- sggqrf
- sggrqf
- sggsvd
- sggsvp
- sgtcon
- sgtrfs
- sgtsv
- sgtsvx
- sgttrf
- sgttrs
- sgtts2
- shgeqz
- shsein
- shseqr
- slabad
- slabrd
- slacn2
- slacon
- slacpy
- sladiv
- slae2
- slaebz
- slaed0
- slaed1
- slaed2
- slaed3
- slaed4

- slaed5
- slaed6
- slaed7
- slaed8
- slaed9
- slaeda
- slaein
- slaev2
- slaexc
- slag2
- slag2d
- slags2
- slagtf
- slagtm
- slagts
- slagv2
- slahqr
- slahr2
- slahrd
- slaic1
- slaln2
- slals0
- slalsa
- slalsd
- slamch
- slamrg
- slangb
- slange
- slangt
- slanhs
- slansb
- slansp
- slanst
- slansy
- slantb
- slantp

- slantr
- slanv2
- slapll
- slapmt
- slapy2
- slapy3
- slaqgb
- slaqge
- slaqp2
- slaqps
- slaqr0
- slaqr1
- slaqr2
- slaqr3
- slaqr4
- slaqr5
- slaqsb
- slaqsp
- slaqsy
- slaqtr
- slar1v
- slar2v
- slarf
- slarfb
- slarfg
- slarft
- slarfx
- slargv
- slarnv
- slarra
- slarrb
- slarrc
- slarrd
- slarre
- slarrf
- slarrj

- slarrk
- slarrr
- slarrv
- slartg
- slartv
- slaruv
- slarz
- slarzb
- slarzt
- slas2
- slascl
- slasd0
- slasd1
- slasd2
- slasd3
- slasd4
- slasd5
- slasd6
- slasd7
- slasd8
- slasda
- slasdq
- slasdt
- slaset
- slasq1
- slasq2
- slasq6
- slasr
- slasrt
- slassq
- slasv2
- slaswp
- slasy2
- slasyf
- slatbs
- slatdf

- slatps
- slatrd
- slatrs
- slatrz
- slatzm
- slauu2
- slauum
- sopgtr
- sopmtr
- sorg2l
- sorg2r
- sorgbr
- sorghr
- sorgl2
- sorglq
- sorgql
- sorgqr
- sorgr2
- sorgrq
- sorgtr
- sorm2l
- sorm2r
- sormbr
- sormhr
- sorml2
- sormlq
- sormql
- sormqr
- sormr2
- sormr3
- sormrq
- sormrz
- sormtr
- spbcon
- spbequ
- spbrfs

- spbstf
- spbsv
- spbsvx
- spbtf2
- spbtrf
- spbtrs
- spocon
- spoequ
- sporfs
- sposv
- sposvx
- spotf2
- spotrf
- spotri
- spotrs
- sppcon
- sppequ
- spprfs
- sppsv
- sppsvx
- spptrf
- spptri
- spptrs
- sptcon
- spteqr
- sptrfs
- sptsv
- sptsvx
- spttrf
- spttrs
- sptts2
- srscl
- ssbev
- ssbevd
- ssbevx
- ssbgst

- ssbgv
- ssbgvd
- ssbgvx
- ssbtrd
- sspcon
- sspev
- sspevd
- sspevx
- sspgst
- sspgv
- sspgvd
- sspgvx
- ssprfs
- sspsv
- sspsvx
- ssptrd
- ssptrf
- ssptri
- ssptrs
- sstebz
- sstedc
- sstegr
- sstein
- sstemr
- ssteqr
- ssterf
- sstev
- sstevd
- sstevr
- sstevx
- ssycon
- ssyev
- ssyevd
- ssyevr
- ssyevx
- ssygs2

- ssygst
- ssygv
- ssygvd
- ssygvx
- ssyrfs
- ssysv
- ssysvx
- ssytd2
- ssytf2
- ssytrd
- ssytrf
- ssytri
- ssytrs
- stbcon
- stbrfs
- stbtrs
- stgevc
- stgex2
- stgexc
- stgsen
- stgsja
- stgsna
- stgsy2
- stgsyl
- stpcon
- stprfs
- stptri
- stptrs
- strcon
- strevc
- strexc
- strrfs
- strsen
- strsna
- strsyl
- strti2

- strtri
- strtrs
- stzrqf
- stzrzf
- zbdsqr
- zdrscl
- zgbbrd
- zgbcon
- zgbequ
- zgbrfs
- zgbsv
- zgbsvx
- zgbtf2
- zgbtrf
- zgbtrs
- zgebak
- zgebal
- zgebd2
- zgebrd
- zgecon
- zgeequ
- zgees
- zgeesx
- zgeev
- zgeevx
- zgegs
- zgegv
- zgehd2
- zgehrd
- zgelq2
- zgelqf
- zgels
- zgelsd
- zgelss
- zgelsx
- zgelsy

- zgeql2
- zgeqlf
- zgeqp3
- zgeqpf
- zgeqr2
- zgeqrf
- zgerfs
- zgerq2
- zgerqf
- zgesc2
- zgesdd
- zgesv
- zgesvd
- zgesvx
- zgetc2
- zgetf2
- zgetrf
- zgetri
- zgetrs
- zggbak
- zggbal
- zgges
- zggesx
- zggev
- zggevx
- zggglm
- zgghrd
- zgglse
- zggqrf
- zggrqf
- zggsvd
- zggsvp
- zgtcon
- zgtrfs
- zgtsv
- zgtsvx

- zgttrf
- zgttrs
- zgtts2
- zhbev
- zhbevd
- zhbevx
- zhbgst
- zhbgv
- zhbgvd
- zhbgvx
- zhbtrd
- zhecon
- zheev
- zheevd
- zheevr
- zheevx
- zhegs2
- zhegst
- zhegv
- zhegvd
- zhegvx
- zherfs
- zhesv
- zhesvx
- zhetd2
- zhetf2
- zhetrd
- zhetrf
- zhetri
- zhetrs
- zhgeqz
- zhpcon
- zhpev
- zhpevd
- zhpevx
- zhpgst

- zhpgv
- zhpgvd
- zhpgvx
- zhprfs
- zhpsv
- zhpsvx
- zhptrd
- zhptrf
- zhptri
- zhptrs
- zhsein
- zhseqr
- zlabrd
- zlacgv
- zlacn2
- zlacon
- zlacp2
- zlacpy
- zlacrm
- zlacrt
- zladiv
- zlaed0
- zlaed7
- zlaed8
- zlaein
- zlaesy
- zlaev2
- zlag2c
- zlags2
- zlagtm
- zlahef
- zlahqr
- zlahr2
- zlahrd
- zlaic1
- zlals0

- zlalsa
- zlalsd
- zlangb
- zlange
- zlangt
- zlanhb
- zlanhe
- zlanhp
- zlanhs
- zlanht
- zlansb
- zlansp
- zlansy
- zlantb
- zlantp
- zlantr
- zlapll
- zlapmt
- zlaqgb
- zlaqge
- zlaqhb
- zlaqhe
- zlaqhp
- zlaqp2
- zlaqps
- zlaqr0
- zlaqr1
- zlaqr2
- zlaqr3
- zlaqr4
- zlaqr5
- zlaqsb
- zlaqsp
- zlaqsy
- zlar1v
- zlar2v

- zlarcm
- zlarf
- zlarfb
- zlarfg
- zlarft
- zlarfx
- zlargv
- zlarnv
- zlarrv
- zlartg
- zlartv
- zlarz
- zlarzb
- zlarzt
- zlascl
- zlaset
- zlasr
- zlassq
- zlaswp
- zlasyf
- zlatbs
- zlatdf
- zlatps
- zlatrd
- zlatrs
- zlatrz
- zlatzm
- zlauu2
- zlauum
- zpbcon
- zpbequ
- zpbrfs
- zpbstf
- zpbsv
- zpbsvx
- zpbtf2

- zpbtrf
- zpbtrs
- zpocon
- zpoequ
- zporfs
- zposv
- zposvx
- zpotf2
- zpotrf
- zpotri
- zpotrs
- zppcon
- zppequ
- zpprfs
- zppsv
- zppsvx
- zpptrf
- zpptri
- zpptrs
- zptcon
- zpteqr
- zptrfs
- zptsv
- zptsvx
- zpttrf
- zpttrs
- zptts2
- zrot
- zspcon
- zspmv
- zspr
- zsprfs
- zspsv
- zspsvx
- zsptrf
- zsptri

- zsptrs
- zstedc
- zstegr
- zstein
- zstemr
- zsteqr
- zsycon
- zsymv
- zsyr
- zsyrfs
- zsysv
- zsysvx
- zsytf2
- zsytrf
- zsytri
- zsytrs
- ztbcon
- ztbrfs
- ztbtrs
- ztgevc
- ztgex2
- ztgexc
- ztgsen
- ztgsja
- ztgsna
- ztgsy2
- ztgsyl
- ztpcon
- ztprfs
- ztptri
- ztptrs
- ztrcon
- ztrevc
- ztrexc
- ztrrfs
- ztrsen

- ztrsna
- ztrsyl
- ztrti2
- ztrtri
- ztrtrs
- ztzrqf
- ztzrzf
- zung2l
- zung2r
- zungbr
- zunghr
- zungl2
- zunglq
- zungql
- zungqr
- zungr2
- zungrq
- zungtr
- zunm2l
- zunm2r
- zunmbr
- zunmhr
- zunml2
- zunmlq
- zunmql
- zunmqr
- zunmr2
- zunmr3
- zunmrq
- zunmrz
- zunmtr
- zupgtr
- zupmtr

5.20 Interpolative matrix decomposition (`scipy.linalg.interpolative`)

New in version 0.13.

An interpolative decomposition (ID) of a matrix $A \in C^{m \times n}$ of rank $k \leq \min\{m, n\}$ is a factorization

$$A\Pi = \begin{bmatrix} A\Pi_1 & A\Pi_2 \end{bmatrix} = A\Pi_1 \begin{bmatrix} I & T \end{bmatrix},$$

where $\Pi = [\Pi_1, \Pi_2]$ is a permutation matrix with $\Pi_1 \in \{0, 1\}^{n \times k}$, i.e., $A\Pi_2 = A\Pi_1 T$. This can equivalently be written as $A = BP$, where $B = A\Pi_1$ and $P = [I, T]\Pi^{\mathsf{T}}$ are the *skeleton* and *interpolation matrices*, respectively.

If A does not have exact rank k, then there exists an approximation in the form of an ID such that $A = BP + E$, where $\|E\| \sim \sigma_{k+1}$ is on the order of the $(k+1)$-th largest singular value of A. Note that σ_{k+1} is the best possible error for a rank-k approximation and, in fact, is achieved by the singular value decomposition (SVD) $A \approx USV^*$, where $U \in C^{m \times k}$ and $V \in C^{n \times k}$ have orthonormal columns and $S = \mathrm{diag}(\sigma_i) \in C^{k \times k}$ is diagonal with nonnegative entries. The principal advantages of using an ID over an SVD are that:

- it is cheaper to construct;
- it preserves the structure of A; and
- it is more efficient to compute with in light of the identity submatrix of P.

5.20.1 Routines

Main functionality:

`interp_decomp`(A, eps_or_k[, rand])	Compute ID of a matrix.
`reconstruct_matrix_from_id`(B, idx, proj)	Reconstruct matrix from its ID.
`reconstruct_interp_matrix`(idx, proj)	Reconstruct interpolation matrix from ID.
`reconstruct_skel_matrix`(A, k, idx)	Reconstruct skeleton matrix from ID.
`id_to_svd`(B, idx, proj)	Convert ID to SVD.
`svd`(A, eps_or_k[, rand])	Compute SVD of a matrix via an ID.
`estimate_spectral_norm`(A[, its])	Estimate spectral norm of a matrix by the randomized power method.
`estimate_spectral_norm_diff`(A, B[, its])	Estimate spectral norm of the difference of two matrices by the randomized po
`estimate_rank`(A, eps)	Estimate matrix rank to a specified relative precision using randomized metho

`scipy.linalg.interpolative.`**`interp_decomp`**(*A*, *eps_or_k*, *rand=True*)

Compute ID of a matrix.

An ID of a matrix *A* is a factorization defined by a rank *k*, a column index array *idx*, and interpolation coefficients *proj* such that:

```
numpy.dot(A[:,idx[:k]], proj) = A[:,idx[k:]]
```

The original matrix can then be reconstructed as:

```
numpy.hstack([A[:,idx[:k]],
                              numpy.dot(A[:,idx[:k]], proj)]
                         )[:,numpy.argsort(idx)]
```

or via the routine `reconstruct_matrix_from_id`. This can equivalently be written as:

```
numpy.dot(A[:,idx[:k]],
                    numpy.hstack([numpy.eye(k), proj])
                  )[:,np.argsort(idx)]
```

in terms of the skeleton and interpolation matrices:

```
B = A[:,idx[:k]]
```

and:

```
P = numpy.hstack([numpy.eye(k), proj])[:,np.argsort(idx)]
```

respectively. See also `reconstruct_interp_matrix` and `reconstruct_skel_matrix`.

The ID can be computed to any relative precision or rank (depending on the value of *eps_or_k*). If a precision is specified (*eps_or_k* < *1*), then this function has the output signature:

```
k, idx, proj = interp_decomp(A, eps_or_k)
```

Otherwise, if a rank is specified (*eps_or_k* >= *1*), then the output signature is:

```
idx, proj = interp_decomp(A, eps_or_k)
```

Parameters

A : `numpy.ndarray` or `scipy.sparse.linalg.LinearOperator` with *rmatvec*

Matrix to be factored

eps_or_k : float or int

Relative error (if *eps_or_k* < *1*) or rank (if *eps_or_k* >= *1*) of approximation.

rand : bool, optional

Whether to use random sampling if *A* is of type `numpy.ndarray` (randomized algorithms are always used if *A* is of type `scipy.sparse.linalg.LinearOperator`).

Returns

k : int

Rank required to achieve specified relative precision if *eps_or_k* < *1*.

idx : `numpy.ndarray`

Column index array.

proj : `numpy.ndarray`

Interpolation coefficients.

`scipy.linalg.interpolative.`**`reconstruct_matrix_from_id`**(*B*, *idx*, *proj*)

Reconstruct matrix from its ID.

A matrix *A* with skeleton matrix *B* and ID indices and coefficients *idx* and *proj*, respectively, can be reconstructed as:

```
numpy.hstack([B, numpy.dot(B, proj)])[:,numpy.argsort(idx)]
```

See also `reconstruct_interp_matrix` and `reconstruct_skel_matrix`.

Parameters

B : `numpy.ndarray`

Skeleton matrix.

idx : `numpy.ndarray`

Column index array.

proj : `numpy.ndarray`

Interpolation coefficients.

Returns

`numpy.ndarray`

Reconstructed matrix.

`scipy.linalg.interpolative.`**`reconstruct_interp_matrix`**(*idx*, *proj*)

Reconstruct interpolation matrix from ID.

The interpolation matrix can be reconstructed from the ID indices and coefficients *idx* and *proj*, respectively, as:

```
P = numpy.hstack([numpy.eye(proj.shape[0]), proj])[:,numpy.argsort(idx)]
```

The original matrix can then be reconstructed from its skeleton matrix *B* via:

```
numpy.dot(B, P)
```

See also `reconstruct_matrix_from_id` and `reconstruct_skel_matrix`.

Parameters	**idx** : `numpy.ndarray` Column index array. **proj** : `numpy.ndarray` Interpolation coefficients.
Returns	`numpy.ndarray` Interpolation matrix.

`scipy.linalg.interpolative.`**`reconstruct_skel_matrix`**(*A*, *k*, *idx*)

Reconstruct skeleton matrix from ID.

The skeleton matrix can be reconstructed from the original matrix *A* and its ID rank and indices *k* and *idx*, respectively, as:

```
B = A[:,idx[:k]]
```

The original matrix can then be reconstructed via:

```
numpy.hstack([B, numpy.dot(B, proj)])[:,numpy.argsort(idx)]
```

See also `reconstruct_matrix_from_id` and `reconstruct_interp_matrix`.

Parameters	**A** : `numpy.ndarray` Original matrix. **k** : int Rank of ID. **idx** : `numpy.ndarray` Column index array.
Returns	`numpy.ndarray` Skeleton matrix.

`scipy.linalg.interpolative.`**`id_to_svd`**(*B*, *idx*, *proj*)

Convert ID to SVD.

The SVD reconstruction of a matrix with skeleton matrix *B* and ID indices and coefficients *idx* and *proj*, respectively, is:

```
U, S, V = id_to_svd(B, idx, proj)
A = numpy.dot(U, numpy.dot(numpy.diag(S), V.conj().T))
```

See also `svd`.

Parameters	**B** : `numpy.ndarray` Skeleton matrix. **idx** : `numpy.ndarray` Column index array. **proj** : `numpy.ndarray` Interpolation coefficients.
Returns	**U** : `numpy.ndarray` Left singular vectors. **S** : `numpy.ndarray` Singular values. **V** : `numpy.ndarray`

Right singular vectors.

`scipy.linalg.interpolative.`**`svd`**`(`*A*, *eps_or_k*, *rand=True*`)`

Compute SVD of a matrix via an ID.

An SVD of a matrix *A* is a factorization:

```
A = numpy.dot(U, numpy.dot(numpy.diag(S), V.conj().T))
```

where *U* and *V* have orthonormal columns and *S* is nonnegative.

The SVD can be computed to any relative precision or rank (depending on the value of *eps_or_k*).

See also `interp_decomp` and `id_to_svd`.

Parameters

A : `numpy.ndarray` or `scipy.sparse.linalg.LinearOperator`

Matrix to be factored, given as either a `numpy.ndarray` or a `scipy.sparse.linalg.LinearOperator` with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

eps_or_k : float or int

Relative error (if *eps_or_k* < *1*) or rank (if *eps_or_k* >= *1*) of approximation.

rand : bool, optional

Whether to use random sampling if *A* is of type `numpy.ndarray` (randomized algorithms are always used if *A* is of type `scipy.sparse.linalg.LinearOperator`).

Returns

U : `numpy.ndarray`

Left singular vectors.

S : `numpy.ndarray`

Singular values.

V : `numpy.ndarray`

Right singular vectors.

`scipy.linalg.interpolative.`**`estimate_spectral_norm`**`(`*A*, *its=20*`)`

Estimate spectral norm of a matrix by the randomized power method.

Parameters

A : `scipy.sparse.linalg.LinearOperator`

Matrix given as a `scipy.sparse.linalg.LinearOperator` with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

its : int, optional

Number of power method iterations.

Returns

float

Spectral norm estimate.

`scipy.linalg.interpolative.`**`estimate_spectral_norm_diff`**`(`*A*, *B*, *its=20*`)`

Estimate spectral norm of the difference of two matrices by the randomized power method.

Parameters

A : `scipy.sparse.linalg.LinearOperator`

First matrix given as a `scipy.sparse.linalg.LinearOperator` with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

B : `scipy.sparse.linalg.LinearOperator`

Second matrix given as a `scipy.sparse.linalg.LinearOperator` with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

its : int, optional

Number of power method iterations.

Returns

float

Spectral norm estimate of matrix difference.

`scipy.linalg.interpolative.`**`estimate_rank`**`(`*A*, *eps*`)`

Estimate matrix rank to a specified relative precision using randomized methods.

The matrix *A* can be given as either a `numpy.ndarray` or a `scipy.sparse.linalg.LinearOperator`, with different algorithms used for each case. If *A* is of type `numpy.ndarray`, then the output rank is typically about 8 higher than the actual numerical rank.

Parameters **A** : `numpy.ndarray` or `scipy.sparse.linalg.LinearOperator`

Matrix whose rank is to be estimated, given as either a `numpy.ndarray` or a `scipy.sparse.linalg.LinearOperator` with the *rmatvec* method (to apply the matrix adjoint).

eps : float

Relative error for numerical rank definition.

Returns int

Estimated matrix rank.

Support functions:

`seed`([seed])	Seed the internal random number generator used in this ID package.
`rand`(*shape)	Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.

`scipy.linalg.interpolative.`**`seed`**`(`*seed=None*`)`

Seed the internal random number generator used in this ID package.

The generator is a lagged Fibonacci method with 55-element internal state.

Parameters **seed** : int, sequence, 'default', optional

If 'default', the random seed is reset to a default value.

If `seed` is a sequence containing 55 floating-point numbers in range [0,1], these are used to set the internal state of the generator.

If the value is an integer, the internal state is obtained from `numpy.random.RandomState` (MT19937) with the integer used as the initial seed.

If `seed` is omitted (None), `numpy.random` is used to initialize the generator.

`scipy.linalg.interpolative.`**`rand`**`(`**shape*`)`

Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.

This routine is used for all random number generation in this package and can affect ID and SVD results.

Parameters **shape**

Shape of output array

5.20.2 References

This module uses the ID software package [R439] by Martinsson, Rokhlin, Shkolnisky, and Tygert, which is a Fortran library for computing IDs using various algorithms, including the rank-revealing QR approach of [R440] and the more recent randomized methods described in [R441], [R442], and [R443]. This module exposes its functionality in a way convenient for Python users. Note that this module does not add any functionality beyond that of organizing a simpler and more consistent interface.

We advise the user to consult also the documentation for the ID package.

5.20.3 Tutorial

Initializing

The first step is to import `scipy.linalg.interpolative` by issuing the command:

```
>>> import scipy.linalg.interpolative as sli
```

Now let's build a matrix. For this, we consider a Hilbert matrix, which is well know to have low rank:

```
>>> from scipy.linalg import hilbert
>>> n = 1000
>>> A = hilbert(n)
```

We can also do this explicitly via:

```
>>> import numpy as np
>>> n = 1000
>>> A = np.empty((n, n), order='F')
>>> for j in range(n):
>>>     for i in range(m):
>>>         A[i,j] = 1. / (i + j + 1)
```

Note the use of the flag `order='F'` in `numpy.empty`. This instantiates the matrix in Fortran-contiguous order and is important for avoiding data copying when passing to the backend.

We then define multiplication routines for the matrix by regarding it as a `scipy.sparse.linalg.LinearOperator`:

```
>>> from scipy.sparse.linalg import aslinearoperator
>>> L = aslinearoperator(A)
```

This automatically sets up methods describing the action of the matrix and its adjoint on a vector.

Computing an ID

We have several choices of algorithm to compute an ID. These fall largely according to two dichotomies:

1. how the matrix is represented, i.e., via its entries or via its action on a vector; and
2. whether to approximate it to a fixed relative precision or to a fixed rank.

We step through each choice in turn below.

In all cases, the ID is represented by three parameters:

1. a rank `k`;
2. an index array `idx`; and
3. interpolation coefficients `proj`.

The ID is specified by the relation `np.dot(A[:,idx[:k]], proj) == A[:,idx[k:]]`.

From matrix entries

We first consider a matrix given in terms of its entries.

To compute an ID to a fixed precision, type:

```
>>> k, idx, proj = sli.interp_decomp(A, eps)
```

where `eps < 1` is the desired precision.

To compute an ID to a fixed rank, use:

```
>>> idx, proj = sli.interp_decomp(A, k)
```

where `k >= 1` is the desired rank.

Both algorithms use random sampling and are usually faster than the corresponding older, deterministic algorithms, which can be accessed via the commands:

```
>>> k, idx, proj = sli.interp_decomp(A, eps, rand=False)
```

and:

```
>>> idx, proj = sli.interp_decomp(A, k, rand=False)
```

respectively.

From matrix action

Now consider a matrix given in terms of its action on a vector as a `scipy.sparse.linalg.LinearOperator`.

To compute an ID to a fixed precision, type:

```
>>> k, idx, proj = sli.interp_decomp(L, eps)
```

To compute an ID to a fixed rank, use:

```
>>> idx, proj = sli.interp_decomp(L, k)
```

These algorithms are randomized.

Reconstructing an ID

The ID routines above do not output the skeleton and interpolation matrices explicitly but instead return the relevant information in a more compact (and sometimes more useful) form. To build these matrices, write:

```
>>> B = sli.reconstruct_skel_matrix(A, k, idx)
```

for the skeleton matrix and:

```
>>> P = sli.reconstruct_interp_matrix(idx, proj)
```

for the interpolation matrix. The ID approximation can then be computed as:

```
>>> C = np.dot(B, P)
```

This can also be constructed directly using:

```
>>> C = sli.reconstruct_matrix_from_id(B, idx, proj)
```

without having to first compute `P`.

Alternatively, this can be done explicitly as well using:

```
>>> B = A[:,idx[:k]]
>>> P = np.hstack([np.eye(k), proj])[:,np.argsort(idx)]
>>> C = np.dot(B, P)
```

Computing an SVD

An ID can be converted to an SVD via the command:

```
>>> U, S, V = sli.id_to_svd(B, idx, proj)
```

The SVD approximation is then:

```
>>> C = np.dot(U, np.dot(np.diag(S), np.dot(V.conj().T)))
```

The SVD can also be computed "fresh" by combining both the ID and conversion steps into one command. Following the various ID algorithms above, there are correspondingly various SVD algorithms that one can employ.

From matrix entries

We consider first SVD algorithms for a matrix given in terms of its entries.

To compute an SVD to a fixed precision, type:

```
>>> U, S, V = sli.svd(A, eps)
```

To compute an SVD to a fixed rank, use:

```
>>> U, S, V = sli.svd(A, k)
```

Both algorithms use random sampling; for the determinstic versions, issue the keyword `rand=False` as above.

From matrix action

Now consider a matrix given in terms of its action on a vector.

To compute an SVD to a fixed precision, type:

```
>>> U, S, V = sli.svd(L, eps)
```

To compute an SVD to a fixed rank, use:

```
>>> U, S, V = sli.svd(L, k)
```

Utility routines

Several utility routines are also available.

To estimate the spectral norm of a matrix, use:

```
>>> snorm = sli.estimate_spectral_norm(A)
```

This algorithm is based on the randomized power method and thus requires only matrix-vector products. The number of iterations to take can be set using the keyword `its` (default: `its=20`). The matrix is interpreted as a `scipy.sparse.linalg.LinearOperator`, but it is also valid to supply it as a `numpy.ndarray`, in which case it is trivially converted using `scipy.sparse.linalg.aslinearoperator`.

The same algorithm can also estimate the spectral norm of the difference of two matrices `A1` and `A2` as follows:

```
>>> diff = sli.estimate_spectral_norm_diff(A1, A2)
```

This is often useful for checking the accuracy of a matrix approximation.

Some routines in `scipy.linalg.interpolative` require estimating the rank of a matrix as well. This can be done with either:

```
>>> k = sli.estimate_rank(A, eps)
```

or:

```
>>> k = sli.estimate_rank(L, eps)
```

depending on the representation. The parameter `eps` controls the definition of the numerical rank.

Finally, the random number generation required for all randomized routines can be controlled via `scipy.linalg.interpolative.seed`. To reset the seed values to their original values, use:

```
>>> sli.seed('default')
```

To specify the seed values, use:

```
>>> sli.seed(s)
```

where `s` must be an integer or array of 55 floats. If an integer, the array of floats is obtained by using `np.random.rand` with the given integer seed.

To simply generate some random numbers, type:

```
>>> sli.rand(n)
```

where `n` is the number of random numbers to generate.

Remarks

The above functions all automatically detect the appropriate interface and work with both real and complex data types, passing input arguments to the proper backend routine.

5.21 Miscellaneous routines (`scipy.misc`)

Various utilities that don't have another home.

Note that the Python Imaging Library (PIL) is not a dependency of SciPy and therefore the `pilutil` module is not available on systems that don't have PIL installed.

`ascent`()	Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos
`bytescale`(data[, cmin, cmax, high, low])	Byte scales an array (image).
`central_diff_weights`(Np[, ndiv])	Return weights for an Np-point central derivative.
`comb`(N, k[, exact, repetition])	The number of combinations of N things taken k at a time.
`derivative`(func, x0[, dx, n, args, order])	Find the n-th derivative of a function at a point.
`face`([gray])	Get a 1024 x 768, color image of a raccoon face.
`factorial`(n[, exact])	The factorial function, n! = special.gamma(n+1).
`factorial2`(n[, exact])	Double factorial.
`factorialk`(n, k[, exact])	n(!!...!) = multifactorial of order k
`fromimage`(im[, flatten])	Return a copy of a PIL image as a numpy array.
`imfilter`(arr, ftype)	Simple filtering of an image.
`imread`(name[, flatten])	Read an image from a file as an array.
`imresize`(arr, size[, interp, mode])	Resize an image.
`imrotate`(arr, angle[, interp])	Rotate an image counter-clockwise by angle degrees.
`imsave`(name, arr[, format])	Save an array as an image.
`imshow`(arr)	Simple showing of an image through an external viewer.
`info`([object, maxwidth, output, toplevel])	Get help information for a function, class, or module.
`lena`()	Get classic image processing example image, Lena, at 8-bit grayscale bit-depth, 512
`logsumexp`(a[, axis, b, keepdims])	Compute the log of the sum of exponentials of input elements.
`pade`(an, m)	Return Pade approximation to a polynomial as the ratio of two polynomials.
`toimage`(arr[, high, low, cmin, cmax, pal, ...])	Takes a numpy array and returns a PIL image.
`who`([vardict])	Print the Numpy arrays in the given dictionary.

`scipy.misc.`**`ascent`**`()`

Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos

The image is derived from accent-to-the-top.jpg at http://www.public-domain-image.com/people-public-domain-images-pictures/

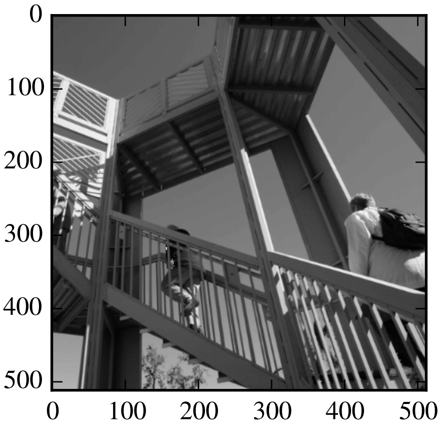
Parameters **None**

Returns **ascent** : ndarray

convenient image to use for testing and demonstration

Examples

```
>>> import scipy.misc
>>> ascent = scipy.misc.ascent()
>>> ascent.shape
(512, 512)
>>> ascent.max()
255

>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(ascent)
>>> plt.show()
```



`scipy.misc.`**`bytescale`**(*data*, *cmin=None*, *cmax=None*, *high=255*, *low=0*)

Byte scales an array (image).

Byte scaling means converting the input image to uint8 dtype and scaling the range to `(low, high)` (default 0-255). If the input image already has dtype uint8, no scaling is done.

Parameters	**data** : ndarray PIL image data array. **cmin** : scalar, optional Bias scaling of small values. Default is `data.min()`. **cmax** : scalar, optional Bias scaling of large values. Default is `data.max()`. **high** : scalar, optional Scale max value to *high*. Default is 255. **low** : scalar, optional Scale min value to *low*. Default is 0.
Returns	**img_array** : uint8 ndarray The byte-scaled array.

Examples

```
>>> img = array([[ 91.06794177,   3.39058326,  84.4221549 ],
                 [ 73.88003259,  80.91433048,   4.88878881],
                 [ 51.53875334,  34.45808177,  27.5873488 ]])
>>> bytescale(img)
array([[255,   0, 236],
       [205, 225,   4],
       [140,  90,  70]], dtype=uint8)
>>> bytescale(img, high=200, low=100)
array([[200, 100, 192],
       [180, 188, 102],
       [155, 135, 128]], dtype=uint8)
>>> bytescale(img, cmin=0, cmax=255)
array([[91,  3, 84],
       [74, 81,  5],
       [52, 34, 28]], dtype=uint8)
```

`scipy.misc.`**`central_diff_weights`**(*Np*, *ndiv=1*)

Return weights for an Np-point central derivative.

Assumes equally-spaced function points.

If weights are in the vector w, then derivative is w[0] * f(x-ho*dx) + ... + w[-1] * f(x+h0*dx)

Parameters **Np** : int

Number of points for the central derivative.

ndiv : int, optional

Number of divisions. Default is 1.

Notes

Can be inaccurate for large number of points.

`scipy.misc.`**`comb`**(*N*, *k*, *exact=False*, *repetition=False*)

The number of combinations of N things taken k at a time.

This is often expressed as "N choose k".

Parameters **N** : int, ndarray

Number of things.

k : int, ndarray

Number of elements taken.

exact : bool, optional

If *exact* is False, then floating point precision is used, otherwise exact long integer is computed.

repetition : bool, optional

If *repetition* is True, then the number of combinations with repetition is computed.

Returns **val** : int, ndarray

The total number of combinations.

Notes

- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

```
>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([ 120.,  210.])
>>> comb(10, 3, exact=True)
120L
>>> comb(10, 3, exact=True, repetition=True)
220L
```

`scipy.misc.`**`derivative`**(*func*, *x0*, *dx=1.0*, *n=1*, *args=()*, *order=3*)

Find the n-th derivative of a function at a point.

Given a function, use a central difference formula with spacing *dx* to compute the *n*-th derivative at *x0*.

Parameters **func** : function

Input function.

x0 : float

The point at which *n*-th derivative is found.

dx : int, optional

Spacing.

n : int, optional
Order of the derivative. Default is 1.

args : tuple, optional
Arguments

order : int, optional
Number of points to use, must be odd.

Notes

Decreasing the step size too small can result in round-off error.

Examples

```
>>> def f(x):
...     return x**3 + x**2
...
>>> derivative(f, 1.0, dx=1e-6)
4.9999999999217337
```

`scipy.misc.`**`face`**`(`*gray=False*`)`

Get a 1024 x 768, color image of a raccoon face.

raccoon-procyon-lotor.jpg at http://www.public-domain-image.com

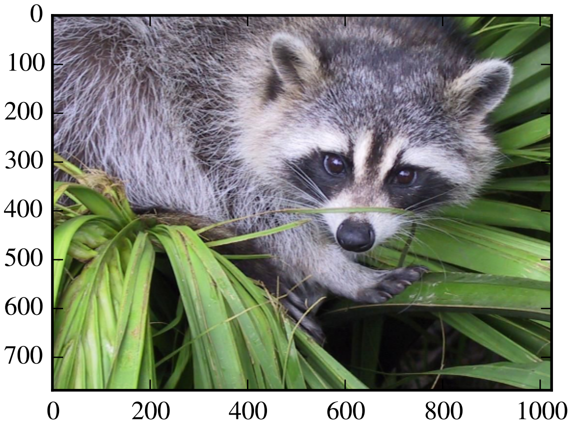
Parameters **gray** : bool, optional
If True then return color image, otherwise return an 8-bit gray-scale

Returns **face** : ndarray
image of a racoon face

Examples

```
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> face.shape
(768, 1024, 3)
>>> face.max()
230
>>> face.dtype
dtype('uint8')
```

```
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(face)
>>> plt.show()
```



`scipy.misc.`**`factorial`**`(`*n*, *exact=False*`)`

The factorial function, n! = special.gamma(n+1).

If exact is 0, then floating point precision is used, otherwise exact long integer is computed.

- Array argument accepted only for exact=False case.
- If n<0, the return value is 0.

Parameters **n** : int or array_like of ints

Calculate `n!`. Arrays are only supported with *exact* set to False. If `n < 0`, the return value is 0.

exact : bool, optional

The result can be approximated rapidly using the gamma-formula above. If *exact* is set to True, calculate the answer exactly using integer arithmetic. Default is False.

Returns **nf** : float or int

Factorial of *n*, as an integer or a float depending on *exact*.

Examples

```
>>> from scipy.special import factorial
>>> arr = np.array([3,4,5])
>>> factorial(arr, exact=False)
array([   6.,   24.,  120.])
>>> factorial(5, exact=True)
120L
```

`scipy.misc.`**`factorial2`**`(`*n*, *exact=False*`)`

Double factorial.

This is the factorial with every second value skipped, i.e., `7!! = 7 * 5 * 3 * 1`. It can be approximated numerically as:

```
n!! = special.gamma(n/2+1)*2**((m+1)/2)/sqrt(pi)  n odd
    = 2**(n/2) * (n/2)!                           n even
```

Parameters **n** : int or array_like

Calculate `n!!`. Arrays are only supported with *exact* set to False. If `n < 0`, the return value is 0.

exact : bool, optional
The result can be approximated rapidly using the gamma-formula above (default). If *exact* is set to True, calculate the answer exactly using integer arithmetic.

Returns **nff** : float or int
Double factorial of *n*, as an int or a float depending on *exact*.

Examples

```
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
array(105.00000000000001)
>>> factorial2(7, exact=True)
105L
```

`scipy.misc.`**`factorialk`**(*n*, *k*, *exact=True*)

n(!!...!) = multifactorial of order k k times

Parameters **n** : int
Calculate multifactorial. If $n < 0$, the return value is 0.

k : int
Order of multifactorial.

exact : bool, optional
If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns **val** : int
Multi factorial of *n*.

Raises **NotImplementedError**
Raises when exact is False

Examples

```
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120L
>>> factorialk(5, 3, exact=True)
10L
```

`scipy.misc.`**`fromimage`**(*im*, *flatten=0*)

Return a copy of a PIL image as a numpy array.

Parameters **im** : PIL image
Input image.

flatten : bool
If true, convert the output to grey-scale.

Returns **fromimage** : ndarray
The different colour bands/channels are stored in the third dimension, such that a grey-image is MxN, an RGB-image MxNx3 and an RGBA-image MxNx4.

`scipy.misc.`**`imfilter`**(*arr*, *ftype*)

Simple filtering of an image.

Parameters **arr** : ndarray
The array of Image in which the filter is to be applied.

ftype : str
The filter that has to be applied. Legal values are: ‘blur’, ‘contour’, ‘detail’, ‘edge_enhance’, ‘edge_enhance_more’, ‘emboss’, ‘find_edges’, ‘smooth’, ‘smooth_more’, ‘sharpen’.

Returns **imfilter** : ndarray
The array with filter applied.

Raises **ValueError**
Unknown filter type. If the filter you are trying to apply is unsupported.

`scipy.misc.`**`imread`**(*name*, *flatten=0*)
Read an image from a file as an array.

Parameters **name** : str or file object
The file name or file object to be read.
flatten : bool, optional
If True, flattens the color layers into a single gray-scale layer.

Returns **imread** : ndarray
The array obtained by reading image from file *imfile*.

Notes

The image is flattened by calling convert('F') on the resulting image object.

`scipy.misc.`**`imresize`**(*arr*, *size*, *interp='bilinear'*, *mode=None*)
Resize an image.

Parameters **arr** : ndarray
The array of image to be resized.
size : int, float or tuple
- int - Percentage of current size.
- float - Fraction of current size.
- tuple - Size of the output image.

interp : str, optional
Interpolation to use for re-sizing ('nearest', 'bilinear', 'bicubic' or 'cubic').
mode : str, optional
The PIL image mode ('P', 'L', etc.) to convert *arr* before resizing.

Returns **imresize** : ndarray
The resized array of image.

See also:

`toimage` Implicitly used to convert *arr* according to *mode*.

`scipy.ndimage.zoom`
More generic implementation that does not use PIL.

`scipy.misc.`**`imrotate`**(*arr*, *angle*, *interp='bilinear'*)
Rotate an image counter-clockwise by angle degrees.

Parameters **arr** : ndarray
Input array of image to be rotated.
angle : float
The angle of rotation.
interp : str, optional
Interpolation
- 'nearest' : for nearest neighbor
- 'bilinear' : for bilinear
- 'cubic' : cubic
- 'bicubic' : for bicubic

Returns **imrotate** : ndarray
The rotated array of image.

`scipy.misc.`**`imsave`**(*name*, *arr*, *format=None*)
Save an array as an image.

Parameters **name** : str or file object
Output file name or file object.
arr : ndarray, MxN or MxNx3 or MxNx4
Array containing image values. If the shape is `MxN`, the array represents a grey-level image. Shape `MxNx3` stores the red, green and blue bands along the last dimension. An alpha layer may be included, specified as the last colour band of an `MxNx4` array.
format : str
Image format. If omitted, the format to use is determined from the file name extension. If a file object was used instead of a file name, this parameter should always be used.

Examples

Construct an array of gradient intensity values and save to file:

```
>>> x = np.zeros((255, 255))
>>> x = np.zeros((255, 255), dtype=np.uint8)
>>> x[:] = np.arange(255)
>>> imsave('/tmp/gradient.png', x)
```

Construct an array with three colour bands (R, G, B) and store to file:

```
>>> rgb = np.zeros((255, 255, 3), dtype=np.uint8)
>>> rgb[..., 0] = np.arange(255)
>>> rgb[..., 1] = 55
>>> rgb[..., 2] = 1 - np.arange(255)
>>> imsave('/tmp/rgb_gradient.png', rgb)
```

`scipy.misc.`**`imshow`**`(`*arr*`)`

Simple showing of an image through an external viewer.

Uses the image viewer specified by the environment variable SCIPY_PIL_IMAGE_VIEWER, or if that is not defined then *see*, to view a temporary file generated from array data.

Parameters **arr** : ndarray
Array of image data to show.
Returns None

Examples

```
>>> a = np.tile(np.arange(255), (255,1))
>>> from scipy import misc
>>> misc.pilutil.imshow(a)
```

`scipy.misc.`**`info`**`(`*object=None, maxwidth=76, output=<open file '<stdout>', mode 'w' at 0x7fa42a301150>, toplevel='scipy'*`)`

Get help information for a function, class, or module.

Parameters **object** : object or str, optional
Input object or name to get information about. If *object* is a numpy object, its docstring is given. If it is a string, available modules are searched for matching objects. If None, information about `info` itself is returned.
maxwidth : int, optional
Printing width.
output : file like object, optional
File like object that the output is written to, default is `stdout`. The object has to be opened in 'w' or 'a' mode.
toplevel : str, optional
Start search at this level.

See also:

`source`, `lookfor`

Notes

When used interactively with an object, `np.info(obj)` is equivalent to `help(obj)` on the Python prompt or `obj?` on the IPython prompt.

Examples

```
>>> np.info(np.polyval)
   polyval(p, x)
     Evaluate the polynomial p at x.
     ...
```

When using a string for *object* it is possible to get multiple results.

```
>>> np.info('fft')
     *** Found in numpy ***
Core FFT routines
...
     *** Found in numpy.fft ***
 fft(a, n=None, axis=-1)
...
     *** Repeat reference found in numpy.fft.fftpack ***
     *** Total of 3 references found. ***
```

`scipy.misc.`**`lena`**`()`

Get classic image processing example image, Lena, at 8-bit grayscale bit-depth, 512 x 512 size.

Parameters	**None**
Returns	**lena** : ndarray Lena image

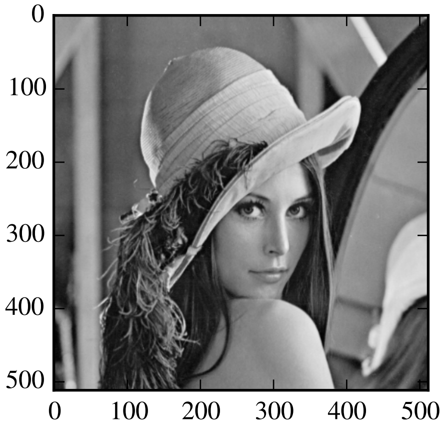
Notes

Though safe for work in most places, this sexualized image is drawn from Playboy and makes some viewers uncomfortable. It has been very widely used as an example in image processing and is therefore made available for compatibility. For new code that needs an example image we recommend `face` or `ascent`.

Examples

```
>>> import scipy.misc
>>> lena = scipy.misc.lena()
>>> lena.shape
(512, 512)
>>> lena.max()
245
>>> lena.dtype
dtype('int32')
```

```
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(lena)
>>> plt.show()
```



`scipy.misc.`**`logsumexp`**`(`*a*, *axis=None*, *b=None*, *keepdims=False*`)`

Compute the log of the sum of exponentials of input elements.

Parameters

a : array_like

Input array.

axis : None or int or tuple of ints, optional

Axis or axes over which the sum is taken. By default *axis* is None, and all elements are summed. Tuple of ints is not accepted if NumPy version is lower than 1.7.0.

New in version 0.11.0.

keepdims : bool, optional

If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array.

New in version 0.15.0.

b : array-like, optional

Scaling factor for exp(*a*) must be of the same shape as *a* or broadcastable to *a*.

New in version 0.12.0.

Returns

res : ndarray

The result, `np.log(np.sum(np.exp(a)))` calculated in a numerically more stable way. If *b* is given then `np.log(np.sum(b*np.exp(a)))` is returned.

See also:

`numpy.logaddexp`, `numpy.logaddexp2`

Notes

Numpy has a logaddexp function which is very similar to `logsumexp`, but only handles two arguments. *logaddexp.reduce* is similar to this function, but may be less stable.

Examples

```
>>> from scipy.misc import logsumexp
>>> a = np.arange(10)
>>> np.log(np.sum(np.exp(a)))
9.4586297444267107
>>> logsumexp(a)
9.4586297444267107
```

With weights

```
>>> a = np.arange(10)
>>> b = np.arange(10, 0, -1)
>>> logsumexp(a, b=b)
9.9170178533034665
>>> np.log(np.sum(b*np.exp(a)))
9.9170178533034647
```

`scipy.misc.`**`pade`**(*an*, *m*)

Return Pade approximation to a polynomial as the ratio of two polynomials.

Parameters **an** : (N,) array_like

Taylor series coefficients.

m : int

The order of the returned approximating polynomials.

Returns **p, q** : Polynomial class

The pade approximation of the polynomial defined by *an* is *p(x)/q(x)*.

Examples

```
>>> from scipy import misc
>>> e_exp = [1.0, 1.0, 1.0/2.0, 1.0/6.0, 1.0/24.0, 1.0/120.0]
>>> p, q = misc.pade(e_exp, 2)

>>> e_exp.reverse()
>>> e_poly = np.poly1d(e_exp)
```

Compare `e_poly(x)` and the pade approximation `p(x)/q(x)`

```
>>> e_poly(1)
2.7166666666666668

>>> p(1)/q(1)
2.7179487179487181
```

`scipy.misc.`**`toimage`**(*arr*, *high=255*, *low=0*, *cmin=None*, *cmax=None*, *pal=None*, *mode=None*, *channel_axis=None*)

Takes a numpy array and returns a PIL image.

The mode of the PIL image depends on the array shape and the *pal* and *mode* keywords.

For 2-D arrays, if *pal* is a valid (N,3) byte-array giving the RGB values (from 0 to 255) then `mode='P'`, otherwise `mode='L'`, unless mode is given as ‘F’ or ‘I’ in which case a float and/or integer array is made.

Notes

For 3-D arrays, the *channel_axis* argument tells which dimension of the array holds the channel data.

For 3-D arrays if one of the dimensions is 3, the mode is ‘RGB’ by default or ‘YCbCr’ if selected.

The numpy array must be either 2 dimensional or 3 dimensional.

`scipy.misc.`**`who`**(*vardict=None*)

Print the Numpy arrays in the given dictionary.

If there is no dictionary passed in or *vardict* is None then returns Numpy arrays in the globals() dictionary (all Numpy arrays in the namespace).

Parameters **vardict** : dict, optional

A dictionary possibly containing ndarrays. Default is globals().

Returns **out** : None

Returns 'None'.

Notes

Prints out the name, shape, bytes and type of all of the ndarrays present in *vardict*.

Examples

```
>>> a = np.arange(10)
>>> b = np.ones(20)
>>> np.who()
Name            Shape            Bytes            Type
===========================================================
a               10               40               int32
b               20               160              float64
Upper bound on total bytes  =       200

>>> d = {'x': np.arange(2.0), 'y': np.arange(3.0), 'txt': 'Some str',
... 'idx':5}
>>> np.who(d)
Name            Shape            Bytes            Type
===========================================================
y               3                24               float64
x               2                16               float64
Upper bound on total bytes  =       40
```

5.22 Multi-dimensional image processing (`scipy.ndimage`)

This package contains various functions for multi-dimensional image processing.

5.22.1 Filters `scipy.ndimage.filters`

`convolve`(input, weights[, output, mode, ...])	Multidimensional convolution.
`convolve1d`(input, weights[, axis, output, ...])	Calculate a one-dimensional convolution along the given axis.
`correlate`(input, weights[, output, mode, ...])	Multi-dimensional correlation.
`correlate1d`(input, weights[, axis, output, ...])	Calculate a one-dimensional correlation along the given axis.
`gaussian_filter`(input, sigma[, order, ...])	Multidimensional Gaussian filter.
`gaussian_filter1d`(input, sigma[, axis, ...])	One-dimensional Gaussian filter.
`gaussian_gradient_magnitude`(input, sigma[, ...])	Multidimensional gradient magnitude using Gaussian derivatives.
`gaussian_laplace`(input, sigma[, output, ...])	Multidimensional Laplace filter using gaussian second derivatives.
`generic_filter`(input, function[, size, ...])	Calculates a multi-dimensional filter using the given function.
`generic_filter1d`(input, function, filter_size)	Calculate a one-dimensional filter along the given axis.
`generic_gradient_magnitude`(input, derivative)	Gradient magnitude using a provided gradient function.
`generic_laplace`(input, derivative2[, ...])	N-dimensional Laplace filter using a provided second derivative functio
`laplace`(input[, output, mode, cval])	N-dimensional Laplace filter based on approximate second derivatives.
`maximum_filter`(input[, size, footprint, ...])	Calculates a multi-dimensional maximum filter.
`maximum_filter1d`(input, size[, axis, ...])	Calculate a one-dimensional maximum filter along the given axis.
`median_filter`(input[, size, footprint, ...])	Calculates a multidimensional median filter.
`minimum_filter`(input[, size, footprint, ...])	Calculates a multi-dimensional minimum filter.
`minimum_filter1d`(input, size[, axis, ...])	Calculate a one-dimensional minimum filter along the given axis.
`percentile_filter`(input, percentile[, size, ...])	Calculates a multi-dimensional percentile filter.

Continued on next pag

Table 5.83 – continued from previous page

`prewitt`(input[, axis, output, mode, cval])	Calculate a Prewitt filter.
`rank_filter`(input, rank[, size, footprint, ...])	Calculates a multi-dimensional rank filter.
`sobel`(input[, axis, output, mode, cval])	Calculate a Sobel filter.
`uniform_filter`(input[, size, output, mode, ...])	Multi-dimensional uniform filter.
`uniform_filter1d`(input, size[, axis, ...])	Calculate a one-dimensional uniform filter along the given axis.

`scipy.ndimage.filters.`**`convolve`**(*input*, *weights*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional convolution.

The array is convolved with the given kernel.

Parameters **input** : array_like

Input array to filter.

weights : array_like

Array of weights, same number of dimensions as input

output : ndarray, optional

The *output* parameter passes an array in which to store the filter output.

mode : {'reflect','constant','nearest','mirror', 'wrap'}, optional

the *mode* parameter determines how the array borders are handled. For 'constant' mode, values beyond borders are set to be *cval*. Default is 'reflect'.

cval : scalar, optional

Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : array_like, optional

The *origin* parameter controls the placement of the filter. Default is 0.

Returns **result** : ndarray

The result of convolution of *input* with *weights*.

See also:

`correlate` Correlate an image with a kernel.

Notes

Each value in result is $C_i = \sum_j I_{i+j-k} W_j$, where W is the *weights* kernel, j is the n-D spatial index over W, I is the *input* and k is the coordinate of the center of W, specified by *origin* in the input parameters.

Examples

Perhaps the simplest case to understand is `mode='constant', cval=0.0`, because in this case borders (i.e. where the *weights* kernel, centered on any one value, extends beyond an edge of *input*.

```
>>> a = np.array([[1, 2, 0, 0],
....     [5, 3, 0, 4],
....     [0, 0, 0, 7],
....     [9, 3, 0, 0]])
>>> k = np.array([[1,1,1],[1,1,0],[1,0,0]])
>>> from scipy import ndimage
>>> ndimage.convolve(a, k, mode='constant', cval=0.0)
array([[11, 10,  7,  4],
       [10,  3, 11, 11],
       [15, 12, 14,  7],
       [12,  3,  7,  0]])
```

Setting `cval=1.0` is equivalent to padding the outer edge of *input* with 1.0's (and then extracting only the original region of the result).

```
>>> ndimage.convolve(a, k, mode='constant', cval=1.0)
array([[13, 11,  8,  7],
       [11,  3, 11, 14],
       [16, 12, 14, 10],
       [15,  6, 10,  5]])
```

With `mode='reflect'` (the default), outer values are reflected at the edge of *input* to fill in missing values.

```
>>> b = np.array([[2, 0, 0],
                  [1, 0, 0],
                  [0, 0, 0]])
>>> k = np.array([[0,1,0],[0,1,0],[0,1,0]])
>>> ndimage.convolve(b, k, mode='reflect')
array([[5, 0, 0],
       [3, 0, 0],
       [1, 0, 0]])
```

This includes diagonally at the corners.

```
>>> k = np.array([[1,0,0],[0,1,0],[0,0,1]])
>>> ndimage.convolve(b, k)
array([[4, 2, 0],
       [3, 2, 0],
       [1, 1, 0]])
```

With `mode='nearest'`, the single nearest value in to an edge in *input* is repeated as many times as needed to match the overlapping *weights*.

```
>>> c = np.array([[2, 0, 1],
                  [1, 0, 0],
                  [0, 0, 0]])
>>> k = np.array([[0, 1, 0],
                  [0, 1, 0],
                  [0, 1, 0],
                  [0, 1, 0],
                  [0, 1, 0]])
>>> ndimage.convolve(c, k, mode='nearest')
array([[7, 0, 3],
       [5, 0, 2],
       [3, 0, 1]])
```

`scipy.ndimage.filters.`**`convolve1d`**(*input*, *weights*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a one-dimensional convolution along the given axis.

The lines of the array along the given axis are convolved with the given weights.

Parameters **input** : array_like

Input array to filter.

weights : ndarray

One-dimensional sequence of numbers.

axis : int, optional

The axis of *input* along which to calculate. Default is -1.

output : array, optional

The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional

The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional

Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional

The *origin* parameter controls the placement of the filter. Default 0.0.

Returns **convolve1d** : ndarray

Convolved array with same shape as input

`scipy.ndimage.filters.`**`correlate`**(*input*, *weights*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional correlation.

The array is correlated with the given kernel.

Parameters **input** : array-like

input array to filter

weights : ndarray

array of weights, same number of dimensions as input

output : array, optional

The `output` parameter passes an array in which to store the filter output.

mode : {'reflect','constant','nearest','mirror', 'wrap'}, optional

The `mode` parameter determines how the array borders are handled, where `cval` is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional

Value to fill past edges of input if `mode` is 'constant'. Default is 0.0

origin : scalar, optional

The `origin` parameter controls the placement of the filter. Default 0

See also:

`convolve`	Convolve an image with a kernel.

`scipy.ndimage.filters.`**`correlate1d`**(*input*, *weights*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a one-dimensional correlation along the given axis.

The lines of the array along the given axis are correlated with the given weights.

Parameters **input** : array_like

Input array to filter.

weights : array

One-dimensional sequence of numbers.

axis : int, optional

The axis of *input* along which to calculate. Default is -1.

output : array, optional

The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional

The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional

Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional

The *origin* parameter controls the placement of the filter. Default 0.0.

`scipy.ndimage.filters.`**`gaussian_filter`**(*input*, *sigma*, *order=0*, *output=None*, *mode='reflect'*, *cval=0.0*, *truncate=4.0*)

Multidimensional Gaussian filter.

Parameters **input** : array_like

Input array to filter.

sigma : scalar or sequence of scalars
Standard deviation for Gaussian kernel. The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.

order : {0, 1, 2, 3} or sequence from same set, optional
The order of the filter along each axis is given as a sequence of integers, or as a single number. An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

truncate : float
Truncate the filter at this many standard deviations. Default is 4.0.

Returns **gaussian_filter** : ndarray
Returned array of same shape as *input*.

Notes

The multidimensional filter is implemented as a sequence of one-dimensional convolution filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

`scipy.ndimage.filters.`**`gaussian_filter1d`**(*input*, *sigma*, *axis=-1*, *order=0*, *output=None*, *mode='reflect'*, *cval=0.0*, *truncate=4.0*)

One-dimensional Gaussian filter.

Parameters **input** : array_like
Input array to filter.

sigma : scalar
standard deviation for Gaussian kernel

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

order : {0, 1, 2, 3}, optional
An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

truncate : float, optional
Truncate the filter at this many standard deviations. Default is 4.0.

Returns **gaussian_filter1d** : ndarray

`scipy.ndimage.filters.`**`gaussian_gradient_magnitude`**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*, ***kwargs*)

Multidimensional gradient magnitude using Gaussian derivatives.

Parameters **input** : array_like
Input array to filter.
sigma : scalar or sequence of scalars
The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes..
output : array, optional
The *output* parameter passes an array in which to store the filter output.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0
Extra keyword arguments will be passed to gaussian_filter().

`scipy.ndimage.filters.`**`gaussian_laplace`**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*, ***kwargs*)

Multidimensional Laplace filter using gaussian second derivatives.

Parameters **input** : array_like
Input array to filter.
sigma : scalar or sequence of scalars
The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.
output : array, optional
The *output* parameter passes an array in which to store the filter output.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0
Extra keyword arguments will be passed to gaussian_filter().

`scipy.ndimage.filters.`**`generic_filter`**(*input*, *function*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*, *extra_arguments=()*, *extra_keywords=None*)

Calculates a multi-dimensional filter using the given function.

At each element the provided function is called. The input values within the filter footprint at that element are passed to the function as a 1D array of double values.

Parameters **input** : array_like
Input array to filter.
function : callable
Function to apply at each element.
size : scalar or tuple, optional
See footprint, below
footprint : array, optional
Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).
output : array, optional
The *output* parameter passes an array in which to store the filter output.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional

The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

extra_arguments : sequence, optional
Sequence of extra positional arguments to pass to passed function

extra_keywords : dict, optional
dict of extra keyword arguments to pass to passed function

`scipy.ndimage.filters.`**`generic_filter1d`**(*input*, *function*, *filter_size*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*, *extra_arguments=()*, *extra_keywords=None*)

Calculate a one-dimensional filter along the given axis.

`generic_filter1d` iterates over the lines of the array, calling the given function at each line. The arguments of the line are the input line, and the output line. The input and output lines are 1D double arrays. The input line is extended appropriately according to the filter size and origin. The output line must be modified in-place with the result.

Parameters

input : array_like
Input array to filter.

function : callable
Function to apply along given axis.

filter_size : scalar
Length of the filter.

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

extra_arguments : sequence, optional
Sequence of extra positional arguments to pass to passed function

extra_keywords : dict, optional
dict of extra keyword arguments to pass to passed function

`scipy.ndimage.filters.`**`generic_gradient_magnitude`**(*input*, *derivative*, *output=None*, *mode='reflect'*, *cval=0.0*, *extra_arguments=()*, *extra_keywords=None*)

Gradient magnitude using a provided gradient function.

Parameters

input : array_like
Input array to filter.

derivative : callable
Callable with the following signature:

```
derivative(input, axis, output, mode, cval,
           *extra_arguments, **extra_keywords)
```

See *extra_arguments*, *extra_keywords* below. *derivative* can assume that *input* and *output* are ndarrays. Note that the output from *derivative* is modified inplace; be careful to copy important inputs before returning them.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

extra_keywords : dict, optional
dict of extra keyword arguments to pass to passed function

extra_arguments : sequence, optional
Sequence of extra positional arguments to pass to passed function

`scipy.ndimage.filters.`**`generic_laplace`**(*input*, *derivative2*, *output=None*, *mode='reflect'*, *cval=0.0*, *extra_arguments=()*, *extra_keywords=None*)

N-dimensional Laplace filter using a provided second derivative function

Parameters

input : array_like
Input array to filter.

derivative2 : callable
Callable with the following signature:

```
derivative2(input, axis, output, mode, cval,
            *extra_arguments, **extra_keywords)
```

See *extra_arguments*, *extra_keywords* below.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

extra_keywords : dict, optional
dict of extra keyword arguments to pass to passed function

extra_arguments : sequence, optional
Sequence of extra positional arguments to pass to passed function

`scipy.ndimage.filters.`**`laplace`**(*input*, *output=None*, *mode='reflect'*, *cval=0.0*)

N-dimensional Laplace filter based on approximate second derivatives.

Parameters

input : array_like
Input array to filter.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

`scipy.ndimage.filters.`**`maximum_filter`**(*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculates a multi-dimensional maximum filter.

Parameters

input : array_like
Input array to filter.

size : scalar or tuple, optional
See footprint, below

footprint : array, optional
Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

`scipy.ndimage.filters.`**`maximum_filter1d`**`(`*input*, *size*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*`)`

Calculate a one-dimensional maximum filter along the given axis.

The lines of the array along the given axis are filtered with a maximum filter of given size.

Parameters

input : array_like
Input array to filter.

size : int
Length along which to calculate the 1-D maximum.

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

Returns

maximum1d : ndarray, None
Maximum-filtered array with same shape as input. None if *output* is not None

Notes

This function implements the MAXLIST algorithm [R102], as described by Richard Harter [R103], and has a guaranteed O(n) performance, *n* being the *input* length, regardless of filter size.

References

[R102], [R103]

`scipy.ndimage.filters.`**`median_filter`**`(`*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*`)`

Calculates a multidimensional median filter.

Parameters

input : array_like
    Input array to filter.
size : scalar or tuple, optional
    See footprint, below
footprint : array, optional
    Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).
output : array, optional
    The *output* parameter passes an array in which to store the filter output.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
    The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval : scalar, optional
    Value to fill past edges of input if *mode* is 'constant'. Default is 0.0
origin : scalar, optional
    The *origin* parameter controls the placement of the filter. Default 0.0.

Returns

median_filter : ndarray
    Return of same shape as *input*.

`scipy.ndimage.filters.`**`minimum_filter`**`(`*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*`)`

Calculates a multi-dimensional minimum filter.

Parameters

input : array_like
    Input array to filter.
size : scalar or tuple, optional
    See footprint, below
footprint : array, optional
    Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).
output : array, optional
    The *output* parameter passes an array in which to store the filter output.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
    The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval : scalar, optional
    Value to fill past edges of input if *mode* is 'constant'. Default is 0.0
origin : scalar, optional
    The *origin* parameter controls the placement of the filter. Default 0.0.

`scipy.ndimage.filters.`**`minimum_filter1d`**(*input*, *size*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a one-dimensional minimum filter along the given axis.

The lines of the array along the given axis are filtered with a minimum filter of given size.

Parameters

input : array_like
Input array to filter.

size : int
length along which to calculate 1D minimum

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

Notes

This function implements the MINLIST algorithm [R104], as described by Richard Harter [R105], and has a guaranteed O(n) performance, *n* being the *input* length, regardless of filter size.

References

[R104], [R105]

`scipy.ndimage.filters.`**`percentile_filter`**(*input*, *percentile*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculates a multi-dimensional percentile filter.

Parameters

input : array_like
Input array to filter.

percentile : scalar
The percentile parameter may be less then zero, i.e., percentile = -20 equals percentile = 80

size : scalar or tuple, optional
See footprint, below

footprint : array, optional
Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

`scipy.ndimage.filters.`**`prewitt`**(*input*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*)
Calculate a Prewitt filter.

Parameters

input : array_like
Input array to filter.

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

`scipy.ndimage.filters.`**`rank_filter`**(*input*, *rank*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)
Calculates a multi-dimensional rank filter.

Parameters

input : array_like
Input array to filter.

rank : int
The rank parameter may be less then zero, i.e., rank = -1 indicates the largest element.

size : scalar or tuple, optional
See footprint, below

footprint : array, optional
Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2).

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

`scipy.ndimage.filters.`**`sobel`**(*input*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*)
Calculate a Sobel filter.

Parameters

input : array_like
Input array to filter.

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional

The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

`scipy.ndimage.filters.`**`uniform_filter`**(*input*, *size=3*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional uniform filter.

Parameters

input : array_like
Input array to filter.

size : int or sequence of ints, optional
The sizes of the uniform filter are given for each axis as a sequence, or as a single number, in which case the size is equal for all axes.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

Notes

The multi-dimensional filter is implemented as a sequence of one-dimensional uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

`scipy.ndimage.filters.`**`uniform_filter1d`**(*input*, *size*, *axis=-1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a one-dimensional uniform filter along the given axis.

The lines of the array along the given axis are filtered with a uniform filter of given size.

Parameters

input : array_like
Input array to filter.

size : int
length of uniform filter

axis : int, optional
The axis of *input* along which to calculate. Default is -1.

output : array, optional
The *output* parameter passes an array in which to store the filter output.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0.0.

5.22.2 Fourier filters `scipy.ndimage.fourier`

`fourier_ellipsoid`(input, size[, n, axis, output])	Multi-dimensional ellipsoid fourier filter.

Continued on next page

Table 5.84 – continued from previous page

`fourier_gaussian`(input, sigma[, n, axis, output])	Multi-dimensional Gaussian fourier filter.
`fourier_shift`(input, shift[, n, axis, output])	Multi-dimensional fourier shift filter.
`fourier_uniform`(input, size[, n, axis, output])	Multi-dimensional uniform fourier filter.

`scipy.ndimage.fourier.`**`fourier_ellipsoid`**(*input*, *size*, *n=-1*, *axis=-1*, *output=None*)

Multi-dimensional ellipsoid fourier filter.

The array is multiplied with the fourier transform of a ellipsoid of given sizes.

Parameters

input : array_like
The input array.

size : float or sequence
The size of the box used for filtering. If a float, *size* is the same for all axes. If a sequence, *size* has to contain one value for each axis.

n : int, optional
If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis : int, optional
The axis of the real transform.

output : ndarray, optional
If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_ellipsoid : ndarray or None
The filtered input. If *output* is given as a parameter, None is returned.

Notes

This function is implemented for arrays of rank 1, 2, or 3.

`scipy.ndimage.fourier.`**`fourier_gaussian`**(*input*, *sigma*, *n=-1*, *axis=-1*, *output=None*)

Multi-dimensional Gaussian fourier filter.

The array is multiplied with the fourier transform of a Gaussian kernel.

Parameters

input : array_like
The input array.

sigma : float or sequence
The sigma of the Gaussian kernel. If a float, *sigma* is the same for all axes. If a sequence, *sigma* has to contain one value for each axis.

n : int, optional
If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis : int, optional
The axis of the real transform.

output : ndarray, optional
If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_gaussian : ndarray or None
The filtered input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.fourier.`**`fourier_shift`**(*input*, *shift*, *n=-1*, *axis=-1*, *output=None*)

Multi-dimensional fourier shift filter.

The array is multiplied with the fourier transform of a shift operation.

Parameters **input** : array_like

The input array.

shift : float or sequence

The size of the box used for filtering. If a float, *shift* is the same for all axes. If a sequence, *shift* has to contain one value for each axis.

n : int, optional

If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis : int, optional

The axis of the real transform.

output : ndarray, optional

If given, the result of shifting the input is placed in this array. None is returned in this case.

Returns **fourier_shift** : ndarray or None

The shifted input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.fourier.`**`fourier_uniform`**(*input*, *size*, *n=-1*, *axis=-1*, *output=None*)

Multi-dimensional uniform fourier filter.

The array is multiplied with the fourier transform of a box of given size.

Parameters **input** : array_like

The input array.

size : float or sequence

The size of the box used for filtering. If a float, *size* is the same for all axes. If a sequence, *size* has to contain one value for each axis.

n : int, optional

If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis : int, optional

The axis of the real transform.

output : ndarray, optional

If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns **fourier_uniform** : ndarray or None

The filtered input. If *output* is given as a parameter, None is returned.

5.22.3 Interpolation `scipy.ndimage.interpolation`

`affine_transform`(input, matrix[, offset, ...])	Apply an affine transformation.
`geometric_transform`(input, mapping[, ...])	Apply an arbitrary geometric transform.
`map_coordinates`(input, coordinates[, ...])	Map the input array to new coordinates by interpolation.
`rotate`(input, angle[, axes, reshape, ...])	Rotate an array.
`shift`(input, shift[, output, order, mode, ...])	Shift an array.
`spline_filter`(input[, order, output])	Multi-dimensional spline filter.
`spline_filter1d`(input[, order, axis, output])	Calculates a one-dimensional spline filter along the given axis.
`zoom`(input, zoom[, output, order, mode, ...])	Zoom an array.

`scipy.ndimage.interpolation.`**`affine_transform`**(*input*, *matrix*, *offset=0.0*, *output_shape=None*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Apply an affine transformation.

The given matrix and offset are used to find for each point in the output the corresponding coordinates in the input by an affine transformation. The value of the input at those coordinates is determined by spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Parameters

input : ndarray
The input array.

matrix : ndarray
The matrix must be two-dimensional or can also be given as a one-dimensional sequence or array. In the latter case, it is assumed that the matrix is diagonal. A more efficient algorithms is then applied that exploits the separability of the problem.

offset : float or sequence, optional
The offset into the array where the transform is applied. If a float, *offset* is the same for each axis. If a sequence, *offset* should contain one value for each axis.

output_shape : tuple of ints, optional
Shape tuple.

output : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array.

order : int, optional
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional
Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns

affine_transform : ndarray or None
The transformed input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.interpolation.`**`geometric_transform`**(*input*, *mapping*, *output_shape=None*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*, *extra_arguments=()*, *extra_keywords={}*)

Apply an arbritrary geometric transform.

The given mapping function is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

Parameters

input : array_like
The input array.

mapping : callable
A callable object that accepts a tuple of length equal to the output array rank, and returns the corresponding input coordinates as a tuple of length equal to the input array rank.

output_shape : tuple of ints, optional
Shape tuple.

output : ndarray or dtype, optional

The array in which to place the output, or the dtype of the returned array.

order : int, optional

The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional

Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional

Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional

The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

extra_arguments : tuple, optional

Extra arguments passed to *mapping*.

extra_keywords : dict, optional

Extra keywords passed to *mapping*.

Returns **return_value** : ndarray or None

The filtered input. If *output* is given as a parameter, None is returned.

See also:

`map_coordinates`, `affine_transform`, `spline_filter1d`

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(12.).reshape((4, 3))
>>> def shift_func(output_coords):
...     return (output_coords[0] - 0.5, output_coords[1] - 0.5)
...
>>> ndimage.geometric_transform(a, shift_func)
array([[ 0.   ,  0.   ,  0.   ],
       [ 0.   ,  1.362,  2.738],
       [ 0.   ,  4.812,  6.187],
       [ 0.   ,  8.263,  9.637]])
```

`scipy.ndimage.interpolation.`**`map_coordinates`**(*input*, *coordinates*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Map the input array to new coordinates by interpolation.

The array of coordinates is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

The shape of the output is derived from that of the coordinate array by dropping the first axis. The values of the array along the first axis are the coordinates in the input array at which the output value is found.

Parameters **input** : ndarray

The input array.

coordinates : array_like

The coordinates at which *input* is evaluated.

output : ndarray or dtype, optional

The array in which to place the output, or the dtype of the returned array.

order : int, optional

The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional

Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns **map_coordinates** : ndarray
The result of transforming the input. The shape of the output is derived from that of *coordinates* by dropping the first axis.

See also:

`spline_filter`, `geometric_transform`, `scipy.interpolate`

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(12.).reshape((4, 3))
>>> a
array([[  0.,   1.,   2.],
       [  3.,   4.,   5.],
       [  6.,   7.,   8.],
       [  9.,  10.,  11.]])
>>> ndimage.map_coordinates(a, [[0.5, 2], [0.5, 1]], order=1)
[ 2.  7.]
```

Above, the interpolated value of a[0.5, 0.5] gives output[0], while a[2, 1] is output[1].

```
>>> inds = np.array([[0.5, 2], [0.5, 4]])
>>> ndimage.map_coordinates(a, inds, order=1, cval=-33.3)
array([  2. , -33.3])
>>> ndimage.map_coordinates(a, inds, order=1, mode='nearest')
array([ 2.,  8.])
>>> ndimage.map_coordinates(a, inds, order=1, cval=0, output=bool)
array([ True, False], dtype=bool)
```

`scipy.ndimage.interpolation.`**`rotate`**(*input*, *angle*, *axes=(1, 0)*, *reshape=True*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Rotate an array.

The array is rotated in the plane defined by the two axes given by the *axes* parameter using spline interpolation of the requested order.

Parameters **input** : ndarray
The input array.

angle : float
The rotation angle in degrees.

axes : tuple of 2 ints, optional
The two axes that define the plane of rotation. Default is the first two axes.

reshape : bool, optional
If *reshape* is true, the output shape is adapted so that the input array is contained completely in the output. Default is True.

output : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array.

order : int, optional
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional

Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns **rotate** : ndarray or None
The rotated input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.interpolation.`**`shift`**(*input*, *shift*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Shift an array.

The array is shifted using spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Parameters **input** : ndarray
The input array.

shift : float or sequence, optional
The shift along the axes. If a float, `shift` is the same for each axis. If a sequence, `shift` should contain one value for each axis.

output : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array.

order : int, optional
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional
Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns **shift** : ndarray or None
The shifted input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.interpolation.`**`spline_filter`**(*input*, *order=3*, *output=<type 'numpy.float64'>*)

Multi-dimensional spline filter.

For more details, see `spline_filter1d`.

See also:

`spline_filter1d`

Notes

The multi-dimensional filter is implemented as a sequence of one-dimensional spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

`scipy.ndimage.interpolation.`**`spline_filter1d`**(*input*, *order=3*, *axis=-1*, *output=<type 'numpy.float64'>*)

Calculates a one-dimensional spline filter along the given axis.

The lines of the array along the given axis are filtered by a spline filter. The order of the spline must be >= 2 and <= 5.

Parameters

input : array_like
The input array.

order : int, optional
The order of the spline, default is 3.

axis : int, optional
The axis along which the spline filter is applied. Default is the last axis.

output : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array. Default is `numpy.float64`.

Returns

spline_filter1d : ndarray or None
The filtered input. If *output* is given as a parameter, None is returned.

`scipy.ndimage.interpolation.`**`zoom`**(*input*, *zoom*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

Parameters

input : ndarray
The input array.

zoom : float or sequence, optional
The zoom factor along the axes. If a float, `zoom` is the same for each axis. If a sequence, `zoom` should contain one value for each axis.

output : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array.

order : int, optional
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional
Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.

cval : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns

zoom : ndarray or None
The zoomed input. If *output* is given as a parameter, None is returned.

5.22.4 Measurements `scipy.ndimage.measurements`

`center_of_mass`(input[, labels, index])	Calculate the center of mass of the values of an array at labels.
`extrema`(input[, labels, index])	Calculate the minimums and maximums of the values of an array at labels, a
`find_objects`(input[, max_label])	Find objects in a labeled array.
`histogram`(input, min, max, bins[, labels, index])	Calculate the histogram of the values of an array, optionally at labels.
`label`(input[, structure, output])	Label features in an array.

Table 5.86 – continued from previous page

`labeled_comprehension`(input, labels, index, ...)	Roughly equivalent to [func(input[labels == i]) for i in index].
`maximum`(input[, labels, index])	Calculate the maximum of the values of an array over labeled regions.
`maximum_position`(input[, labels, index])	Find the positions of the maximums of the values of an array at labels.
`mean`(input[, labels, index])	Calculate the mean of the values of an array at labels.
`minimum`(input[, labels, index])	Calculate the minimum of the values of an array over labeled regions.
`minimum_position`(input[, labels, index])	Find the positions of the minimums of the values of an array at labels.
`standard_deviation`(input[, labels, index])	Calculate the standard deviation of the values of an n-D image array, option
`sum`(input[, labels, index])	Calculate the sum of the values of the array.
`variance`(input[, labels, index])	Calculate the variance of the values of an n-D image array, optionally at spe
`watershed_ift`(input, markers[, structure, ...])	Apply watershed from markers using image foresting transform algorithm.

`scipy.ndimage.measurements.`**`center_of_mass`**(*input*, *labels=None*, *index=None*)

Calculate the center of mass of the values of an array at labels.

Parameters **input** : ndarray

Data from which to calculate center-of-mass.

labels : ndarray, optional

Labels for objects in *input*, as generated by *ndimage.label*. Only used with *index*. Dimensions must be the same as *input*.

index : int or sequence of ints, optional

Labels for which to calculate centers-of-mass. If not specified, all labels greater than zero are used. Only used with *labels*.

Returns **center_of_mass** : tuple, or list of tuples

Coordinates of centers-of-mass.

Examples

```
>>> a = np.array(([0,0,0,0],
                  [0,1,1,0],
                  [0,1,1,0],
                  [0,1,1,0]))
>>> from scipy import ndimage
>>> ndimage.measurements.center_of_mass(a)
(2.0, 1.5)
```

Calculation of multiple objects in an image

```
>>> b = np.array(([0,1,1,0],
                  [0,1,0,0],
                  [0,0,0,0],
                  [0,0,1,1],
                  [0,0,1,1]))
>>> lbl = ndimage.label(b)[0]
>>> ndimage.measurements.center_of_mass(b, lbl, [1,2])
[(0.33333333333333331, 1.3333333333333333), (3.5, 2.5)]
```

`scipy.ndimage.measurements.`**`extrema`**(*input*, *labels=None*, *index=None*)

Calculate the minimums and maximums of the values of an array at labels, along with their positions.

Parameters **input** : ndarray

Nd-image data to process.

labels : ndarray, optional

Labels of features in input. If not None, must be same shape as *input*.

index : int or sequence of ints, optional

Labels to include in output. If None (default), all values where non-zero *labels* are used.

Returns **minimums, maximums** : int or ndarray
Values of minimums and maximums in each feature.
min_positions, max_positions : tuple or list of tuples
Each tuple gives the n-D coordinates of the corresponding minimum or maximum.

See also:

`maximum`, `minimum`, `maximum_position`, `minimum_position`, `center_of_mass`

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.extrema(a)
(0, 9, (0, 2), (3, 0))
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.extrema(a, lbl, index=np.arange(1, nlbl+1))
(array([1, 4, 3]),
 array([5, 7, 9]),
 [(0, 0), (1, 3), (3, 1)],
 [(1, 0), (2, 3), (3, 0)])
```

If no index is given, non-zero *labels* are processed:

```
>>> ndimage.extrema(a, lbl)
(1, 9, (0, 0), (3, 0))
```

`scipy.ndimage.measurements.`**`find_objects`**(*input*, *max_label=0*)
Find objects in a labeled array.

Parameters **input** : ndarray of ints
Array containing objects defined by different labels. Labels with value 0 are ignored.
max_label : int, optional
Maximum label to be searched for in *input*. If max_label is not given, the positions of all objects are returned.

Returns **object_slices** : list of tuples
A list of tuples, with each tuple containing N slices (with N the dimension of the input array). Slices correspond to the minimal parallelepiped that contains the object. If a number is missing, None is returned instead of a slice.

See also:

`label`, `center_of_mass`

Notes

This function is very useful for isolating a volume of interest inside a 3-D array, that cannot be “seen through”.

Examples

```
>>> a = np.zeros((6,6), dtype=np.int)
>>> a[2:4, 2:4] = 1
>>> a[4, 4] = 1
>>> a[:2, :3] = 2
>>> a[0, 5] = 3
```

```
>>> a
array([[2, 2, 2, 0, 0, 3],
       [2, 2, 2, 0, 0, 0],
       [0, 0, 1, 1, 0, 0],
       [0, 0, 1, 1, 0, 0],
       [0, 0, 0, 0, 1, 0],
       [0, 0, 0, 0, 0, 0]])
>>> ndimage.find_objects(a)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3, None)), (slice(0, 1, No
>>> ndimage.find_objects(a, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3, None))]
>>> ndimage.find_objects(a == 1, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), None]

>>> loc = ndimage.find_objects(a)[0]
>>> a[loc]
array([[1, 1, 0]
       [1, 1, 0]
       [0, 0, 1]])
```

`scipy.ndimage.measurements.`**`histogram`**`(`*input*, *min*, *max*, *bins*, *labels=None*, *index=None*`)`

Calculate the histogram of the values of an array, optionally at labels.

Histogram calculates the frequency of values in an array within bins determined by *min*, *max*, and *bins*. The *labels* and *index* keywords can limit the scope of the histogram to specified sub-regions within the array.

Parameters

input : array_like
Data for which to calculate histogram.

min, max : int
Minimum and maximum values of range of histogram bins.

bins : int
Number of bins.

labels : array_like, optional
Labels for objects in *input*. If not None, must be same shape as *input*.

index : int or sequence of ints, optional
Label or labels for which to calculate histogram. If None, all values where label is greater than zero are used

Returns

hist : ndarray
Histogram counts.

Examples

```
>>> a = np.array([[ 0.    ,  0.2146,  0.5962,  0.    ],
                  [ 0.    ,  0.7778,  0.    ,  0.    ],
                  [ 0.    ,  0.    ,  0.    ,  0.    ],
                  [ 0.    ,  0.    ,  0.7181,  0.2787],
                  [ 0.    ,  0.    ,  0.6573,  0.3094]])
>>> from scipy import ndimage
>>> ndimage.measurements.histogram(a, 0, 1, 10)
array([13,  0,  2,  1,  0,  1,  1,  2,  0,  0])
```

With labels and no indices, non-zero elements are counted:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl)
array([0, 0, 2, 1, 0, 1, 1, 2, 0, 0])
```

Indices can be used to count only certain objects:

```
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl, 2)
array([0, 0, 1, 1, 0, 0, 1, 1, 0, 0])
```

`scipy.ndimage.measurements.`**`label`**(*input*, *structure=None*, *output=None*)

Label features in an array.

Parameters **input** : array_like

An array-like object to be labeled. Any non-zero values in *input* are counted as features and zero values are considered the background.

structure : array_like, optional

A structuring element that defines feature connections. *structure* must be symmetric. If no structuring element is provided, one is automatically generated with a squared connectivity equal to one. That is, for a 2-D *input* array, the default structuring element is:

```
[[0,1,0],
 [1,1,1],
 [0,1,0]]
```

output : (None, data-type, array_like), optional

If *output* is a data type, it specifies the type of the resulting labeled feature array If *output* is an array-like object, then *output* will be updated with the labeled features from this function. This function can operate in-place, by passing output=input. Note that the output must be able to store the largest label, or this function will raise an Exception.

Returns **label** : ndarray or int

An integer ndarray where each unique feature in *input* has a unique label in the returned array.

num_features : int

How many objects were found.

If *output* is None, this function returns a tuple of (*labeled_array*, *num_features*).

If *output* is a ndarray, then it will be updated with values in *labeled_array* and only *num_features* will be returned by this function.

See also:

`find_objects`

generate a list of slices for the labeled features (or objects); useful for finding features' position or dimensions

Examples

Create an image with some features, then label it using the default (cross-shaped) structuring element:

```
>>> a = np.array([[0,0,1,1,0,0],
...               [0,0,0,1,0,0],
...               [1,1,0,0,1,0],
...               [0,0,0,1,0,0]])
>>> labeled_array, num_features = label(a)
```

Each of the 4 features are labeled with a different integer:

```
>>> print(num_features)
4
>>> print(labeled_array)
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
```

```
       [2, 2, 0, 0, 3, 0],
       [0, 0, 0, 4, 0, 0]])
```

Generate a structuring element that will consider features connected even if they touch diagonally:

```
>>> s = generate_binary_structure(2,2)
```

or,

```
>>> s = [[1,1,1],
         [1,1,1],
         [1,1,1]]
```

Label the image using the new structuring element:

```
>>> labeled_array, num_features = label(a, structure=s)
```

Show the 2 labeled features (note that features 1, 3, and 4 from above are now considered a single feature):

```
>>> print(num_features)
2
>>> print(labeled_array)
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [2, 2, 0, 0, 1, 0],
       [0, 0, 0, 1, 0, 0]])
```

`scipy.ndimage.measurements.`**`labeled_comprehension`**(*input*, *labels*, *index*, *func*, *out_dtype*, *default*, *pass_positions=False*)

Roughly equivalent to [func(input[labels == i]) for i in index].

Sequentially applies an arbitrary function (that works on array_like input) to subsets of an n-D image array specified by *labels* and *index*. The option exists to provide the function with positional parameters as the second argument.

Parameters **input** : array_like

Data from which to select *labels* to process.

labels : array_like or None

Labels to objects in *input*. If not None, array must be same shape as *input*. If None, *func* is applied to raveled *input*.

index : int, sequence of ints or None

Subset of *labels* to which to apply *func*. If a scalar, a single value is returned. If None, *func* is applied to all non-zero values of *labels*.

func : callable

Python function to apply to *labels* from *input*.

out_dtype : dtype

Dtype to use for *result*.

default : int, float or None

Default return value when a element of *index* does not exist in *labels*.

pass_positions : bool, optional

If True, pass linear indices to *func* as a second argument. Default is False.

Returns **result** : ndarray

Result of applying *func* to each of *labels* to *input* in *index*.

Examples

```
>>> a = np.array([[1, 2, 0, 0],
                  [5, 3, 0, 4],
                  [0, 0, 0, 7],
```

```
                  [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> lbl, nlbl = ndimage.label(a)
>>> lbls = np.arange(1, nlbl+1)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, 0)
array([ 2.75,  5.5 ,  6.  ])
```

Falling back to *default*:

```
>>> lbls = np.arange(1, nlbl+2)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, -1)
array([ 2.75,  5.5 ,  6.  , -1.  ])
```

Passing positions:

```
>>> def fn(val, pos):
...     print("fn says: %s : %s" % (val, pos))
...     return (val.sum()) if (pos.sum() % 2 == 0) else (-val.sum())
...
>>> ndimage.labeled_comprehension(a, lbl, lbls, fn, float, 0, True)
fn says: [1 2 5 3] : [0 1 4 5]
fn says: [4 7] : [7 11]
fn says: [9 3] : [12 13]
array([ 11.,  11., -12.])
```

`scipy.ndimage.measurements.`**`maximum`**`(`*input*, *labels=None*, *index=None*`)`

Calculate the maximum of the values of an array over labeled regions.

Parameters

input : array_like

Array_like of values. For each region specified by *labels*, the maximal values of *input* over the region is computed.

labels : array_like, optional

An array of integers marking different regions over which the maximum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the maximum over the whole array is returned.

index : array_like, optional

A list of region labels that are taken into account for computing the maxima. If index is None, the maximum over all elements where *labels* is non-zero is returned.

Returns

output : float or list of floats

List of maxima of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the maximal value of *input* if *labels* is None, and the maximal value of elements where *labels* is greater than zero if *index* is None.

See also:

`label`, `minimum`, `median`, `maximum_position`, `extrema`, `sum`, `mean`, `variance`, `standard_deviation`

Notes

The function returns a Python list and not a Numpy array, use `np.array` to convert the list to an array.

Examples

```
>>> a = np.arange(16).reshape((4,4))
>>> a
array([[ 0,  1,  2,  3],
       [ 4,  5,  6,  7],
```

```
       [ 8,  9, 10, 11],
       [12, 13, 14, 15]])
>>> labels = np.zeros_like(a)
>>> labels[:2,:2] = 1
>>> labels[2:, 1:3] = 2
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 0],
       [0, 2, 2, 0],
       [0, 2, 2, 0]])
>>> from scipy import ndimage
>>> ndimage.maximum(a)
15.0
>>> ndimage.maximum(a, labels=labels, index=[1,2])
[5.0, 14.0]
>>> ndimage.maximum(a, labels=labels)
14.0

>>> b = np.array([[1, 2, 0, 0],
                  [5, 3, 0, 4],
                  [0, 0, 0, 7],
                  [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(b)
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.maximum(b, labels=labels, index=np.arange(1, labels_nb + 1))
[5.0, 7.0, 9.0]
```

scipy.ndimage.measurements.**maximum_position**(*input*, *labels=None*, *index=None*)

Find the positions of the maximums of the values of an array at labels.

For each region specified by *labels*, the position of the maximum value of *input* within the region is returned.

Parameters

input : array_like
Array_like of values.

labels : array_like, optional
An array of integers marking different regions over which the position of the maximum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the location of the first maximum over the whole array is returned.
The *labels* argument only works when *index* is specified.

index : array_like, optional
A list of region labels that are taken into account for finding the location of the maxima. If *index* is None, the first maximum over all elements where *labels* is non-zero is returned.
The *index* argument only works when *labels* is specified.

Returns

output : list of tuples of ints
List of tuples of ints that specify the location of maxima of *input* over the regions determined by *labels* and whose index is in *index*.
If *index* or *labels* are not specified, a tuple of ints is returned specifying the location of the `first` maximal value of *input*.

See also:

`label`, `minimum`, `median`, `maximum_position`, `extrema`, `sum`, `mean`, `variance`, `standard_deviation`

`scipy.ndimage.measurements.`**`mean`**`(`*input*, *labels=None*, *index=None*`)`

Calculate the mean of the values of an array at labels.

Parameters **input** : array_like

Array on which to compute the mean of elements over distinct regions.

labels : array_like, optional

Array of labels of same shape, or broadcastable to the same shape as *input*. All elements sharing the same label form one region over which the mean of the elements is computed.

index : int or sequence of ints, optional

Labels of the objects over which the mean is to be computed. Default is None, in which case the mean for all values where label is greater than 0 is calculated.

Returns **out** : list

Sequence of same length as *index*, with the mean of the different regions labeled by the labels in *index*.

See also:

`ndimage.variance`, `ndimage.standard_deviation`, `ndimage.minimum`, `ndimage.maximum`, `ndimage.sum`, `ndimage.label`

Examples

```
>>> a = np.arange(25).reshape((5,5))
>>> labels = np.zeros_like(a)
>>> labels[3:5,3:5] = 1
>>> index = np.unique(labels)
>>> labels
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 1, 1],
       [0, 0, 0, 1, 1]])
>>> index
array([0, 1])
>>> ndimage.mean(a, labels=labels, index=index)
[10.285714285714286, 21.0]
```

`scipy.ndimage.measurements.`**`minimum`**`(`*input*, *labels=None*, *index=None*`)`

Calculate the minimum of the values of an array over labeled regions.

Parameters **input** : array_like

Array_like of values. For each region specified by *labels*, the minimal values of *input* over the region is computed.

labels : array_like, optional

An array_like of integers marking different regions over which the minimum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the minimum over the whole array is returned.

index : array_like, optional

A list of region labels that are taken into account for computing the minima. If index is None, the minimum over all elements where *labels* is non-zero is returned.

Returns **minimum** : float or list of floats

List of minima of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the minimal value of *input* if *labels* is None, and the minimal value of elements where *labels* is greater than zero if *index* is None.

See also:

`label`, `maximum`, `median`, `minimum_position`, `extrema`, `sum`, `mean`, `variance`, `standard_deviation`

Notes

The function returns a Python list and not a Numpy array, use `np.array` to convert the list to an array.

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(a)
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.minimum(a, labels=labels, index=np.arange(1, labels_nb + 1))
[1.0, 4.0, 3.0]
>>> ndimage.minimum(a)
0.0
>>> ndimage.minimum(a, labels=labels)
1.0
```

`scipy.ndimage.measurements.`**`minimum_position`**`(`*input*, *labels=None*, *index=None*`)`

Find the positions of the minimums of the values of an array at labels.

Parameters **input** : array_like

Array_like of values.

labels : array_like, optional

An array of integers marking different regions over which the position of the minimum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the location of the first minimum over the whole array is returned.

The *labels* argument only works when *index* is specified.

index : array_like, optional

A list of region labels that are taken into account for finding the location of the minima. If *index* is None, the `first` minimum over all elements where *labels* is non-zero is returned.

The *index* argument only works when *labels* is specified.

Returns **output** : list of tuples of ints

Tuple of ints or list of tuples of ints that specify the location of minima of *input* over the regions determined by *labels* and whose index is in *index*.

If *index* or *labels* are not specified, a tuple of ints is returned specifying the location of the first minimal value of *input*.

See also:

`label`, `minimum`, `median`, `maximum_position`, `extrema`, `sum`, `mean`, `variance`, `standard_deviation`

`scipy.ndimage.measurements.`**`standard_deviation`**`(`*input*, *labels=None*, *index=None*`)`

Calculate the standard deviation of the values of an n-D image array, optionally at specified sub-regions.

Parameters	**input** : array_like Nd-image data to process. **labels** : array_like, optional Labels to identify sub-regions in *input*. If not None, must be same shape as *input*. **index** : int or sequence of ints, optional *labels* to include in output. If None (default), all values where *labels* is non-zero are used.
Returns	**standard_deviation** : float or ndarray Values of standard deviation, for each sub-region if *labels* and *index* are specified.

See also:

`label`, `variance`, `maximum`, `minimum`, `extrema`

Examples

```
>>> a = np.array([[1, 2, 0, 0],
                  [5, 3, 0, 4],
                  [0, 0, 0, 7],
                  [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.standard_deviation(a)
2.7585095613392387
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.standard_deviation(a, lbl, index=np.arange(1, nlbl+1))
array([ 1.479,  1.5  ,  3.   ])
```

If no index is given, non-zero *labels* are processed:

```
>>> ndimage.standard_deviation(a, lbl)
2.4874685927665499
```

`scipy.ndimage.measurements.`**`sum`**`(`*input*, *labels=None*, *index=None*`)`

Calculate the sum of the values of the array.

Parameters	**input** : array_like Values of *input* inside the regions defined by *labels* are summed together. **labels** : array_like of ints, optional Assign labels to the values of the array. Has to have the same shape as *input*. **index** : array_like, optional A single label number or a sequence of label numbers of the objects to be measured.
Returns	**sum** : ndarray or scalar An array of the sums of values of *input* inside the regions defined by *labels* with the same shape as *index*. If 'index' is None or scalar, a scalar is returned.

See also:

`mean`, `median`

Examples

```
>>> input =  [0,1,2,3]
>>> labels = [1,1,2,2]
>>> sum(input, labels, index=[1,2])
[1.0, 5.0]
>>> sum(input, labels, index=1)
1
```

```
>>> sum(input, labels)
6
```

`scipy.ndimage.measurements.`**`variance`**(*input*, *labels=None*, *index=None*)

Calculate the variance of the values of an n-D image array, optionally at specified sub-regions.

Parameters

input : array_like
Nd-image data to process.

labels : array_like, optional
Labels defining sub-regions in *input*. If not None, must be same shape as *input*.

index : int or sequence of ints, optional
labels to include in output. If None (default), all values where *labels* is non-zero are used.

Returns

variance : float or ndarray
Values of variance, for each sub-region if *labels* and *index* are specified.

See also:

`label`, `standard_deviation`, `maximum`, `minimum`, `extrema`

Examples

```
>>> a = np.array([[1, 2, 0, 0],
                  [5, 3, 0, 4],
                  [0, 0, 0, 7],
                  [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.variance(a)
7.609375
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.variance(a, lbl, index=np.arange(1, nlbl+1))
array([ 2.1875,  2.25  ,  9.    ])
```

If no index is given, all non-zero *labels* are processed:

```
>>> ndimage.variance(a, lbl)
6.1875
```

`scipy.ndimage.measurements.`**`watershed_ift`**(*input*, *markers*, *structure=None*, *output=None*)

Apply watershed from markers using image foresting transform algorithm.

Parameters

input : array_like
Input.

markers : array_like
Markers are points within each watershed that form the beginning of the process. Negative markers are considered background markers which are processed after the other markers.

structure : structure element, optional
A structuring element defining the connectivity of the object can be provided. If None, an element is generated with a squared connectivity equal to one.

output : ndarray, optional
An output array can optionally be provided. The same shape as input.

Returns

watershed_ift : ndarray
Output. Same shape as *input*.

References

[R106]

5.22.5 Morphology `scipy.ndimage.morphology`

`binary_closing`(input[, structure, ...])	Multi-dimensional binary closing with the given structuring element.
`binary_dilation`(input[, structure, ...])	Multi-dimensional binary dilation with the given structuring element.
`binary_erosion`(input[, structure, ...])	Multi-dimensional binary erosion with a given structuring element.
`binary_fill_holes`(input[, structure, ...])	Fill the holes in binary objects.
`binary_hit_or_miss`(input[, structure1, ...])	Multi-dimensional binary hit-or-miss transform.
`binary_opening`(input[, structure, ...])	Multi-dimensional binary opening with the given structuring element.
`binary_propagation`(input[, structure, mask, ...])	Multi-dimensional binary propagation with the given structuring element.
`black_tophat`(input[, size, footprint, ...])	Multi-dimensional black tophat filter.
`distance_transform_bf`(input[, metric, ...])	Distance transform function by a brute force algorithm.
`distance_transform_cdt`(input[, metric, ...])	Distance transform for chamfer type of transforms.
`distance_transform_edt`(input[, sampling, ...])	Exact euclidean distance transform.
`generate_binary_structure`(rank, connectivity)	Generate a binary structure for binary morphological operations.
`grey_closing`(input[, size, footprint, ...])	Multi-dimensional greyscale closing.
`grey_dilation`(input[, size, footprint, ...])	Calculate a greyscale dilation, using either a structuring element, or a foot
`grey_erosion`(input[, size, footprint, ...])	Calculate a greyscale erosion, using either a structuring element, or a foot
`grey_opening`(input[, size, footprint, ...])	Multi-dimensional greyscale opening.
`iterate_structure`(structure, iterations[, ...])	Iterate a structure by dilating it with itself.
`morphological_gradient`(input[, size, ...])	Multi-dimensional morphological gradient.
`morphological_laplace`(input[, size, ...])	Multi-dimensional morphological laplace.
`white_tophat`(input[, size, footprint, ...])	Multi-dimensional white tophat filter.

`scipy.ndimage.morphology.`**`binary_closing`**(*input*, *structure=None*, *iterations=1*, *output=None*, *origin=0*)

Multi-dimensional binary closing with the given structuring element.

The *closing* of an input image by a structuring element is the *erosion* of the *dilation* of the image by the structuring element.

Parameters

input : array_like

Binary array_like to be closed. Non-zero (True) elements form the subset to be closed.

structure : array_like, optional

Structuring element used for the closing. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).

iterations : {int, float}, optional

The dilation step of the closing, then the erosion step are each repeated *iterations* times (one, by default). If iterations is less than 1, each operations is repeated until the result does not change anymore.

output : ndarray, optional

Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin : int or tuple of ints, optional

Placement of the filter, by default 0.

Returns

binary_closing : ndarray of bools

Closing of the input by the structuring element.

See also:

`grey_closing`, `binary_opening`, `binary_dilation`, `binary_erosion`, `generate_binary_structure`

Notes

Closing [R107] is a mathematical morphology operation [R108] that consists in the succession of a dilation and an erosion of the input with the same structuring element. Closing therefore fills holes smaller than the structuring element.

Together with *opening* (`binary_opening`), closing can be used for noise removal.

References

[R107], [R108]

Examples

```
>>> a = np.zeros((5,5), dtype=np.int)
>>> a[1:-1, 1:-1] = 1; a[2,2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing removes small holes
>>> ndimage.binary_closing(a).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing is the erosion of the dilation of the input
>>> ndimage.binary_dilation(a).astype(np.int)
array([[0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0]])
>>> ndimage.binary_erosion(ndimage.binary_dilation(a)).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
```

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1:6, 2:5] = 1; a[1:3,3] = 0
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # In addition to removing holes, closing can also
>>> # coarsen boundaries with fine hollows.
```

```
>>> ndimage.binary_closing(a).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_closing(a, structure=np.ones((2,2))).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`binary_dilation`**(*input*, *structure=None*, *iterations=1*, *mask=None*, *output=None*, *border_value=0*, *origin=0*, *brute_force=False*)

Multi-dimensional binary dilation with the given structuring element.

Parameters

input : array_like
    Binary array_like to be dilated. Non-zero (True) elements form the subset to be dilated.

structure : array_like, optional
    Structuring element used for the dilation. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one.

iterations : {int, float}, optional
    The dilation is repeated *iterations* times (one, by default). If iterations is less than 1, the dilation is repeated until the result does not change anymore.

mask : array_like, optional
    If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.

output : ndarray, optional
    Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin : int or tuple of ints, optional
    Placement of the filter, by default 0.

border_value : int (cast to 0 or 1), optional
    Value at the border in the output array.

Returns

binary_dilation : ndarray of bools
    Dilation of the input by the structuring element.

See also:

`grey_dilation`, `binary_erosion`, `binary_closing`, `binary_opening`, `generate_binary_structure`

Notes

Dilation [R109] is a mathematical morphology operation [R110] that uses a structuring element for expanding the shapes in an image. The binary dilation of an image by a structuring element is the locus of the points covered by the structuring element, when its center lies within the non-zero points of the image.

References

[R109], [R110]

Examples

```
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a)
array([[False, False, False, False, False],
       [False, False,  True, False, False],
       [False,  True,  True,  True, False],
       [False, False,  True, False, False],
       [False, False, False, False, False]], dtype=bool)
>>> ndimage.binary_dilation(a).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> # 3x3 structuring element with connectivity 1, used by default
>>> struct1 = ndimage.generate_binary_structure(2, 1)
>>> struct1
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> # 3x3 structuring element with connectivity 2
>>> struct2 = ndimage.generate_binary_structure(2, 2)
>>> struct2
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
>>> ndimage.binary_dilation(a, structure=struct1).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a, structure=struct2).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a, structure=struct1,\
... iterations=2).astype(a.dtype)
array([[ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 1.,  1.,  1.,  1.,  1.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.]])
```

`scipy.ndimage.morphology.`**`binary_erosion`**(*input*, *structure=None*, *iterations=1*, *mask=None*, *output=None*, *border_value=0*, *origin=0*, *brute_force=False*)

Multi-dimensional binary erosion with a given structuring element.

Binary erosion is a mathematical morphology operation used for image processing.

Parameters **input** : array_like

Binary image to be eroded. Non-zero (True) elements form the subset to be eroded.

structure : array_like, optional

Structuring element used for the erosion. Non-zero elements are considered True. If no structuring element is provided, an element is generated with a square connectivity equal to one.

iterations : {int, float}, optional

The erosion is repeated *iterations* times (one, by default). If iterations is less than 1, the erosion is repeated until the result does not change anymore.

mask : array_like, optional

If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.

output : ndarray, optional

Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin : int or tuple of ints, optional

Placement of the filter, by default 0.

border_value : int (cast to 0 or 1), optional

Value at the border in the output array.

Returns **binary_erosion** : ndarray of bools

Erosion of the input by the structuring element.

See also:

`grey_erosion`, `binary_dilation`, `binary_closing`, `binary_opening`, `generate_binary_structure`

Notes

Erosion [R111] is a mathematical morphology operation [R112] that uses a structuring element for shrinking the shapes in an image. The binary erosion of an image by a structuring element is the locus of the points where a superimposition of the structuring element centered on the point is entirely contained in the set of non-zero elements of the image.

References

[R111], [R112]

Examples

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1:6, 2:5] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_erosion(a).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
```

```
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> #Erosion removes objects smaller than the structure
>>> ndimage.binary_erosion(a, structure=np.ones((5,5))).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`binary_fill_holes`**`(`*input*, *structure=None*, *output=None*, *origin=0*`)`

Fill the holes in binary objects.

Parameters

input : array_like
  n-dimensional binary array with holes to be filled

structure : array_like, optional
  Structuring element used in the computation; large-size elements make computations faster but may miss holes separated from the background by thin regions. The default element (with a square connectivity equal to one) yields the intuitive result where all holes in the input have been filled.

output : ndarray, optional
  Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin : int, tuple of ints, optional
  Position of the structuring element.

Returns

out : ndarray
  Transformation of the initial image *input* where holes have been filled.

See also:

`binary_dilation`, `binary_propagation`, `label`

Notes

The algorithm used in this function consists in invading the complementary of the shapes in *input* from the outer boundary of the image, using binary dilations. Holes are not connected to the boundary and are therefore not invaded. The result is the complementary subset of the invaded region.

References

[R113]

Examples

```
>>> a = np.zeros((5, 5), dtype=int)
>>> a[1:4, 1:4] = 1
>>> a[2,2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
```

```
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_fill_holes(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Too big structuring element
>>> ndimage.binary_fill_holes(a, structure=np.ones((5,5))).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`binary_hit_or_miss`**(*input*, *structure1=None*, *structure2=None*, *output=None*, *origin1=0*, *origin2=None*)

Multi-dimensional binary hit-or-miss transform.

The hit-or-miss transform finds the locations of a given pattern inside the input image.

Parameters

input : array_like (cast to booleans)
Binary image where a pattern is to be detected.

structure1 : array_like (cast to booleans), optional
Part of the structuring element to be fitted to the foreground (non-zero elements) of *input*. If no value is provided, a structure of square connectivity 1 is chosen.

structure2 : array_like (cast to booleans), optional
Second part of the structuring element that has to miss completely the foreground. If no value is provided, the complementary of *structure1* is taken.

output : ndarray, optional
Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin1 : int or tuple of ints, optional
Placement of the first part of the structuring element *structure1*, by default 0 for a centered structure.

origin2 : int or tuple of ints, optional
Placement of the second part of the structuring element *structure2*, by default 0 for a centered structure. If a value is provided for *origin1* and not for *origin2*, then *origin2* is set to *origin1*.

Returns

binary_hit_or_miss : ndarray
Hit-or-miss transform of *input* with the given structuring element (*structure1*, *structure2*).

See also:

`ndimage.morphology`, `binary_erosion`

References

[R114]

Examples

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1, 1] = 1; a[2:4, 2:4] = 1; a[4:6, 4:6] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0, 0],
```

```
              [0, 0, 1, 1, 0, 0, 0],
              [0, 0, 1, 1, 0, 0, 0],
              [0, 0, 0, 0, 1, 1, 0],
              [0, 0, 0, 0, 1, 1, 0],
              [0, 0, 0, 0, 0, 0, 0]])
>>> structure1 = np.array([[1, 0, 0], [0, 1, 1], [0, 1, 1]])
>>> structure1
array([[1, 0, 0],
       [0, 1, 1],
       [0, 1, 1]])
>>> # Find the matches of structure1 in the array a
>>> ndimage.binary_hit_or_miss(a, structure1=structure1).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # Change the origin of the filter
>>> # origin1=1 is equivalent to origin1=(1,1) here
>>> ndimage.binary_hit_or_miss(a, structure1=structure1,\
... origin1=1).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`binary_opening`**(*input*, *structure=None*, *iterations=1*, *output=None*, *origin=0*)

Multi-dimensional binary opening with the given structuring element.

The *opening* of an input image by a structuring element is the *dilation* of the *erosion* of the image by the structuring element.

Parameters

input : array_like

Binary array_like to be opened. Non-zero (True) elements form the subset to be opened.

structure : array_like, optional

Structuring element used for the opening. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).

iterations : {int, float}, optional

The erosion step of the opening, then the dilation step are each repeated *iterations* times (one, by default). If *iterations* is less than 1, each operation is repeated until the result does not change anymore.

output : ndarray, optional

Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin : int or tuple of ints, optional

Placement of the filter, by default 0.

Returns

binary_opening : ndarray of bools

Opening of the input by the structuring element.

See also:

`grey_opening`, `binary_closing`, `binary_erosion`, `binary_dilation`, `generate_binary_structure`

Notes

Opening [R115] is a mathematical morphology operation [R116] that consists in the succession of an erosion and a dilation of the input with the same structuring element. Opening therefore removes objects smaller than the structuring element.

Together with *closing* (`binary_closing`), opening can be used for noise removal.

References

[R115], [R116]

Examples

```
>>> a = np.zeros((5,5), dtype=np.int)
>>> a[1:4, 1:4] = 1; a[4, 4] = 1
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 1]])
>>> # Opening removes small objects
>>> ndimage.binary_opening(a, structure=np.ones((3,3))).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening can also smooth corners
>>> ndimage.binary_opening(a).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening is the dilation of the erosion of the input
>>> ndimage.binary_erosion(a).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_dilation(ndimage.binary_erosion(a)).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`binary_propagation`**(*input*, *structure=None*, *mask=None*, *output=None*, *border_value=0*, *origin=0*)

Multi-dimensional binary propagation with the given structuring element.

Parameters **input** : array_like

Binary image to be propagated inside *mask*.

structure : array_like, optional

Structuring element used in the successive dilations. The output may depend on the structuring element, especially if *mask* has several connex components. If no structuring element is provided, an element is generated with a squared connectivity equal to one.

mask : array_like, optional

Binary mask defining the region into which *input* is allowed to propagate.

output : ndarray, optional

Array of the same shape as input, into which the output is placed. By default, a new array is created.

border_value : int (cast to 0 or 1), optional

Value at the border in the output array.

origin : int or tuple of ints, optional

Placement of the filter, by default 0.

Returns **binary_propagation** : ndarray

Binary propagation of *input* inside *mask*.

Notes

This function is functionally equivalent to calling binary_dilation with the number of iterations less then one: iterative dilation until the result does not change anymore.

The succession of an erosion and propagation inside the original image can be used instead of an *opening* for deleting small objects while keeping the contours of larger objects untouched.

References

[R117], [R118]

Examples

```
>>> input = np.zeros((8, 8), dtype=np.int)
>>> input[2, 2] = 1
>>> mask = np.zeros((8, 8), dtype=np.int)
>>> mask[1:4, 1:4] = mask[4, 4]  = mask[6:8, 6:8] = 1
>>> input
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
>>> mask
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 1, 1],
       [0, 0, 0, 0, 0, 0, 1, 1]])
>>> ndimage.binary_propagation(input, mask=mask).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
```

```
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_propagation(input, mask=mask,\
... structure=np.ones((3,3))).astype(np.int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])

>>> # Comparison between opening and erosion+propagation
>>> a = np.zeros((6,6), dtype=np.int)
>>> a[2:5, 2:5] = 1; a[0, 0] = 1; a[5, 5] = 1
>>> a
array([[1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 1]])
>>> ndimage.binary_opening(a).astype(np.int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0]])
>>> b = ndimage.binary_erosion(a)
>>> b.astype(int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_propagation(b, mask=a).astype(np.int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`black_tophat`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional black tophat filter.

Parameters **input** : array_like

Input.

size : tuple of ints, optional

Shape of a flat and full structuring element used for the filter. Optional if *footprint* or *structure* is provided.

footprint : array of ints, optional
Positions of non-infinite elements of a flat structuring element used for the black tophat filter.

structure : array of ints, optional
Structuring element used for the filter. *structure* may be a non-flat structuring element.

output : array, optional
An array used for storing the output of the filter may be provided.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0

Returns **black_tophat** : ndarray
Result of the filter of *input* with *structure*.

See also:

`white_tophat`, `grey_opening`, `grey_closing`

`scipy.ndimage.morphology.`**`distance_transform_bf`**`(`*input*, *metric='euclidean'*, *sampling=None*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*`)`

Distance transform function by a brute force algorithm.

This function calculates the distance transform of the *input*, by replacing each background element (zero values), with its shortest distance to the foreground (any element non-zero).

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result.

Parameters **input** : array_like
Input

metric : str, optional
Three types of distance metric are supported: 'euclidean', 'taxicab' and 'chessboard'.

sampling : {int, sequence of ints}, optional
This parameter is only used in the case of the euclidean *metric* distance transform.
The sampling along each axis can be given by the *sampling* parameter which should be a sequence of length equal to the input rank, or a single number in which the *sampling* is assumed to be equal along all axes.

return_distances : bool, optional
The *return_distances* flag can be used to indicate if the distance transform is returned.
The default is True.

return_indices : bool, optional
The *return_indices* flags can be used to indicate if the feature transform is returned.
The default is False.

distances : float64 ndarray, optional
Optional output array to hold distances (if *return_distances* is True).

indices : int64 ndarray, optional
Optional output array to hold indices (if *return_indices* is True).

Returns **distances** : ndarray
Distance array if *return_distances* is True.

indices : ndarray
Indices array if *return_indices* is True.

Notes

This function employs a slow brute force algorithm, see also the function distance_transform_cdt for more efficient taxicab and chessboard algorithms.

`scipy.ndimage.morphology.`**`distance_transform_cdt`**(*input*, *metric='chessboard'*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*)

Distance transform for chamfer type of transforms.

Parameters

input : array_like

Input

metric : {'chessboard', 'taxicab'}, optional

The *metric* determines the type of chamfering that is done. If the *metric* is equal to 'taxicab' a structure is generated using generate_binary_structure with a squared distance equal to 1. If the *metric* is equal to 'chessboard', a *metric* is generated using generate_binary_structure with a squared distance equal to the dimensionality of the array. These choices correspond to the common interpretations of the 'taxicab' and the 'chessboard' distance metrics in two dimensions.

The default for *metric* is 'chessboard'.

return_distances, return_indices : bool, optional

The *return_distances*, and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

If the feature transform is returned (`return_indices=True`), the index of the closest background element is returned along the first axis of the result.

The *return_distances* default is True, and the *return_indices* default is False.

distances, indices : ndarrays of int32, optional

The *distances* and *indices* arguments can be used to give optional output arrays that must be the same shape as *input*.

`scipy.ndimage.morphology.`**`distance_transform_edt`**(*input*, *sampling=None*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*)

Exact euclidean distance transform.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result.

Parameters

input : array_like

Input data to transform. Can be any type but will be converted into binary: 1 wherever input equates to True, 0 elsewhere.

sampling : float or int, or sequence of same, optional

Spacing of elements along each dimension. If a sequence, must be of length equal to the input rank; if a single number, this is used for all axes. If not specified, a grid spacing of unity is implied.

return_distances : bool, optional

Whether to return distance matrix. At least one of return_distances/return_indices must be True. Default is True.

return_indices : bool, optional

Whether to return indices matrix. Default is False.

distances : ndarray, optional

Used for output of distance array, must be of type float64.

indices : ndarray, optional

Used for output of indices, must be of type int32.

Returns

distance_transform_edt : ndarray or list of ndarrays

Either distance matrix, index matrix, or a list of the two, depending on *return_x* flags and *distance* and *indices* input parameters.

Notes

The euclidean distance transform gives values of the euclidean distance:

```
              n
y_i = sqrt(sum (x[i]-b[i])**2)
              i
```

where b[i] is the background point (value 0) with the smallest Euclidean distance to input points x[i], and n is the number of dimensions.

Examples

```
>>> a = np.array(([0,1,1,1,1],
                  [0,0,1,1,1],
                  [0,1,1,1,1],
                  [0,1,1,1,0],
                  [0,1,1,0,0]))
>>> from scipy import ndimage
>>> ndimage.distance_transform_edt(a)
array([[ 0.    ,  1.    ,  1.4142,  2.2361,  3.    ],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  2.    ],
       [ 0.    ,  1.    ,  1.4142,  1.4142,  1.    ],
       [ 0.    ,  1.    ,  1.4142,  1.    ,  0.    ],
       [ 0.    ,  1.    ,  1.    ,  0.    ,  0.    ]])
```

With a sampling of 2 units along x, 1 along y:

```
>>> ndimage.distance_transform_edt(a, sampling=[2,1])
array([[ 0.    ,  1.    ,  2.    ,  2.8284,  3.6056],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  3.    ],
       [ 0.    ,  1.    ,  2.    ,  2.2361,  2.    ],
       [ 0.    ,  1.    ,  2.    ,  1.    ,  0.    ],
       [ 0.    ,  1.    ,  1.    ,  0.    ,  0.    ]])
```

Asking for indices as well:

```
>>> edt, inds = ndimage.distance_transform_edt(a, return_indices=True)
>>> inds
array([[[0, 0, 1, 1, 3],
        [1, 1, 1, 1, 3],
        [2, 2, 1, 3, 3],
        [3, 3, 4, 4, 3],
        [4, 4, 4, 4, 4]],
       [[0, 0, 1, 1, 4],
        [0, 1, 1, 1, 4],
        [0, 0, 1, 4, 4],
        [0, 0, 3, 3, 4],
        [0, 0, 3, 3, 4]]])
```

With arrays provided for inplace outputs:

```
>>> indices = np.zeros(((np.ndim(a),) + a.shape), dtype=np.int32)
>>> ndimage.distance_transform_edt(a, return_indices=True, indices=indices)
array([[ 0.    ,  1.    ,  1.4142,  2.2361,  3.    ],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  2.    ],
       [ 0.    ,  1.    ,  1.4142,  1.4142,  1.    ],
       [ 0.    ,  1.    ,  1.4142,  1.    ,  0.    ],
```

```
        [ 0.     ,  1.     ,  1.     ,  0.     ,  0.     ]])
>>> indices
array([[[0, 0, 1, 1, 3],
         [1, 1, 1, 1, 3],
         [2, 2, 1, 3, 3],
         [3, 3, 4, 4, 3],
         [4, 4, 4, 4, 4]],
        [[0, 0, 1, 1, 4],
         [0, 1, 1, 1, 4],
         [0, 0, 1, 4, 4],
         [0, 0, 3, 3, 4],
         [0, 0, 3, 3, 4]]])
```

`scipy.ndimage.morphology.`**`generate_binary_structure`**`(`*rank*, *connectivity*`)`

Generate a binary structure for binary morphological operations.

Parameters **rank** : int

Number of dimensions of the array to which the structuring element will be applied, as returned by *np.ndim*.

connectivity : int

connectivity determines which elements of the output array belong to the structure, i.e. are considered as neighbors of the central element. Elements up to a squared distance of *connectivity* from the center are considered neighbors. *connectivity* may range from 1 (no diagonal elements are neighbors) to *rank* (all elements are neighbors).

Returns **output** : ndarray of bools

Structuring element which may be used for binary morphological operations, with *rank* dimensions and all dimensions equal to 3.

See also:

`iterate_structure`, `binary_dilation`, `binary_erosion`

Notes

`generate_binary_structure` can only create structuring elements with dimensions equal to 3, i.e. minimal dimensions. For larger structuring elements, that are useful e.g. for eroding large objects, one may either use `iterate_structure`, or create directly custom arrays with numpy functions such as `numpy.ones`.

Examples

```
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> a = np.zeros((5,5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> b = ndimage.binary_dilation(a, structure=struct).astype(a.dtype)
>>> b
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
```

```
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(b, structure=struct).astype(a.dtype)
array([[ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 1.,  1.,  1.,  1.,  1.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.]])
>>> struct = ndimage.generate_binary_structure(2, 2)
>>> struct
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
>>> struct = ndimage.generate_binary_structure(3, 1)
>>> struct # no diagonal elements
array([[[False, False, False],
        [False,  True, False],
        [False, False, False]],
       [[False,  True, False],
        [ True,  True,  True],
        [False,  True, False]],
       [[False, False, False],
        [False,  True, False],
        [False, False, False]]], dtype=bool)
```

`scipy.ndimage.morphology.`**`grey_closing`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional greyscale closing.

A greyscale closing consists in the succession of a greyscale dilation, and a greyscale erosion.

Parameters

input : array_like
  Array over which the grayscale closing is to be computed.

size : tuple of ints
  Shape of a flat and full structuring element used for the grayscale closing. Optional if *footprint* or *structure* is provided.

footprint : array of ints, optional
  Positions of non-infinite elements of a flat structuring element used for the grayscale closing.

structure : array of ints, optional
  Structuring element used for the grayscale closing. *structure* may be a non-flat structuring element.

output : array, optional
  An array used for storing the ouput of the closing may be provided.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
  The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
  Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional
  The *origin* parameter controls the placement of the filter. Default 0

Returns

grey_closing : ndarray
  Result of the grayscale closing of *input* with *structure*.

See also:

`binary_closing`, `grey_dilation`, `grey_erosion`, `grey_opening`, `generate_binary_structure`

Notes

The action of a grayscale closing with a flat structuring element amounts to smoothen deep local minima, whereas binary closing fills small holes.

References

[R119]

Examples

```
>>> a = np.arange(36).reshape((6,6))
>>> a[3,3] = 0
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20,  0, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_closing(a, size=(3,3))
array([[ 7,  7,  8,  9, 10, 11],
       [ 7,  7,  8,  9, 10, 11],
       [13, 13, 14, 15, 16, 17],
       [19, 19, 20, 20, 22, 23],
       [25, 25, 26, 27, 28, 29],
       [31, 31, 32, 33, 34, 35]])
>>> # Note that the local minimum a[3,3] has disappeared
```

`scipy.ndimage.morphology.`**`grey_dilation`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a greyscale dilation, using either a structuring element, or a footprint corresponding to a flat structuring element.

Grayscale dilation is a mathematical morphology operation. For the simple case of a full and flat structuring element, it can be viewed as a maximum filter over a sliding window.

Parameters

input : array_like
  Array over which the grayscale dilation is to be computed.

size : tuple of ints
  Shape of a flat and full structuring element used for the grayscale dilation. Optional if *footprint* or *structure* is provided.

footprint : array of ints, optional
  Positions of non-infinite elements of a flat structuring element used for the grayscale dilation. Non-zero values give the set of neighbors of the center over which the maximum is chosen.

structure : array of ints, optional
  Structuring element used for the grayscale dilation. *structure* may be a non-flat structuring element.

output : array, optional
  An array used for storing the ouput of the dilation may be provided.

mode : {'reflect','constant','nearest','mirror', 'wrap'}, optional
  The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
  Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional
  The *origin* parameter controls the placement of the filter. Default 0

Returns **grey_dilation** : ndarray
Grayscale dilation of *input*.

See also:

`binary_dilation`, `grey_erosion`, `grey_closing`, `grey_opening`, `generate_binary_structure`, `ndimage.maximum_filter`

Notes

The grayscale dilation of an image input by a structuring element s defined over a domain E is given by:

(input+s)(x) = max {input(y) + s(x-y), for y in E}

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale dilation computes the maximum of the input image inside a sliding window defined by E.

Grayscale dilation [R120] is a *mathematical morphology* operation [R121].

References

[R120], [R121]

Examples

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[2:5, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, footprint=np.ones((3,3)))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> s = ndimage.generate_binary_structure(2,1)
>>> s
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> ndimage.grey_dilation(a, footprint=s)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
```

```
           [0, 1, 1, 3, 2, 1, 0],
           [0, 1, 1, 2, 2, 2, 0],
           [0, 0, 1, 1, 2, 0, 0],
           [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, size=(3,3), structure=np.ones((3,3)))
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 4, 3, 1],
       [1, 2, 2, 3, 3, 3, 1],
       [1, 2, 2, 3, 3, 3, 1],
       [1, 1, 1, 1, 1, 1, 1]])
```

`scipy.ndimage.morphology.`**`grey_erosion`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a greyscale erosion, using either a structuring element, or a footprint corresponding to a flat structuring element.

Grayscale erosion is a mathematical morphology operation. For the simple case of a full and flat structuring element, it can be viewed as a minimum filter over a sliding window.

Parameters

input : array_like
  Array over which the grayscale erosion is to be computed.

size : tuple of ints
  Shape of a flat and full structuring element used for the grayscale erosion. Optional if *footprint* or *structure* is provided.

footprint : array of ints, optional
  Positions of non-infinite elements of a flat structuring element used for the grayscale erosion. Non-zero values give the set of neighbors of the center over which the minimum is chosen.

structure : array of ints, optional
  Structuring element used for the grayscale erosion. *structure* may be a non-flat structuring element.

output : array, optional
  An array used for storing the ouput of the erosion may be provided.

mode : {'reflect','constant','nearest','mirror', 'wrap'}, optional
  The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
  Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional
  The *origin* parameter controls the placement of the filter. Default 0

Returns

output : ndarray
  Grayscale erosion of *input*.

See also:

`binary_erosion`, `grey_dilation`, `grey_opening`, `grey_closing`, `generate_binary_structure`, `ndimage.minimum_filter`

Notes

The grayscale erosion of an image input by a structuring element s defined over a domain E is given by:

(input+s)(x) = min {input(y) - s(x-y), for y in E}

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale erosion computes the minimum of the input image inside a sliding window defined by E.

Grayscale erosion [R122] is a *mathematical morphology* operation [R123].

References

[R122], [R123]

Examples

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1:6, 1:6] = 3
>>> a[4,4] = 2; a[2,3] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 1, 3, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 3, 2, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> footprint = ndimage.generate_binary_structure(2, 1)
>>> footprint
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> # Diagonally-connected elements are not considered neighbors
>>> ndimage.grey_erosion(a, size=(3,3), footprint=footprint)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 1, 2, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`grey_opening`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional greyscale opening.

A greyscale opening consists in the succession of a greyscale erosion, and a greyscale dilation.

Parameters **input** : array_like

Array over which the grayscale opening is to be computed.

size : tuple of ints

Shape of a flat and full structuring element used for the grayscale opening. Optional if *footprint* or *structure* is provided.

footprint : array of ints, optional

Positions of non-infinite elements of a flat structuring element used for the grayscale opening.

structure : array of ints, optional

Structuring element used for the grayscale opening. *structure* may be a non-flat structuring element.

output : array, optional
An array used for storing the ouput of the opening may be provided.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default 0

Returns **grey_opening** : ndarray
Result of the grayscale opening of *input* with *structure*.

See also:

`binary_opening`, `grey_dilation`, `grey_erosion`, `grey_closing`, `generate_binary_structure`

Notes

The action of a grayscale opening with a flat structuring element amounts to smoothen high local maxima, whereas binary opening erases small objects.

References

[R124]

Examples

```
>>> a = np.arange(36).reshape((6,6))
>>> a[3, 3] = 50
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 50, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_opening(a, size=(3,3))
array([[ 0,  1,  2,  3,  4,  4],
       [ 6,  7,  8,  9, 10, 10],
       [12, 13, 14, 15, 16, 16],
       [18, 19, 20, 22, 22, 22],
       [24, 25, 26, 27, 28, 28],
       [24, 25, 26, 27, 28, 28]])
>>> # Note that the local maximum a[3,3] has disappeared
```

`scipy.ndimage.morphology.`**`iterate_structure`**(*structure*, *iterations*, *origin=None*)

Iterate a structure by dilating it with itself.

Parameters **structure** : array_like
Structuring element (an array of bools, for example), to be dilated with itself.

iterations : int
number of dilations performed on the structure with itself

origin : optional
If origin is None, only the iterated structure is returned. If not, a tuple of the iterated structure and the modified origin is returned.

Returns **iterate_structure** : ndarray of bools
A new structuring element obtained by dilating *structure* (*iterations* - 1) times with itself.

See also:

`generate_binary_structure`

Examples

```
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct.astype(int)
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
>>> ndimage.iterate_structure(struct, 2).astype(int)
array([[0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0]])
>>> ndimage.iterate_structure(struct, 3).astype(int)
array([[0, 0, 0, 1, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1, 1, 1],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`morphological_gradient`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional morphological gradient.

The morphological gradient is calculated as the difference between a dilation and an erosion of the input with a given structuring element.

Parameters **input** : array_like

Array over which to compute the morphlogical gradient.

size : tuple of ints

Shape of a flat and full structuring element used for the mathematical morphology operations. Optional if *footprint* or *structure* is provided. A larger *size* yields a more blurred gradient.

footprint : array of ints, optional

Positions of non-infinite elements of a flat structuring element used for the morphology operations. Larger footprints give a more blurred morphological gradient.

structure : array of ints, optional

Structuring element used for the morphology operations. *structure* may be a non-flat structuring element.

output : array, optional

An array used for storing the ouput of the morphological gradient may be provided.

mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional

The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval : scalar, optional

Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin : scalar, optional

The *origin* parameter controls the placement of the filter. Default 0

Returns **morphological_gradient** : ndarray

Morphological gradient of *input*.

See also:

`grey_dilation`, `grey_erosion`, `ndimage.gaussian_gradient_magnitude`

Notes

For a flat structuring element, the morphological gradient computed at a given point corresponds to the maximal difference between elements of the input among the elements covered by the structuring element centered on the point.

References

[R125]

Examples

```
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[2:5, 2:5] = 1
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 0, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # The morphological gradient is computed as the difference
>>> # between a dilation and an erosion
>>> ndimage.grey_dilation(a, size=(3,3)) -\
...  ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 0, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[2:5, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 2, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

`scipy.ndimage.morphology.`**`morphological_laplace`**(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)

Multi-dimensional morphological laplace.

Parameters **input** : array_like
Input.
size : int or sequence of ints, optional
See *structure*.
footprint : bool or ndarray, optional
See *structure*.
structure : structure, optional
Either *size*, *footprint*, or the *structure* must be provided.
output : ndarray, optional
An output array can optionally be provided.
mode : {'reflect','constant','nearest','mirror', 'wrap'}, optional
The mode parameter determines how the array borders are handled. For 'constant' mode, values beyond borders are set to be *cval*. Default is 'reflect'.
cval : scalar, optional
Value to fill past edges of input if mode is 'constant'. Default is 0.0
origin : origin, optional
The origin parameter controls the placement of the filter.

Returns **morphological_laplace** : ndarray
Output

`scipy.ndimage.morphology.`**`white_tophat`**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multi-dimensional white tophat filter.

Parameters **input** : array_like
Input.
size : tuple of ints
Shape of a flat and full structuring element used for the filter. Optional if *footprint* or *structure* is provided.
footprint : array of ints, optional
Positions of elements of a flat structuring element used for the white tophat filter.
structure : array of ints, optional
Structuring element used for the filter. *structure* may be a non-flat structuring element.
output : array, optional
An array used for storing the output of the filter may be provided.
mode : {'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional
The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval : scalar, optional
Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.
origin : scalar, optional
The *origin* parameter controls the placement of the filter. Default is 0.

Returns **output** : ndarray
Result of the filter of *input* with *structure*.

See also:

`black_tophat`

5.22.6 Utility

`imread`(fname[, flatten, mode])	Read an image from a file as an array.

`scipy.ndimage.`**`imread`**(*fname*, *flatten=False*, *mode=None*)

Read an image from a file as an array.

Parameters **fname** : str

Image file name, e.g. `test.jpg`, or a file object.

flatten : bool, optional

If true, convert the output to grey-scale. Default is False.

mode : str, optional

mode to convert image to, e.g. `RGB`.

Returns **img_array** : ndarray

The different colour bands/channels are stored in the third dimension, such that a grey-image is MxN, an RGB-image MxNx3 and an RGBA-image MxNx4.

Raises **ImportError**

If the Python Imaging Library (PIL) can not be imported.

5.23 Orthogonal distance regression (`scipy.odr`)

5.23.1 Package Content

`Data`(x[, y, we, wd, fix, meta])	The data to fit.
`RealData`(x[, y, sx, sy, covx, covy, fix, meta])	The data, with weightings as actual standard deviations and/or covariances.
`Model`(fcn[, fjacb, fjacd, extra_args, ...])	The Model class stores information about the function you wish to fit.
`ODR`(data, model[, beta0, delta0, ifixb, ...])	The ODR class gathers all information and coordinates the running of the main fitti
`Output`(output)	The Output class stores the output of an ODR run.
`odr`(fcn, beta0, y, x[, we, wd, fjacb, ...])	Low-level function for ODR.
`odr_error`	Exception indicating an error in fitting.
`odr_stop`	Exception stopping fitting.

class `scipy.odr.`**`Data`**(*x*, *y=None*, *we=None*, *wd=None*, *fix=None*, *meta={}*)

The data to fit.

Parameters **x** : array_like

Input data for regression.

y : array_like, optional

Input data for regression.

we : array_like, optional

If *we* is a scalar, then that value is used for all data points (and all dimensions of the response variable). If *we* is a rank-1 array of length q (the dimensionality of the response variable), then this vector is the diagonal of the covariant weighting matrix for all data points. If *we* is a rank-1 array of length n (the number of data points), then the i'th element is the weight for the i'th response variable observation (single-dimensional only). If *we* is a rank-2 array of shape (q, q), then this is the full covariant weighting matrix broadcast to each observation. If *we* is a rank-2 array of shape (q, n), then *we[:,i]* is the diagonal of the covariant weighting matrix for the i'th observation. If *we* is a rank-3 array of shape (q, q, n), then *we[:,:,i]* is the full specification of the covariant weighting matrix for each observation. If the fit is implicit, then only a positive scalar value is used.

wd : array_like, optional

If *wd* is a scalar, then that value is used for all data points (and all dimensions of the input variable). If *wd* = 0, then the covariant weighting matrix for each observation is set to the identity matrix (so each dimension of each observation has the same weight). If *wd* is a rank-1 array of length m (the dimensionality of the input variable), then this vector is the diagonal of the covariant weighting matrix for all data points. If *wd* is a rank-1 array of length n (the number of data points), then the i'th element is the weight for the i'th input variable observation (single-dimensional only). If *wd* is a rank-2 array of shape (m, m), then this is the full covariant weighting matrix broadcast to each observation. If *wd* is a rank-2 array of shape (m, n), then *wd[:,i]* is the diagonal of the covariant weighting matrix for the i'th observation. If *wd* is a rank-3 array of shape (m, m, n), then *wd[:,:,i]* is the full specification of the covariant weighting matrix for each observation.

fix : array_like of ints, optional

The *fix* argument is the same as ifixx in the class ODR. It is an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

meta : dict, optional

Free-form dictionary for metadata.

Notes

Each argument is attached to the member of the instance of the same name. The structures of *x* and *y* are described in the Model class docstring. If *y* is an integer, then the Data instance can only be used to fit with implicit models where the dimensionality of the response is equal to the specified value of *y*.

The *we* argument weights the effect a deviation in the response variable has on the fit. The *wd* argument weights the effect a deviation in the input variable has on the fit. To handle multidimensional inputs and responses easily, the structure of these arguments has the n'th dimensional axis first. These arguments heavily use the structured arguments feature of ODRPACK to conveniently and flexibly support all options. See the ODRPACK User's Guide for a full explanation of how these weights are used in the algorithm. Basically, a higher value of the weight for a particular data point makes a deviation at that point more detrimental to the fit.

Methods

`set_meta`(**kwds)	Update the metadata dictionary with the keywords and data provided by keywords.

`Data.`**`set_meta`**`(`***kwds*`)`

Update the metadata dictionary with the keywords and data provided by keywords.

Examples

```
>>> data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

class `scipy.odr.`**`RealData`**`(`*x*, *y=None*, *sx=None*, *sy=None*, *covx=None*, *covy=None*, *fix=None*, *meta={}*`)`

The data, with weightings as actual standard deviations and/or covariances.

Parameters

x : array_like

x

y : array_like, optional

y

sx, sy : array_like, optional

Standard deviations of *x*. *sx* are standard deviations of *x* and are converted to weights by dividing 1.0 by their squares.

sy : array_like, optional

Standard deviations of *y*. *sy* are standard deviations of *y* and are converted to weights by dividing 1.0 by their squares.

covx : array_like, optional
Covariance of *x covx* is an array of covariance matrices of *x* and are converted to weights by performing a matrix inversion on each observation's covariance matrix.

covy : array_like, optional
Covariance of *y covy* is an array of covariance matrices and are converted to weights by performing a matrix inversion on each observation's covariance matrix.

fix : array_like, optional
The argument and member fix is the same as Data.fix and ODR.ifixx: It is an array of integers with the same shape as *x* that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

meta : dict, optional
Free-form dictionary for metadata.

Notes

The weights *wd* and *we* are computed from provided values as follows:

sx and *sy* are converted to weights by dividing 1.0 by their squares. For example, `wd = 1./numpy.power('sx', 2)`.

covx and *covy* are arrays of covariance matrices and are converted to weights by performing a matrix inversion on each observation's covariance matrix. For example, `we[i] = numpy.linalg.inv(covy[i])`.

These arguments follow the same structured argument conventions as wd and we only restricted by their natures: *sx* and *sy* can't be rank-3, but *covx* and *covy* can be.

Only set *either sx* or *covx* (not both). Setting both will raise an exception. Same with *sy* and *covy*.

Methods

`set_meta`(**kwds)	Update the metadata dictionary with the keywords and data provided by keywords.

`RealData.`**`set_meta`**`(`***kwds*`)`
Update the metadata dictionary with the keywords and data provided by keywords.

Examples

```
>>> data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

class `scipy.odr.`**`Model`**(*fcn*, *fjacb=None*, *fjacd=None*, *extra_args=None*, *estimate=None*, *implicit=0*, *meta=None*)
The Model class stores information about the function you wish to fit.

It stores the function itself, at the least, and optionally stores functions which compute the Jacobians used during fitting. Also, one can provide a function that will provide reasonable starting values for the fit parameters possibly given the set of data.

Parameters

fcn : function
fcn(beta, x) –> y

fjacb : function
Jacobian of fcn wrt the fit parameters beta.
fjacb(beta, x) –> @f_i(x,B)/@B_j

fjacd : function
Jacobian of fcn wrt the (possibly multidimensional) input variable.
fjacd(beta, x) –> @f_i(x,B)/@x_j

extra_args : tuple, optional

If specified, *extra_args* should be a tuple of extra arguments to pass to *fcn*, *fjacb*, and *fjacd*. Each will be called by *apply(fcn, (beta, x) + extra_args)*

estimate : array_like of rank-1
Provides estimates of the fit parameters from the data
estimate(data) –> estbeta

implicit : boolean
If TRUE, specifies that the model is implicit; i.e *fcn(beta, x)* ~= 0 and there is no y data to fit against

meta : dict, optional
freeform dictionary of metadata for the model

Notes

Note that the *fcn*, *fjacb*, and *fjacd* operate on NumPy arrays and return a NumPy array. The *estimate* object takes an instance of the Data class.

Here are the rules for the shapes of the argument and return arrays of the callback functions:

x	if the input data is single-dimensional, then *x* is rank-1 array; i.e. `x = array([1, 2, 3, ...]); x.shape = (n,)` If the input data is multi-dimensional, then *x* is a rank-2 array; i.e., `x = array([[1, 2, ...], [2, 4, ...]]); x.shape = (m, n)`. In all cases, it has the same shape as the input data array passed to `odr`. *m* is the dimensionality of the input data, *n* is the number of observations.
y	if the response variable is single-dimensional, then *y* is a rank-1 array, i.e., `y = array([2, 4, ...]); y.shape = (n,)`. If the response variable is multi-dimensional, then *y* is a rank-2 array, i.e., `y = array([[2, 4, ...], [3, 6, ...]]); y.shape = (q, n)` where *q* is the dimensionality of the response variable.
beta	rank-1 array of length *p* where *p* is the number of parameters; i.e. `beta = array([B_1, B_2, ..., B_p])`
fjacb	if the response variable is multi-dimensional, then the return array's shape is *(q, p, n)* such that `fjacb(x,beta)[l,k,i] = d f_l(X,B)/d B_k` evaluated at the i'th data point. If *q == 1*, then the return array is only rank-2 and with shape *(p, n)*.
fjacd	as with fjacb, only the return array's shape is *(q, m, n)* such that `fjacd(x,beta)[l,j,i] = d f_l(X,B)/d X_j` at the i'th data point. If *q == 1*, then the return array's shape is *(m, n)*. If *m == 1*, the shape is (q, n). If *m == q == 1*, the shape is *(n,)*.

Methods

`set_meta`(**kwds)	Update the metadata dictionary with the keywords and data provided here.

`Model.`**`set_meta`**`(`***kwds*`)`
Update the metadata dictionary with the keywords and data provided here.

Examples

set_meta(name="Exponential", equation="y = a exp(b x) + c")

class `scipy.odr.`**`ODR`**`(`*data*, *model*, *beta0=None*, *delta0=None*, *ifixb=None*, *ifixx=None*, *job=None*, *iprint=None*, *errfile=None*, *rptfile=None*, *ndigit=None*, *taufac=None*, *sstol=None*, *partol=None*, *maxit=None*, *stpb=None*, *stpd=None*, *sclb=None*, *scld=None*, *work=None*, *iwork=None*`)`

The ODR class gathers all information and coordinates the running of the main fitting routine.

Members of instances of the ODR class have the same names as the arguments to the initialization routine.

Parameters **data** : Data class instance

instance of the Data class

model : Model class instance

instance of the Model class

Other Parameters

beta0 : array_like of rank-1

a rank-1 sequence of initial parameter values. Optional if model provides an "estimate" function to estimate these values.

delta0 : array_like of floats of rank-1, optional

a (double-precision) float array to hold the initial values of the errors in the input variables. Must be same shape as data.x

ifixb : array_like of ints of rank-1, optional

sequence of integers with the same length as beta0 that determines which parameters are held fixed. A value of 0 fixes the parameter, a value > 0 makes the parameter free.

ifixx : array_like of ints with same shape as data.x, optional

an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

job : int, optional

an integer telling ODRPACK what tasks to perform. See p. 31 of the ODRPACK User's Guide if you absolutely must set the value here. Use the method set_job post-initialization for a more readable interface.

iprint : int, optional

an integer telling ODRPACK what to print. See pp. 33-34 of the ODRPACK User's Guide if you absolutely must set the value here. Use the method set_iprint post-initialization for a more readable interface.

errfile : str, optional

string with the filename to print ODRPACK errors to. *Do Not Open This File Yourself!*

rptfile : str, optional

string with the filename to print ODRPACK summaries to. *Do Not Open This File Yourself!*

ndigit : int, optional

integer specifying the number of reliable digits in the computation of the function.

taufac : float, optional

float specifying the initial trust region. The default value is 1. The initial trust region is equal to taufac times the length of the first computed Gauss-Newton step. taufac must be less than 1.

sstol : float, optional

float specifying the tolerance for convergence based on the relative change in the sum-of-squares. The default value is eps**(1/2) where eps is the smallest value such that 1 + eps > 1 for double precision computation on the machine. sstol must be less than 1.

partol : float, optional

float specifying the tolerance for convergence based on the relative change in the estimated parameters. The default value is eps**(2/3) for explicit models and `eps**(1/3)` for implicit models. partol must be less than 1.

maxit : int, optional

integer specifying the maximum number of iterations to perform. For first runs, maxit is the total number of iterations performed and defaults to 50. For restarts, maxit is the number of additional iterations to perform and defaults to 10.

stpb : array_like, optional

sequence (`len(stpb) == len(beta0)`) of relative step sizes to compute finite difference derivatives wrt the parameters.

stpd : optional

array (`stpd.shape == data.x.shape` or `stpd.shape == (m,)`) of relative step sizes to compute finite difference derivatives wrt the input variable errors. If stpd is a rank-1 array with length m (the dimensionality of the input variable), then the values are broadcast to all observations.

sclb : array_like, optional

sequence (`len(stpb) == len(beta0)`) of scaling factors for the parameters. The purpose of these scaling factors are to scale all of the parameters to around unity. Normally appropriate scaling factors are computed if this argument is not specified. Specify them yourself if the automatic procedure goes awry.

scld : array_like, optional

array (scld.shape == data.x.shape or scld.shape == (m,)) of scaling factors for the *errors* in the input variables. Again, these factors are automatically computed if you do not provide them. If scld.shape == (m,), then the scaling factors are broadcast to all observations.

work : ndarray, optional

array to hold the double-valued working data for ODRPACK. When restarting, takes the value of self.output.work.

iwork : ndarray, optional

array to hold the integer-valued working data for ODRPACK. When restarting, takes the value of self.output.iwork.

Attributes

data	(Data) The data for this fit
model	(Model) The model used in fit
output	(Output) An instance if the Output class containing all of the returned data from an invocation of ODR.run() or ODR.restart()

Methods

`restart`([iter])	Restarts the run with iter more iterations.
`run`()	Run the fitting routine with all of the information given.
`set_iprint`([init, so_init, iter, so_iter, ...])	Set the iprint parameter for the printing of computation reports.
`set_job`([fit_type, deriv, var_calc, ...])	Sets the “job” parameter is a hopefully comprehensible way.

`ODR.`**`restart`**(*iter=None*)

Restarts the run with iter more iterations.

Parameters **iter** : int, optional

ODRPACK’s default for the number of new iterations is 10.

Returns **output** : Output instance

This object is also assigned to the attribute .output .

`ODR.`**`run`**()

Run the fitting routine with all of the information given.

Returns **output** : Output instance

This object is also assigned to the attribute .output .

`ODR.`**`set_iprint`**(*init=None*, *so_init=None*, *iter=None*, *so_iter=None*, *iter_step=None*, *final=None*, *so_final=None*)

Set the iprint parameter for the printing of computation reports.

If any of the arguments are specified here, then they are set in the iprint member. If iprint is not set manually or with this method, then ODRPACK defaults to no printing. If no filename is specified with the member rptfile, then ODRPACK prints to stdout. One can tell ODRPACK to print to stdout in addition to the specified filename by setting the so_* arguments to this function, but one cannot specify to print to stdout but not a file since one can do that by not specifying a rptfile filename.

There are three reports: initialization, iteration, and final reports. They are represented by the arguments init, iter, and final respectively. The permissible values are 0, 1, and 2 representing "no report", "short report", and "long report" respectively.

The argument iter_step (0 <= iter_step <= 9) specifies how often to make the iteration report; the report will be made for every iter_step'th iteration starting with iteration one. If iter_step == 0, then no iteration report is made, regardless of the other arguments.

If the rptfile is None, then any so_* arguments supplied will raise an exception.

`ODR.`**`set_job`**(*fit_type=None*, *deriv=None*, *var_calc=None*, *del_init=None*, *restart=None*)

Sets the "job" parameter is a hopefully comprehensible way.

If an argument is not specified, then the value is left as is. The default value from class initialization is for all of these options set to 0.

Parameters **fit_type** : {0, 1, 2} int

0 -> explicit ODR
1 -> implicit ODR
2 -> ordinary least-squares

deriv : {0, 1, 2, 3} int

0 -> forward finite differences
1 -> central finite differences
2 -> user-supplied derivatives (Jacobians) with results
checked by ODRPACK
3 -> user-supplied derivatives, no checking

var_calc : {0, 1, 2} int

0 -> calculate asymptotic covariance matrix and fit
parameter uncertainties (V_B, s_B) using derivatives recomputed at the final solution
1 -> calculate V_B and s_B using derivatives from last iteration
2 -> do not calculate V_B and s_B

del_init : {0, 1} int

0 -> initial input variable offsets set to 0
1 -> initial offsets provided by user in variable "work"

restart : {0, 1} int

0 -> fit is not a restart
1 -> fit is a restart

Notes

The permissible values are different from those given on pg. 31 of the ODRPACK User's Guide only in that one cannot specify numbers greater than the last value for each variable.

If one does not supply functions to compute the Jacobians, the fitting procedure will change deriv to 0, finite differences, as a default. To initialize the input variable offsets by yourself, set del_init to 1 and put the offsets into the "work" variable correctly.

class `scipy.odr.`**`Output`**(*output*)

The Output class stores the output of an ODR run.

Notes

Takes one argument for initialization, the return value from the function `odr`. The attributes listed as "optional" above are only present if `odr` was run with `full_output=1`.

Attributes

beta	(ndarray) Estimated parameter values, of shape (q,).
sd_beta	(ndarray) Standard errors of the estimated parameters, of shape (p,).
cov_beta	(ndarray) Covariance matrix of the estimated parameters, of shape (p,p).
delta	(ndarray, optional) Array of estimated errors in input variables, of same shape as *x*.
eps	(ndarray, optional) Array of estimated errors in response variables, of same shape as *y*.
xplus	(ndarray, optional) Array of `x + delta`.
y	(ndarray, optional) Array `y = fcn(x + delta)`.
res_var	(float, optional) Residual variance.
sum_sqare	(float, optional) Sum of squares error.
sum_square_delta	(float, optional) Sum of squares of delta error.
sum_square_eps	(float, optional) Sum of squares of eps error.
inv_condnum	(float, optional) Inverse condition number (cf. ODRPACK UG p. 77).
rel_error	(float, optional) Relative error in function values computed within fcn.
work	(ndarray, optional) Final work array.
work_ind	(dict, optional) Indices into work for drawing out values (cf. ODRPACK UG p. 83).
info	(int, optional) Reason for returning, as output by ODRPACK (cf. ODRPACK UG p. 38).
stopreason	(list of str, optional) *info* interpreted into English.

Methods

`pprint`()	Pretty-print important results.

`Output.`**`pprint`**`()`

Pretty-print important results.

`scipy.odr.`**`odr`**`(`*fcn*, *beta0*, *y*, *x*, *we=None*, *wd=None*, *fjacb=None*, *fjacd=None*, *extra_args=None*, *ifixx=None*, *ifixb=None*, *job=0*, *iprint=0*, *errfile=None*, *rptfile=None*, *ndigit=0*, *taufac=0.0*, *sstol=-1.0*, *partol=-1.0*, *maxit=-1*, *stpb=None*, *stpd=None*, *sclb=None*, *scld=None*, *work=None*, *iwork=None*, *full_output=0*`)`

Low-level function for ODR.

See also:

`ODR`, `Model`, `Data`, `RealData`

Notes

This is a function performing the same operation as the `ODR`, `Model` and `Data` classes together. The parameters of this function are explained in the class documentation.

exception `scipy.odr.`**`odr_error`**

Exception indicating an error in fitting.

This is raised by `scipy.odr` if an error occurs during fitting.

exception `scipy.odr.`**`odr_stop`**

Exception stopping fitting.

You can raise this exception in your objective function to tell `scipy.odr` to stop fitting.

5.23.2 Usage information

Introduction

Why Orthogonal Distance Regression (ODR)? Sometimes one has measurement errors in the explanatory (a.k.a., “independent”) variable(s), not just the response (a.k.a., “dependent”) variable(s). Ordinary Least Squares (OLS) fitting procedures treat the data for explanatory variables as fixed, i.e., not subject to error of any kind. Furthermore, OLS procedures require that the response variables be an explicit function of the explanatory variables; sometimes making the equation explicit is impractical and/or introduces errors. ODR can handle both of these cases with ease, and can even reduce to the OLS case if that is sufficient for the problem.

ODRPACK is a FORTRAN-77 library for performing ODR with possibly non-linear fitting functions. It uses a modified trust-region Levenberg-Marquardt-type algorithm [R468] to estimate the function parameters. The fitting functions are provided by Python functions operating on NumPy arrays. The required derivatives may be provided by Python functions as well, or may be estimated numerically. ODRPACK can do explicit or implicit ODR fits, or it can do OLS. Input and output variables may be multi-dimensional. Weights can be provided to account for different variances of the observations, and even covariances between dimensions of the variables.

The `scipy.odr` package offers an object-oriented interface to ODRPACK, in addition to the low-level `odr` function.

Additional background information about ODRPACK can be found in the ODRPACK User’s Guide, reading which is recommended.

Basic usage

1. Define the function you want to fit against.:

```
def f(B, x):
    '''Linear function y = m*x + b'''
    # B is a vector of the parameters.
    # x is an array of the current x values.
    # x is in the same format as the x passed to Data or RealData.
    #
    # Return an array in the same format as y passed to Data or RealData.
    return B[0]*x + B[1]
```

2. Create a Model.:

```
linear = Model(f)
```

3. Create a Data or RealData instance.:

```
mydata = Data(x, y, wd=1./power(sx,2), we=1./power(sy,2))
```

   or, when the actual covariances are known:

```
mydata = RealData(x, y, sx=sx, sy=sy)
```

4. Instantiate ODR with your data, model and initial parameter estimate.:

```
myodr = ODR(mydata, linear, beta0=[1., 2.])
```

5. Run the fit.:

```
myoutput = myodr.run()
```

6. Examine output.:

```
myoutput.pprint()
```

References

5.24 Optimization and root finding (`scipy.optimize`)

5.24.1 Optimization

Local Optimization

`minimize`(fun, x0[, args, method, jac, hess, ...])	Minimization of scalar function of one or more variables.
`minimize_scalar`(fun[, bracket, bounds, ...])	Minimization of scalar function of one variable.
`OptimizeResult`	Represents the optimization result.

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method=None*, *jac=None*, *hess=None*, *hessp=None*, *bounds=None*, *constraints=()*, *tol=None*, *callback=None*, *options=None*)

Minimization of scalar function of one or more variables.

In general, the optimization problems are of the form:

minimize f(x)

subject to:

`g_i(x) >= 0`, i = 1,...,m `h_j(x) = 0`, j = 1,...,p

Where x is a vector of one or more variables. `g_i(x)` are the inequality constraints. `h_j(x)` are the equality constrains.

Optionally, the lower and upper bounds for each element in x can also be specified using the *bounds* argument.

Parameters

fun : callable
Objective function.

x0 : ndarray
Initial guess.

args : tuple, optional
Extra arguments passed to the objective function and its derivatives (Jacobian, Hessian).

method : str or callable, optional
Type of solver. Should be one of

- ‘Nelder-Mead’ *(see here)*
- ‘Powell’ *(see here)*
- ‘CG’ *(see here)*
- ‘BFGS’ *(see here)*
- ‘Newton-CG’ *(see here)*
- ‘L-BFGS-B’ *(see here)*
- ‘TNC’ *(see here)*
- ‘COBYLA’ *(see here)*
- ‘SLSQP’ *(see here)*
- ‘dogleg’ *(see here)*
- ‘trust-ncg’ *(see here)*
- custom - a callable object (added in version 0.14.0), see below for description.

If not given, chosen to be one of `BFGS`, `L-BFGS-B`, `SLSQP`, depending if the problem has constraints or bounds.

jac : bool or callable, optional

Jacobian (gradient) of objective function. Only for CG, BFGS, Newton-CG, L-BFGS-B, TNC, SLSQP, dogleg, trust-ncg. If *jac* is a Boolean and is True, *fun* is assumed to return the gradient along with the objective function. If False, the gradient will be estimated numerically. *jac* can also be a callable returning the gradient of the objective. In this case, it must accept the same arguments as *fun*.

hess, hessp : callable, optional

Hessian (matrix of second-order derivatives) of objective function or Hessian of objective function times an arbitrary vector p. Only for Newton-CG, dogleg, trust-ncg. Only one of *hessp* or *hess* needs to be given. If *hess* is provided, then *hessp* will be ignored. If neither *hess* nor *hessp* is provided, then the Hessian product will be approximated using finite differences on *jac*. *hessp* must compute the Hessian times an arbitrary vector.

bounds : sequence, optional

Bounds for variables (only for L-BFGS-B, TNC and SLSQP). `(min, max)` pairs for each element in `x`, defining the bounds on that parameter. Use None for one of `min` or `max` when there is no bound in that direction.

constraints : dict or sequence of dict, optional

Constraints definition (only for COBYLA and SLSQP). Each constraint is defined in a dictionary with fields:

type	[str] Constraint type: 'eq' for equality, 'ineq' for inequality.
fun	[callable] The function defining the constraint.
jac	[callable, optional] The Jacobian of *fun* (only for SLSQP).
args	[sequence, optional] Extra arguments to be passed to the function and Jacobian.

Equality constraint means that the constraint function result is to be zero whereas inequality means that it is to be non-negative. Note that COBYLA only supports inequality constraints.

tol : float, optional

Tolerance for termination. For detailed control, use solver-specific options.

options : dict, optional

A dictionary of solver options. All methods accept the following generic options:

maxiter	[int] Maximum number of iterations to perform.
disp	[bool] Set to True to print convergence messages.

For method-specific options, see `show_options`.

callback : callable, optional

Called after each iteration, as `callback(xk)`, where `xk` is the current parameter vector.

Returns **res** : OptimizeResult

The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

`minimize_scalar`

Interface to minimization algorithms for scalar univariate functions

`show_options`

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *BFGS*.

Unconstrained minimization

Method *Nelder-Mead* uses the Simplex algorithm [R142], [R143]. This algorithm has been successful in many applications but other algorithms using the first and/or second derivatives information might be preferred for their better performances and robustness in general.

Method *Powell* is a modification of Powell's method [R144], [R145] which is a conjugate direction method. It performs sequential one-dimensional minimizations along each vector of the directions set (*direc* field in *options* and *info*), which is updated at each iteration of the main minimization loop. The function need not be differentiable, and no derivatives are taken.

Method *CG* uses a nonlinear conjugate gradient algorithm by Polak and Ribiere, a variant of the Fletcher-Reeves method described in [R146] pp. 120-122. Only the first derivatives are used.

Method *BFGS* uses the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS) [R146] pp. 136. It uses the first derivatives only. BFGS has proven good performance even for non-smooth optimizations. This method also returns an approximation of the Hessian inverse, stored as *hess_inv* in the OptimizeResult object.

Method *Newton-CG* uses a Newton-CG algorithm [R146] pp. 168 (also known as the truncated Newton method). It uses a CG method to the compute the search direction. See also *TNC* method for a box-constrained minimization with a similar algorithm.

Method *dogleg* uses the dog-leg trust-region algorithm [R146] for unconstrained minimization. This algorithm requires the gradient and Hessian; furthermore the Hessian is required to be positive definite.

Method *trust-ncg* uses the Newton conjugate gradient trust-region algorithm [R146] for unconstrained minimization. This algorithm requires the gradient and either the Hessian or a function that computes the product of the Hessian with a given vector.

Constrained minimization

Method *L-BFGS-B* uses the L-BFGS-B algorithm [R147], [R148] for bound constrained minimization.

Method *TNC* uses a truncated Newton algorithm [R146], [R149] to minimize a function with variables subject to bounds. This algorithm uses gradient information; it is also called Newton Conjugate-Gradient. It differs from the *Newton-CG* method described above as it wraps a C implementation and allows each variable to be given upper and lower bounds.

Method *COBYLA* uses the Constrained Optimization BY Linear Approximation (COBYLA) method [R150], [1], [2]. The algorithm is based on linear approximations to the objective function and each constraint. The method wraps a FORTRAN implementation of the algorithm. The constraints functions 'fun' may return either a single number or an array or list of numbers.

Method *SLSQP* uses Sequential Least SQuares Programming to minimize a function of several variables with any combination of bounds, equality and inequality constraints. The method wraps the SLSQP Optimization subroutine originally implemented by Dieter Kraft [3]. Note that the wrapper handles infinite values in bounds by converting them into large floating values.

Custom minimizers

---

[1] Powell M J D. Direct search algorithms for optimization calculations. 1998. Acta Numerica 7: 287-336.

[2] Powell M J D. A view of algorithms for optimization without derivatives. 2007.Cambridge University Technical Report DAMTP 2007/NA03

[3] Kraft, D. A software package for sequential quadratic programming. 1988. Tech. Rep. DFVLR-FB 88-28, DLR German Aerospace Center – Institute for Flight Mechanics, Koln, Germany.

It may be useful to pass a custom minimization method, for example when using a frontend to this method such as `scipy.optimize.basinhopping` or a different library. You can simply pass a callable as the `method` parameter.

The callable is called as `method(fun, x0, args, **kwargs, **options)` where `kwargs` corresponds to any other parameters passed to `minimize` (such as *callback*, *hess*, etc.), except the *options* dict, which has its contents also passed as *method* parameters pair by pair. Also, if *jac* has been passed as a bool type, *jac* and *fun* are mangled so that *fun* returns just the function values and *jac* is converted to a function returning the Jacobian. The method shall return an `OptimizeResult` object.

The provided *method* callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by `minimize` may expand in future versions and then these parameters will be passed to the method. You can find an example in the scipy.optimize tutorial.

New in version 0.11.0.

References

[R142], [R143], [R144], [R145], [R146], [R147], [R148], [R149], [R150], [10], [11], [12]

Examples

Let us consider the problem of minimizing the Rosenbrock function. This function (and its respective derivatives) is implemented in `rosen` (resp. `rosen_der`, `rosen_hess`) in the `scipy.optimize`.

```
>>> from scipy.optimize import minimize, rosen, rosen_der
```

A simple application of the *Nelder-Mead* method is:

```
>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> res = minimize(rosen, x0, method='Nelder-Mead')
>>> res.x
[ 1.  1.  1.  1.  1.]
```

Now using the *BFGS* algorithm, using the first derivative and a few options:

```
>>> res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
...                 options={'gtol': 1e-6, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 52
         Function evaluations: 64
         Gradient evaluations: 64
>>> res.x
array([ 1.  1.  1.  1.  1.])
>>> print(res.message)
Optimization terminated successfully.
>>> res.hess_inv
[[ 0.00749589  0.01255155  0.02396251  0.04750988  0.09495377]
 [ 0.01255155  0.02510441  0.04794055  0.09502834  0.18996269]
 [ 0.02396251  0.04794055  0.09631614  0.19092151  0.38165151]
 [ 0.04750988  0.09502834  0.19092151  0.38341252  0.7664427 ]
 [ 0.09495377  0.18996269  0.38165151  0.7664427   1.53713523]]
```

Next, consider a minimization problem with several constraints (namely Example 16.4 from [R146]). The objective function is:

```
>>> fun = lambda x: (x[0] - 1)**2 + (x[1] - 2.5)**2
```

There are three constraints defined as:

```
>>> cons = ({'type': 'ineq', 'fun': lambda x:  x[0] - 2 * x[1] + 2},
...         {'type': 'ineq', 'fun': lambda x: -x[0] - 2 * x[1] + 6},
...         {'type': 'ineq', 'fun': lambda x: -x[0] + 2 * x[1] + 2})
```

And variables must be positive, hence the following bounds:

```
>>> bnds = ((0, None), (0, None))
```

The optimization problem is solved using the SLSQP method as:

```
>>> res = minimize(fun, (2, 0), method='SLSQP', bounds=bnds,
...                constraints=cons)
```

It should converge to the theoretical solution (1.4 ,1.7).

`scipy.optimize.`**`minimize_scalar`**(*fun*, *bracket=None*, *bounds=None*, *args=()*, *method='brent'*, *tol=None*, *options=None*)

Minimization of scalar function of one variable.

Parameters

fun : callable

Objective function. Scalar function, must return a scalar.

bracket : sequence, optional

For methods 'brent' and 'golden', `bracket` defines the bracketing interval and can either have three items *(a, b, c)* so that $a < b < c$ and $fun(b) < fun(a), fun(c)$ or two items *a* and *c* which are assumed to be a starting interval for a downhill bracket search (see `bracket`); it doesn't always mean that the obtained solution will satisfy $a <= x <= c$.

bounds : sequence, optional

For method 'bounded', *bounds* is mandatory and must have two items corresponding to the optimization bounds.

args : tuple, optional

Extra arguments passed to the objective function.

method : str or callable, optional

Type of solver. Should be one of

- 'Brent' *(see here)*
- 'Bounded' *(see here)*
- 'Golden' *(see here)*
- custom - a callable object (added in version 0.14.0), see below

tol : float, optional

Tolerance for termination. For detailed control, use solver-specific options.

options : dict, optional

A dictionary of solver options.

maxiter	[int] Maximum number of iterations to perform.
disp	[bool] Set to True to print convergence messages.

See `show_options` for solver-specific options.

Returns

res : OptimizeResult

The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

`minimize`	Interface to minimization algorithms for scalar multivariate functions

show_options
Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *Brent*.

Method *Brent* uses Brent's algorithm to find a local minimum. The algorithm uses inverse parabolic interpolation when possible to speed up convergence of the golden section method.

Method *Golden* uses the golden section search technique. It uses analog of the bisection method to decrease the bracketed interval. It is usually preferable to use the *Brent* method.

Method *Bounded* can perform bounded minimization. It uses the Brent method to find a local minimum in the interval x1 < xopt < x2.

Custom minimizers

It may be useful to pass a custom minimization method, for example when using some library frontend to minimize_scalar. You can simply pass a callable as the `method` parameter.

The callable is called as `method(fun, args, **kwargs, **options)` where `kwargs` corresponds to any other parameters passed to `minimize` (such as `bracket`, *tol*, etc.), except the *options* dict, which has its contents also passed as *method* parameters pair by pair. The method shall return an `OptimizeResult` object.

The provided *method* callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by `minimize` may expand in future versions and then these parameters will be passed to the method. You can find an example in the scipy.optimize tutorial.

New in version 0.11.0.

Examples

Consider the problem of minimizing the following function.

```
>>> def f(x):
...     return (x - 2) * x * (x + 2)**2
```

Using the *Brent* method, we find the local minimum as:

```
>>> from scipy.optimize import minimize_scalar
>>> res = minimize_scalar(f)
>>> res.x
1.28077640403
```

Using the *Bounded* method, we find a local minimum with specified bounds as:

```
>>> res = minimize_scalar(f, bounds=(-3, -1), method='bounded')
>>> res.x
-2.0000002026
```

class `scipy.optimize.`**`OptimizeResult`**
Represents the optimization result.

Notes

There may be additional attributes not listed above depending of the specific solver. Since this class is essentially a subclass of dict with attribute accessors, one can see which attributes are available using the *keys()* method.

Attributes

x	(ndarray) The solution of the optimization.
success	(bool) Whether or not the optimizer exited successfully.
status	(int) Termination status of the optimizer. Its value depends on the underlying solver. Refer to *message* for details.
message	(str) Description of the cause of the termination.
fun, jac, hess, hess_inv	(ndarray) Values of objective function, Jacobian, Hessian or its inverse (if available). The Hessians may be approximations, see the documentation of the function in question.
nfev, njev, nhev	(int) Number of evaluations of the objective functions and of its Jacobian and Hessian.
nit	(int) Number of iterations performed by the optimizer.
maxcv	(float) The maximum constraint violation.

Methods

`clear`(() -> None. Remove all items from D.)	
`copy`(() -> a shallow copy of D)	
`fromkeys`(...)	v defaults to None.
`get`((k[,d]) -> D[k] if k in D, ...)	
`has_key`((k) -> True if D has a key k, else False)	
`items`(() -> list of D's (key, value) pairs, ...)	
`iteritems`(() -> an iterator over the (key, ...)	
`iterkeys`(() -> an iterator over the keys of D)	
`itervalues`(...)	
`keys`(() -> list of D's keys)	
`pop`((k[,d]) -> v, ...)	If key is not found, d is returned if given, otherwise KeyError is raised
`popitem`(() -> (k, v), ...)	2-tuple; but raise KeyError if D is empty.
`setdefault`((k[,d]) -> D.get(k,d), ...)	
`update`(([E, ...)	If E present and has a .keys() method, does: for k in E: D[k] = E[k]
`values`(() -> list of D's values)	
`viewitems`(...)	
`viewkeys`(...)	
`viewvalues`(...)	

`OptimizeResult.`**`clear`**`()` → None. Remove all items from D.

`OptimizeResult.`**`copy`**`()` → a shallow copy of D

static `OptimizeResult.`**`fromkeys`**`(`*S*[, *v*]`)` → New dict with keys from S and values equal to v.
v defaults to None.

`OptimizeResult.`**`get`**`(`*k*[, *d*]`)` → D[k] if k in D, else d. d defaults to None.

`OptimizeResult.`**`has_key`**`(`*k*`)` → True if D has a key k, else False

`OptimizeResult.`**`items`**`()` → list of D's (key, value) pairs, as 2-tuples

`OptimizeResult.`**`iteritems`**`()` → an iterator over the (key, value) items of D

`OptimizeResult.`**`iterkeys`**`()` → an iterator over the keys of D

`OptimizeResult.`**`itervalues`**`()` → an iterator over the values of D

`OptimizeResult.`**`keys`**`()` → list of D's keys

`OptimizeResult.`**`pop`**`(`*k*[, *d*]`)` → v, remove specified key and return the corresponding value.
If key is not found, d is returned if given, otherwise KeyError is raised

`OptimizeResult.`**`popitem`**`()` → (k, v), remove and return some (key, value) pair as a
2-tuple; but raise KeyError if D is empty.

`OptimizeResult.`**`setdefault`**`(`*k*[, *d*]`)` → D.get(k,d), also set D[k]=d if k not in D

`OptimizeResult.`**`update`**`(`[*E*], ***F*`)` → None. Update D from dict/iterable E and F.
If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

`OptimizeResult.`**`values`**`()` → list of D's values

`OptimizeResult.`**`viewitems`**`()` → a set-like object providing a view on D's items

`OptimizeResult.`**`viewkeys`**`()` → a set-like object providing a view on D's keys

`OptimizeResult.`**`viewvalues`**`()` → an object providing a view on D's values

The `minimize` function supports the following methods:

minimize(method='Nelder-Mead')

`scipy.optimize.`**`minimize`**`(`*fun*, *x0*, *args=()*, *method='Nelder-Mead'*, *tol=None*, *callback=None*, *options={'disp': False, 'maxiter': None, 'return_all': False, 'func': None, 'maxfev': None, 'xtol': 0.0001, 'ftol': 0.0001}*`)`

Minimization of scalar function of one or more variables using the Nelder-Mead algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
Set to True to print convergence messages.

xtol : float
Relative error in solution *xopt* acceptable for convergence.

ftol : float
Relative error in `fun(xopt)` acceptable for convergence.

maxiter : int
Maximum number of iterations to perform.

maxfev : int
Maximum number of function evaluations to make.

minimize(method='Powell')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='Powell'*, *tol=None*, *callback=None*, *options={'disp': False, 'return_all': False, 'maxiter': None, 'direc': None, 'func': None, 'maxfev': None, 'xtol': 0.0001, 'ftol': 0.0001}*)

Minimization of scalar function of one or more variables using the modified Powell algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
  Set to True to print convergence messages.

xtol : float
  Relative error in solution *xopt* acceptable for convergence.

ftol : float
  Relative error in `fun(xopt)` acceptable for convergence.

maxiter : int
  Maximum number of iterations to perform.

maxfev : int
  Maximum number of function evaluations to make.

direc : ndarray
  Initial set of direction vectors for the Powell method.

minimize(method='CG')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='CG'*, *jac=None*, *tol=None*, *callback=None*, *options={'disp': False, 'gtol': 1e-05, 'eps': 1.4901161193847656e-08, 'return_all': False, 'maxiter': None, 'norm': inf}*)

Minimization of scalar function of one or more variables using the conjugate gradient algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
  Set to True to print convergence messages.

maxiter : int
  Maximum number of iterations to perform.

gtol : float
  Gradient norm must be less than *gtol* before successful termination.

norm : float
  Order of norm (Inf is max, -Inf is min).

eps : float or ndarray
  If *jac* is approximated, use this value for the step size.

minimize(method='BFGS')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='BFGS'*, *jac=None*, *tol=None*, *callback=None*, *options={'disp': False, 'gtol': 1e-05, 'eps': 1.4901161193847656e-08, 'return_all': False, 'maxiter': None, 'norm': inf}*)

Minimization of scalar function of one or more variables using the BFGS algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
  Set to True to print convergence messages.

maxiter : int
Maximum number of iterations to perform.
gtol : float
Gradient norm must be less than *gtol* before successful termination.
norm : float
Order of norm (Inf is max, -Inf is min).
eps : float or ndarray
If *jac* is approximated, use this value for the step size.

minimize(method='Newton-CG')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='Newton-CG'*, *jac=None*, *hess=None*, *hessp=None*, *tol=None*, *callback=None*, *options={'disp': False*, *'xtol': 1e-05*, *'eps': 1.4901161193847656e-08*, *'return_all': False*, *'maxiter': None}*)

Minimization of scalar function of one or more variables using the Newton-CG algorithm.

Note that the *jac* parameter (Jacobian) is required.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
Set to True to print convergence messages.
xtol : float
Average relative error in solution *xopt* acceptable for convergence.
maxiter : int
Maximum number of iterations to perform.
eps : float or ndarray
If *jac* is approximated, use this value for the step size.

minimize(method='L-BFGS-B')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='L-BFGS-B'*, *jac=None*, *bounds=None*, *tol=None*, *callback=None*, *options={'disp': None*, *'iprint': -1*, *'gtol': 1e-05*, *'eps': 1e-08*, *'maxiter': 15000*, *'ftol': 2.220446049250313e-09*, *'maxcor': 10*, *'maxfun': 15000}*)

Minimize a scalar function of one or more variables using the L-BFGS-B algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

disp : bool
Set to True to print convergence messages.
maxcor : int
The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)
factr : float
The iteration stops when `(f^k - f^{k+1})/max{|f^k|,|f^{k+1}|,1} <= factr * eps`, where `eps` is the machine precision, which is automatically generated by the code. Typical values for *factr* are: 1e12 for low accuracy; 1e7 for moderate accuracy; 10.0 for extremely high accuracy.
ftol : float
The iteration stops when `(f^k - f^{k+1})/max{|f^k|,|f^{k+1}|,1} <= ftol`.

gtol : float
The iteration will stop when `max{|proj g_i | i = 1, ..., n} <= gtol` where `pg_i` is the i-th component of the projected gradient.

eps : float
Step size used for numerical approximation of the jacobian.

disp : int
Set to True to print convergence messages.

maxfun : int
Maximum number of function evaluations.

maxiter : int
Maximum number of iterations.

minimize(method='TNC')

`scipy.optimize.`**`minimize`** (*fun*, *x0*, *args=()*, *method='TNC'*, *jac=None*, *bounds=None*, *tol=None*, *callback=None*, *options={'disp': False, 'minfev': 0, 'scale': None, 'rescale': -1, 'offset': None, 'gtol': -1, 'eps': 1e-08, 'eta': -1, 'maxiter': None, 'maxCGit': -1, 'mesg_num': None, 'ftol': -1, 'xtol': -1, 'stepmx': 0, 'accuracy': 0}*)

Minimize a scalar function of one or more variables using a truncated Newton (TNC) algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

eps : float
Step size used for numerical approximation of the jacobian.

scale : list of floats
Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x] fo the others. Defaults to None

offset : float
Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

disp : bool
Set to True to print convergence messages.

maxCGit : int
Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1,min(50,n/2)). Defaults to -1.

maxiter : int
Maximum number of function evaluation. if None, *maxiter* is set to max(100, 10*len(x0)). Defaults to None.

eta : float
Severity of the line search. if < 0 or > 1, set to 0.25. Defaults to -1.

stepmx : float
Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

accuracy : float
Relative precision for finite difference calculations. If <= machine_precision, set to sqrt(machine_precision). Defaults to 0.

minfev : float
Minimum function value estimate. Defaults to 0.

ftol : float
Precision goal for the value of f in the stoping criterion. If ftol < 0.0, ftol is set to 0.0 defaults to -1.

xtol : float

Precision goal for the value of x in the stopping criterion (after applying x scaling factors). If xtol < 0.0, xtol is set to sqrt(machine_precision). Defaults to -1.

gtol : float
Precision goal for the value of the projected gradient in the stopping criterion (after applying x scaling factors). If gtol < 0.0, gtol is set to 1e-2 * sqrt(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.

rescale : float
Scaling factor (in log10) used to trigger f value rescaling. If 0, rescale at each iteration. If a large value, never rescale. If < 0, rescale is set to 1.3.

minimize(method='COBYLA')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='COBYLA'*, *constraints=()*, *tol=None*, *callback=None*, *options={'iprint': 1*, *'disp': False*, *'maxiter': 1000*, *'catol': 0.0002*, *'rhobeg': 1.0}*)

Minimize a scalar function of one or more variables using the Constrained Optimization BY Linear Approximation (COBYLA) algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

rhobeg : float
Reasonable initial changes to the variables.

tol : float
Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.

disp : bool
Set to True to print convergence messages. If False, *verbosity* is ignored as set to 0.

maxiter : int
Maximum number of function evaluations.

catol : float
Tolerance (absolute) for constraint violations

minimize(method='SLSQP')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='SLSQP'*, *jac=None*, *bounds=None*, *constraints=()*, *tol=None*, *callback=None*, *options={'disp': False*, *'iprint': 1*, *'eps': 1.4901161193847656e-08*, *'func': None*, *'maxiter': 100*, *'ftol': 1e-06}*)

Minimize a scalar function of one or more variables using Sequential Least SQuares Programming (SLSQP).

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

ftol : float
Precision goal for the value of f in the stopping criterion.

eps : float
Step size used for numerical approximation of the jacobian.

disp : bool
Set to True to print convergence messages. If False, *verbosity* is ignored and set to 0.

maxiter : int
Maximum number of iterations.

minimize(method='dogleg')

`scipy.optimize.`**`minimize`** (*fun*, *x0*, *args=()*, *method='dogleg'*, *jac=None*, *hess=None*, *tol=None*, *callback=None*, *options={}*)

Minimization of scalar function of one or more variables using the dog-leg trust-region algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

initial_trust_radius : float
Initial trust-region radius.

max_trust_radius : float
Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.

eta : float
Trust region related acceptance stringency for proposed steps.

gtol : float
Gradient norm must be less than *gtol* before successful termination.

minimize(method='trust-ncg')

`scipy.optimize.`**`minimize`** (*fun*, *x0*, *args=()*, *method='trust-ncg'*, *jac=None*, *hess=None*, *hessp=None*, *tol=None*, *callback=None*, *options={}*)

Minimization of scalar function of one or more variables using the Newton conjugate gradient trust-region algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

Options

initial_trust_radius : float
Initial trust-region radius.

max_trust_radius : float
Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.

eta : float
Trust region related acceptance stringency for proposed steps.

gtol : float
Gradient norm must be less than *gtol* before successful termination.

The `minimize_scalar` function supports the following methods:

minimize_scalar(method='brent')

`scipy.optimize.`**`minimize_scalar`** (*fun*, *args=()*, *method='brent'*, *tol=None*, *options={'xtol': 1.48e-08*, *'brack': None*, *'func': None*, *'maxiter': 500}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

Options

maxiter : int
Maximum number of iterations to perform.

xtol : float
Relative error in solution *xopt* acceptable for convergence.

Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

minimize_scalar(method='bounded')

`scipy.optimize.`**`minimize_scalar`**(*fun*, *bounds=None*, *args=()*, *method='bounded'*, *tol=None*, *options={'disp': 0*, *'maxiter': 500*, *'func': None*, *'xatol': 1e-05}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

Options **maxiter** : int
Maximum number of iterations to perform.
disp : bool
Set to True to print convergence messages.
xatol : float
Absolute error in solution *xopt* acceptable for convergence.

minimize_scalar(method='golden')

`scipy.optimize.`**`minimize_scalar`**(*fun*, *args=()*, *method='golden'*, *tol=None*, *options={'xtol': 1.4901161193847656e-08*, *'brack': None*, *'func': None}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

Options **maxiter** : int
Maximum number of iterations to perform.
xtol : float
Relative error in solution *xopt* acceptable for convergence.

The specific optimization method interfaces below in this subsection are not recommended for use in new scripts; all of these methods are accessible via a newer, more consistent interface provided by the functions above.

General-purpose multivariate methods:

`fmin`(func, x0[, args, xtol, ftol, maxiter, ...])	Minimize a function using the downhill simplex algorithm.
`fmin_powell`(func, x0[, args, xtol, ftol, ...])	Minimize a function using modified Powell's method.
`fmin_cg`(f, x0[, fprime, args, gtol, norm, ...])	Minimize a function using a nonlinear conjugate gradient algorithm.
`fmin_bfgs`(f, x0[, fprime, args, gtol, norm, ...])	Minimize a function using the BFGS algorithm.
`fmin_ncg`(f, x0, fprime[, fhess_p, fhess, ...])	Unconstrained minimization of a function using the Newton-CG method.

`scipy.optimize.`**`fmin`**(*func*, *x0*, *args=()*, *xtol=0.0001*, *ftol=0.0001*, *maxiter=None*, *maxfun=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Minimize a function using the downhill simplex algorithm.

This algorithm only uses function values, not derivatives or second derivatives.

Parameters **func** : callable func(x,*args)
The objective function to be minimized.
x0 : ndarray
Initial guess.
args : tuple, optional
Extra arguments passed to func, i.e. `f(x,*args)`.
callback : callable, optional

Called after each iteration, as callback(xk), where xk is the current parameter vector.

xtol : float, optional
Relative error in xopt acceptable for convergence.

ftol : number, optional
Relative error in func(xopt) acceptable for convergence.

maxiter : int, optional
Maximum number of iterations to perform.

maxfun : number, optional
Maximum number of function evaluations to make.

full_output : bool, optional
Set to True if fopt and warnflag outputs are desired.

disp : bool, optional
Set to True to print convergence messages.

retall : bool, optional
Set to True to return list of solutions at each iteration.

Returns **xopt** : ndarray
Parameter that minimizes function.

fopt : float
Value of function at minimum: `fopt = func(xopt)`.

iter : int
Number of iterations performed.

funcalls : int
Number of function calls made.

warnflag : int
1 : Maximum number of function evaluations made. 2 : Maximum number of iterations reached.

allvecs : list
Solution at each iteration.

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'Nelder-Mead' *method* in particular.

Notes

Uses a Nelder-Mead simplex algorithm to find the minimum of function of one or more variables.

This algorithm has a long history of successful use in applications. But it will usually be slower than an algorithm that uses first or second derivative information. In practice it can have poor performance in high-dimensional problems and is not robust to minimizing complicated functions. Additionally, there currently is no complete theory describing when the algorithm will successfully converge to the minimum, or how fast it will if it does.

References

[R136], [R137]

`scipy.optimize.`**`fmin_powell`**(*func*, *x0*, *args=()*, *xtol=0.0001*, *ftol=0.0001*, *maxiter=None*, *maxfun=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*, *direc=None*)

Minimize a function using modified Powell's method. This method only uses function values, not derivatives.

Parameters **func** : callable f(x,*args)
Objective function to be minimized.

x0 : ndarray
Initial guess.

args : tuple, optional

Extra arguments passed to func.

callback : callable, optional

An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current parameter vector.

direc : ndarray, optional

Initial direction set.

xtol : float, optional

Line-search error tolerance.

ftol : float, optional

Relative error in `func(xopt)` acceptable for convergence.

maxiter : int, optional

Maximum number of iterations to perform.

maxfun : int, optional

Maximum number of function evaluations to make.

full_output : bool, optional

If True, fopt, xi, direc, iter, funcalls, and warnflag are returned.

disp : bool, optional

If True, print convergence messages.

retall : bool, optional

If True, return a list of the solution at each iteration.

Returns

xopt : ndarray

Parameter which minimizes *func*.

fopt : number

Value of function at minimum: `fopt = func(xopt)`.

direc : ndarray

Current direction set.

iter : int

Number of iterations.

funcalls : int

Number of function calls made.

warnflag : int

Integer warning flag:

1 : Maximum number of function evaluations. 2 : Maximum number of iterations.

allvecs : list

List of solutions at each iteration.

See also:

`minimize`	Interface to unconstrained minimization algorithms for multivariate functions. See the 'Powell' *method* in particular.

Notes

Uses a modification of Powell's method to find the minimum of a function of N variables. Powell's method is a conjugate direction method.

The algorithm has two loops. The outer loop merely iterates over the inner loop. The inner loop minimizes over each current direction in the direction set. At the end of the inner loop, if certain conditions are met, the direction that gave the largest decrease is dropped and replaced with the difference between the current estiamted x and the estimated x from the beginning of the inner-loop.

The technical conditions for replacing the direction of greatest increase amount to checking that

1. No further gain can be made along the direction of greatest increase from that iteration.

2. The direction of greatest increase accounted for a large sufficient fraction of the decrease in the function value from that iteration of the inner loop.

References

Powell M.J.D. (1964) An efficient method for finding the minimum of a function of several variables without calculating derivatives, Computer Journal, 7 (2):155-162.

Press W., Teukolsky S.A., Vetterling W.T., and Flannery B.P.: Numerical Recipes (any edition), Cambridge University Press

`scipy.optimize.`**`fmin_cg`**(*f*, *x0*, *fprime=None*, *args=()*, *gtol=1e-05*, *norm=inf*, *epsilon=1.4901161193847656e-08*, *maxiter=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Minimize a function using a nonlinear conjugate gradient algorithm.

Parameters

f : callable, `f(x, *args)`
Objective function to be minimized. Here *x* must be a 1-D array of the variables that are to be changed in the search for a minimum, and *args* are the other (fixed) parameters of *f*.

x0 : ndarray
A user-supplied initial estimate of *xopt*, the optimal value of *x*. It must be a 1-D array of values.

fprime : callable, `fprime(x, *args)`, optional
A function that returns the gradient of *f* at *x*. Here *x* and *args* are as described above for *f*. The returned value must be a 1-D array. Defaults to None, in which case the gradient is approximated numerically (see *epsilon*, below).

args : tuple, optional
Parameter values passed to *f* and *fprime*. Must be supplied whenever additional fixed parameters are needed to completely specify the functions *f* and *fprime*.

gtol : float, optional
Stop when the norm of the gradient is less than *gtol*.

norm : float, optional
Order to use for the norm of the gradient (`-np.Inf` is min, `np.Inf` is max).

epsilon : float or ndarray, optional
Step size(s) to use when *fprime* is approximated numerically. Can be a scalar or a 1-D array. Defaults to `sqrt(eps)`, with eps the floating point machine precision. Usually `sqrt(eps)` is about 1.5e-8.

maxiter : int, optional
Maximum number of iterations to perform. Default is `200 * len(x0)`.

full_output : bool, optional
If True, return *fopt*, *func_calls*, *grad_calls*, and *warnflag* in addition to *xopt*. See the Returns section below for additional information on optional return values.

disp : bool, optional
If True, return a convergence message, followed by *xopt*.

retall : bool, optional
If True, add to the returned values the results of each iteration.

callback : callable, optional
An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current value of *x0*.

Returns

xopt : ndarray
Parameters which minimize f, i.e. `f(xopt) == fopt`.

fopt : float, optional
Minimum value found, f(xopt). Only returned if *full_output* is True.

func_calls : int, optional
The number of function_calls made. Only returned if *full_output* is True.

grad_calls : int, optional
The number of gradient calls made. Only returned if *full_output* is True.

warnflag : int, optional
Integer value with warning status, only returned if *full_output* is True.
0 : Success.
1 : The maximum number of iterations was exceeded.

2	[Gradient and/or function calls were not changing. May indicate] that precision was lost, i.e., the routine did not converge.

allvecs : list of ndarray, optional
List of arrays, containing the results at each iteration. Only returned if *retall* is True.

See also:

`minimize`	common interface to all `scipy.optimize` algorithms for unconstrained and constrained minimization of multivariate functions. It provides an alternative way to call `fmin_cg`, by specifying `method='CG'`.

Notes

This conjugate gradient algorithm is based on that of Polak and Ribiere [R138].

Conjugate gradient methods tend to work better when:

1. *f* has a unique global minimizing point, and no local minima or other stationary points,
2. *f* is, at least locally, reasonably well approximated by a quadratic function of the variables,
3. *f* is continuous and has a continuous gradient,
4. *fprime* is not too large, e.g., has a norm less than 1000,
5. The initial guess, *x0*, is reasonably close to *f* 's global minimizing point, *xopt*.

References

[R138]

Examples

Example 1: seek the minimum value of the expression `a*u**2 + b*u*v + c*v**2 + d*u + e*v + f` for given values of the parameters and an initial guess `(u, v) = (0, 0)`.

```
>>> args = (2, 3, 7, 8, 9, 10)  # parameter values
>>> def f(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     return a*u**2 + b*u*v + c*v**2 + d*u + e*v + f
>>> def gradf(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     gu = 2*a*u + b*v + d     # u-component of the gradient
...     gv = b*u + 2*c*v + e     # v-component of the gradient
...     return np.asarray((gu, gv))
>>> x0 = np.asarray((0, 0))  # Initial guess.
>>> from scipy import optimize
>>> res1 = optimize.fmin_cg(f, x0, fprime=gradf, args=args)
>>> print('res1 = ', res1)
Optimization terminated successfully.
         Current function value: 1.617021
         Iterations: 2
         Function evaluations: 5
```

```
          Gradient evaluations: 5
res1 =  [-1.80851064 -0.25531915]
```

Example 2: solve the same problem using the `minimize` function. (This *myopts* dictionary shows all of the available options, although in practice only non-default values would be needed. The returned value will be a dictionary.)

```
>>> opts = {'maxiter' : None,    # default value.
...         'disp' : True,    # non-default value.
...         'gtol' : 1e-5,    # default value.
...         'norm' : np.inf,  # default value.
...         'eps' : 1.4901161193847656e-08}  # default value.
>>> res2 = optimize.minimize(f, x0, jac=gradf, args=args,
...                          method='CG', options=opts)
Optimization terminated successfully.
        Current function value: 1.617021
        Iterations: 2
        Function evaluations: 5
        Gradient evaluations: 5
>>> res2.x  # minimum found
array([-1.80851064 -0.25531915])
```

`scipy.optimize.`**`fmin_bfgs`**(*f, x0, fprime=None, args=(), gtol=1e-05, norm=inf, epsilon=1.4901161193847656e-08, maxiter=None, full_output=0, disp=1, retall=0, callback=None*)

Minimize a function using the BFGS algorithm.

Parameters

f : callable f(x,*args)
Objective function to be minimized.

x0 : ndarray
Initial guess.

fprime : callable f'(x,*args), optional
Gradient of f.

args : tuple, optional
Extra arguments passed to f and fprime.

gtol : float, optional
Gradient norm must be less than gtol before successful termination.

norm : float, optional
Order of norm (Inf is max, -Inf is min)

epsilon : int or ndarray, optional
If fprime is approximated, use this value for the step size.

callback : callable, optional
An optional user-supplied function to call after each iteration. Called as callback(xk), where xk is the current parameter vector.

maxiter : int, optional
Maximum number of iterations to perform.

full_output : bool, optional
If True,return fopt, func_calls, grad_calls, and warnflag in addition to xopt.

disp : bool, optional
Print convergence message if True.

retall : bool, optional
Return a list of results at each iteration if True.

Returns

xopt : ndarray
Parameters which minimize f, i.e. f(xopt) == fopt.

fopt : float
Minimum value.

gopt : ndarray
Value of gradient at minimum, f'(xopt), which should be near 0.
Bopt : ndarray
Value of 1/f''(xopt), i.e. the inverse hessian matrix.
func_calls : int
Number of function_calls made.
grad_calls : int
Number of gradient calls made.
warnflag : integer
1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing.
allvecs : list
`OptimizeResult` at each iteration. Only returned if retall is True.

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'BFGS' *method* in particular.

Notes

Optimize the function, f, whose gradient is given by fprime using the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS)

References

Wright, and Nocedal 'Numerical Optimization', 1999, pg. 198.

`scipy.optimize.`**`fmin_ncg`**(*f*, *x0*, *fprime*, *fhess_p=None*, *fhess=None*, *args=()*, *avextol=1e-05*, *epsilon=1.4901161193847656e-08*, *maxiter=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Unconstrained minimization of a function using the Newton-CG method.

Parameters

f : callable `f(x, *args)`
Objective function to be minimized.
x0 : ndarray
Initial guess.
fprime : callable `f'(x, *args)`
Gradient of f.
fhess_p : callable `fhess_p(x, p, *args)`, optional
Function which computes the Hessian of f times an arbitrary vector, p.
fhess : callable `fhess(x, *args)`, optional
Function to compute the Hessian matrix of f.
args : tuple, optional
Extra arguments passed to f, fprime, fhess_p, and fhess (the same set of extra arguments is supplied to all of these functions).
epsilon : float or ndarray, optional
If fhess is approximated, use this value for the step size.
callback : callable, optional
An optional user-supplied function which is called after each iteration. Called as callback(xk), where xk is the current parameter vector.
avextol : float, optional
Convergence is assumed when the average relative error in the minimizer falls below this amount.
maxiter : int, optional
Maximum number of iterations to perform.
full_output : bool, optional

If True, return the optional outputs.

disp : bool, optional

If True, print convergence message.

retall : bool, optional

If True, return a list of results at each iteration.

Returns

xopt : ndarray

Parameters which minimize f, i.e. `f(xopt) == fopt`.

fopt : float

Value of the function at xopt, i.e. `fopt = f(xopt)`.

fcalls : int

Number of function calls made.

gcalls : int

Number of gradient calls made.

hcalls : int

Number of hessian calls made.

warnflag : int

Warnings generated by the algorithm. 1 : Maximum number of iterations exceeded.

allvecs : list

The result at each iteration, if retall is True (see below).

See also:

`minimize` Interface to minimization algorithms for multivariate functions. See the 'Newton-CG' *method* in particular.

Notes

Only one of *fhess_p* or *fhess* need to be given. If *fhess* is provided, then *fhess_p* will be ignored. If neither *fhess* nor *fhess_p* is provided, then the hessian product will be approximated using finite differences on *fprime*. *fhess_p* must compute the hessian times an arbitrary vector. If it is not given, finite-differences on *fprime* are used to compute it.

Newton-CG methods are also called truncated Newton methods. This function differs from scipy.optimize.fmin_tnc because

1. ***scipy.optimize.fmin_ncg is written purely in python using numpy***
   and scipy while scipy.optimize.fmin_tnc calls a C function.
2. ***scipy.optimize.fmin_ncg is only for unconstrained minimization***
   while scipy.optimize.fmin_tnc is for unconstrained minimization or box constrained minimization. (Box constraints give lower and upper bounds for each variable separately.)

References

Wright & Nocedal, 'Numerical Optimization', 1999, pg. 140.

Constrained multivariate methods:

`fmin_l_bfgs_b`(func, x0[, fprime, args, ...])	Minimize a function func using the L-BFGS-B algorithm.
`fmin_tnc`(func, x0[, fprime, args, ...])	Minimize a function with variables subject to bounds, using gradient info
`fmin_cobyla`(func, x0, cons[, args, ...])	Minimize a function using the Constrained Optimization BY Linear Appr
`fmin_slsqp`(func, x0[, eqcons, f_eqcons, ...])	Minimize a function using Sequential Least SQuares Programming
`differential_evolution`(func, bounds[, args, ...])	Finds the global minimum of a multivariate function.

`scipy.optimize.`**`fmin_l_bfgs_b`**(*func*, *x0*, *fprime=None*, *args=()*, *approx_grad=0*, *bounds=None*,
m=10, *factr=10000000.0*, *pgtol=1e-05*, *epsilon=1e-08*, *iprint=-1*,
maxfun=15000, *maxiter=15000*, *disp=None*, *callback=None*)

Minimize a function func using the L-BFGS-B algorithm.

Parameters

func : callable f(x,*args)
Function to minimise.

x0 : ndarray
Initial guess.

fprime : callable fprime(x,*args), optional
The gradient of *func*. If None, then *func* returns the function value and the gradient (`f, g = func(x, *args)`), unless *approx_grad* is True in which case *func* returns only `f`.

args : sequence, optional
Arguments to pass to *func* and *fprime*.

approx_grad : bool, optional
Whether to approximate the gradient numerically (in which case *func* returns only the function value).

bounds : list, optional
`(min, max)` pairs for each element in `x`, defining the bounds on that parameter. Use None or +-inf for one of `min` or `max` when there is no bound in that direction.

m : int, optional
The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)

factr : float, optional
The iteration stops when `(f^k - f^{k+1})/max{|f^k|,|f^{k+1}|,1} <= factr * eps`, where `eps` is the machine precision, which is automatically generated by the code. Typical values for *factr* are: 1e12 for low accuracy; 1e7 for moderate accuracy; 10.0 for extremely high accuracy.

pgtol : float, optional
The iteration will stop when `max{|proj g_i | i = 1, ..., n} <= pgtol` where `pg_i` is the i-th component of the projected gradient.

epsilon : float, optional
Step size used when *approx_grad* is True, for numerically calculating the gradient

iprint : int, optional
Controls the frequency of output. `iprint < 0` means no output; `iprint == 0` means write messages to stdout; `iprint > 1` in addition means write logging information to a file named `iterate.dat` in the current working directory.

disp : int, optional
If zero, then no output. If a positive number, then this over-rides *iprint* (i.e., *iprint* gets the value of *disp*).

maxfun : int, optional
Maximum number of function evaluations.

maxiter : int, optional
Maximum number of iterations.

callback : callable, optional
Called after each iteration, as `callback(xk)`, where `xk` is the current parameter vector.

Returns

x : array_like
Estimated position of the minimum.

f : float
Value of *func* at the minimum.

d : dict
Information dictionary.

- d['warnflag'] is
  - 0 if converged,

- –1 if too many function evaluations or too many iterations,
- –2 if stopped for another reason, given in d['task']
- d['grad'] is the gradient at the minimum (should be 0 ish)
- d['funcalls'] is the number of function calls made.
- d['nit'] is the number of iterations.

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'L-BFGS-B' *method* in particular.

Notes

License of L-BFGS-B (FORTRAN code):

The version included here (in fortran code) is 3.0 (released April 25, 2011). It was written by Ciyou Zhu, Richard Byrd, and Jorge Nocedal <nocedal@ece.nwu.edu>. It carries the following condition for use:

This software is freely available, but we expect that all publications describing work using this software, or all commercial products using it, quote at least one of the references given below. This software is released under the BSD License.

References

- R. H. Byrd, P. Lu and J. Nocedal. A Limited Memory Algorithm for Bound Constrained Optimization, (1995), SIAM Journal on Scientific and Statistical Computing, 16, 5, pp. 1190-1208.
- C. Zhu, R. H. Byrd and J. Nocedal. L-BFGS-B: Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization (1997), ACM Transactions on Mathematical Software, 23, 4, pp. 550 - 560.
- J.L. Morales and J. Nocedal. L-BFGS-B: Remark on Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization (2011), ACM Transactions on Mathematical Software, 38, 1.

`scipy.optimize.`**`fmin_tnc`**(*func*, *x0*, *fprime=None*, *args=()*, *approx_grad=0*, *bounds=None*, *epsilon=1e-08*, *scale=None*, *offset=None*, *messages=15*, *maxCGit=-1*, *maxfun=None*, *eta=-1*, *stepmx=0*, *accuracy=0*, *fmin=0*, *ftol=-1*, *xtol=-1*, *pgtol=-1*, *rescale=-1*, *disp=None*, *callback=None*)

Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm. This method wraps a C implementation of the algorithm.

Parameters

func : callable `func(x, *args)`

Function to minimize. Must do one of:

1. Return f and g, where f is the value of the function and g its gradient (a list of floats).
2. Return the function value but supply gradient function separately as *fprime*.
3. Return the function value and set `approx_grad=True`.

If the function returns None, the minimization is aborted.

x0 : array_like

Initial estimate of minimum.

fprime : callable `fprime(x, *args)`, optional

Gradient of *func*. If None, then either *func* must return the function value and the gradient (`f,g = func(x, *args)`) or *approx_grad* must be True.

args : tuple, optional

Arguments to pass to function.

approx_grad : bool, optional

If true, approximate the gradient numerically.

bounds : list, optional
  (min, max) pairs for each element in x0, defining the bounds on that parameter. Use None or +/-inf for one of min or max when there is no bound in that direction.

epsilon : float, optional
  Used if approx_grad is True. The stepsize in a finite difference approximation for fprime.

scale : array_like, optional
  Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x| for the others. Defaults to None.

offset : array_like, optional
  Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

messages : int, optional
  Bit mask used to select messages display during minimization values defined in the MSGS dict. Defaults to MGS_ALL.

disp : int, optional
  Integer interface to messages. 0 = no message, 5 = all messages

maxCGit : int, optional
  Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1,min(50,n/2)). Defaults to -1.

maxfun : int, optional
  Maximum number of function evaluation. if None, maxfun is set to max(100, 10*len(x0)). Defaults to None.

eta : float, optional
  Severity of the line search. if < 0 or > 1, set to 0.25. Defaults to -1.

stepmx : float, optional
  Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

accuracy : float, optional
  Relative precision for finite difference calculations. If <= machine_precision, set to sqrt(machine_precision). Defaults to 0.

fmin : float, optional
  Minimum function value estimate. Defaults to 0.

ftol : float, optional
  Precision goal for the value of f in the stoping criterion. If ftol < 0.0, ftol is set to 0.0 defaults to -1.

xtol : float, optional
  Precision goal for the value of x in the stopping criterion (after applying x scaling factors). If xtol < 0.0, xtol is set to sqrt(machine_precision). Defaults to -1.

pgtol : float, optional
  Precision goal for the value of the projected gradient in the stopping criterion (after applying x scaling factors). If pgtol < 0.0, pgtol is set to 1e-2 * sqrt(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.

rescale : float, optional
  Scaling factor (in log10) used to trigger f value rescaling. If 0, rescale at each iteration. If a large value, never rescale. If < 0, rescale is set to 1.3.

callback : callable, optional
  Called after each iteration, as callback(xk), where xk is the current parameter vector.

Returns

x : ndarray
  The solution.

nfeval : int
  The number of function evaluations.

rc : int

Return code, see below

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'TNC' *method* in particular.

Notes

The underlying algorithm is truncated Newton, also called Newton Conjugate-Gradient. This method differs from scipy.optimize.fmin_ncg in that

1. It wraps a C implementation of the algorithm
2. It allows each variable to be given an upper and lower bound.

The algorithm incoporates the bound constraints by determining the descent direction as in an unconstrained truncated Newton, but never taking a step-size large enough to leave the space of feasible x's. The algorithm keeps track of a set of currently active constraints, and ignores them when computing the minimum allowable step size. (The x's associated with the active constraint are kept fixed.) If the maximum allowable step size is zero then a new constraint is added. At the end of each iteration one of the constraints may be deemed no longer active and removed. A constraint is considered no longer active is if it is currently active but the gradient for that variable points inward from the constraint. The specific constraint removed is the one associated with the variable of largest index whose constraint is no longer active.

Return codes are defined as follows:

```
-1 : Infeasible (lower bound > upper bound)
 0 : Local minimum reached (|pg| ~= 0)
 1 : Converged (|f_n-f_(n-1)| ~= 0)
 2 : Converged (|x_n-x_(n-1)| ~= 0)
 3 : Max. number of function evaluations reached
 4 : Linear search failed
 5 : All lower bounds are equal to the upper bounds
 6 : Unable to progress
 7 : User requested end of minimization
```

References

Wright S., Nocedal J. (2006), 'Numerical Optimization'

Nash S.G. (1984), "Newton-Type Minimization Via the Lanczos Method", SIAM Journal of Numerical Analysis 21, pp. 770-778

`scipy.optimize.`**`fmin_cobyla`**(*func*, *x0*, *cons*, *args=()*, *consargs=None*, *rhobeg=1.0*, *rhoend=0.0001*, *iprint=1*, *maxfun=1000*, *disp=None*, *catol=0.0002*)

Minimize a function using the Constrained Optimization BY Linear Approximation (COBYLA) method. This method wraps a FORTRAN implentation of the algorithm.

Parameters

func : callable

Function to minimize. In the form func(x, *args).

x0 : ndarray

Initial guess.

cons : sequence

Constraint functions; must all be `>=0` (a single function if only 1 constraint). Each function takes the parameters *x* as its first argument, and it can return either a single number or an array or list of numbers.

args : tuple, optional

Extra arguments to pass to function.

consargs : tuple, optional

Extra arguments to pass to constraint functions (default of None means use same extra arguments as those passed to func). Use `()` for no extra arguments.

rhobeg : float, optional

Reasonable initial changes to the variables.

rhoend : float, optional

Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.

iprint : {0, 1, 2, 3}, optional

Controls the frequency of output; 0 implies no output. Deprecated.

disp : {0, 1, 2, 3}, optional

Over-rides the iprint interface. Preferred.

maxfun : int, optional

Maximum number of function evaluations.

catol : float, optional

Absolute tolerance for constraint violations.

Returns **x** : ndarray

The argument that minimises *f*.

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'COBYLA' *method* in particular.

Notes

This algorithm is based on linear approximations to the objective function and each constraint. We briefly describe the algorithm.

Suppose the function is being minimized over k variables. At the jth iteration the algorithm has k+1 points v_1, ..., v_(k+1), an approximate solution x_j, and a radius RHO_j. (i.e. linear plus a constant) approximations to the objective function and constraint functions such that their function values agree with the linear approximation on the k+1 points v_1,.., v_(k+1). This gives a linear program to solve (where the linear approximations of the constraint functions are constrained to be non-negative).

However the linear approximations are likely only good approximations near the current simplex, so the linear program is given the further requirement that the solution, which will become x_(j+1), must be within RHO_j from x_j. RHO_j only decreases, never increases. The initial RHO_j is rhobeg and the final RHO_j is rhoend. In this way COBYLA's iterations behave like a trust region algorithm.

Additionally, the linear program may be inconsistent, or the approximation may give poor improvement. For details about how these issues are resolved, as well as how the points v_i are updated, refer to the source code or the references below.

References

Powell M.J.D. (1994), "A direct search optimization method that models the objective and constraint functions by linear interpolation.", in Advances in Optimization and Numerical Analysis, eds. S. Gomez and J-P Hennart, Kluwer Academic (Dordrecht), pp. 51-67

Powell M.J.D. (1998), "Direct search algorithms for optimization calculations", Acta Numerica 7, 287-336

Powell M.J.D. (2007), "A view of algorithms for optimization without derivatives", Cambridge University Technical Report DAMTP 2007/NA03

Examples

Minimize the objective function f(x,y) = x*y subject to the constraints x**2 + y**2 < 1 and y > 0:

```
>>> def objective(x):
...     return x[0]*x[1]
...
>>> def constr1(x):
...     return 1 - (x[0]**2 + x[1]**2)
...
>>> def constr2(x):
...     return x[1]
...
>>> from scipy.optimize import fmin_cobyla
>>> fmin_cobyla(objective, [0.0, 0.1], [constr1, constr2], rhoend=1e-7)

   Normal return from subroutine COBYLA

   NFVALS =   64   F =-5.000000E-01    MAXCV = 1.998401E-14
   X =-7.071069E-01   7.071067E-01
array([-0.70710685,  0.70710671])
```

The exact solution is (-sqrt(2)/2, sqrt(2)/2).

`scipy.optimize.`**`fmin_slsqp`**(*func, x0, eqcons=(), f_eqcons=None, ieqcons=(), f_ieqcons=None, bounds=(), fprime=None, fprime_eqcons=None, fprime_ieqcons=None, args=(), iter=100, acc=1e-06, iprint=1, disp=None, full_output=0, epsilon=1.4901161193847656e-08, callback=None*)

Minimize a function using Sequential Least SQuares Programming

Python interface function for the SLSQP Optimization subroutine originally implemented by Dieter Kraft.

Parameters

func : callable f(x,*args)

Objective function.

x0 : 1-D ndarray of float

Initial guess for the independent variable(s).

eqcons : list, optional

A list of functions of length n such that eqcons[j](x,*args) == 0.0 in a successfully optimized problem.

f_eqcons : callable f(x,*args), optional

Returns a 1-D array in which each element must equal 0.0 in a successfully optimized problem. If f_eqcons is specified, eqcons is ignored.

ieqcons : list, optional

A list of functions of length n such that ieqcons[j](x,*args) >= 0.0 in a successfully optimized problem.

f_ieqcons : callable f(x,*args), optional

Returns a 1-D ndarray in which each element must be greater or equal to 0.0 in a successfully optimized problem. If f_ieqcons is specified, ieqcons is ignored.

bounds : list, optional

A list of tuples specifying the lower and upper bound for each independent variable [(xl0, xu0),(xl1, xu1),...] Infinite values will be interpreted as large floating values.

fprime : callable *f(x,*args)*, optional

A function that evaluates the partial derivatives of func.

fprime_eqcons : callable *f(x,*args)*, optional

A function of the form *f(x, *args)* that returns the m by n array of equality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_eqcons should be sized as (len(eqcons), len(x0)).

fprime_ieqcons : callable *f(x,*args)*, optional

A function of the form *f(x, *args)* that returns the m by n array of inequality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_ieqcons should be sized as (len(ieqcons), len(x0)).

args : sequence, optional
Additional arguments passed to func and fprime.

iter : int, optional
The maximum number of iterations.

acc : float, optional
Requested accuracy.

iprint : int, optional
The verbosity of fmin_slsqp :

- iprint <= 0 : Silent operation
- iprint == 1 : Print summary upon completion (default)
- iprint >= 2 : Print status of each iterate and summary

disp : int, optional
Over-rides the iprint interface (preferred).

full_output : bool, optional
If False, return only the minimizer of func (default). Otherwise, output final objective function and summary information.

epsilon : float, optional
The step size for finite-difference derivative estimates.

callback : callable, optional
Called after each iteration, as `callback(x)`, where `x` is the current parameter vector.

Returns

out : ndarray of float
The final minimizer of func.

fx : ndarray of float, if full_output is true
The final value of the objective function.

its : int, if full_output is true
The number of iterations.

imode : int, if full_output is true
The exit mode from the optimizer (see below).

smode : string, if full_output is true
Message describing the exit mode from the optimizer.

See also:

`minimize`	Interface to minimization algorithms for multivariate functions. See the 'SLSQP' *method* in particular.

Notes

Exit modes are defined as follows

```
-1 : Gradient evaluation required (g & a)
 0 : Optimization terminated successfully.
 1 : Function evaluation required (f & c)
 2 : More equality constraints than independent variables
 3 : More than 3*n iterations in LSQ subproblem
 4 : Inequality constraints incompatible
 5 : Singular matrix E in LSQ subproblem
 6 : Singular matrix C in LSQ subproblem
 7 : Rank-deficient equality constraint subproblem HFTI
 8 : Positive directional derivative for linesearch
 9 : Iteration limit exceeded
```

Examples

Examples are given *in the tutorial*.

`scipy.optimize.`**`differential_evolution`**(*func*, *bounds*, *args=()*, *strategy='best1bin'*, *maxiter=None*, *popsize=15*, *tol=0.01*, *mutation=(0.5, 1)*, *recombination=0.7*, *seed=None*, *callback=None*, *disp=False*, *polish=True*, *init='latinhypercube'*)

Finds the global minimum of a multivariate function. Differential Evolution is stochastic in nature (does not use gradient methods) to find the minimium, and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

The algorithm is due to Storn and Price [R133].

Parameters

func : callable

The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

bounds : sequence

Bounds for variables. `(min, max)` pairs for each element in `x`, defining the lower and upper bounds for the optimizing argument of *func*. It is required to have `len(bounds) == len(x)`. `len(bounds)` is used to determine the number of parameters in `x`.

args : tuple, optional

Any additional fixed parameters needed to completely specify the objective function.

strategy : str, optional

The differential evolution strategy to use. Should be one of:

- 'best1bin'
- 'best1exp'
- 'rand1exp'
- 'randtobest1exp'
- 'best2exp'
- 'rand2exp'
- 'randtobest1bin'
- 'best2bin'
- 'rand2bin'
- 'rand1bin'

The default is 'best1bin'.

maxiter : int, optional

The maximum number of times the entire population is evolved. The maximum number of function evaluations is: `maxiter * popsize * len(x)`

popsize : int, optional

A multiplier for setting the total population size. The population has `popsize * len(x)` individuals.

tol : float, optional

When the mean of the population energies, multiplied by tol, divided by the standard deviation of the population energies is greater than 1 the solving process terminates: `convergence = mean(pop) * tol / stdev(pop) > 1`

mutation : float or tuple(float, float), optional

The mutation constant. If specified as a float it should be in the range [0, 2]. If specified as a tuple `(min, max)` dithering is employed. Dithering randomly changes the mutation constant on a generation by generation basis. The mutation constant for that generation is taken from `U[min, max)`. Dithering can help speed convergence significantly. Increasing the mutation constant increases the search radius, but will slow down convergence.

recombination : float, optional

The recombination constant, should be in the range [0, 1]. Increasing this value allows a larger number of mutants to progress into the next generation, but at the risk of population stability.

seed : int or *np.random.RandomState*, optional

If *seed* is not specified the *np.RandomState* singleton is used. If *seed* is an int, a new *np.random.RandomState* instance is used, seeded with seed. If *seed* is already a *np.random.RandomState instance*, then that *np.random.RandomState* instance is used. Specify *seed* for repeatable minimizations.

disp : bool, optional

Display status messages

callback : callable, *callback(xk, convergence=val)*, optional

A function to follow the progress of the minimization. `xk` is the current value of `x0`. `val` represents the fractional value of the population convergence. When `val` is greater than one the function halts. If callback returns *True*, then the minimization is halted (any polishing is still carried out).

polish : bool, optional

If True (default), then `scipy.optimize.minimize` with the *L-BFGS-B* method is used to polish the best population member at the end, which can improve the minimization slightly.

init : string, optional

Specify how the population initialization is performed. Should be one of:

- 'latinhypercube'
- 'random'

The default is 'latinhypercube'. Latin Hypercube sampling tries to maximize coverage of the available parameter space. 'random' initializes the population randomly - this has the drawback that clustering can occur, preventing the whole of parameter space being covered.

Returns **res** : OptimizeResult

The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes. If *polish* was employed, then OptimizeResult also contains the *jac* attribute.

Notes

Differential evolution is a stochastic population based method that is useful for global optimization problems. At each pass through the population the algorithm mutates each candidate solution by mixing with other candidate solutions to create a trial candidate. There are several strategies [R134] for creating trial candidates, which suit some problems more than others. The 'best1bin' strategy is a good starting point for many systems. In this strategy two members of the population are randomly chosen. Their difference is used to mutate the best member (the *best* in *best1bin*), b_0, so far:

$$b' = b_0 + mutation * (population[rand0] - population[rand1])$$

A trial vector is then constructed. Starting with a randomly chosen 'i'th parameter the trial is sequentially filled (in modulo) with parameters from *b'* or the original candidate. The choice of whether to use *b'* or the original candidate is made with a binomial distribution (the 'bin' in 'best1bin') - a random number in [0, 1) is generated. If this number is less than the *recombination* constant then the parameter is loaded from *b'*, otherwise it is loaded from the original candidate. The final parameter is always loaded from *b'*. Once the trial candidate is built its fitness is assessed. If the trial is better than the original candidate then it takes its place. If it is also better than the best overall candidate it also replaces that. To improve your chances of finding a global minimum use higher *popsize* values, with higher *mutation* and (dithering), but lower *recombination* values. This has the effect of widening the search radius, but slowing convergence.

New in version 0.15.0.

References

[R133], [R134], [R135]

Examples

Let us consider the problem of minimizing the Rosenbrock function. This function is implemented in `rosen` in `scipy.optimize`.

```
>>> from scipy.optimize import rosen, differential_evolution
>>> bounds = [(0,2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Next find the minimum of the Ackley function (http://en.wikipedia.org/wiki/Test_functions_for_optimization).

```
>>> from scipy.optimize import differential_evolution
>>> import numpy as np
>>> def ackley(x):
...     arg1 = -0.2 * np.sqrt(0.5 * (x[0] ** 2 + x[1] ** 2))
...     arg2 = 0.5 * (np.cos(2. * np.pi * x[0]) + np.cos(2. * np.pi * x[1]))
...     return -20. * np.exp(arg1) - np.exp(arg2) + 20. + np.e
>>> bounds = [(-5, 5), (-5, 5)]
>>> result = differential_evolution(ackley, bounds)
>>> result.x, result.fun
(array([ 0.,  0.]), 4.4408920985006262e-16)
```

Univariate (scalar) minimization methods:

`fminbound`(func, x1, x2[, args, xtol, ...])	Bounded minimization for scalar functions.
`brent`(func[, args, brack, tol, full_output, ...])	Given a function of one-variable and a possible bracketing interval, return the minim
`golden`(func[, args, brack, tol, full_output])	Return the minimum of a function of one variable.

`scipy.optimize.`**`fminbound`**(*func*, *x1*, *x2*, *args=()*, *xtol=1e-05*, *maxfun=500*, *full_output=0*, *disp=1*)

Bounded minimization for scalar functions.

Parameters

func : callable f(x,*args)
Objective function to be minimized (must accept and return scalars).

x1, x2 : float or array scalar
The optimization bounds.

args : tuple, optional
Extra arguments passed to function.

xtol : float, optional
The convergence tolerance.

maxfun : int, optional
Maximum number of function evaluations allowed.

full_output : bool, optional
If True, return optional outputs.

disp : int, optional
If non-zero, print messages.
0 : no message printing. 1 : non-convergence notification messages only. 2 : print a message on convergence too. 3 : print iteration results.

Returns

xopt : ndarray
Parameters (over given interval) which minimize the objective function.

fval : number
The function value at the minimum point.

ierr : int
An error flag (0 if converged, 1 if maximum number of function calls reached).
numfunc : int
The number of function calls made.

See also:

minimize_scalar
Interface to minimization algorithms for scalar univariate functions. See the 'Bounded' *method* in particular.

Notes

Finds a local minimizer of the scalar function *func* in the interval x1 < xopt < x2 using Brent's method. (See `brent` for auto-bracketing).

`scipy.optimize.`**`brent`**(*func*, *args=()*, *brack=None*, *tol=1.48e-08*, *full_output=0*, *maxiter=500*)
Given a function of one-variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

Parameters
func : callable f(x,*args)
Objective function.
args : tuple, optional
Additional arguments (if present).
brack : tuple, optional
Triple (a,b,c) where (a<b<c) and func(b) < func(a),func(c). If bracket consists of two numbers (a,c) then they are assumed to be a starting interval for a downhill bracket search (see `bracket`); it doesn't always mean that the obtained solution will satisfy a<=x<=c.
tol : float, optional
Stop if between iteration change is less than *tol*.
full_output : bool, optional
If True, return all output args (xmin, fval, iter, funcalls).
maxiter : int, optional
Maximum number of iterations in solution.

Returns
xmin : ndarray
Optimum point.
fval : float
Optimum value.
iter : int
Number of iterations.
funcalls : int
Number of objective function evaluations made.

See also:

minimize_scalar
Interface to minimization algorithms for scalar univariate functions. See the 'Brent' *method* in particular.

Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

`scipy.optimize.`**`golden`**(*func*, *args=()*, *brack=None*, *tol=1.4901161193847656e-08*, *full_output=0*)
Return the minimum of a function of one variable.

Given a function of one variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

Parameters **func** : callable func(x,*args)

Objective function to minimize.

args : tuple, optional

Additional arguments (if present), passed to func.

brack : tuple, optional

Triple (a,b,c), where (a<b<c) and func(b) < func(a),func(c). If bracket consists of two numbers (a, c), then they are assumed to be a starting interval for a downhill bracket search (see `bracket`); it doesn't always mean that obtained solution will satisfy a<=x<=c.

tol : float, optional

x tolerance stop criterion

full_output : bool, optional

If True, return optional outputs.

See also:

`minimize_scalar`

Interface to minimization algorithms for scalar univariate functions. See the 'Golden' *method* in particular.

Notes

Uses analog of bisection method to decrease the bracketed interval.

Equation (Local) Minimizers

`leastsq`(func, x0[, args, Dfun, full_output, ...])	Minimize the sum of squares of a set of equations.
`nnls`(A, b)	Solve `argmin_x || Ax - b ||_2` for `x>=0`.

`scipy.optimize.`**`leastsq`**(*func*, *x0*, *args=()*, *Dfun=None*, *full_output=0*, *col_deriv=0*, *ftol=1.49012e-08*, *xtol=1.49012e-08*, *gtol=0.0*, *maxfev=0*, *epsfcn=None*, *factor=100*, *diag=None*)

Minimize the sum of squares of a set of equations.

```
x = arg min(sum(func(y)**2,axis=0))
         y
```

Parameters **func** : callable

should take at least one (possibly length N vector) argument and returns M floating point numbers. It must not return NaNs or fitting might fail.

x0 : ndarray

The starting estimate for the minimization.

args : tuple, optional

Any extra arguments to func are placed in this tuple.

Dfun : callable, optional

A function or method to compute the Jacobian of func with derivatives across the rows. If this is None, the Jacobian will be estimated.

full_output : bool, optional

non-zero to return all optional outputs.

col_deriv : bool, optional

non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

ftol : float, optional

Relative error desired in the sum of squares.

xtol : float, optional

Relative error desired in the approximate solution.

gtol : float, optional

Orthogonality desired between the function vector and the columns of the Jacobian.

maxfev : int, optional

The maximum number of calls to the function. If *Dfun* is provided then the default *maxfev* is 100*(N+1) where N is the number of elements in x0, otherwise the default *maxfev* is 200*(N+1).

epsfcn : float, optional

A variable used in determining a suitable step length for the forward- difference approximation of the Jacobian (for Dfun=None). Normally the actual step length will be sqrt(epsfcn)*x If epsfcn is less than the machine precision, it is assumed that the relative errors are of the order of the machine precision.

factor : float, optional

A parameter determining the initial step bound (`factor * || diag * x||`). Should be in interval `(0.1, 100)`.

diag : sequence, optional

N positive entries that serve as a scale factors for the variables.

Returns **x** : ndarray

The solution (or the result of the last iteration for an unsuccessful call).

cov_x : ndarray

Uses the fjac and ipvt optional outputs to construct an estimate of the jacobian around the solution. None if a singular matrix encountered (indicates very flat curvature in some direction). This matrix must be multiplied by the residual variance to get the covariance of the parameter estimates – see curve_fit.

infodict : dict

a dictionary of optional outputs with the key s:

nfev	The number of function calls
fvec	The function evaluated at the output
fjac	A permutation of the R matrix of a QR factorization of the final approximate Jacobian matrix, stored column wise. Together with ipvt, the covariance of the estimate can be approximated.
ipvt	An integer array of length N which defines a permutation matrix, p, such that fjac*p = q*r, where r is upper triangular with diagonal elements of nonincreasing magnitude. Column j of p is column ipvt(j) of the identity matrix.
qtf	The vector (transpose(q) * fvec).

mesg : str

A string message giving information about the cause of failure.

ier : int

An integer flag. If it is equal to 1, 2, 3 or 4, the solution was found. Otherwise, the solution was not found. In either case, the optional output variable 'mesg' gives more information.

Notes

"leastsq" is a wrapper around MINPACK's lmdif and lmder algorithms.

cov_x is a Jacobian approximation to the Hessian of the least squares objective function. This approximation assumes that the objective function is based on the difference between some observed target data (ydata) and a (non-linear) function of the parameters *f(xdata, params)*

```
func(params) = ydata - f(xdata, params)
```

so that the objective function is

```
  min   sum((ydata - f(xdata, params))**2, axis=0)
params
```

`scipy.optimize.`**`nnls`**(*A*, *b*)

Solve `argmin_x || Ax - b ||_2` for `x>=0`. This is a wrapper for a FORTAN non-negative least squares solver.

Parameters

A : ndarray
  Matrix `A` as shown above.

b : ndarray
  Right-hand side vector.

Returns

x : ndarray
  Solution vector.

rnorm : float
  The residual, `|| Ax-b ||_2`.

Notes

The FORTRAN code was published in the book below. The algorithm is an active set method. It solves the KKT (Karush-Kuhn-Tucker) conditions for the non-negative least squares problem.

References

Lawson C., Hanson R.J., (1987) Solving Least Squares Problems, SIAM

Global Optimization

`basinhopping`(func, x0[, niter, T, stepsize, ...])	Find the global minimum of a function using the basin-hopping algorithm
`brute`(func, ranges[, args, Ns, full_output, ...])	Minimize a function over a given range by brute force.
`differential_evolution`(func, bounds[, args, ...])	Finds the global minimum of a multivariate function.

`scipy.optimize.`**`basinhopping`**(*func*, *x0*, *niter=100*, *T=1.0*, *stepsize=0.5*, *minimizer_kwargs=None*, *take_step=None*, *accept_test=None*, *callback=None*, *interval=50*, *disp=False*, *niter_success=None*)

Find the global minimum of a function using the basin-hopping algorithm

Parameters

func : callable `f(x, *args)`
  Function to be optimized. `args` can be passed as an optional item in the dict `minimizer_kwargs`

x0 : ndarray
  Initial guess.

niter : integer, optional
  The number of basin hopping iterations

T : float, optional
  The "temperature" parameter for the accept or reject criterion. Higher "temperatures" mean that larger jumps in function value will be accepted. For best results `T` should be comparable to the separation (in function value) between local minima.

stepsize : float, optional
  initial step size for use in the random displacement.

minimizer_kwargs : dict, optional

Extra keyword arguments to be passed to the minimizer `scipy.optimize.minimize()` Some important options could be:

method	[str] The minimization method (e.g. `"L-BFGS-B"`)
args	[tuple] Extra arguments passed to the objective function (`func`) and its derivatives (Jacobian, Hessian).

take_step : callable `take_step(x)`, optional

Replace the default step taking routine with this routine. The default step taking routine is a random displacement of the coordinates, but other step taking algorithms may be better for some systems. `take_step` can optionally have the attribute `take_step.stepsize`. If this attribute exists, then `basinhopping` will adjust `take_step.stepsize` in order to try to optimize the global minimum search.

accept_test : callable, `accept_test(f_new=f_new, x_new=x_new, f_old=fold, x_old=x_old)`, optional

Define a test which will be used to judge whether or not to accept the step. This will be used in addition to the Metropolis test based on "temperature" `T`. The acceptable return values are True, False, or `"force accept"`. If the latter, then this will override any other tests in order to accept the step. This can be used, for example, to forcefully escape from a local minimum that `basinhopping` is trapped in.

callback : callable, `callback(x, f, accept)`, optional

A callback function which will be called for all minima found. `x` and `f` are the coordinates and function value of the trial minimum, and `accept` is whether or not that minimum was accepted. This can be used, for example, to save the lowest N minima found. Also, `callback` can be used to specify a user defined stop criterion by optionally returning True to stop the `basinhopping` routine.

interval : integer, optional

interval for how often to update the `stepsize`

disp : bool, optional

Set to True to print status messages

niter_success : integer, optional

Stop the run if the global minimum candidate remains the same for this number of iterations.

Returns **res** : OptimizeResult

The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `fun` the value of the function at the solution, and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

`minimize`	The local minimization function called once for each basinhopping step. `minimizer_kwargs` is passed to this routine.

Notes

Basin-hopping is a stochastic algorithm which attempts to find the global minimum of a smooth scalar function of one or more variables [R127] [R128] [R129] [R130]. The algorithm in its current form was described by David Wales and Jonathan Doye [R128] http://www-wales.ch.cam.ac.uk/.

The algorithm is iterative with each cycle composed of the following features

1. random perturbation of the coordinates
2. local minimization
3. accept or reject the new coordinates based on the minimized function value

The acceptance test used here is the Metropolis criterion of standard Monte Carlo algorithms, although there are many other possibilities [R129].

This global minimization method has been shown to be extremely efficient for a wide variety of problems in physics and chemistry. It is particularly useful when the function has many minima separated by large barriers. See the Cambridge Cluster Database http://www-wales.ch.cam.ac.uk/CCD.html for databases of molecular systems that have been optimized primarily using basin-hopping. This database includes minimization problems exceeding 300 degrees of freedom.

See the free software program GMIN (http://www-wales.ch.cam.ac.uk/GMIN) for a Fortran implementation of basin-hopping. This implementation has many different variations of the procedure described above, including more advanced step taking algorithms and alternate acceptance criterion.

For stochastic global optimization there is no way to determine if the true global minimum has actually been found. Instead, as a consistency check, the algorithm can be run from a number of different random starting points to ensure the lowest minimum found in each example has converged to the global minimum. For this reason `basinhopping` will by default simply run for the number of iterations `niter` and return the lowest minimum found. It is left to the user to ensure that this is in fact the global minimum.

Choosing `stepsize`: This is a crucial parameter in `basinhopping` and depends on the problem being solved. Ideally it should be comparable to the typical separation between local minima of the function being optimized. `basinhopping` will, by default, adjust `stepsize` to find an optimal value, but this may take many iterations. You will get quicker results if you set a sensible value for `stepsize`.

Choosing `T`: The parameter `T` is the temperature used in the metropolis criterion. Basinhopping steps are accepted with probability `1` if `func(xnew) < func(xold)`, or otherwise with probability:

```
exp( -(func(xnew) - func(xold)) / T )
```

So, for best results, `T` should to be comparable to the typical difference in function values between local minima.

New in version 0.12.0.

References

[R127], [R128], [R129], [R130]

Examples

The following example is a one-dimensional minimization problem, with many local minima superimposed on a parabola.

```
>>> from scipy.optimize import basinhopping
>>> func = lambda x: np.cos(14.5 * x - 0.3) + (x + 0.2) * x
>>> x0=[1.]
```

Basinhopping, internally, uses a local minimization algorithm. We will use the parameter `minimizer_kwargs` to tell basinhopping which algorithm to use and how to set up that minimizer. This parameter will be passed to `scipy.optimize.minimize()`.

```
>>> minimizer_kwargs = {"method": "BFGS"}
>>> ret = basinhopping(func, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=200)
>>> print("global minimum: x = %.4f, f(x0) = %.4f" % (ret.x, ret.fun))
global minimum: x = -0.1951, f(x0) = -1.0009
```

Next consider a two-dimensional minimization problem. Also, this time we will use gradient information to significantly speed up the search.

```
>>> def func2d(x):
...     f = np.cos(14.5 * x[0] - 0.3) + (x[1] + 0.2) * x[1] + (x[0] +
...                                                             0.2) * x[0]
...     df = np.zeros(2)
...     df[0] = -14.5 * np.sin(14.5 * x[0] - 0.3) + 2. * x[0] + 0.2
...     df[1] = 2. * x[1] + 0.2
...     return f, df
```

We'll also use a different local minimization algorithm. Also we must tell the minimizer that our function returns both energy and gradient (jacobian)

```
>>> minimizer_kwargs = {"method":"L-BFGS-B", "jac":True}
>>> x0 = [1.0, 1.0]
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=200)
>>> print("global minimum: x = [%.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
...                                                           ret.x[1],
...                                                           ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Here is an example using a custom step taking routine. Imagine you want the first coordinate to take larger steps then the rest of the coordinates. This can be implemented like so:

```
>>> class MyTakeStep(object):
...    def __init__(self, stepsize=0.5):
...        self.stepsize = stepsize
...    def __call__(self, x):
...        s = self.stepsize
...        x[0] += np.random.uniform(-2.*s, 2.*s)
...        x[1:] += np.random.uniform(-s, s, x[1:].shape)
...        return x
```

Since `MyTakeStep.stepsize` exists basinhopping will adjust the magnitude of `stepsize` to optimize the search. We'll use the same 2-D function as before

```
>>> mytakestep = MyTakeStep()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=200, take_step=mytakestep)
>>> print("global minimum: x = [%.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
...                                                           ret.x[1],
...                                                           ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Now let's do an example using a custom callback function which prints the value of every minimum found

```
>>> def print_fun(x, f, accepted):
...         print("at minimum %.4f accepted %d" % (f, int(accepted)))
```

We'll run it for only 10 basinhopping steps this time.

```
>>> np.random.seed(1)
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=10, callback=print_fun)
at minimum 0.4159 accepted 1
at minimum -0.9073 accepted 1
at minimum -0.1021 accepted 1
at minimum -0.1021 accepted 1
at minimum 0.9102 accepted 1
at minimum 0.9102 accepted 1
at minimum 2.2945 accepted 0
```

```
at minimum -0.1021 accepted 1
at minimum -1.0109 accepted 1
at minimum -1.0109 accepted 1
```

The minimum at -1.0109 is actually the global minimum, found already on the 8th iteration.

Now let's implement bounds on the problem using a custom `accept_test`:

```
>>> class MyBounds(object):
...     def __init__(self, xmax=[1.1,1.1], xmin=[-1.1,-1.1] ):
...         self.xmax = np.array(xmax)
...         self.xmin = np.array(xmin)
...     def __call__(self, **kwargs):
...         x = kwargs["x_new"]
...         tmax = bool(np.all(x <= self.xmax))
...         tmin = bool(np.all(x >= self.xmin))
...         return tmax and tmin

>>> mybounds = MyBounds()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=10, accept_test=mybounds)
```

`scipy.optimize.`**`brute`**(*func*, *ranges*, *args=()*, *Ns=20*, *full_output=0*, *finish=<function fmin at 0x7fa41234d9b0>*, *disp=False*)

Minimize a function over a given range by brute force.

Uses the "brute force" method, i.e. computes the function's value at each point of a multidimensional grid of points, to find the global minimum of the function.

The function is evaluated everywhere in the range with the datatype of the first call to the function, as enforced by the `vectorize` NumPy function. The value and type of the function evaluation returned when `full_output=True` are affected in addition by the `finish` argument (see Notes).

Parameters

func : callable
: The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

ranges : tuple
: Each component of the *ranges* tuple must be either a "slice object" or a range tuple of the form `(low, high)`. The program uses these to create the grid of points on which the objective function will be computed. See *Note 2* for more detail.

args : tuple, optional
: Any additional fixed parameters needed to completely specify the function.

Ns : int, optional
: Number of grid points along the axes, if not otherwise specified. See *Note2*.

full_output : bool, optional
: If True, return the evaluation grid and the objective function's values on it.

finish : callable, optional
: An optimization function that is called with the result of brute force minimization as initial guess. *finish* should take *func* and the initial guess as positional arguments, and take *args* as keyword arguments. It may additionally take *full_output* and/or *disp* as keyword arguments. Use None if no "polishing" function is to be used. See Notes for more details.

disp : bool, optional
: Set to True to print convergence messages.

Returns

x0 : ndarray
: A 1-D array containing the coordinates of a point at which the objective function had its minimum value. (See *Note 1* for which point is returned.)

fval : float
Function value at the point *x0*. (Returned when *full_output* is True.)

grid : tuple
Representation of the evaluation grid. It has the same length as *x0*. (Returned when *full_output* is True.)

Jout : ndarray
Function values at each point of the evaluation grid, *i.e.*, `Jout = func(*grid)`. (Returned when *full_output* is True.)

See also:

`basinhopping`, `differential_evolution`

Notes

Note 1: The program finds the gridpoint at which the lowest value of the objective function occurs. If *finish* is None, that is the point returned. When the global minimum occurs within (or not very far outside) the grid's boundaries, and the grid is fine enough, that point will be in the neighborhood of the gobal minimum.

However, users often employ some other optimization program to "polish" the gridpoint values, *i.e.*, to seek a more precise (local) minimum near *brute's* best gridpoint. The `brute` function's *finish* option provides a convenient way to do that. Any polishing program used must take *brute's* output as its initial guess as a positional argument, and take *brute's* input values for *args* as keyword arguments, otherwise an error will be raised. It may additionally take *full_output* and/or *disp* as keyword arguments.

`brute` assumes that the *finish* function returns either an `OptimizeResult` object or a tuple in the form: `(xmin, Jmin, ... , statuscode)`, where `xmin` is the minimizing value of the argument, `Jmin` is the minimum value of the objective function, "..." may be some other returned values (which are not used by `brute`), and `statuscode` is the status code of the *finish* program.

Note that when *finish* is not None, the values returned are those of the *finish* program, *not* the gridpoint ones. Consequently, while `brute` confines its search to the input grid points, the *finish* program's results usually will not coincide with any gridpoint, and may fall outside the grid's boundary.

Note 2: The grid of points is a `numpy.mgrid` object. For `brute` the *ranges* and *Ns* inputs have the following effect. Each component of the *ranges* tuple can be either a slice object or a two-tuple giving a range of values, such as (0, 5). If the component is a slice object, `brute` uses it directly. If the component is a two-tuple range, `brute` internally converts it to a slice object that interpolates *Ns* points from its low-value to its high-value, inclusive.

Examples

We illustrate the use of `brute` to seek the global minimum of a function of two variables that is given as the sum of a positive-definite quadratic and two deep "Gaussian-shaped" craters. Specifically, define the objective function *f* as the sum of three other functions, `f = f1 + f2 + f3`. We suppose each of these has a signature `(z, *params)`, where `z = (x, y)`, and `params` and the functions are as defined below.

```
>>> params = (2, 3, 7, 8, 9, 10, 44, -1, 2, 26, 1, -2, 0.5)
>>> def f1(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (a * x**2 + b * x * y + c * y**2 + d*x + e*y + f)

>>> def f2(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-g*np.exp(-((x-h)**2 + (y-i)**2) / scale))
```

```
>>> def f3(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-j*np.exp(-((x-k)**2 + (y-l)**2) / scale))

>>> def f(z, *params):
...     return f1(z, *params) + f2(z, *params) + f3(z, *params)
```

Thus, the objective function may have local minima near the minimum of each of the three functions of which it is composed. To use `fmin` to polish its gridpoint result, we may then continue as follows:

```
>>> rranges = (slice(-4, 4, 0.25), slice(-4, 4, 0.25))
>>> from scipy import optimize
>>> resbrute = optimize.brute(f, rranges, args=params, full_output=True,
...                           finish=optimize.fmin)
>>> resbrute[0]  # global minimum
array([-1.05665192,  1.80834843])
>>> resbrute[1]  # function value at global minimum
-3.4085818767
```

Note that if *finish* had been set to None, we would have gotten the gridpoint [-1.0 1.75] where the rounded function value is -2.892.

`scipy.optimize.`**`differential_evolution`**(*func*, *bounds*, *args=()*, *strategy='best1bin'*, *maxiter=None*, *popsize=15*, *tol=0.01*, *mutation=(0.5, 1)*, *recombination=0.7*, *seed=None*, *callback=None*, *disp=False*, *polish=True*, *init='latinhypercube'*)

Finds the global minimum of a multivariate function. Differential Evolution is stochastic in nature (does not use gradient methods) to find the minimium, and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

The algorithm is due to Storn and Price [R133].

Parameters

func : callable

The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

bounds : sequence

Bounds for variables. `(min, max)` pairs for each element in `x`, defining the lower and upper bounds for the optimizing argument of *func*. It is required to have `len(bounds) == len(x)`. `len(bounds)` is used to determine the number of parameters in `x`.

args : tuple, optional

Any additional fixed parameters needed to completely specify the objective function.

strategy : str, optional

The differential evolution strategy to use. Should be one of:

- 'best1bin'
- 'best1exp'
- 'rand1exp'
- 'randtobest1exp'
- 'best2exp'
- 'rand2exp'
- 'randtobest1bin'
- 'best2bin'
- 'rand2bin'
- 'rand1bin'

The default is 'best1bin'.

maxiter : int, optional

The maximum number of times the entire population is evolved. The maximum number of function evaluations is: `maxiter * popsize * len(x)`

popsize : int, optional

A multiplier for setting the total population size. The population has `popsize * len(x)` individuals.

tol : float, optional

When the mean of the population energies, multiplied by tol, divided by the standard deviation of the population energies is greater than 1 the solving process terminates: `convergence = mean(pop) * tol / stdev(pop) > 1`

mutation : float or tuple(float, float), optional

The mutation constant. If specified as a float it should be in the range [0, 2]. If specified as a tuple `(min, max)` dithering is employed. Dithering randomly changes the mutation constant on a generation by generation basis. The mutation constant for that generation is taken from `U[min, max)`. Dithering can help speed convergence significantly. Increasing the mutation constant increases the search radius, but will slow down convergence.

recombination : float, optional

The recombination constant, should be in the range [0, 1]. Increasing this value allows a larger number of mutants to progress into the next generation, but at the risk of population stability.

seed : int or *np.random.RandomState*, optional

If *seed* is not specified the *np.RandomState* singleton is used. If *seed* is an int, a new *np.random.RandomState* instance is used, seeded with seed. If *seed* is already a *np.random.RandomState instance*, then that *np.random.RandomState* instance is used. Specify *seed* for repeatable minimizations.

disp : bool, optional

Display status messages

callback : callable, *callback(xk, convergence=val)*, optional

A function to follow the progress of the minimization. `xk` is the current value of `x0`. `val` represents the fractional value of the population convergence. When `val` is greater than one the function halts. If callback returns *True*, then the minimization is halted (any polishing is still carried out).

polish : bool, optional

If True (default), then `scipy.optimize.minimize` with the *L-BFGS-B* method is used to polish the best population member at the end, which can improve the minimization slightly.

init : string, optional

Specify how the population initialization is performed. Should be one of:

- 'latinhypercube'
- 'random'

The default is 'latinhypercube'. Latin Hypercube sampling tries to maximize coverage of the available parameter space. 'random' initializes the population randomly - this has the drawback that clustering can occur, preventing the whole of parameter space being covered.

Returns **res** : OptimizeResult

The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes. If *polish* was employed, then OptimizeResult also contains the *jac* attribute.

Notes

Differential evolution is a stochastic population based method that is useful for global optimization problems. At each pass through the population the algorithm mutates each candidate solution by mixing with other candidate solutions to create a trial candidate. There are several strategies [R134] for creating trial candidates, which suit some problems more than others. The 'best1bin' strategy is a good starting point for many systems. In this strategy two members of the population are randomly chosen. Their difference is used to mutate the best member (the *best* in *best1bin*), b_0, so far:

$$b' = b_0 + mutation * (population[rand0] - population[rand1])$$

A trial vector is then constructed. Starting with a randomly chosen 'i'th parameter the trial is sequentially filled (in modulo) with parameters from *b'* or the original candidate. The choice of whether to use *b'* or the original candidate is made with a binomial distribution (the 'bin' in 'best1bin') - a random number in [0, 1) is generated. If this number is less than the *recombination* constant then the parameter is loaded from *b'*, otherwise it is loaded from the original candidate. The final parameter is always loaded from *b'*. Once the trial candidate is built its fitness is assessed. If the trial is better than the original candidate then it takes its place. If it is also better than the best overall candidate it also replaces that. To improve your chances of finding a global minimum use higher *popsize* values, with higher *mutation* and (dithering), but lower *recombination* values. This has the effect of widening the search radius, but slowing convergence.

New in version 0.15.0.

References

[R133], [R134], [R135]

Examples

Let us consider the problem of minimizing the Rosenbrock function. This function is implemented in `rosen` in `scipy.optimize`.

```
>>> from scipy.optimize import rosen, differential_evolution
>>> bounds = [(0,2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Next find the minimum of the Ackley function (http://en.wikipedia.org/wiki/Test_functions_for_optimization).

```
>>> from scipy.optimize import differential_evolution
>>> import numpy as np
>>> def ackley(x):
...     arg1 = -0.2 * np.sqrt(0.5 * (x[0] ** 2 + x[1] ** 2))
...     arg2 = 0.5 * (np.cos(2. * np.pi * x[0]) + np.cos(2. * np.pi * x[1]))
...     return -20. * np.exp(arg1) - np.exp(arg2) + 20. + np.e
>>> bounds = [(-5, 5), (-5, 5)]
>>> result = differential_evolution(ackley, bounds)
>>> result.x, result.fun
(array([ 0.,  0.]), 4.4408920985006262e-16)
```

Rosenbrock function

`rosen`(x)	The Rosenbrock function.
`rosen_der`(x)	The derivative (i.e.
`rosen_hess`(x)	The Hessian matrix of the Rosenbrock function.
`rosen_hess_prod`(x, p)	Product of the Hessian matrix of the Rosenbrock function with a vector.

`scipy.optimize.`**`rosen`**`(x)`

The Rosenbrock function.

The function computed is:

```
sum(100.0*(x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0
```

Parameters	**x** : array_like 1-D array of points at which the Rosenbrock function is to be computed.
Returns	**f** : float The value of the Rosenbrock function.

See also:

`rosen_der`, `rosen_hess`, `rosen_hess_prod`

`scipy.optimize.`**`rosen_der`**`(x)`

The derivative (i.e. gradient) of the Rosenbrock function.

Parameters	**x** : array_like 1-D array of points at which the derivative is to be computed.
Returns	**rosen_der** : (N,) ndarray The gradient of the Rosenbrock function at *x*.

See also:

`rosen`, `rosen_hess`, `rosen_hess_prod`

`scipy.optimize.`**`rosen_hess`**`(x)`

The Hessian matrix of the Rosenbrock function.

Parameters	**x** : array_like 1-D array of points at which the Hessian matrix is to be computed.
Returns	**rosen_hess** : ndarray The Hessian matrix of the Rosenbrock function at *x*.

See also:

`rosen`, `rosen_der`, `rosen_hess_prod`

`scipy.optimize.`**`rosen_hess_prod`**`(x, p)`

Product of the Hessian matrix of the Rosenbrock function with a vector.

Parameters	**x** : array_like 1-D array of points at which the Hessian matrix is to be computed. **p** : array_like 1-D array, the vector to be multiplied by the Hessian matrix.
Returns	**rosen_hess_prod** : ndarray The Hessian matrix of the Rosenbrock function at *x* multiplied by the vector *p*.

See also:

`rosen`, `rosen_der`, `rosen_hess`

5.24.2 Fitting

`curve_fit`(f, xdata, ydata[, p0, sigma, ...])	Use non-linear least squares to fit a function, f, to data.

`scipy.optimize.`**`curve_fit`**(*f*, *xdata*, *ydata*, *p0=None*, *sigma=None*, *absolute_sigma=False*, *check_finite=True*, ***kw*)

Use non-linear least squares to fit a function, f, to data.

Assumes `ydata = f(xdata, *params) + eps`

Parameters **f** : callable

The model function, f(x, ...). It must take the independent variable as the first argument and the parameters to fit as separate remaining arguments.

xdata : An M-length sequence or an (k,M)-shaped array

for functions with k predictors. The independent variable where the data is measured.

ydata : M-length sequence

The dependent data — nominally f(xdata, ...)

p0 : None, scalar, or N-length sequence, optional

Initial guess for the parameters. If None, then the initial values will all be 1 (if the number of parameters for the function can be determined using introspection, otherwise a ValueError is raised).

sigma : None or M-length sequence, optional

If not None, the uncertainties in the ydata array. These are used as weights in the least-squares problem i.e. minimising `np.sum( ((f(xdata, *popt) - ydata) / sigma)**2 )` If None, the uncertainties are assumed to be 1.

absolute_sigma : bool, optional

If False, *sigma* denotes relative weights of the data points. The returned covariance matrix *pcov* is based on *estimated* errors in the data, and is not affected by the overall magnitude of the values in *sigma*. Only the relative magnitudes of the *sigma* values matter.

If True, *sigma* describes one standard deviation errors of the input data points. The estimated covariance in *pcov* is based on these values.

check_finite : bool, optional

If True, check that the input arrays do not contain nans of infs, and raise a ValueError if they do. Setting this parameter to False may silently produce nonsensical results if the input arrays do contain nans. Default is True.

Returns **popt** : array

Optimal values for the parameters so that the sum of the squared error of `f(xdata, *popt) - ydata` is minimized

pcov : 2d array

The estimated covariance of popt. The diagonals provide the variance of the parameter estimate. To compute one standard deviation errors on the parameters use `perr = np.sqrt(np.diag(pcov))`.

How the *sigma* parameter affects the estimated covariance depends on *absolute_sigma* argument, as described above.

Raises **OptimizeWarning**

if covariance of the parameters can not be estimated.

ValueError

if ydata and xdata contain NaNs.

See also:

`leastsq`

Notes

The algorithm uses the Levenberg-Marquardt algorithm through `leastsq`. Additional keyword arguments are passed directly to that algorithm.

Examples

```
>>> import numpy as np
>>> from scipy.optimize import curve_fit
>>> def func(x, a, b, c):
...     return a * np.exp(-b * x) + c

>>> xdata = np.linspace(0, 4, 50)
>>> y = func(xdata, 2.5, 1.3, 0.5)
>>> ydata = y + 0.2 * np.random.normal(size=len(xdata))

>>> popt, pcov = curve_fit(func, xdata, ydata)
```

5.24.3 Root finding

Scalar functions

`brentq`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find a root of a function in given interval.
`brenth`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find root of f in [a,b].
`ridder`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find a root of a function in an interval.
`bisect`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find root of a function within an interval.
`newton`(func, x0[, fprime, args, tol, ...])	Find a zero using the Newton-Raphson or secant method.

`scipy.optimize.`**`brentq`**(*f*, *a*, *b*, *args=()*, *xtol=1e-12*, *rtol=4.4408920985006262e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a root of a function in given interval.

Return float, a zero of *f* between *a* and *b*. *f* must be a continuous function, and [a,b] must be a sign changing interval.

Description: Uses the classic Brent (1973) method to find a zero of the function *f* on the sign changing interval [a , b]. Generally considered the best of the rootfinding routines here. It is a safe version of the secant method that uses inverse quadratic extrapolation. Brent's method combines root bracketing, interval bisection, and inverse quadratic interpolation. It is sometimes known as the van Wijngaarden-Dekker-Brent method. Brent (1973) claims convergence is guaranteed for functions computable within [a,b].

[Brent1973] provides the classic description of the algorithm. Another description can be found in a recent edition of Numerical Recipes, including [PressEtal1992]. Another description is at http://mathworld.wolfram.com/BrentsMethod.html. It should be easy to understand the algorithm just by reading our code. Our code diverges a bit from standard presentations: we choose a different formula for the extrapolation step.

Parameters **f** : function

Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.

a : number

One end of the bracketing interval [a,b].

b : number

The other end of the bracketing interval [a,b].

xtol : number, optional

The routine converges when a root is known to lie within xtol of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

rtol : number, optional

The routine converges when a root is known to lie within *rtol* times the value returned of the value returned. Should be >= 0. Defaults to `np.finfo(float).eps * 2`.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : bool, optional

If True, raise RuntimeError if the algorithm didn't converge.

Returns **x0** : float

Zero of *f* between *a* and *b*.

r : RootResults (present if `full_output = True`)

Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

`multivariate` `fmin`, `fmin_powell`, `fmin_cg`, `fmin_bfgs`, `fmin_ncg`

`nonlinear` `leastsq`

`constrained` `fmin_l_bfgs_b`, `fmin_tnc`, `fmin_cobyla`

`global` `basinhopping`, `brute`, `differential_evolution`

`local` `fminbound`, `brent`, `golden`, `bracket`

`n-dimensional` `fsolve`

`one-dimensional` `brentq`, `brenth`, `ridder`, `bisect`, `newton`

`scalar` `fixed_point`

Notes

f must be continuous. f(a) and f(b) must have opposite signs.

References

[Brent1973], [PressEtal1992]

`scipy.optimize.`**`brenth`**(*f*, *a*, *b*, *args=()*, *xtol=1e-12*, *rtol=4.4408920985006262e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find root of f in [a,b].

A variation on the classic Brent routine to find a zero of the function f between the arguments a and b that uses hyperbolic extrapolation instead of inverse quadratic extrapolation. There was a paper back in the 1980's ... f(a) and f(b) cannot have the same signs. Generally on a par with the brent routine, but not as heavily tested. It is a safe version of the secant method that uses hyperbolic extrapolation. The version here is by Chuck Harris.

Parameters **f** : function

Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.

a : number

One end of the bracketing interval [a,b].

b : number

The other end of the bracketing interval [a,b].

xtol : number, optional

The routine converges when a root is known to lie within xtol of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

rtol : number, optional

The routine converges when a root is known to lie within *rtol* times the value returned of the value returned. Should be >= 0. Defaults to `np.finfo(float).eps * 2`.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : bool, optional

If True, raise RuntimeError if the algorithm didn't converge.

Returns **x0** : float

Zero of *f* between *a* and *b*.

r : RootResults (present if `full_output = True`)

Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

`fmin`, `fmin_powell`, `fmin_cg`

`leastsq`	nonlinear least squares minimizer

`fmin_l_bfgs_b`, `fmin_tnc`, `fmin_cobyla`, `basinhopping`, `differential_evolution`, `brute`, `fminbound`, `brent`, `golden`, `bracket`

`fsolve`	n-dimensional root-finding

`brentq`, `brenth`, `ridder`, `bisect`, `newton`

`fixed_point`

scalar fixed-point finder

`scipy.optimize.`**`ridder`**(*f*, *a*, *b*, *args=()*, *xtol=1e-12*, *rtol=4.4408920985006262e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a root of a function in an interval.

Parameters **f** : function

Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.

a : number

One end of the bracketing interval [a,b].

b : number

The other end of the bracketing interval [a,b].

xtol : number, optional

The routine converges when a root is known to lie within xtol of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

rtol : number, optional

The routine converges when a root is known to lie within *rtol* times the value returned of the value returned. Should be >= 0. Defaults to `np.finfo(float).eps * 2`.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : bool, optional

If True, raise RuntimeError if the algorithm didn't converge.

Returns

x0 : float

Zero of *f* between *a* and *b*.

r : RootResults (present if `full_output = True`)

Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

`brentq`, `brenth`, `bisect`, `newton`

`fixed_point`

scalar fixed-point finder

Notes

Uses [Ridders1979] method to find a zero of the function *f* between the arguments *a* and *b*. Ridders' method is faster than bisection, but not generally as fast as the Brent rountines. [Ridders1979] provides the classic description and source of the algorithm. A description can also be found in any recent edition of Numerical Recipes.

The routine used here diverges slightly from standard presentations in order to be a bit more careful of tolerance.

References

[Ridders1979]

`scipy.optimize.`**`bisect`**(*f*, *a*, *b*, *args=()*, *xtol=1e-12*, *rtol=4.4408920985006262e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find root of a function within an interval.

Basic bisection routine to find a zero of the function *f* between the arguments *a* and *b*. *f(a)* and *f(b)* cannot have the same signs. Slow but sure.

Parameters

f : function

Python function returning a number. *f* must be continuous, and f(a) and f(b) must have opposite signs.

a : number

One end of the bracketing interval [a,b].

b : number

The other end of the bracketing interval [a,b].

xtol : number, optional

The routine converges when a root is known to lie within *xtol* of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

rtol : number, optional

The routine converges when a root is known to lie within *rtol* times the value returned of the value returned. Should be >= 0. Defaults to `np.finfo(float).eps * 2`.

maxiter : number, optional
: if convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.

args : tuple, optional
: containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional
: If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where x is the root, and r is a *RootResults* object.

disp : bool, optional
: If True, raise RuntimeError if the algorithm didn't converge.

Returns

x0 : float
: Zero of *f* between *a* and *b*.

r : RootResults (present if `full_output = True`)
: Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

`brentq`, `brenth`, `bisect`, `newton`

`fixed_point`	scalar fixed-point finder
`fsolve`	n-dimensional root-finding

`scipy.optimize.`**`newton`**(*func*, *x0*, *fprime=None*, *args=()*, *tol=1.48e-08*, *maxiter=50*, *fprime2=None*)

Find a zero using the Newton-Raphson or secant method.

Find a zero of the function *func* given a nearby starting point *x0*. The Newton-Raphson method is used if the derivative *fprime* of *func* is provided, otherwise the secant method is used. If the second order derivate *fprime2* of *func* is provided, parabolic Halley's method is used.

Parameters

func : function
: The function whose zero is wanted. It must be a function of a single variable of the form f(x,a,b,c...), where a,b,c... are extra arguments that can be passed in the *args* parameter.

x0 : float
: An initial estimate of the zero that should be somewhere near the actual zero.

fprime : function, optional
: The derivative of the function when available and convenient. If it is None (default), then the secant method is used.

args : tuple, optional
: Extra arguments to be used in the function call.

tol : float, optional
: The allowable error of the zero value.

maxiter : int, optional
: Maximum number of iterations.

fprime2 : function, optional
: The second order derivative of the function when available and convenient. If it is None (default), then the normal Newton-Raphson or the secant method is used. If it is given, parabolic Halley's method is used.

Returns

zero : float
: Estimated location where function is zero.

See also:

`brentq`, `brenth`, `ridder`, `bisect`

`fsolve`	find zeroes in n dimensions.

Notes

The convergence rate of the Newton-Raphson method is quadratic, the Halley method is cubic, and the secant method is sub-quadratic. This means that if the function is well behaved the actual error in the estimated zero is approximately the square (cube for Halley) of the requested tolerance up to roundoff error. However, the stopping criterion used here is the step size and there is no guarantee that a zero has been found. Consequently the result should be verified. Safer algorithms are brentq, brenth, ridder, and bisect, but they all require that the root first be bracketed in an interval where the function changes sign. The brentq algorithm is recommended for general use in one dimensional problems when such an interval has been found.

Fixed point finding:

`fixed_point`(func, x0[, args, xtol, maxiter])	Find a fixed point of the function.

`scipy.optimize.`**`fixed_point`**(*func*, *x0*, *args=()*, *xtol=1e-08*, *maxiter=500*)

Find a fixed point of the function.

Given a function of one or more variables and a starting point, find a fixed-point of the function: i.e. where `func(x0) == x0`.

Parameters **func** : function

Function to evaluate.

x0 : array_like

Fixed point of function.

args : tuple, optional

Extra arguments to *func*.

xtol : float, optional

Convergence tolerance, defaults to 1e-08.

maxiter : int, optional

Maximum number of iterations, defaults to 500.

Notes

Uses Steffensen's Method using Aitken's `Del^2` convergence acceleration. See Burden, Faires, "Numerical Analysis", 5th edition, pg. 80

Examples

```
>>> from scipy import optimize
>>> def func(x, c1, c2):
...     return np.sqrt(c1/(x+c2))
>>> c1 = np.array([10,12.])
>>> c2 = np.array([3, 5.])
>>> optimize.fixed_point(func, [1.2, 1.3], args=(c1,c2))
array([ 1.4920333 ,  1.37228132])
```

Multidimensional

General nonlinear solvers:

`root`(fun, x0[, args, method, jac, tol, ...])	Find a root of a vector function.
`fsolve`(func, x0[, args, fprime, ...])	Find the roots of a function.
`broyden1`(F, xin[, iter, alpha, ...])	Find a root of a function, using Broyden's first Jacobian approximation.
`broyden2`(F, xin[, iter, alpha, ...])	Find a root of a function, using Broyden's second Jacobian approximation.

`scipy.optimize.`**`root`**(*fun*, *x0*, *args=()*, *method='hybr'*, *jac=None*, *tol=None*, *callback=None*, *options=None*)

Find a root of a vector function.

Parameters **fun** : callable

A vector function to find a root of.

x0 : ndarray

Initial guess.

args : tuple, optional

Extra arguments passed to the objective function and its Jacobian.

method : str, optional

Type of solver. Should be one of

- 'hybr' *(see here)*
- 'lm' *(see here)*
- 'broyden1' *(see here)*
- 'broyden2' *(see here)*
- 'anderson' *(see here)*
- 'linearmixing' *(see here)*
- 'diagbroyden' *(see here)*
- 'excitingmixing' *(see here)*
- 'krylov' *(see here)*
- 'df-sane' *(see here)*

jac : bool or callable, optional

If *jac* is a Boolean and is True, *fun* is assumed to return the value of Jacobian along with the objective function. If False, the Jacobian will be estimated numerically. *jac* can also be a callable returning the Jacobian of *fun*. In this case, it must accept the same arguments as *fun*.

tol : float, optional

Tolerance for termination. For detailed control, use solver-specific options.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual. For all methods but 'hybr' and 'lm'.

options : dict, optional

A dictionary of solver options. E.g. *xtol* or *maxiter*, see `show_options()` for details.

Returns **sol** : OptimizeResult

The solution represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the algorithm exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

`show_options`

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *hybr*.

Method *hybr* uses a modification of the Powell hybrid method as implemented in MINPACK [R153].

Method *lm* solves the system of nonlinear equations in a least squares sense using a modification of the Levenberg-Marquardt algorithm as implemented in MINPACK [R153].

Method *df-sane* is a derivative-free spectral method. [R155]

Methods *broyden1*, *broyden2*, *anderson*, *linearmixing*, *diagbroyden*, *excitingmixing*, *krylov* are inexact Newton methods, with backtracking or full line searches [R154]. Each method corresponds to a particular Jacobian approximations. See `nonlin` for details.

- Method *broyden1* uses Broyden's first Jacobian approximation, it is known as Broyden's good method.
- Method *broyden2* uses Broyden's second Jacobian approximation, it is known as Broyden's bad method.
- Method *anderson* uses (extended) Anderson mixing.
- Method *Krylov* uses Krylov approximation for inverse Jacobian. It is suitable for large-scale problem.
- Method *diagbroyden* uses diagonal Broyden Jacobian approximation.
- Method *linearmixing* uses a scalar Jacobian approximation.
- Method *excitingmixing* uses a tuned diagonal Jacobian approximation.

> **Warning:** The algorithms implemented for methods *diagbroyden*, *linearmixing* and *excitingmixing* may be useful for specific problems, but whether they will work may depend strongly on the problem.

New in version 0.11.0.

References

[R153], [R154], [R155]

Examples

The following functions define a system of nonlinear equations and its jacobian.

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]

>>> def jac(x):
...     return np.array([[1 + 1.5 * (x[0] - x[1])**2,
...                       -1.5 * (x[0] - x[1])**2],
...                      [-1.5 * (x[1] - x[0])**2,
...                       1 + 1.5 * (x[1] - x[0])**2]])
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.root(fun, [0, 0], jac=jac, method='hybr')
>>> sol.x
array([ 0.8411639,  0.1588361])
```

`scipy.optimize.`**`fsolve`**(*func*, *x0*, *args=()*, *fprime=None*, *full_output=0*, *col_deriv=0*, *xtol=1.49012e-08*, *maxfev=0*, *band=None*, *epsfcn=None*, *factor=100*, *diag=None*)

Find the roots of a function.

Return the roots of the (non-linear) equations defined by `func(x) = 0` given a starting estimate.

Parameters

func : callable `f(x, *args)`

A function that takes at least one (possibly vector) argument.

x0 : ndarray

The starting estimate for the roots of `func(x) = 0`.

args : tuple, optional

Any extra arguments to *func*.

fprime : callable(x), optional

A function to compute the Jacobian of *func* with derivatives across the rows. By default, the Jacobian will be estimated.

full_output : bool, optional

If True, return optional outputs.

col_deriv : bool, optional

Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

xtol : float, optional

The calculation will terminate if the relative error between two consecutive iterates is at most *xtol*.

maxfev : int, optional

The maximum number of calls to the function. If zero, then `100*(N+1)` is the maximum where N is the number of elements in *x0*.

band : tuple, optional

If set to a two-sequence containing the number of sub- and super-diagonals within the band of the Jacobi matrix, the Jacobi matrix is considered banded (only for `fprime=None`).

epsfcn : float, optional

A suitable step length for the forward-difference approximation of the Jacobian (for `fprime=None`). If *epsfcn* is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

factor : float, optional

A parameter determining the initial step bound (`factor * || diag * x||`). Should be in the interval `(0.1, 100)`.

diag : sequence, optional

N positive entries that serve as a scale factors for the variables.

Returns

x : ndarray

The solution (or the result of the last iteration for an unsuccessful call).

infodict : dict

A dictionary of optional outputs with the keys:

nfev	number of function calls
njev	number of Jacobian calls
fvec	function evaluated at the output
fjac	the orthogonal matrix, q, produced by the QR factorization of the final approximate Jacobian matrix, stored column wise
r	upper triangular matrix produced by QR factorization of the same matrix
qtf	the vector `(transpose(q) * fvec)`

ier : int

An integer flag. Set to 1 if a solution was found, otherwise refer to *mesg* for more information.

mesg : str

If no solution is found, *mesg* details the cause of failure.

See also:

root	Interface to root finding algorithms for multivariate

`functions.`

Notes

`fsolve` is a wrapper around MINPACK's hybrd and hybrj algorithms.

`scipy.optimize.`**`broyden1`**`(`*F*, *xin*, *iter=None*, *alpha=None*, *reduction_method='restart'*, *max_rank=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*`)`

Find a root of a function, using Broyden's first Jacobian approximation.

This method is also known as "Broyden's good method".

Parameters

F : function(x) -> f

Function whose root to find; should take and return an array-like object.

x0 : array_like

Initial guess for the solution

alpha : float, optional

Initial guess for the Jacobian is `(-1/alpha)`.

reduction_method : str or tuple, optional

Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.

Methods available:

- `restart`: drop all matrix columns. Has no extra parameters.
- `simple`: drop oldest matrix column. Has no extra parameters.
- `svd`: keep only the most significant SVD components. Takes an extra parameter, `to_retain`, which determines the number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank : int, optional

Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional

Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol : ndarray

An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**

When a solution was not found.

Notes

This algorithm implements the inverse Jacobian Quasi-Newton update

$$H_+ = H + (dx - Hdf)dx^\dagger H/(dx^\dagger Hdf)$$

which corresponds to Broyden's first Jacobian update

$$J_+ = J + (df - Jdx)dx^\dagger/dx^\dagger dx$$

References

[R131]

`scipy.optimize.`**`broyden2`**`(`*F*, *xin*, *iter=None*, *alpha=None*, *reduction_method='restart'*, *max_rank=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*`)`

Find a root of a function, using Broyden's second Jacobian approximation.

This method is also known as "Broyden's bad method".

Parameters

F : function(x) -> f

Function whose root to find; should take and return an array-like object.

x0 : array_like

Initial guess for the solution

alpha : float, optional

Initial guess for the Jacobian is `(-1/alpha)`.

reduction_method : str or tuple, optional

Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.

Methods available:

- `restart`: drop all matrix columns. Has no extra parameters.
- `simple`: drop oldest matrix column. Has no extra parameters.
- `svd`: keep only the most significant SVD components. Takes an extra parameter, `to_retain`, which determines the number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank : int, optional

Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional

Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns **sol** : ndarray

An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**

When a solution was not found.

Notes

This algorithm implements the inverse Jacobian Quasi-Newton update

$$H_+ = H + (dx - H df) df^\dagger / (df^\dagger df)$$

corresponding to Broyden's second method.

References

[R132]

The `root` function supports the following methods:

root(method='hybr')

`scipy.optimize.`**`root`**(*fun*, *x0*, *args=()*, *method='hybr'*, *jac=None*, *tol=None*, *callback=None*, *options={'full_output': 0*, *'col_deriv': 0*, *'diag': None*, *'factor': 100*, *'eps': None*, *'band': None*, *'func': None*, *'maxfev': 0*, *'xtol': 1.49012e-08}*)

Find the roots of a multivariate function using MINPACK's hybrd and hybrj routines (modified Powell method).

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options **col_deriv** : bool

Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

xtol : float

The calculation will terminate if the relative error between two consecutive iterates is at most *xtol*.

maxfev : int

The maximum number of calls to the function. If zero, then `100*(N+1)` is the maximum where N is the number of elements in *x0*.

band : tuple

If set to a two-sequence containing the number of sub- and super-diagonals within the band of the Jacobi matrix, the Jacobi matrix is considered banded (only for `fprime=None`).

eps : float

A suitable step length for the forward-difference approximation of the Jacobian (for `fprime=None`). If *eps* is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

factor : float

A parameter determining the initial step bound (`factor * || diag * x||`). Should be in the interval `(0.1, 100)`.

diag : sequence

N positive entries that serve as a scale factors for the variables.

root(method='lm')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='lm'*, *jac=None*, *tol=None*, *callback=None*, *options={'col_deriv': 0, 'diag': None, 'factor': 100, 'gtol': 0.0, 'eps': 0.0, 'func': None, 'maxiter': 0, 'xtol': 1.49012e-08, 'ftol': 1.49012e-08}*)

Solve for least squares with Levenberg-Marquardt

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

col_deriv : bool

non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

ftol : float

Relative error desired in the sum of squares.

xtol : float

Relative error desired in the approximate solution.

gtol : float

Orthogonality desired between the function vector and the columns of the Jacobian.

maxiter : int

The maximum number of calls to the function. If zero, then 100*(N+1) is the maximum where N is the number of elements in x0.

epsfcn : float

A suitable step length for the forward-difference approximation of the Jacobian (for Dfun=None). If epsfcn is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

factor : float

A parameter determining the initial step bound (`factor * || diag * x||`). Should be in interval `(0.1, 100)`.

diag : sequence

N positive entries that serve as a scale factors for the variables.

root(method='broyden1')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='broyden1'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional

Relative tolerance for the residual. If omitted, not used.

fatol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional

Relative minimum step size. If omitted, not used.

xatol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional

Options for the respective Jacobian approximation.

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

reduction_method

[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.

Methods available:

- ***`restart`: drop all matrix columns. Has no***

  extra parameters.
- ***`simple`: drop oldest matrix column. Has no***

  extra parameters.
- ***`svd`: keep only the most significant SVD***

  components.

Extra parameters:

- ***`to_retain`: number of SVD compo***

  retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

root(method='broyden2')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='broyden2'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit : int, optional
Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional
Print status to stdout on every iteration.

maxiter : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional
Relative tolerance for the residual. If omitted, not used.

fatol : float, optional
Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional
Relative minimum step size. If omitted, not used.

xatol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional
Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional
Options for the respective Jacobian approximation.

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

reduction_method

[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.

Methods available:

- ***`restart`**: drop all matrix columns. Has no* extra parameters.
- ***`simple`**: drop oldest matrix column. Has no* extra parameters.

- ***`svd`**: keep only the most significant SVD* components.

Extra parameters:

- ***`to_retain`**: number of SVD compo* retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

root(method='anderson')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='anderson'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit : int, optional
Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional
Print status to stdout on every iteration.

maxiter : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional
Relative tolerance for the residual. If omitted, not used.

fatol : float, optional
Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional
Relative minimum step size. If omitted, not used.

xatol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional
Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional

Options for the respective Jacobian approximation.

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

M [float, optional] Number of previous vectors to retain. Defaults to 5.

w0 [float, optional] Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.

root(method='linearmixing')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='linearmixing'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options **nit** : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.

ftol : float, optional

Relative tolerance for the residual. If omitted, not used.

fatol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional

Relative minimum step size. If omitted, not used.

xatol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional

Options for the respective Jacobian approximation.

alpha [float, optional] initial guess for the jacobian is (-1/alpha).

root(method='diagbroyden')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='diagbroyden'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options **nit** : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional
Relative tolerance for the residual. If omitted, not used.

fatol : float, optional
Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional
Relative minimum step size. If omitted, not used.

xatol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional
Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional
Options for the respective Jacobian approximation.

alpha [float, optional] initial guess for the jacobian is (-1/alpha).

root(method='excitingmixing')

`scipy.optimize.`**`root`**(*fun*, *x0*, *args=()*, *method='excitingmixing'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit : int, optional
Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional
Print status to stdout on every iteration.

maxiter : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional
Relative tolerance for the residual. If omitted, not used.

fatol : float, optional
Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional
Relative minimum step size. If omitted, not used.

xatol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional

Options for the respective Jacobian approximation.

alpha	[float, optional] Initial Jacobian approximation is (-1/alpha).
alphamax	[float, optional] The entries of the diagonal Jacobian are kept in the range `[alpha, alphamax]`.

root(method='krylov')

`scipy.optimize.`**`root`** (*fun*, *x0*, *args=()*, *method='krylov'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol : float, optional

Relative tolerance for the residual. If omitted, not used.

fatol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol : float, optional

Relative minimum step size. If omitted, not used.

xatol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options : dict, optional

Options for the respective Jacobian approximation.

rdiff [float, optional] Relative step size to use in numerical differentiation.

method [{'lgmres', 'gmres', 'bicgstab', 'cgs', 'minres'} or function] Krylov method to use to approximate the Jacobian. Can be a string, or a function implementing the same interface as the iterative solvers in `scipy.sparse.linalg`.

The default is `scipy.sparse.linalg.lgmres`.

inner_M [LinearOperator or InverseJacobian] Preconditioner for the inner Krylov iteration. Note that you can use also inverse Jacobians as (adaptive) preconditioners. For example,

```
>>> jac = BroydenFirst()
>>> kjac = KrylovJacobian(inner_M=jac.inverse).
```

If the preconditioner has a method named 'update', it will be called as `update(x, f)` after each nonlinear step, with `x` giving the current point, and `f` the current function value.

inner_tol, inner_maxiter, ...
Parameters to pass on to the "inner" Krylov solver. See `scipy.sparse.linalg.gmres` for details.

outer_k [int, optional] Size of the subspace kept across LGMRES nonlinear iterations.
See `scipy.sparse.linalg.lgmres` for details.

root(method='df-sane')

`scipy.optimize.root` (*fun*, *x0*, *args=()*, *method='df-sane'*, *tol=None*, *callback=None*, *options={'disp': False*, *'fnorm': None*, *'sigma_0': 1.0*, *'eta_strategy': None*, *'sigma_eps': 1e-10*, *'M': 10*, *'line_search': 'cruz'*, *'fatol': 1e-300*, *'func': None*, *'maxfev': 1000*, *'ftol': 1e-08}*)

Solve nonlinear equation with the DF-SANE method

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

ftol : float, optional
Relative norm tolerance.

fatol : float, optional
Absolute norm tolerance. Algorithm terminates when `||func(x)|| < fatol + ftol ||func(x_0)||`.

fnorm : callable, optional
Norm to use in the convergence check. If None, 2-norm is used.

maxfev : int, optional
Maximum number of function evaluations.

disp : bool, optional
Whether to print convergence process to stdout.

eta_strategy : callable, optional
Choice of the `eta_k` parameter, which gives slack for growth of `||F||**2`. Called as `eta_k = eta_strategy(k, x, F)` with *k* the iteration number, *x* the current iterate and *F* the current residual. Should satisfy `eta_k > 0` and `sum(eta, k=0..inf) < inf`. Default: `||F||**2 / (1 + k)**2`.

sigma_eps : float, optional
The spectral coefficient is constrained to `sigma_eps < sigma < 1/sigma_eps`. Default: 1e-10

sigma_0 : float, optional
Initial spectral coefficient. Default: 1.0

M : int, optional
Number of iterates to include in the nonmonotonic line search. Default: 10

line_search : {'cruz', 'cheng'}
Type of line search to employ. 'cruz' is the original one defined in [Martinez & Raydan. Math. Comp. 75, 1429 (2006)], 'cheng' is a modified search defined in [Cheng & Li. IMA J. Numer. Anal. 29, 814 (2009)]. Default: 'cruz'

References

[R509], [R510], [R511]

Large-scale nonlinear solvers:

`newton_krylov`(F, xin[, iter, rdiff, method, ...])	Find a root of a function, using Krylov approximation for inverse Jacobian.
`anderson`(F, xin[, iter, alpha, w0, M, ...])	Find a root of a function, using (extended) Anderson mixing.

`scipy.optimize.`**`newton_krylov`**(*F*, *xin*, *iter=None*, *rdiff=None*, *method='lgmres'*, *inner_maxiter=20*, *inner_M=None*, *outer_k=10*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using Krylov approximation for inverse Jacobian.

This method is suitable for solving large-scale problems.

Parameters

F : function(x) -> f

Function whose root to find; should take and return an array-like object.

x0 : array_like

Initial guess for the solution

rdiff : float, optional

Relative step size to use in numerical differentiation.

method : {'lgmres', 'gmres', 'bicgstab', 'cgs', 'minres'} or function

Krylov method to use to approximate the Jacobian. Can be a string, or a function implementing the same interface as the iterative solvers in `scipy.sparse.linalg`.

The default is `scipy.sparse.linalg.lgmres`.

inner_M : LinearOperator or InverseJacobian

Preconditioner for the inner Krylov iteration. Note that you can use also inverse Jacobians as (adaptive) preconditioners. For example,

```
>>> from scipy.optimize.nonlin import BroydenFirst, KrylovJacobian
>>> from scipy.optimize.nonlin import InverseJacobian
>>> jac = BroydenFirst()
>>> kjac = KrylovJacobian(inner_M=InverseJacobian(jac))
```

If the preconditioner has a method named 'update', it will be called as `update(x, f)` after each nonlinear step, with `x` giving the current point, and `f` the current function value.

inner_tol, inner_maxiter, ...

Parameters to pass on to the "inner" Krylov solver. See `scipy.sparse.linalg.gmres` for details.

outer_k : int, optional

Size of the subspace kept across LGMRES nonlinear iterations. See `scipy.sparse.linalg.lgmres` for details.

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional
Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional
Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional
Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns **sol** : ndarray
An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**
When a solution was not found.

See also:

`scipy.sparse.linalg.gmres`, `scipy.sparse.linalg.lgmres`

Notes

This function implements a Newton-Krylov solver. The basic idea is to compute the inverse of the Jacobian with an iterative Krylov method. These methods require only evaluating the Jacobian-vector products, which are conveniently approximated by a finite difference:

$$Jv \approx (f(x + \omega * v/|v|) - f(x))/\omega$$

Due to the use of iterative matrix inverses, these methods can deal with large nonlinear problems.

Scipy's `scipy.sparse.linalg` module offers a selection of Krylov solvers to choose from. The default here is *lgmres*, which is a variant of restarted GMRES iteration that reuses some of the information obtained in the previous Newton steps to invert Jacobians in subsequent steps.

For a review on Newton-Krylov methods, see for example [R151], and for the LGMRES sparse inverse method, see [R152].

References

[R151], [R152]

`scipy.optimize.`**`anderson`**(*F*, *xin*, *iter=None*, *alpha=None*, *w0=0.01*, *M=5*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using (extended) Anderson mixing.

The Jacobian is formed by for a 'best' solution in the space spanned by last *M* vectors. As a result, only a MxM matrix inversions and MxN multiplications are required. [Ey]

Parameters **F** : function(x) -> f
Function whose root to find; should take and return an array-like object.

x0 : array_like
Initial guess for the solution

alpha : float, optional
Initial guess for the Jacobian is (-1/alpha).

M : float, optional

Number of previous vectors to retain. Defaults to 5.

w0 : float, optional

Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional

Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns **sol** : ndarray

An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**

When a solution was not found.

References

[Ey]

Simple iterations:

`excitingmixing`(F, xin[, iter, alpha, ...])	Find a root of a function, using a tuned diagonal Jacobian approximation.
`linearmixing`(F, xin[, iter, alpha, verbose, ...])	Find a root of a function, using a scalar Jacobian approximation.
`diagbroyden`(F, xin[, iter, alpha, verbose, ...])	Find a root of a function, using diagonal Broyden Jacobian approximation.

`scipy.optimize.`**`excitingmixing`**(*F*, *xin*, *iter=None*, *alpha=None*, *alphamax=1.0*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using a tuned diagonal Jacobian approximation.

The Jacobian matrix is diagonal and is tuned on each iteration.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

F : function(x) -> f

Function whose root to find; should take and return an array-like object.

x0 : array_like

Initial guess for the solution

alpha : float, optional

Initial Jacobian approximation is (-1/alpha).

alphamax : float, optional

The entries of the diagonal Jacobian are kept in the range `[alpha, alphamax]`.

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional

Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol : ndarray

An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence

When a solution was not found.

`scipy.optimize.`**`linearmixing`**(*F*, *xin*, *iter=None*, *alpha=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using a scalar Jacobian approximation.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

F : function(x) -> f

Function whose root to find; should take and return an array-like object.

x0 : array_like
Initial guess for the solution

alpha : float, optional
The Jacobian approximation is (-1/alpha).

iter : int, optional
Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional
Print status to stdout on every iteration.

maxiter : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional
Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional
Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional
Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional
Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional
Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional
Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional
Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns **sol** : ndarray
An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**
When a solution was not found.

`scipy.optimize.`**`diagbroyden`**(*F*, *xin*, *iter=None*, *alpha=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using diagonal Broyden Jacobian approximation.

The Jacobian approximation is derived from previous iterations, by retaining only the diagonal of Broyden matrices.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters **F** : function(x) -> f
Function whose root to find; should take and return an array-like object.

x0 : array_like
Initial guess for the solution

alpha : float, optional
Initial guess for the Jacobian is (-1/alpha).

iter : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose : bool, optional

Print status to stdout on every iteration.

maxiter : int, optional

Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol : float, optional

Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol : float, optional

Relative tolerance for the residual. If omitted, not used.

x_tol : float, optional

Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol : float, optional

Relative minimum step size. If omitted, not used.

tol_norm : function(vector) -> scalar, optional

Norm to use in convergence check. Default is the maximum norm.

line_search : {None, 'armijo' (default), 'wolfe'}, optional

Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback : function, optional

Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns **sol** : ndarray

An array (of similar array type as *x0*) containing the final solution.

Raises **NoConvergence**

When a solution was not found.

Additional information on the nonlinear solvers

5.24.4 Linear Programming

Simplex Algorithm:

`linprog`(c[, A_ub, b_ub, A_eq, b_eq, bounds, ...])	Minimize a linear objective function subject to linear equality and inequality c

`scipy.optimize.`**`linprog`**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='simplex'*, *callback=None*, *options=None*)

Minimize a linear objective function subject to linear equality and inequality constraints.

Linear Programming is intended to solve the following problem form:

Minimize: c^T * x

Subject to: A_ub * x <= b_ub

A_eq * x == b_eq

Parameters **c** : array_like

Coefficients of the linear objective function to be minimized.

A_ub : array_like, optional

2-D array which, when matrix-multiplied by x, gives the values of the upper-bound inequality constraints at x.

b_ub : array_like, optional

1-D array of values representing the upper-bound of each inequality constraint (row) in A_ub.

A_eq : array_like, optional

2-D array which, when matrix-multiplied by x, gives the values of the equality constraints at x.

b_eq : array_like, optional

1-D array of values representing the RHS of each equality constraint (row) in A_eq.

bounds : sequence, optional

`(min, max)` pairs for each element in `x`, defining the bounds on that parameter. Use None for one of `min` or `max` when there is no bound in that direction. By default bounds are `(0, None)` (non-negative) If a sequence containing a single tuple is provided, then `min` and `max` will be applied to all variables in the problem.

method : str, optional

Type of solver. At this time only 'simplex' is supported *(see here)*.

callback : callable, optional

If a callback function is provide, it will be called within each iteration of the simplex algorithm. The callback must have the signature *callback(xk, **kwargs)* where xk is the current solution vector and kwargs is a dictionary containing the following:

```
"tableau" : The current Simplex algorithm tableau
"nit" : The current iteration.
"pivot" : The pivot (row, column) used for the next iteration.
"phase" : Whether the algorithm is in Phase 1 or Phase 2.
"basis" : The indices of the columns of the basic variables.
```

options : dict, optional

A dictionary of solver options. All methods accept the following generic options:

maxiter [int] Maximum number of iterations to perform.

disp [bool] Set to True to print convergence messages.

For method-specific options, see *show_options('linprog')*.

Returns A `scipy.optimize.OptimizeResult` consisting of the following fields:

x [ndarray] The independent variable vector which optimizes the linear programming problem.

slack [ndarray] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, then the corresponding constraint is active.

success [bool] Returns True if the algorithm succeeded in finding an optimal solution.

status [int] An integer representing the exit status of the optimization:

```
0 : Optimization terminated successfully
1 : Iteration limit reached
2 : Problem appears to be infeasible
3 : Problem appears to be unbounded
```

nit [int] The number of iterations performed.

message [str] A string descriptor of the exit status of the optimization.

See also:

`show_options`

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *Simplex*.

Method *Simplex* uses the Simplex algorithm (as it relates to Linear Programming, NOT the Nelder-Mead Simplex) [R139], [R140]. This algorithm should be reasonably reliable and fast.

New in version 0.15.0.

References

[R139], [R140], [R141]

Examples

Consider the following problem:

Minimize: f = -1*x[0] + 4*x[1]
Subject to: -3*x[0] + 1*x[1] <= 6

1*x[0] + 2*x[1] <= 4
x[1] >= -3
where: -inf <= x[0] <= inf

This problem deviates from the standard linear programming problem. In standard form, linear programming problems assume the variables x are non-negative. Since the variables don't have standard bounds where 0 <= x <= inf, the bounds of the variables must be explicitly set.

There are two upper-bound constraints, which can be expressed as

dot(A_ub, x) <= b_ub

The input for this problem is as follows:

```
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bounds = (None, None)
>>> x1_bounds = (-3, None)
>>> from scipy.optimize import linprog
>>> res = linprog(c, A_ub=A, b_ub=b, bounds=(x0_bounds, x1_bounds),
...               options={"disp": True})
>>> print(res)
Optimization terminated successfully.
     Current function value: -11.428571
     Iterations: 2
status: 0
success: True
fun: -11.428571428571429
x: array([-1.14285714,  2.57142857])
message: 'Optimization terminated successfully.'
nit: 2
```

Note the actual objective value is 11.428571. In this case we minimized the negative of the objective function.

The `linprog` function supports the following methods:

linprog(method='Simplex')

`scipy.optimize.`**`linprog`**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='simplex'*, *callback=None*, *options={'disp': False*, *'bland': False*, *'tol': 1e-12*, *'maxiter': 1000}*)

Solve the following linear programming problem via a two-phase simplex algorithm.

maximize: c^T * x

subject to: A_ub * x <= b_ub

A_eq * x == b_eq

Parameters

c : array_like

Coefficients of the linear objective function to be maximized.

A_ub : array_like

2-D array which, when matrix-multiplied by x, gives the values of the upper-bound inequality constraints at x.

b_ub : array_like

1-D array of values representing the upper-bound of each inequality constraint (row) in A_ub.

A_eq : array_like

2-D array which, when matrix-multiplied by x, gives the values of the equality constraints at x.

b_eq : array_like

1-D array of values representing the RHS of each equality constraint (row) in A_eq.

bounds : array_like

The bounds for each independent variable in the solution, which can take one of three forms:: None : The default bounds, all variables are non-negative. (lb, ub) : If a 2-element sequence is provided, the same

lower bound (lb) and upper bound (ub) will be applied to all variables.

[(lb_0, ub_0), (lb_1, ub_1), ...]

[If an n x 2 sequence is provided,] each variable x_i will be bounded by lb[i] and ub[i].

Infinite bounds are specified using -np.inf (negative) or np.inf (positive).

callback : callable

If a callback function is provide, it will be called within each iteration of the simplex algorithm. The callback must have the signature *callback(xk, **kwargs)* where xk is the current solution vector and kwargs is a dictionary containing the following:: "tableau" : The current Simplex algorithm tableau "nit" : The current iteration. "pivot" : The pivot (row, column) used for the next iteration. "phase" : Whether the algorithm is in Phase 1 or Phase 2. "bv" : A structured array containing a string representation of each

basic variable and its current value.

Returns

A scipy.optimize.OptimizeResult consisting of the following fields:

```
x : ndarray
    The independent variable vector which optimizes the linear
    programming problem.
slack : ndarray
    The values of the slack variables.  Each slack variable corresponds
    to an inequality constraint.  If the slack is zero, then the
    corresponding constraint is active.
success : bool
```

```
    Returns True if the algorithm succeeded in finding an optimal
    solution.
status : int
    An integer representing the exit status of the optimization::
     0 : Optimization terminated successfully
     1 : Iteration limit reached
     2 : Problem appears to be infeasible
     3 : Problem appears to be unbounded
nit : int
    The number of iterations performed.
message : str
    A string descriptor of the exit status of the optimization.
```

See also:

For documentation for the rest of the parameters, see `scipy.optimize.linprog`

Options

maxiter : int
The maximum number of iterations to perform.

disp : bool
If True, print exit status message to sys.stdout

tol : float
The tolerance which determines when a solution is "close enough" to zero in Phase 1 to be considered a basic feasible solution or close enough to positive to to serve as an optimal solution.

bland : bool
If True, use Bland's anti-cycling rule [3] to choose pivots to prevent cycling. If False, choose pivots which should lead to a converged solution more quickly. The latter method is subject to cycling (non-convergence) in rare instances.

References

[R502], [R503], [R504]

Examples

Consider the following problem:

Minimize: f = -1*x[0] + 4*x[1]
Subject to: -3*x[0] + 1*x[1] <= 6

1*x[0] + 2*x[1] <= 4
x[1] >= -3
where: -inf <= x[0] <= inf

This problem deviates from the standard linear programming problem. In standard form, linear programming problems assume the variables x are non-negative. Since the variables don't have standard bounds where 0 <= x <= inf, the bounds of the variables must be explicitly set.

There are two upper-bound constraints, which can be expressed as

dot(A_ub, x) <= b_ub

The input for this problem is as follows:

```
>>> from scipy.optimize import linprog
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bnds = (None, None)
>>> x1_bnds = (-3, None)
>>> res = linprog(c, A, b, bounds=(x0_bnds, x1_bnds))
>>> print(res)
Optimization terminated successfully.
     Current function value: -22.000000
     Iterations: 1
status: 0
x: array([ 10.,  -3.])
slack: array([ 39.,   0.])
nit: 1
message: 'Optimization terminated successfully.'
fun: -22.0
success: True
```

5.24.5 Utilities

`approx_fprime`(xk, f, epsilon, *args)	Finite-difference approximation of the gradient of a scalar function.
`bracket`(func[, xa, xb, args, grow_limit, ...])	Bracket the minimum of the function.
`check_grad`(func, grad, x0, *args, **kwargs)	Check the correctness of a gradient function by comparing it against a (forward) fir
`line_search`(f, myfprime, xk, pk[, gfk, ...])	Find alpha that satisfies strong Wolfe conditions.
`show_options`([solver, method, disp])	Show documentation for additional options of optimization solvers.
`LbfgsInvHessProduct`(sk, yk)	Linear operator for the L-BFGS approximate inverse Hessian.

`scipy.optimize.`**`approx_fprime`**(*xk*, *f*, *epsilon*, **args*)

Finite-difference approximation of the gradient of a scalar function.

Parameters

xk : array_like

The coordinate vector at which to determine the gradient of *f*.

f : callable

The function of which to determine the gradient (partial derivatives). Should take *xk* as first argument, other arguments to *f* can be supplied in `*args`. Should return a scalar, the value of the function at *xk*.

epsilon : array_like

Increment to *xk* to use for determining the function gradient. If a scalar, uses the same finite difference delta for all partial derivatives. If an array, should contain one value per element of *xk*.

***args** : args, optional

Any other arguments that are to be passed to *f*.

Returns

grad : ndarray

The partial derivatives of *f* to *xk*.

See also:

`check_grad` Check correctness of gradient function against approx_fprime.

Notes

The function gradient is determined by the forward finite difference formula:

```
          f(xk[i] + epsilon[i]) - f(xk[i])
f'[i] = ---------------------------------
                    epsilon[i]
```

The main use of `approx_fprime` is in scalar function optimizers like `fmin_bfgs`, to determine numerically the Jacobian of a function.

Examples

```
>>> from scipy import optimize
>>> def func(x, c0, c1):
...     "Coordinate vector `x` should be an array of size two."
...     return c0 * x[0]**2 + c1*x[1]**2
```

```
>>> x = np.ones(2)
>>> c0, c1 = (1, 200)
>>> eps = np.sqrt(np.finfo(np.float).eps)
>>> optimize.approx_fprime(x, func, [eps, np.sqrt(200) * eps], c0, c1)
array([   2.        ,  400.00004198])
```

`scipy.optimize.`**`bracket`**(*func*, *xa=0.0*, *xb=1.0*, *args=()*, *grow_limit=110.0*, *maxiter=1000*)

Bracket the minimum of the function.

Given a function and distinct initial points, search in the downhill direction (as defined by the initital points) and return new points xa, xb, xc that bracket the minimum of the function f(xa) > f(xb) < f(xc). It doesn't always mean that obtained solution will satisfy xa<=x<=xb

Parameters

func : callable f(x,*args)
Objective function to minimize.

xa, xb : float, optional
Bracketing interval. Defaults *xa* to 0.0, and *xb* to 1.0.

args : tuple, optional
Additional arguments (if present), passed to *func*.

grow_limit : float, optional
Maximum grow limit. Defaults to 110.0

maxiter : int, optional
Maximum number of iterations to perform. Defaults to 1000.

Returns

xa, xb, xc : float
Bracket.

fa, fb, fc : float
Objective function values in bracket.

funcalls : int
Number of function evaluations made.

`scipy.optimize.`**`check_grad`**(*func*, *grad*, *x0*, **args*, ***kwargs*)

Check the correctness of a gradient function by comparing it against a (forward) finite-difference approximation of the gradient.

Parameters

func : callable `func(x0, *args)`
Function whose derivative is to be checked.

grad : callable `grad(x0, *args)`
Gradient of *func*.

x0 : ndarray
Points to check *grad* against forward difference approximation of grad using *func*.

args : *args, optional

Extra arguments passed to *func* and *grad*.

epsilon : float, optional

Step size used for the finite difference approximation. It defaults to `sqrt(numpy.finfo(float).eps)`, which is approximately 1.49e-08.

Returns **err** : float

The square root of the sum of squares (i.e. the 2-norm) of the difference between `grad(x0, *args)` and the finite difference approximation of *grad* using func at the points *x0*.

See also:

`approx_fprime`

Examples

```
>>> def func(x):
...     return x[0]**2 - 0.5 * x[1]**3
>>> def grad(x):
...     return [2 * x[0], -1.5 * x[1]**2]
>>> from scipy.optimize import check_grad
>>> check_grad(func, grad, [1.5, -1.5])
2.9802322387695312e-08
```

`scipy.optimize.`**`line_search`**(*f*, *myfprime*, *xk*, *pk*, *gfk=None*, *old_fval=None*, *old_old_fval=None*, *args=()*, *c1=0.0001*, *c2=0.9*, *amax=50*)

Find alpha that satisfies strong Wolfe conditions.

Parameters **f** : callable f(x,*args)

Objective function.

myfprime : callable f'(x,*args)

Objective function gradient.

xk : ndarray

Starting point.

pk : ndarray

Search direction.

gfk : ndarray, optional

Gradient value for x=xk (xk being the current parameter estimate). Will be recomputed if omitted.

old_fval : float, optional

Function value for x=xk. Will be recomputed if omitted.

old_old_fval : float, optional

Function value for the point preceding x=xk

args : tuple, optional

Additional arguments passed to objective function.

c1 : float, optional

Parameter for Armijo condition rule.

c2 : float, optional

Parameter for curvature condition rule.

amax : float, optional

Maximum step size

Returns **alpha** : float or None

Alpha for which `x_new = x0 + alpha * pk`, or None if the line search algorithm did not converge.

fc : int

Number of function evaluations made.

gc : int

Number of gradient evaluations made.

new_fval : float or None

New function value `f(x_new)=f(x0+alpha*pk)`, or None if the line search algorithm did not converge.

old_fval : float

Old function value `f(x0)`.

new_slope : float or None

The local slope along the search direction at the new value `<myfprime(x_new), pk>`, or None if the line search algorithm did not converge.

Notes

Uses the line search algorithm to enforce strong Wolfe conditions. See Wright and Nocedal, 'Numerical Optimization', 1999, pg. 59-60.

For the zoom phase it uses an algorithm by [...].

`scipy.optimize.`**`show_options`**`(`*solver=None*, *method=None*, *disp=True*`)`

Show documentation for additional options of optimization solvers.

These are method-specific options that can be supplied through the `options` dict.

Parameters

solver : str

Type of optimization solver. One of 'minimize', 'minimize_scalar', 'root', or 'linprog'.

method : str, optional

If not given, shows all methods of the specified solver. Otherwise, show only the options for the specified method. Valid values corresponds to methods' names of respective solver (e.g. 'BFGS' for 'minimize').

disp : bool, optional

Whether to print the result rather than returning it.

Returns

text

Either None (for disp=False) or the text string (disp=True)

Notes

The solver-specific methods are:

`scipy.optimize.minimize`

- *Nelder-Mead*
- *Powell*
- *CG*
- *BFGS*
- *Newton-CG*
- *L-BFGS-B*
- *TNC*
- *COBYLA*
- *SLSQP*
- *dogleg*
- *trust-ncg*

`scipy.optimize.root`

- *hybr*
- *lm*
- *broyden1*
- *broyden2*
- *anderson*
- *linearmixing*

- *diagbroyden*
- *excitingmixing*
- *krylov*
- *df-sane*

`scipy.optimize.minimize_scalar`

- *brent*
- *golden*
- *bounded*

`scipy.optimize.linprog`

- *simplex*

class `scipy.optimize.`**`LbfgsInvHessProduct`**(*sk*, *yk*)

Linear operator for the L-BFGS approximate inverse Hessian.

This operator computes the product of a vector with the approximate inverse of the Hessian of the objective function, using the L-BFGS limited memory approximation to the inverse Hessian, accumulated during the optimization.

Parameters **sk** : array_like, shape=(n_corr, n)

Array of *n_corr* most recent updates to the solution vector. (See [1]).

yk : array_like, shape=(n_corr, n)

Array of *n_corr* most recent updates to the gradient. (See [1]).

References

[R126]

Attributes

`H`	Hermitian adjoint.
`T`	Transpose this linear operator.

`LbfgsInvHessProduct.`**`H`**

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** : LinearOperator

Hermitian adjoint of self.

`LbfgsInvHessProduct.`**`T`**

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

Methods

`__call__`(x)	
`adjoint`()	Hermitian adjoint.
`dot`(x)	Matrix-matrix or matrix-vector multiplication.
`matmat`(X)	Matrix-matrix multiplication.
`matvec`(x)	Matrix-vector multiplication.
`rmatvec`(x)	Adjoint matrix-vector multiplication.

Continued on next page

Table 5.112 – continued from previous page

todense()	Return a dense array representation of this operator.
transpose()	Transpose this linear operator.

LbfgsInvHessProduct.**__call__**(*x*)

LbfgsInvHessProduct.**adjoint**()

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** : LinearOperator

Hermitian adjoint of self.

LbfgsInvHessProduct.**dot**(*x*)

Matrix-matrix or matrix-vector multiplication.

Parameters **x** : array_like

1-d or 2-d array, representing a vector or matrix.

Returns **Ax** : array

1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

LbfgsInvHessProduct.**matmat**(*X*)

Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** : {matrix, ndarray}

An array with shape (N,K).

Returns **Y** : {matrix, ndarray}

A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

LbfgsInvHessProduct.**matvec**(*x*)

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** : {matrix, ndarray}

An array with shape (N,) or (N,1).

Returns **y** : {matrix, ndarray}

A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

LbfgsInvHessProduct.**rmatvec**(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters	**x** : {matrix, ndarray} An array with shape (M,) or (M,1).
Returns	**y** : {matrix, ndarray} A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

`LbfgsInvHessProduct.`**`todense`**`()`

Return a dense array representation of this operator.

Returns	**arr** : ndarray, shape=(n, n) An array with the same shape and containing the same data represented by this *LinearOperator*.

`LbfgsInvHessProduct.`**`transpose`**`()`

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

This is a collection of general-purpose nonlinear multidimensional solvers. These solvers find *x* for which *F(x) = 0*. Both *x* and *F* can be multidimensional.

5.25 Routines

Large-scale nonlinear solvers:

`newton_krylov`(F, xin[, iter, rdiff, method, ...])	Find a root of a function, using Krylov approximation for inverse Jacobian.
`anderson`(F, xin[, iter, alpha, w0, M, ...])	Find a root of a function, using (extended) Anderson mixing.

General nonlinear solvers:

`broyden1`(F, xin[, iter, alpha, ...])	Find a root of a function, using Broyden's first Jacobian approximation.
`broyden2`(F, xin[, iter, alpha, ...])	Find a root of a function, using Broyden's second Jacobian approximation.

Simple iterations:

`excitingmixing`(F, xin[, iter, alpha, ...])	Find a root of a function, using a tuned diagonal Jacobian approximation.
`linearmixing`(F, xin[, iter, alpha, verbose, ...])	Find a root of a function, using a scalar Jacobian approximation.
`diagbroyden`(F, xin[, iter, alpha, verbose, ...])	Find a root of a function, using diagonal Broyden Jacobian approximation.

5.26 Examples

5.26.1 Small problem

```
>>> def F(x):
...     return np.cos(x) + x[::-1] - [1, 2, 3, 4]
>>> import scipy.optimize
>>> x = scipy.optimize.broyden1(F, [1,1,1,1], f_tol=1e-14)
>>> x
array([ 4.04674914,  3.91158389,  2.71791677,  1.61756251])
>>> np.cos(x) + x[::-1]
array([ 1.,  2.,  3.,  4.])
```

5.26.2 Large problem

Suppose that we needed to solve the following integrodifferential equation on the square $[0, 1] \times [0, 1]$:

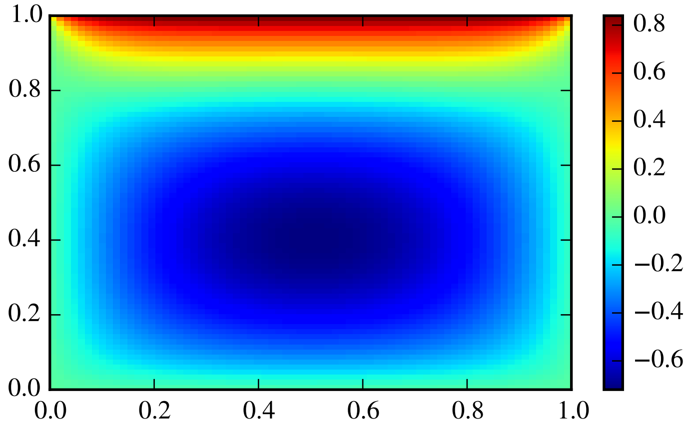
$$\nabla^2 P = 10 \left(\int_0^1 \int_0^1 \cosh(P) \, dx \, dy \right)^2$$

with $P(x, 1) = 1$ and $P = 0$ elsewhere on the boundary of the square.

The solution can be found using the `newton_krylov` solver:

```
import numpy as np
from scipy.optimize import newton_krylov
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def residual(P):
    d2x = zeros_like(P)
    d2y = zeros_like(P)

    d2x[1:-1] = (P[2:]   - 2*P[1:-1] + P[:-2]) / hx/hx
    d2x[0]    = (P[1]    - 2*P[0]    + P_left)/hx/hx
    d2x[-1]   = (P_right - 2*P[-1]   + P[-2])/hx/hx

    d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
    d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
    d2y[:,-1]   = (P_top   - 2*P[:,-1]   + P[:,-2])/hy/hy

    return d2x + d2y - 10*cosh(P).mean()**2

# solve
guess = zeros((nx, ny), float)
sol = newton_krylov(residual, guess, method='lgmres', verbose=1)
print('Residual: %g' % abs(residual(sol)).max())

# visualize
```

```
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolor(x, y, sol)
plt.colorbar()
plt.show()
```



5.27 Signal processing (`scipy.signal`)

5.27.1 Convolution

`convolve`(in1, in2[, mode])	Convolve two N-dimensional arrays.
`correlate`(in1, in2[, mode])	Cross-correlate two N-dimensional arrays.
`fftconvolve`(in1, in2[, mode])	Convolve two N-dimensional arrays using FFT.
`convolve2d`(in1, in2[, mode, boundary, fillvalue])	Convolve two 2-dimensional arrays.
`correlate2d`(in1, in2[, mode, boundary, ...])	Cross-correlate two 2-dimensional arrays.
`sepfir2d`((input, hrow, hcol) -> output)	Description:

`scipy.signal.`**`convolve`**(*in1*, *in2*, *mode='full'*)

Convolve two N-dimensional arrays.

Convolve *in1* and *in2*, with the output size determined by the *mode* argument.

Parameters **in1** : array_like

First input.

in2 : array_like

Second input. Should have the same number of dimensions as *in1*; if sizes of *in1* and *in2* are not equal then *in1* has to be the larger array.

mode : str {'full', 'valid', 'same'}, optional

A string indicating the size of the output:

`full` The output is the full discrete linear convolution of the inputs. (Default)

`valid` The output consists only of those elements that do not rely on the zero-padding.

	same	The output is the same size as *in1*, centered with respect to the 'full' output.

Returns **convolve** : array

An N-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

See also:

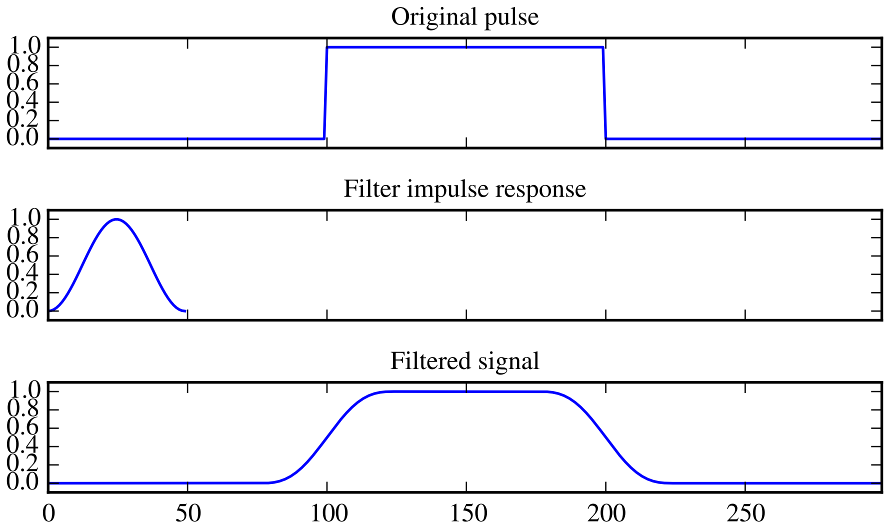
numpy.polymul
performs polynomial multiplication (same operation, but also accepts poly1d objects)

Examples

Smooth a square pulse using a Hann window:

```
>>> from scipy import signal
>>> sig = np.repeat([0., 1., 0.], 100)
>>> win = signal.hann(50)
>>> filtered = signal.convolve(sig, win, mode='same') / sum(win)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_win, ax_filt) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('Original pulse')
>>> ax_orig.margins(0, 0.1)
>>> ax_win.plot(win)
>>> ax_win.set_title('Filter impulse response')
>>> ax_win.margins(0, 0.1)
>>> ax_filt.plot(filtered)
>>> ax_filt.set_title('Filtered signal')
>>> ax_filt.margins(0, 0.1)
>>> fig.tight_layout()
>>> fig.show()
```



scipy.signal.**correlate**(*in1*, *in2*, *mode='full'*)
Cross-correlate two N-dimensional arrays.

Cross-correlate *in1* and *in2*, with the output size determined by the *mode* argument.

Parameters **in1** : array_like

First input.

in2 : array_like

Second input. Should have the same number of dimensions as *in1*; if sizes of *in1* and *in2* are not equal then *in1* has to be the larger array.

mode : str {'full', 'valid', 'same'}, optional

A string indicating the size of the output:

full	The output is the full discrete linear cross-correlation of the inputs. (Default).
valid	The output consists only of those elements that do not rely on the zero-padding.
same	The output is the same size as *in1*, centered with respect to the 'full' output.

Returns **correlate** : array

An N-dimensional array containing a subset of the discrete linear cross-correlation of *in1* with *in2*.

Notes

The correlation z of two d-dimensional arrays x and y is defined as:

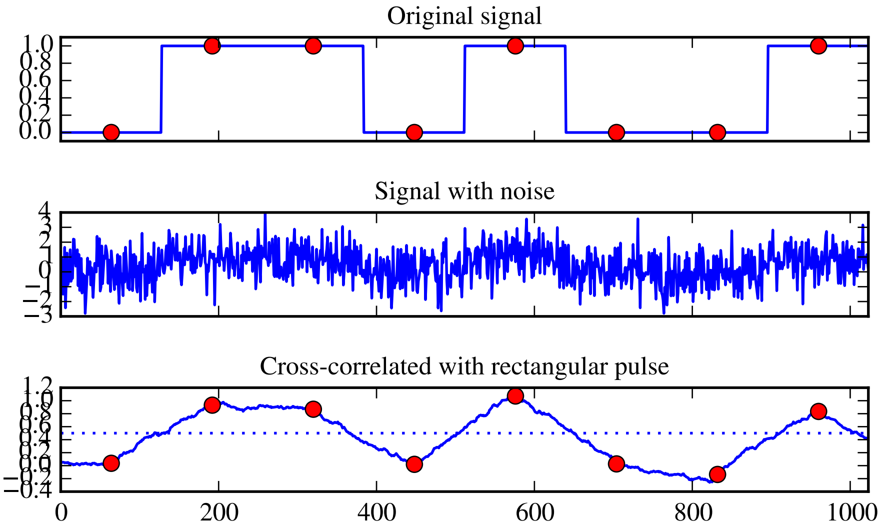
z[...,k,...] = sum[..., i_l, ...]
x[..., i_l,...] * conj(y[..., i_l + k,...])

Examples

Implement a matched filter using cross-correlation, to recover a signal that has passed through a noisy channel.

```
>>> from scipy import signal
>>> sig = np.repeat([0., 1., 1., 0., 1., 0., 0., 1.], 128)
>>> sig_noise = sig + np.random.randn(len(sig))
>>> corr = signal.correlate(sig_noise, np.ones(128), mode='same') / 128
```

```
>>> import matplotlib.pyplot as plt
>>> clock = np.arange(64, len(sig), 128)
>>> fig, (ax_orig, ax_noise, ax_corr) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.plot(clock, sig[clock], 'ro')
>>> ax_orig.set_title('Original signal')
>>> ax_noise.plot(sig_noise)
>>> ax_noise.set_title('Signal with noise')
>>> ax_corr.plot(corr)
>>> ax_corr.plot(clock, corr[clock], 'ro')
>>> ax_corr.axhline(0.5, ls=':')
>>> ax_corr.set_title('Cross-correlated with rectangular pulse')
>>> ax_orig.margins(0, 0.1)
>>> fig.tight_layout()
>>> fig.show()
```



`scipy.signal.`**`fftconvolve`**(*in1*, *in2*, *mode='full'*)

Convolve two N-dimensional arrays using FFT.

Convolve *in1* and *in2* using the fast Fourier transform method, with the output size determined by the *mode* argument.

This is generally much faster than `convolve` for large arrays (n > ~500), but can be slower when only a few output values are needed, and can only output float arrays (int or object array inputs will be cast to float).

Parameters

in1 : array_like

First input.

in2 : array_like

Second input. Should have the same number of dimensions as *in1*; if sizes of *in1* and *in2* are not equal then *in1* has to be the larger array.

mode : str {'full', 'valid', 'same'}, optional

A string indicating the size of the output:

`full`	The output is the full discrete linear convolution of the inputs. (Default)
`valid`	The output consists only of those elements that do not rely on the zero-padding.
`same`	The output is the same size as *in1*, centered with respect to the 'full' output.

Returns

out : array

An N-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

Examples

Autocorrelation of white noise is an impulse. (This is at least 100 times as fast as `convolve`.)

```
>>> from scipy import signal
>>> sig = np.random.randn(1000)
>>> autocorr = signal.fftconvolve(sig, sig[::-1], mode='full')
```

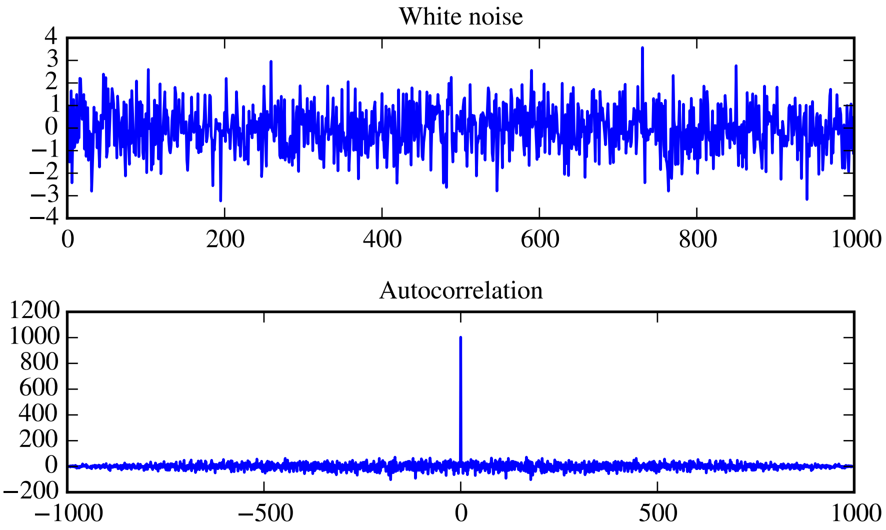
```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag) = plt.subplots(2, 1)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('White noise')
>>> ax_mag.plot(np.arange(-len(sig)+1,len(sig)), autocorr)
```

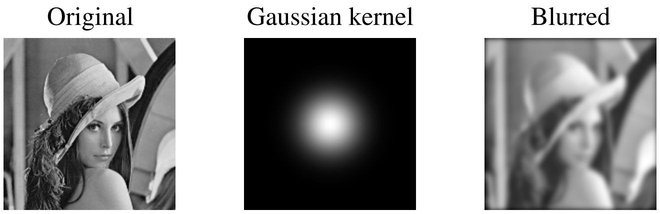
```
>>> ax_mag.set_title('Autocorrelation')
>>> fig.tight_layout()
>>> fig.show()
```

Gaussian blur implemented using FFT convolution. Notice the dark borders around the image, due to the zero-padding beyond its boundaries. The `convolve2d` function allows for other types of image boundaries, but is far slower.

```
>>> from scipy import misc
>>> lena = misc.lena()
>>> kernel = np.outer(signal.gaussian(70, 8), signal.gaussian(70, 8))
>>> blurred = signal.fftconvolve(lena, kernel, mode='same')
```

```
>>> fig, (ax_orig, ax_kernel, ax_blurred) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_kernel.imshow(kernel, cmap='gray')
>>> ax_kernel.set_title('Gaussian kernel')
>>> ax_kernel.set_axis_off()
>>> ax_blurred.imshow(blurred, cmap='gray')
>>> ax_blurred.set_title('Blurred')
>>> ax_blurred.set_axis_off()
>>> fig.show()
```





`scipy.signal.`**`convolve2d`**(*in1*, *in2*, *mode='full'*, *boundary='fill'*, *fillvalue=0*)

Convolve two 2-dimensional arrays.

Convolve *in1* and *in2* with output size determined by *mode*, and boundary conditions determined by *boundary* and *fillvalue*.

Parameters

in1, in2 : array_like

Two-dimensional input arrays to be convolved.

mode : str {'full', 'valid', 'same'}, optional

A string indicating the size of the output:

`full`	The output is the full discrete linear convolution of the inputs. (Default)
`valid`	The output consists only of those elements that do not rely on the zero-padding.
`same`	The output is the same size as *in1*, centered with respect to the 'full' output.

boundary : str {'fill', 'wrap', 'symm'}, optional

A flag indicating how to handle boundaries:

`fill`	pad input arrays with fillvalue. (default)
`wrap`	circular boundary conditions.
`symm`	symmetrical boundary conditions.

fillvalue : scalar, optional

Value to fill pad input arrays with. Default is 0.

Returns

out : ndarray

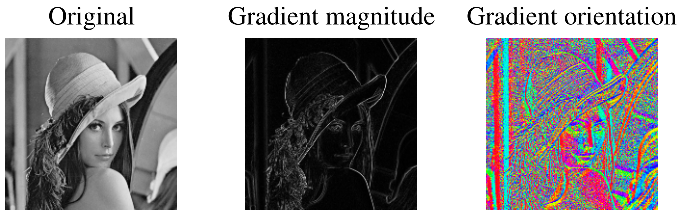
A 2-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

Examples

Compute the gradient of an image by 2D convolution with a complex Scharr operator. (Horizontal operator is real, vertical is imaginary.) Use symmetric boundary condition to avoid creating edges at the image boundaries.

```
>>> from scipy import signal
>>> from scipy import misc
>>> lena = misc.lena()
>>> scharr = np.array([[ -3-3j, 0-10j,  +3 -3j],
...                    [-10+0j, 0+ 0j, +10 +0j],
...                    [ -3+3j, 0+10j,  +3 +3j]]) # Gx + j*Gy
>>> grad = signal.convolve2d(lena, scharr, boundary='symm', mode='same')
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag, ax_ang) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_mag.imshow(np.absolute(grad), cmap='gray')
>>> ax_mag.set_title('Gradient magnitude')
>>> ax_mag.set_axis_off()
>>> ax_ang.imshow(np.angle(grad), cmap='hsv') # hsv is cyclic, like angles
>>> ax_ang.set_title('Gradient orientation')
>>> ax_ang.set_axis_off()
>>> fig.show()
```



`scipy.signal.`**`correlate2d`**(*in1*, *in2*, *mode='full'*, *boundary='fill'*, *fillvalue=0*)

Cross-correlate two 2-dimensional arrays.

Cross correlate *in1* and *in2* with output size determined by *mode*, and boundary conditions determined by *boundary* and *fillvalue*.

Parameters **in1, in2** : array_like

Two-dimensional input arrays to be convolved.

mode : str {'full', 'valid', 'same'}, optional

A string indicating the size of the output:

full	The output is the full discrete linear cross-correlation of the inputs. (Default)
valid	The output consists only of those elements that do not rely on the zero-padding.
same	The output is the same size as *in1*, centered with respect to the 'full' output.

boundary : str {'fill', 'wrap', 'symm'}, optional

A flag indicating how to handle boundaries:

fill	pad input arrays with fillvalue. (default)
wrap	circular boundary conditions.
symm	symmetrical boundary conditions.

fillvalue : scalar, optional

Value to fill pad input arrays with. Default is 0.

Returns **correlate2d** : ndarray

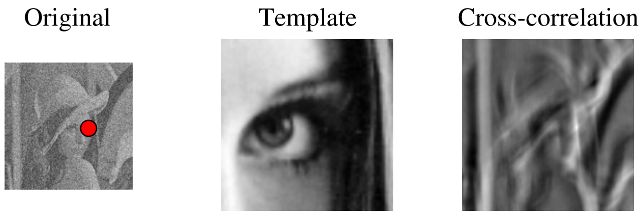
A 2-dimensional array containing a subset of the discrete linear cross-correlation of *in1* with *in2*.

Examples

Use 2D cross-correlation to find the location of a template in a noisy image:

```
>>> from scipy import signal
>>> from scipy import misc
>>> lena = misc.lena() - misc.lena().mean()
>>> template = np.copy(lena[235:295, 310:370]) # right eye
>>> template -= template.mean()
>>> lena = lena + np.random.randn(*lena.shape) * 50 # add noise
>>> corr = signal.correlate2d(lena, template, boundary='symm', mode='same')
>>> y, x = np.unravel_index(np.argmax(corr), corr.shape) # find the match
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_template, ax_corr) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_template.imshow(template, cmap='gray')
>>> ax_template.set_title('Template')
>>> ax_template.set_axis_off()
>>> ax_corr.imshow(corr, cmap='gray')
>>> ax_corr.set_title('Cross-correlation')
>>> ax_corr.set_axis_off()
>>> ax_orig.plot(x, y, 'ro')
>>> fig.show()
```



`scipy.signal.`**`sepfir2d`**(*input*, *hrow*, *hcol*) → output

Description:

Convolve the rank-2 input array with the separable filter defined by the rank-1 arrays hrow, and hcol. Mirror symmetric boundary conditions are assumed. This function can be used to find an image given its B-spline representation.

5.27.2 B-splines

`bspline`(x, n)	B-spline basis function of order n.
`cubic`(x)	A cubic B-spline.
`quadratic`(x)	A quadratic B-spline.
`gauss_spline`(x, n)	Gaussian approximation to B-spline basis function of order n.
`cspline1d`(signal[, lamb])	Compute cubic spline coefficients for rank-1 array.
`qspline1d`(signal[, lamb])	Compute quadratic spline coefficients for rank-1 array.
`cspline2d`((input {, lambda, precision}) -> ck)	Description:
`qspline2d`((input {, lambda, precision}) -> qk)	Description:
`cspline1d_eval`(cj, newx[, dx, x0])	Evaluate a spline at the new set of points.
`qspline1d_eval`(cj, newx[, dx, x0])	Evaluate a quadratic spline at the new set of points.
`spline_filter`(Iin[, lmbda])	Smoothing spline (cubic) filtering of a rank-2 array.

`scipy.signal.`**`bspline`**(*x*, *n*)

B-spline basis function of order n.

Notes

Uses numpy.piecewise and automatic function-generator.

`scipy.signal.`**`cubic`**(*x*)

A cubic B-spline.

This is a special case of `bspline`, and equivalent to `bspline(x, 3)`.

`scipy.signal.`**`quadratic`**(*x*)

A quadratic B-spline.

This is a special case of `bspline`, and equivalent to `bspline(x, 2)`.

`scipy.signal.`**`gauss_spline`**(*x*, *n*)

Gaussian approximation to B-spline basis function of order n.

`scipy.signal.`**`cspline1d`**(*signal*, *lamb=0.0*)

Compute cubic spline coefficients for rank-1 array.

Find the cubic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window [1.0, 4.0, 1.0]/ 6.0 .

Parameters	**signal** : ndarray	
		A rank-1 array representing samples of a signal.
	lamb : float, optional	
		Smoothing coefficient, default is 0.0.
Returns	**c** : ndarray	
		Cubic spline coefficients.

`scipy.signal.`**`qspline1d`**(*signal*, *lamb=0.0*)

Compute quadratic spline coefficients for rank-1 array.

Find the quadratic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window [1.0, 6.0, 1.0]/ 8.0 .

Parameters	**signal** : ndarray	
		A rank-1 array representing samples of a signal.
	lamb : float, optional	
		Smoothing coefficient (must be zero for now).
Returns	**c** : ndarray	
		Cubic spline coefficients.

`scipy.signal.`**`cspline2d`**(*input {, lambda, precision}*) → ck
Description:

> Return the third-order B-spline coefficients over a regularly spacedi input grid for the two-dimensional input image. The lambda argument specifies the amount of smoothing. The precision argument allows specifying the precision used when computing the infinite sum needed to apply mirror- symmetric boundary conditions.

`scipy.signal.`**`qspline2d`**(*input {, lambda, precision}*) → qk
Description:

> Return the second-order B-spline coefficients over a regularly spaced input grid for the two-dimensional input image. The lambda argument specifies the amount of smoothing. The precision argument allows specifying the precision used when computing the infinite sum needed to apply mirror- symmetric boundary conditions.

`scipy.signal.`**`cspline1d_eval`**(*cj*, *newx*, *dx=1.0*, *x0=0*)
Evaluate a spline at the new set of points.

dx is the old sample-spacing while *x0* was the old origin. In other-words the old-sample points (knot-points) for which the *cj* represent spline coefficients were at equally-spaced points of:

> oldx = x0 + j*dx j=0...N-1, with N=len(cj)

Edges are handled using mirror-symmetric boundary conditions.

`scipy.signal.`**`qspline1d_eval`**(*cj*, *newx*, *dx=1.0*, *x0=0*)
Evaluate a quadratic spline at the new set of points.

dx is the old sample-spacing while *x0* was the old origin. In other-words the old-sample points (knot-points) for which the *cj* represent spline coefficients were at equally-spaced points of:

```
oldx = x0 + j*dx  j=0...N-1, with N=len(cj)
```

Edges are handled using mirror-symmetric boundary conditions.

`scipy.signal.`**`spline_filter`**(*Iin*, *lmbda=5.0*)
Smoothing spline (cubic) filtering of a rank-2 array.

Filter an input data set, *Iin*, using a (cubic) smoothing spline of fall-off *lmbda*.

5.27.3 Filtering

`order_filter`(a, domain, rank)	Perform an order filter on an N-dimensional array.
`medfilt`(volume[, kernel_size])	Perform a median filter on an N-dimensional array.
`medfilt2d`(input[, kernel_size])	Median filter a 2-dimensional array.
`wiener`(im[, mysize, noise])	Perform a Wiener filter on an N-dimensional array.
`symiirorder1`((input, c0, z1 {, ...)	Implement a smoothing IIR filter with mirror-symmetric boundary conditio
`symiirorder2`((input, r, omega {, ...)	Implement a smoothing IIR filter with mirror-symmetric boundary conditio
`lfilter`(b, a, x[, axis, zi])	Filter data along one-dimension with an IIR or FIR filter.
`lfiltic`(b, a, y[, x])	Construct initial conditions for lfilter.
`lfilter_zi`(b, a)	Compute an initial state *zi* for the lfilter function that corresponds to the stea
`filtfilt`(b, a, x[, axis, padtype, padlen, ...])	A forward-backward filter.
`savgol_filter`(x, window_length, polyorder[, ...])	Apply a Savitzky-Golay filter to an array.
`deconvolve`(signal, divisor)	Deconvolves `divisor` out of `signal`.
`sosfilt`(sos, x[, axis, zi])	Filter data along one dimension using cascaded second-order sections

Table 5.118 – continued from previous page

`sosfilt_zi`(sos)	Compute an initial state *zi* for the sosfilt function that corresponds to the stea
`hilbert`(x[, N, axis])	Compute the analytic signal, using the Hilbert transform.
`hilbert2`(x[, N])	Compute the '2-D' analytic signal of *x*
`decimate`(x, q[, n, ftype, axis])	Downsample the signal by using a filter.
`detrend`(data[, axis, type, bp])	Remove linear trend along axis from data.
`resample`(x, num[, t, axis, window])	Resample *x* to *num* samples using Fourier method along the given axis.

`scipy.signal.`**`order_filter`**(*a*, *domain*, *rank*)

Perform an order filter on an N-dimensional array.

Perform an order filter on the array in. The domain argument acts as a mask centered over each pixel. The non-zero elements of domain are used to select elements surrounding each input pixel which are placed in a list. The list is sorted, and the output for that pixel is the element corresponding to rank in the sorted list.

Parameters **a** : ndarray

The N-dimensional input array.

domain : array_like

A mask array with the same number of dimensions as *in*. Each dimension should have an odd number of elements.

rank : int

A non-negative integer which selects the element from the sorted list (0 corresponds to the smallest element, 1 is the next smallest element, etc.).

Returns **out** : ndarray

The results of the order filter in an array with the same shape as *in*.

Examples

```
>>> from scipy import signal
>>> x = np.arange(25).reshape(5, 5)
>>> domain = np.identity(3)
>>> x
array([[ 0,  1,  2,  3,  4],
       [ 5,  6,  7,  8,  9],
       [10, 11, 12, 13, 14],
       [15, 16, 17, 18, 19],
       [20, 21, 22, 23, 24]])
>>> signal.order_filter(x, domain, 0)
array([[  0.,   0.,   0.,   0.,   0.],
       [  0.,   0.,   1.,   2.,   0.],
       [  0.,   5.,   6.,   7.,   0.],
       [  0.,  10.,  11.,  12.,   0.],
       [  0.,   0.,   0.,   0.,   0.]])
>>> signal.order_filter(x, domain, 2)
array([[  6.,   7.,   8.,   9.,   4.],
       [ 11.,  12.,  13.,  14.,   9.],
       [ 16.,  17.,  18.,  19.,  14.],
       [ 21.,  22.,  23.,  24.,  19.],
       [ 20.,  21.,  22.,  23.,  24.]])
```

`scipy.signal.`**`medfilt`**(*volume*, *kernel_size=None*)

Perform a median filter on an N-dimensional array.

Apply a median filter to the input array using a local window-size given by *kernel_size*.

Parameters **volume** : array_like

An N-dimensional input array.

kernel_size : array_like, optional

A scalar or an N-length list giving the size of the median filter window in each dimension. Elements of *kernel_size* should be odd. If *kernel_size* is a scalar, then this scalar is used as the size in each dimension. Default size is 3 for each dimension.

Returns **out** : ndarray

An array the same size as input containing the median filtered result.

`scipy.signal.`**`medfilt2d`**`(`*input*, *kernel_size=3*`)`

Median filter a 2-dimensional array.

Apply a median filter to the *input* array using a local window-size given by *kernel_size* (must be odd).

Parameters **input** : array_like

A 2-dimensional input array.

kernel_size : array_like, optional

A scalar or a list of length 2, giving the size of the median filter window in each dimension. Elements of *kernel_size* should be odd. If *kernel_size* is a scalar, then this scalar is used as the size in each dimension. Default is a kernel of size (3, 3).

Returns **out** : ndarray

An array the same size as input containing the median filtered result.

`scipy.signal.`**`wiener`**`(`*im*, *mysize=None*, *noise=None*`)`

Perform a Wiener filter on an N-dimensional array.

Apply a Wiener filter to the N-dimensional array *im*.

Parameters **im** : ndarray

An N-dimensional array.

mysize : int or arraylike, optional

A scalar or an N-length list giving the size of the Wiener filter window in each dimension. Elements of mysize should be odd. If mysize is a scalar, then this scalar is used as the size in each dimension.

noise : float, optional

The noise-power to use. If None, then noise is estimated as the average of the local variance of the input.

Returns **out** : ndarray

Wiener filtered result with the same shape as *im*.

`scipy.signal.`**`symiirorder1`**`(`*input*, *c0*, *z1 {*, *precision}*`)` → output

Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of first-order sections. The second section uses a reversed sequence. This implements a system with the following transfer function and mirror-symmetric boundary conditions:

```
                  c0
H(z) = ---------------------
         (1-z1/z) (1 - z1 z)
```

The resulting signal will have mirror symmetric boundary conditions as well.

Parameters **input** : ndarray

The input signal.

c0, z1 : scalar

Parameters in the transfer function.

precision :

Specifies the precision for calculating initial conditions of the recursive filter based on mirror-symmetric input.

Returns **output** : ndarray

The filtered signal.

`scipy.signal.`**`symiirorder2`**(*input*, *r*, *omega {*, *precision}*) → output

Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of second-order sections. The second section uses a reversed sequence. This implements the following transfer function:

```
                      cs^2
H(z) = ---------------------------------------
       (1 - a2/z - a3/z^2) (1 - a2 z - a3 z^2 )
```

where:

```
a2 = (2 r cos omega)
a3 = - r^2
cs = 1 - 2 r cos omega + r^2
```

Parameters **input** : ndarray

The input signal.

r, omega : scalar

Parameters in the transfer function.

precision :

Specifies the precision for calculating initial conditions of the recursive filter based on mirror-symmetric input.

Returns **output** : ndarray

The filtered signal.

`scipy.signal.`**`lfilter`**(*b*, *a*, *x*, *axis=-1*, *zi=None*)

Filter data along one-dimension with an IIR or FIR filter.

Filter a data sequence, *x*, using a digital filter. This works for many fundamental data types (including Object type). The filter is a direct form II transposed implementation of the standard difference equation (see Notes).

Parameters **b** : array_like

The numerator coefficient vector in a 1-D sequence.

a : array_like

The denominator coefficient vector in a 1-D sequence. If `a[0]` is not 1, then both *a* and *b* are normalized by `a[0]`.

x : array_like

An N-dimensional input array.

axis : int, optional

The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

zi : array_like, optional

Initial conditions for the filter delays. It is a vector (or array of vectors for an N-dimensional input) of length `max(len(a),len(b))-1`. If *zi* is None or is not given then initial rest is assumed. See `lfiltic` for more information.

Returns **y** : array

The output of the digital filter.

zf : array, optional

If *zi* is None, this is not returned, otherwise, *zf* holds the final filter delay values.

Notes

The filter function is implemented as a direct II transposed structure. This means that the filter implements:

```
a[0]*y[n] = b[0]*x[n] + b[1]*x[n-1] + ... + b[nb]*x[n-nb]
                        - a[1]*y[n-1] - ... - a[na]*y[n-na]
```

using the following difference equations:

```
y[m] = b[0]*x[m] + z[0,m-1]
z[0,m] = b[1]*x[m] + z[1,m-1] - a[1]*y[m]
...
z[n-3,m] = b[n-2]*x[m] + z[n-2,m-1] - a[n-2]*y[m]
z[n-2,m] = b[n-1]*x[m] - a[n-1]*y[m]
```

where m is the output sample number and n=max(len(a),len(b)) is the model order.

The rational transfer function describing this filter in the z-transform domain is:

```
                    -1               -nb
        b[0] + b[1]z  + ... + b[nb] z
Y(z) = ---------------------------------- X(z)
                    -1               -na
        a[0] + a[1]z  + ... + a[na] z
```

`scipy.signal.`**`lfiltic`**(*b*, *a*, *y*, *x=None*)

Construct initial conditions for lfilter.

Given a linear filter (b, a) and initial conditions on the output *y* and the input *x*, return the initial conditions on the state vector zi which is used by `lfilter` to generate the output given the input.

Parameters

b : array_like

Linear filter term.

a : array_like

Linear filter term.

y : array_like

Initial conditions.
If `N=len(a) - 1`, then `y = {y[-1], y[-2], ..., y[-N]}`.
If *y* is too short, it is padded with zeros.

x : array_like, optional

Initial conditions.
If `M=len(b) - 1`, then `x = {x[-1], x[-2], ..., x[-M]}`.
If *x* is not given, its initial conditions are assumed zero.
If *x* is too short, it is padded with zeros.

Returns

zi : ndarray

The state vector `zi`. `zi = {z_0[-1], z_1[-1], ..., z_K-1[-1]}`, where `K = max(M,N)`.

See also:

`lfilter`

`scipy.signal.`**`lfilter_zi`**(*b*, *a*)

Compute an initial state *zi* for the lfilter function that corresponds to the steady state of the step response.

A typical use of this function is to set the initial state so that the output of the filter starts at the same value as the first element of the signal to be filtered.

Parameters

b, a : array_like (1-D)

The IIR filter coefficients. See `lfilter` for more information.

Returns

zi : 1-D ndarray

The initial state for the filter.

Notes

A linear filter with order m has a state space representation (A, B, C, D), for which the output y of the filter can be expressed as:

```
z(n+1) = A*z(n) + B*x(n)
y(n)   = C*z(n) + D*x(n)
```

where z(n) is a vector of length m, A has shape (m, m), B has shape (m, 1), C has shape (1, m) and D has shape (1, 1) (assuming x(n) is a scalar). lfilter_zi solves:

```
zi = A*zi + B
```

In other words, it finds the initial condition for which the response to an input of all ones is a constant.

Given the filter coefficients *a* and *b*, the state space matrices for the transposed direct form II implementation of the linear filter, which is the implementation used by scipy.signal.lfilter, are:

```
A = scipy.linalg.companion(a).T
B = b[1:] - a[1:]*b[0]
```

assuming *a[0]* is 1.0; if *a[0]* is not 1, *a* and *b* are first divided by a[0].

Examples

The following code creates a lowpass Butterworth filter. Then it applies that filter to an array whose values are all 1.0; the output is also all 1.0, as expected for a lowpass filter. If the *zi* argument of `lfilter` had not been given, the output would have shown the transient signal.

```
>>> from numpy import array, ones
>>> from scipy.signal import lfilter, lfilter_zi, butter
>>> b, a = butter(5, 0.25)
>>> zi = lfilter_zi(b, a)
>>> y, zo = lfilter(b, a, ones(10), zi=zi)
>>> y
array([1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.])
```

Another example:

```
>>> x = array([0.5, 0.5, 0.5, 0.0, 0.0, 0.0, 0.0])
>>> y, zf = lfilter(b, a, x, zi=zi*x[0])
>>> y
array([ 0.5       ,  0.5       ,  0.5       ,  0.49836039,  0.48610528,
    0.44399389,  0.35505241])
```

Note that the *zi* argument to `lfilter` was computed using `lfilter_zi` and scaled by *x[0]*. Then the output *y* has no transient until the input drops from 0.5 to 0.0.

`scipy.signal.`**`filtfilt`**(*b*, *a*, *x*, *axis=-1*, *padtype='odd'*, *padlen=None*, *method='pad'*, *irlen=None*)

A forward-backward filter.

This function applies a linear filter twice, once forward and once backwards. The combined filter has linear phase.

The function provides options for handling the edges of the signal.

When *method* is "pad", the function pads the data along the given axis in one of three ways: odd, even or constant. The odd and even extensions have the corresponding symmetry about the end point of the data. The constant extension extends the data with the values at the end points. On both the forward and backward passes, the initial condition of the filter is found by using `lfilter_zi` and scaling it by the end point of the extended data.

When *method* is "gust", Gustafsson's method [R173] is used. Initial conditions are chosen for the forward and backward passes so that the forward-backward filter gives the same result as the backward-forward filter.

Parameters

b : (N,) array_like

The numerator coefficient vector of the filter.

a : (N,) array_like

The denominator coefficient vector of the filter. If `a[0]` is not 1, then both *a* and *b* are normalized by `a[0]`.

x : array_like

The array of data to be filtered.

axis : int, optional

The axis of *x* to which the filter is applied. Default is -1.

padtype : str or None, optional

Must be 'odd', 'even', 'constant', or None. This determines the type of extension to use for the padded signal to which the filter is applied. If *padtype* is None, no padding is used. The default is 'odd'.

padlen : int or None, optional

The number of elements by which to extend *x* at both ends of *axis* before applying the filter. This value must be less than `x.shape[axis] - 1`. `padlen=0` implies no padding. The default value is `3 * max(len(a), len(b))`.

method : str, optional

Determines the method for handling the edges of the signal, either "pad" or "gust". When *method* is "pad", the signal is padded; the type of padding is determined by *padtype* and *padlen*, and *irlen* is ignored. When *method* is "gust", Gustafsson's method is used, and *padtype* and *padlen* are ignored.

irlen : int or None, optional

When *method* is "gust", *irlen* specifies the length of the impulse response of the filter. If *irlen* is None, no part of the impulse response is ignored. For a long signal, specifying *irlen* can significantly improve the performance of the filter.

Returns

y : ndarray

The filtered output, an array of type numpy.float64 with the same shape as *x*.

See also:

`lfilter_zi`, `lfilter`

Notes

The option to use Gustaffson's method was added in scipy version 0.16.0.

References

[R173]

Examples

The examples will use several functions from `scipy.signal`.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

First we create a one second signal that is the sum of two pure sine waves, with frequencies 5 Hz and 250 Hz, sampled at 2000 Hz.

```
>>> t = np.linspace(0, 1.0, 2001)
>>> xlow = np.sin(2 * np.pi * 5 * t)
>>> xhigh = np.sin(2 * np.pi * 250 * t)
>>> x = xlow + xhigh
```

Now create a lowpass Butterworth filter with a cutoff of 0.125 times the Nyquist rate, or 125 Hz, and apply it to `x` with `filtfilt`. The result should be approximately `xlow`, with no phase shift.

```
>>> b, a = signal.butter(8, 0.125)
>>> y = signal.filtfilt(b, a, x, padlen=150)
>>> np.abs(y - xlow).max()
9.1086182074789912e-06
```

We get a fairly clean result for this artificial example because the odd extension is exact, and with the moderately long padding, the filter's transients have dissipated by the time the actual data is reached. In general, transient effects at the edges are unavoidable.

The following example demonstrates the option `method="gust"`.

First, create a filter.

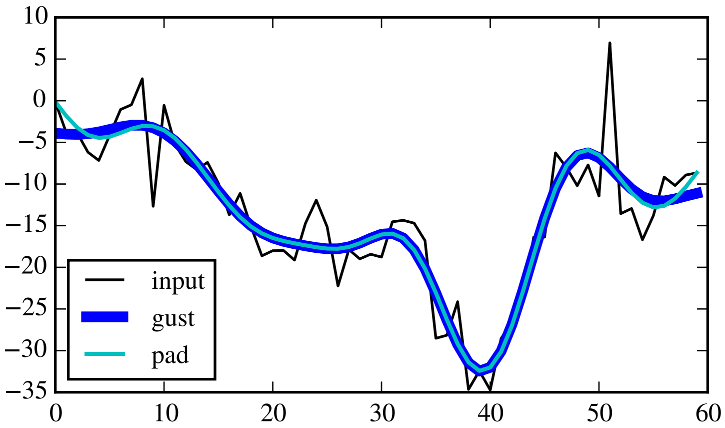
```
>>> b, a = signal.ellip(4, 0.01, 120, 0.125)  # Filter to be applied.
>>> np.random.seed(123456)
```

sig is a random input signal to be filtered.

```
>>> n = 60
>>> sig = np.random.randn(n)**3 + 3*np.random.randn(n).cumsum()
```

Apply `filtfilt` to *sig*, once using the Gustafsson method, and once using padding, and plot the results for comparison.

```
>>> fgust = signal.filtfilt(b, a, sig, method="gust")
>>> fpad = signal.filtfilt(b, a, sig, padlen=50)
>>> plt.plot(sig, 'k-', label='input')
>>> plt.plot(fgust, 'b-', linewidth=4, label='gust')
>>> plt.plot(fpad, 'c-', linewidth=1.5, label='pad')
>>> plt.legend(loc='best')
>>> plt.show()
```



The *irlen* argument can be used to improve the performance of Gustafsson's method.

Estimate the impulse response length of the filter.

```
>>> z, p, k = signal.tf2zpk(b, a)
>>> eps = 1e-9
>>> r = np.max(np.abs(p))
>>> approx_impulse_len = int(np.ceil(np.log(eps) / np.log(r)))
>>> approx_impulse_len
137
```

Apply the filter to a longer signal, with and without the *irlen* argument. The difference between *y1* and *y2* is small. For long signals, using *irlen* gives a significant performance improvement.

```
>>> x = np.random.randn(5000)
>>> y1 = signal.filtfilt(b, a, x, method='gust')
>>> y2 = signal.filtfilt(b, a, x, method='gust', irlen=approx_impulse_len)
>>> print(np.max(np.abs(y1 - y2)))
1.80056858312e-10
```

`scipy.signal.`**`savgol_filter`**`(`*x*, *window_length*, *polyorder*, *deriv=0*, *delta=1.0*, *axis=-1*, *mode='interp'*, *cval=0.0*`)`

Apply a Savitzky-Golay filter to an array.

This is a 1-d filter. If *x* has dimension greater than 1, *axis* determines the axis along which the filter is applied.

Parameters

x : array_like

The data to be filtered. If *x* is not a single or double precision floating point array, it will be converted to type `numpy.float64` before filtering.

window_length : int

The length of the filter window (i.e. the number of coefficients). *window_length* must be a positive odd integer.

polyorder : int

The order of the polynomial used to fit the samples. *polyorder* must be less than *window_length*.

deriv : int, optional

The order of the derivative to compute. This must be a nonnegative integer. The default is 0, which means to filter the data without differentiating.

delta : float, optional

The spacing of the samples to which the filter will be applied. This is only used if deriv > 0. Default is 1.0.

axis : int, optional

The axis of the array *x* along which the filter is to be applied. Default is -1.

mode : str, optional

Must be 'mirror', 'constant', 'nearest', 'wrap' or 'interp'. This determines the type of extension to use for the padded signal to which the filter is applied. When *mode* is 'constant', the padding value is given by *cval*. See the Notes for more details on 'mirror', 'constant', 'wrap', and 'nearest'. When the 'interp' mode is selected (the default), no extension is used. Instead, a degree *polyorder* polynomial is fit to the last *window_length* values of the edges, and this polynomial is used to evaluate the last *window_length // 2* output values.

cval : scalar, optional

Value to fill past the edges of the input if *mode* is 'constant'. Default is 0.0.

Returns **y** : ndarray, same shape as *x*

The filtered data.

See also:

`savgol_coeffs`

Notes

Details on the *mode* options:

'mirror':	Repeats the values at the edges in reverse order. The value closest to the edge is not included.
'nearest':	The extension contains the nearest input value.
'constant':	The extension contains the value given by the *cval* argument.
'wrap':	The extension contains the values from the other end of the array.

For example, if the input is [1, 2, 3, 4, 5, 6, 7, 8], and *window_length* is 7, the following shows the extended data for the various *mode* options (assuming *cval* is 0):

```
mode       |   Ext   |         Input         |   Ext
-----------+---------+-----------------------+---------
'mirror'   | 4  3  2 | 1  2  3  4  5  6  7  8 | 7  6  5
'nearest'  | 1  1  1 | 1  2  3  4  5  6  7  8 | 8  8  8
'constant' | 0  0  0 | 1  2  3  4  5  6  7  8 | 0  0  0
'wrap'     | 6  7  8 | 1  2  3  4  5  6  7  8 | 1  2  3
```

New in version 0.14.0.

Examples

```
>>> np.set_printoptions(precision=2)  # For compact display.
>>> x = np.array([2, 2, 5, 2, 1, 0, 1, 4, 9])
```

Filter with a window length of 5 and a degree 2 polynomial. Use the defaults for all other parameters.

```
>>> y = savgol_filter(x, 5, 2)
array([ 1.66,  3.17,  3.54,  2.86,  0.66,  0.17,  1.  ,  4.  ,  9.  ])
```

Note that the last five values in x are samples of a parabola, so when mode='interp' (the default) is used with polyorder=2, the last three values are unchanged. Compare that to, for example, *mode='nearest'*:

```
>>> savgol_filter(x, 5, 2, mode='nearest')
array([ 1.74,  3.03,  3.54,  2.86,  0.66,  0.17,  1.  ,  4.6 ,  7.97])
```

`scipy.signal.`**`deconvolve`**`(`*signal*, *divisor*`)`

Deconvolves `divisor` out of `signal`.

Returns the quotient and remainder such that `signal = convolve(divisor, quotient) + remainder`

Parameters **signal** : array_like

Signal data, typically a recorded signal

divisor : array_like

Divisor data, typically an impulse response or filter that was applied to the original signal

Returns **quotient** : ndarray

Quotient, typically the recovered original signal

remainder : ndarray

Remainder

See also:

`numpy.polydiv`

performs polynomial division (same operation, but also accepts poly1d objects)

Examples

Deconvolve a signal that's been filtered:

```
>>> from scipy import signal
>>> original = [0, 1, 0, 0, 1, 1, 0, 0]
>>> impulse_response = [2, 1]
>>> recorded = signal.convolve(impulse_response, original)
>>> recorded
array([0, 2, 1, 0, 2, 3, 1, 0, 0])
>>> recovered, remainder = signal.deconvolve(recorded, impulse_response)
>>> recovered
array([ 0.,  1.,  0.,  0.,  1.,  1.,  0.,  0.])
```

`scipy.signal.`**`sosfilt`**`(`*sos*, *x*, *axis=-1*, *zi=None*`)`

Filter data along one dimension using cascaded second-order sections

Filter a data sequence, *x*, using a digital IIR filter defined by *sos*. This is implemented by performing `lfilter` for each second-order section. See `lfilter` for details.

Parameters **sos** : array_like

Array of second-order filter coefficients, must have shape `(n_sections, 6)`. Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

x : array_like

An N-dimensional input array.

axis : int, optional

The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

zi : array_like, optional

Initial conditions for the cascaded filter delays. It is a (at least 2D) vector of shape `(n_sections, ..., 2, ...)`, where `..., 2, ...` denotes the shape of *x*, but with `x.shape[axis]` replaced by 2. If *zi* is None or is not given then initial rest (i.e. all zeros) is assumed. Note that these initial conditions are *not* the same as the initial conditions given by `lfiltic` or `lfilter_zi`.

Returns **y** : ndarray

The output of the digital filter.

zf : ndarray, optional

If *zi* is None, this is not returned, otherwise, *zf* holds the final filter delay values.

See also:

`zpk2sos`, `sos2zpk`, `sosfilt_zi`

Notes

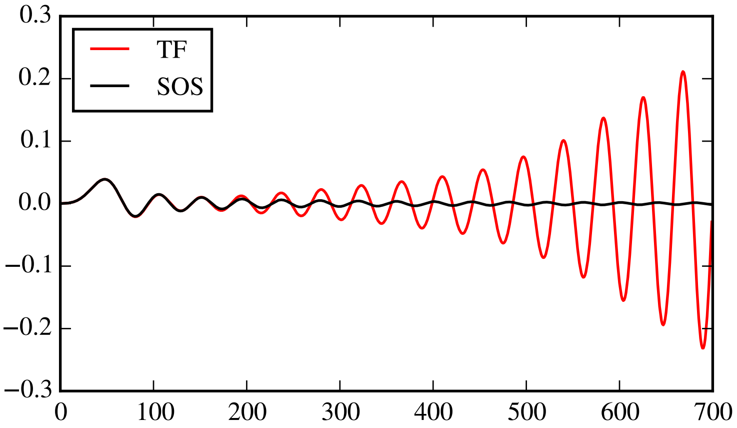
The filter function is implemented as a series of second-order filters with direct-form II transposed structure. It is designed to minimize numerical precision errors for high-order filters.

New in version 0.16.0.

Examples

Plot a 13th-order filter's impulse response using both `lfilter` and `sosfilt`, showing the instability that results from trying to do a 13th-order filter in a single stage (the numerical error pushes some poles outside of the unit circle):

```
>>> import matplotlib.pyplot as plt
>>> from scipy import signal
>>> b, a = signal.ellip(13, 0.009, 80, 0.05, output='ba')
>>> sos = signal.ellip(13, 0.009, 80, 0.05, output='sos')
>>> x = np.zeros(700)
>>> x[0] = 1.
>>> y_tf = signal.lfilter(b, a, x)
>>> y_sos = signal.sosfilt(sos, x)
>>> plt.plot(y_tf, 'r', label='TF')
>>> plt.plot(y_sos, 'k', label='SOS')
>>> plt.legend(loc='best')
>>> plt.show()
```



`scipy.signal.`**`sosfilt_zi`**(*sos*)

Compute an initial state *zi* for the sosfilt function that corresponds to the steady state of the step response.

A typical use of this function is to set the initial state so that the output of the filter starts at the same value as the first element of the signal to be filtered.

Parameters	**sos** : array_like	Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.
Returns	**zi** : ndarray	Initial conditions suitable for use with `sosfilt`, shape `(n_sections, 2)`.

See also:

`sosfilt`, `zpk2sos`

Notes

New in version 0.16.0.

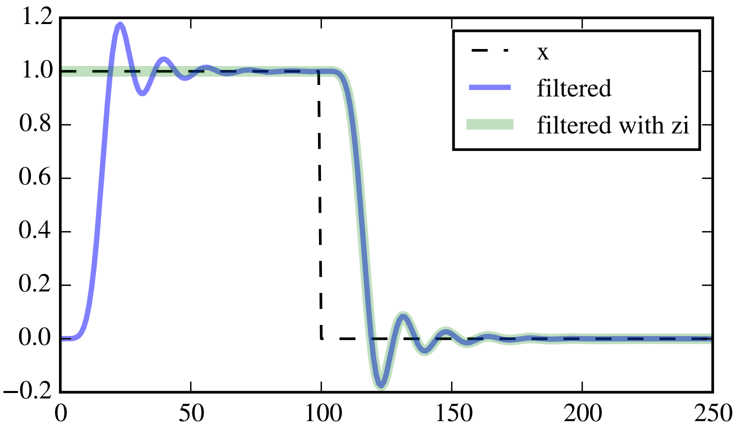
Examples

Filter a rectangular pulse that begins at time 0, with and without the use of the *zi* argument of `scipy.signal.sosfilt`.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> sos = signal.butter(9, 0.125, output='sos')
>>> zi = signal.sosfilt_zi(sos)
>>> x = (np.arange(250) < 100).astype(int)
>>> f1 = signal.sosfilt(sos, x)
>>> f2, zo = signal.sosfilt(sos, x, zi=zi)
```

```
>>> plt.plot(x, 'k--', label='x')
>>> plt.plot(f1, 'b', alpha=0.5, linewidth=2, label='filtered')
>>> plt.plot(f2, 'g', alpha=0.25, linewidth=4, label='filtered with zi')
>>> plt.legend(loc='best')
>>> plt.show()
```



`scipy.signal.`**`hilbert`**(*x*, *N=None*, *axis=-1*)

Compute the analytic signal, using the Hilbert transform.

The transformation is done along the last axis by default.

Parameters **x** : array_like

Signal data. Must be real.

N : int, optional

Number of Fourier components. Default: `x.shape[axis]`

axis : int, optional

Axis along which to do the transformation. Default: -1.

Returns **xa** : ndarray

Analytic signal of *x*, of each 1-D array along *axis*

Notes

The analytic signal `x_a(t)` of signal `x(t)` is:

$$x_a = F^{-1}(F(x)2U) = x + iy$$

where *F* is the Fourier transform, *U* the unit step function, and *y* the Hilbert transform of *x*. [R186]

In other words, the negative half of the frequency spectrum is zeroed out, turning the real-valued signal into a complex signal. The Hilbert transformed signal can be obtained from `np.imag(hilbert(x))`, and the original signal from `np.real(hilbert(x))`.

References

[R186]

`scipy.signal.`**`hilbert2`**(*x*, *N=None*)

Compute the '2-D' analytic signal of *x*

Parameters **x** : array_like

2-D signal data.

N : int or tuple of two ints, optional

Number of Fourier components. Default is `x.shape`

Returns **xa** : ndarray

Analytic signal of *x* taken along axes (0,1).

References

[R187]

`scipy.signal.`**`decimate`**(*x*, *q*, *n=None*, *ftype='iir'*, *axis=-1*)

Downsample the signal by using a filter.

By default, an order 8 Chebyshev type I filter is used. A 30 point FIR filter with hamming window is used if *ftype* is 'fir'.

Parameters **x** : ndarray

The signal to be downsampled, as an N-dimensional array.

q : int

The downsampling factor.

n : int, optional

The order of the filter (1 less than the length for 'fir').

ftype : str {'iir', 'fir'}, optional

The type of the lowpass filter.

axis : int, optional

The axis along which to decimate.

Returns **y** : ndarray

The down-sampled signal.

See also:

`resample`

`scipy.signal.`**`detrend`**`(`*data*, *axis=-1*, *type='linear'*, *bp=0*`)`

Remove linear trend along axis from data.

Parameters	**data** : array_like The input data. **axis** : int, optional The axis along which to detrend the data. By default this is the last axis (-1). **type** : {'linear', 'constant'}, optional The type of detrending. If `type == 'linear'` (default), the result of a linear least-squares fit to *data* is subtracted from *data*. If `type == 'constant'`, only the mean of *data* is subtracted. **bp** : array_like of ints, optional A sequence of break points. If given, an individual linear fit is performed for each part of *data* between two break points. Break points are specified as indices into *data*.
Returns	**ret** : ndarray The detrended input data.

Examples

```
>>> from scipy import signal
>>> randgen = np.random.RandomState(9)
>>> npoints = 1e3
>>> noise = randgen.randn(npoints)
>>> x = 3 + 2*np.linspace(0, 1, npoints) + noise
>>> (signal.detrend(x) - noise).max() < 0.01
True
```

`scipy.signal.`**`resample`**`(`*x*, *num*, *t=None*, *axis=0*, *window=None*`)`

Resample *x* to *num* samples using Fourier method along the given axis.

The resampled signal starts at the same value as *x* but is sampled with a spacing of `len(x) / num * (spacing of x)`. Because a Fourier method is used, the signal is assumed to be periodic.

Parameters	**x** : array_like The data to be resampled. **num** : int The number of samples in the resampled signal. **t** : array_like, optional If *t* is given, it is assumed to be the sample positions associated with the signal data in *x*. **axis** : int, optional The axis of *x* that is resampled. Default is 0. **window** : array_like, callable, string, float, or tuple, optional Specifies the window applied to the signal in the Fourier domain. See below for details.
Returns	resampled_x or (resampled_x, resampled_t) Either the resampled array, or, if *t* was given, a tuple containing the resampled array and the corresponding resampled positions.

Notes

The argument *window* controls a Fourier-domain window that tapers the Fourier spectrum before zero-padding to alleviate ringing in the resampled values for sampled signals you didn't intend to be interpreted as band-limited.

If *window* is a function, then it is called with a vector of inputs indicating the frequency bins (i.e. fftfreq(x.shape[axis])).

If *window* is an array of the same length as *x.shape[axis]* it is assumed to be the window to be applied directly in the Fourier domain (with dc and low-frequency first).

For any other type of *window*, the function `scipy.signal.get_window` is called to generate the window.

The first sample of the returned vector is the same as the first sample of the input vector. The spacing between samples is changed from `dx` to `dx * len(x) / num`.

If *t* is not None, then it represents the old sample positions, and the new sample positions will be returned as well as the new samples.

As noted, `resample` uses FFT transformations, which can be very slow if the number of input samples is large and prime, see `scipy.fftpack.fft`.

5.27.4 Filter design

`bilinear`(b, a[, fs])	Return a digital filter from an analog one using a bilinear transform.
`findfreqs`(num, den, N)	Find an array of frequencies for computing the response of a filter.
`firwin`(numtaps, cutoff[, width, window, ...])	FIR filter design using the window method.
`firwin2`(numtaps, freq, gain[, nfreqs, ...])	FIR filter design using the window method.
`freqs`(b, a[, worN, plot])	Compute frequency response of analog filter.
`freqz`(b[, a, worN, whole, plot])	Compute the frequency response of a digital filter.
`group_delay`(system[, w, whole])	Compute the group delay of a digital filter.
`iirdesign`(wp, ws, gpass, gstop[, analog, ...])	Complete IIR digital and analog filter design.
`iirfilter`(N, Wn[, rp, rs, btype, analog, ...])	IIR digital and analog filter design given order and critical points.
`kaiser_atten`(numtaps, width)	Compute the attenuation of a Kaiser FIR filter.
`kaiser_beta`(a)	Compute the Kaiser parameter *beta*, given the attenuation *a*.
`kaiserord`(ripple, width)	Design a Kaiser window to limit ripple and width of transition region.
`savgol_coeffs`(window_length, polyorder[, ...])	Compute the coefficients for a 1-d Savitzky-Golay FIR filter.
`remez`(numtaps, bands, desired[, weight, Hz, ...])	Calculate the minimax optimal filter using the Remez exchange algorithm.
`unique_roots`(p[, tol, rtype])	Determine unique roots and their multiplicities from a list of roots.
`residue`(b, a[, tol, rtype])	Compute partial-fraction expansion of b(s) / a(s).
`residuez`(b, a[, tol, rtype])	Compute partial-fraction expansion of b(z) / a(z).
`invres`(r, p, k[, tol, rtype])	Compute b(s) and a(s) from partial fraction expansion.
`invresz`(r, p, k[, tol, rtype])	Compute b(z) and a(z) from partial fraction expansion.

`scipy.signal.`**`bilinear`**(*b*, *a*, *fs=1.0*)

Return a digital filter from an analog one using a bilinear transform.

The bilinear transform substitutes `(z-1) / (z+1)` for `s`.

`scipy.signal.`**`findfreqs`**(*num*, *den*, *N*)

Find an array of frequencies for computing the response of a filter.

Parameters **num, den** : array_like, 1-D

The polynomial coefficients of the numerator and denominator of the transfer function of the filter or LTI system. The coefficients are ordered from highest to lowest degree.

N : int

The length of the array to be computed.

Returns **w** : (N,) ndarray

A 1-D array of frequencies, logarithmically spaced.

Examples

Find a set of nine frequencies that span the "interesting part" of the frequency response for the filter with the transfer function

H(s) = s / (s^2 + 8s + 25)

```
>>> findfreqs([1, 0], [1, 8, 25], N=9)
array([  1.00000000e-02,   3.16227766e-02,   1.00000000e-01,
         3.16227766e-01,   1.00000000e+00,   3.16227766e+00,
         1.00000000e+01,   3.16227766e+01,   1.00000000e+02])
```

`scipy.signal.`**`firwin`**(*numtaps*, *cutoff*, *width=None*, *window='hamming'*, *pass_zero=True*, *scale=True*, *nyq=1.0*)

FIR filter design using the window method.

This function computes the coefficients of a finite impulse response filter. The filter will have linear phase; it will be Type I if *numtaps* is odd and Type II if *numtaps* is even.

Type II filters always have zero response at the Nyquist rate, so a ValueError exception is raised if firwin is called with *numtaps* even and having a passband whose right end is at the Nyquist rate.

Parameters **numtaps** : int

Length of the filter (number of coefficients, i.e. the filter order + 1). *numtaps* must be even if a passband includes the Nyquist frequency.

cutoff : float or 1D array_like

Cutoff frequency of filter (expressed in the same units as *nyq*) OR an array of cutoff frequencies (that is, band edges). In the latter case, the frequencies in *cutoff* should be positive and monotonically increasing between 0 and *nyq*. The values 0 and *nyq* must not be included in *cutoff*.

width : float or None, optional

If *width* is not None, then assume it is the approximate width of the transition region (expressed in the same units as *nyq*) for use in Kaiser FIR filter design. In this case, the *window* argument is ignored.

window : string or tuple of string and parameter values, optional

Desired window to use. See `scipy.signal.get_window` for a list of windows and required parameters.

pass_zero : bool, optional

If True, the gain at the frequency 0 (i.e. the "DC gain") is 1. Otherwise the DC gain is 0.

scale : bool, optional

Set to True to scale the coefficients so that the frequency response is exactly unity at a certain frequency. That frequency is either:

- 0 (DC) if the first passband starts at 0 (i.e. pass_zero is True)
- *nyq* (the Nyquist rate) if the first passband ends at *nyq* (i.e the filter is a single band highpass filter); center of first passband otherwise

nyq : float, optional

Nyquist frequency. Each frequency in *cutoff* must be between 0 and *nyq*.

Returns **h** : (numtaps,) ndarray

Coefficients of length *numtaps* FIR filter.

Raises **ValueError**

If any value in *cutoff* is less than or equal to 0 or greater than or equal to *nyq*, if the values in *cutoff* are not strictly monotonically increasing, or if *numtaps* is even but a passband includes the Nyquist frequency.

See also:

`scipy.signal.firwin2`

Examples

Low-pass from 0 to f:

```
>>> from scipy import signal
>>> signal.firwin(numtaps, f)
```

Use a specific window function:

```
>>> signal.firwin(numtaps, f, window='nuttall')
```

High-pass ('stop' from 0 to f):

```
>>> signal.firwin(numtaps, f, pass_zero=False)
```

Band-pass:

```
>>> signal.firwin(numtaps, [f1, f2], pass_zero=False)
```

Band-stop:

```
>>> signal.firwin(numtaps, [f1, f2])
```

Multi-band (passbands are [0, f1], [f2, f3] and [f4, 1]):

```
>>> signal.firwin(numtaps, [f1, f2, f3, f4])
```

Multi-band (passbands are [f1, f2] and [f3,f4]):

```
>>> signal.firwin(numtaps, [f1, f2, f3, f4], pass_zero=False)
```

`scipy.signal.`**`firwin2`**(*numtaps*, *freq*, *gain*, *nfreqs=None*, *window='hamming'*, *nyq=1.0*, *antisymmetric=False*)

FIR filter design using the window method.

From the given frequencies *freq* and corresponding gains *gain*, this function constructs an FIR filter with linear phase and (approximately) the given frequency response.

Parameters

numtaps : int

The number of taps in the FIR filter. *numtaps* must be less than *nfreqs*.

freq : array_like, 1D

The frequency sampling points. Typically 0.0 to 1.0 with 1.0 being Nyquist. The Nyquist frequency can be redefined with the argument *nyq*. The values in *freq* must be nondecreasing. A value can be repeated once to implement a discontinuity. The first value in *freq* must be 0, and the last value must be *nyq*.

gain : array_like

The filter gains at the frequency sampling points. Certain constraints to gain values, depending on the filter type, are applied, see Notes for details.

nfreqs : int, optional

The size of the interpolation mesh used to construct the filter. For most efficient behavior, this should be a power of 2 plus 1 (e.g, 129, 257, etc). The default is one more than the smallest power of 2 that is not less than *numtaps*. *nfreqs* must be greater than *numtaps*.

window : string or (string, float) or float, or None, optional

Window function to use. Default is "hamming". See `scipy.signal.get_window` for the complete list of possible values. If None, no window function is applied.

nyq : float, optional

Nyquist frequency. Each frequency in *freq* must be between 0 and *nyq* (inclusive).

antisymmetric : bool, optional

Whether resulting impulse response is symmetric/antisymmetric. See Notes for more details.

Returns **taps** : ndarray

The filter coefficients of the FIR filter, as a 1-D array of length *numtaps*.

See also:

`scipy.signal.firwin`

Notes

From the given set of frequencies and gains, the desired response is constructed in the frequency domain. The inverse FFT is applied to the desired response to create the associated convolution kernel, and the first *numtaps* coefficients of this kernel, scaled by *window*, are returned.

The FIR filter will have linear phase. The type of filter is determined by the value of 'numtaps' and *antisymmetric* flag. There are four possible combinations:

- odd *numtaps*, *antisymmetric* is False, type I filter is produced
- even *numtaps*, *antisymmetric* is False, type II filter is produced
- odd *numtaps*, *antisymmetric* is True, type III filter is produced
- even *numtaps*, *antisymmetric* is True, type IV filter is produced

Magnitude response of all but type I filters are subjects to following constraints:

- type II – zero at the Nyquist frequency
- type III – zero at zero and Nyquist frequencies
- type IV – zero at zero frequency

New in version 0.9.0.

References

[R175], [R176]

Examples

A lowpass FIR filter with a response that is 1 on [0.0, 0.5], and that decreases linearly on [0.5, 1.0] from 1 to 0:

```
>>> from scipy import signal
>>> taps = signal.firwin2(150, [0.0, 0.5, 1.0], [1.0, 1.0, 0.0])
>>> print(taps[72:78])
[-0.02286961 -0.06362756  0.57310236  0.57310236 -0.06362756 -0.02286961]
```

`scipy.signal.`**`freqs`**`(`*b*, *a*, *worN=None*, *plot=None*`)`

Compute frequency response of analog filter.

Given the numerator *b* and denominator *a* of a filter, compute its frequency response:

```
        b[0]*(jw)**(nb-1) + b[1]*(jw)**(nb-2) + ... + b[nb-1]
H(w) = -------------------------------------------------------
        a[0]*(jw)**(na-1) + a[1]*(jw)**(na-2) + ... + a[na-1]
```

Parameters

b : ndarray
: Numerator of a linear filter.

a : ndarray
: Denominator of a linear filter.

worN : {None, int}, optional
: If None, then compute at 200 frequencies around the interesting parts of the response curve (determined by pole-zero locations). If a single integer, then compute at that many frequencies. Otherwise, compute the response at the angular frequencies (e.g. rad/s) given in *worN*.

plot : callable, optional
: A callable that takes two arguments. If given, the return parameters *w* and *h* are passed to plot. Useful for plotting the frequency response inside `freqs`.

Returns

w : ndarray
: The angular frequencies at which h was computed.

h : ndarray
: The frequency response.

See also:

`freqz`	Compute the frequency response of a digital filter.

Notes

Using Matplotlib's "plot" function as the callable for *plot* produces unexpected results, this plots the real part of the complex transfer function, not the magnitude. Try `lambda w, h: plot(w, abs(h))`.

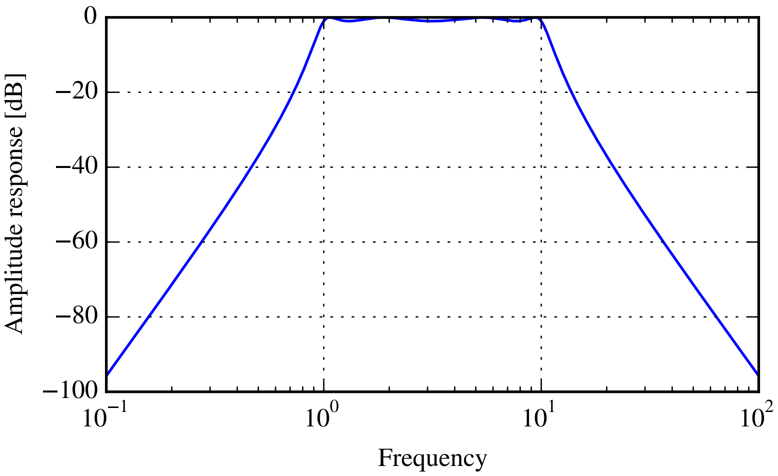
Examples

```
>>> from scipy.signal import freqs, iirfilter
```

```
>>> b, a = iirfilter(4, [1, 10], 1, 60, analog=True, ftype='cheby1')
```

```
>>> w, h = freqs(b, a, worN=np.logspace(-1, 2, 1000))
```

```
>>> import matplotlib.pyplot as plt
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude response [dB]')
>>> plt.grid()
>>> plt.show()
```



`scipy.signal.`**`freqz`**(*b*, *a=1*, *worN=None*, *whole=0*, *plot=None*)

Compute the frequency response of a digital filter.

Given the numerator *b* and denominator *a* of a digital filter, compute its frequency response:

```
        jw               -jw            -jmw
 jw  B(e)    b[0] + b[1]e + .... + b[m]e
H(e) = ---- = -----------------------------------
        jw               -jw            -jnw
     A(e)    a[0] + a[1]e + .... + a[n]e
```

Parameters

b : ndarray
numerator of a linear filter

a : ndarray
denominator of a linear filter

worN : {None, int, array_like}, optional
If None (default), then compute at 512 frequencies equally spaced around the unit circle. If a single integer, then compute at that many frequencies. If an array_like, compute the response at the frequencies given (in radians/sample).

whole : bool, optional
Normally, frequencies are computed from 0 to the Nyquist frequency, pi radians/sample (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to 2*pi radians/sample.

plot : callable
A callable that takes two arguments. If given, the return parameters *w* and *h* are passed to plot. Useful for plotting the frequency response inside `freqz`.

Returns

w : ndarray
The normalized frequencies at which h was computed, in radians/sample.

h : ndarray
The frequency response.

Notes

Using Matplotlib's "plot" function as the callable for *plot* produces unexpected results, this plots the real part of the complex transfer function, not the magnitude. Try `lambda w, h: plot(w, abs(h))`.

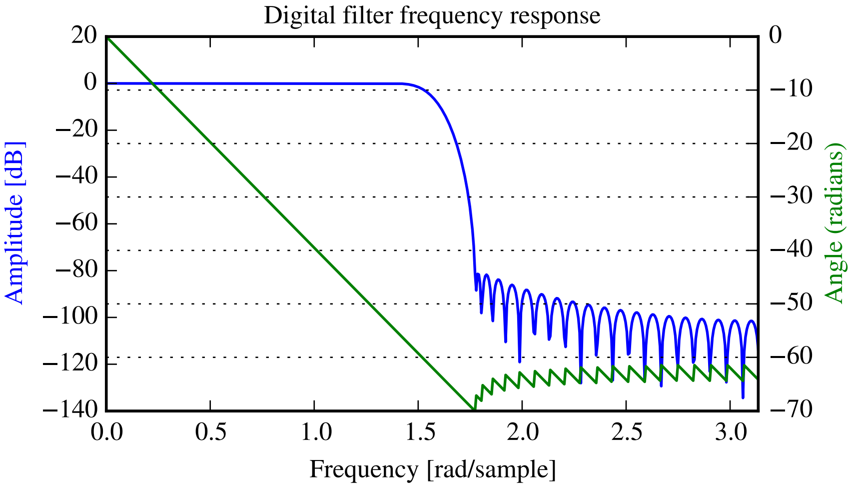
Examples

```
>>> from scipy import signal
>>> b = signal.firwin(80, 0.5, window=('kaiser', 8))
>>> w, h = signal.freqz(b)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.title('Digital filter frequency response')
>>> ax1 = fig.add_subplot(111)
```

```
>>> plt.plot(w, 20 * np.log10(abs(h)), 'b')
>>> plt.ylabel('Amplitude [dB]', color='b')
>>> plt.xlabel('Frequency [rad/sample]')
```

```
>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> plt.plot(w, angles, 'g')
>>> plt.ylabel('Angle (radians)', color='g')
>>> plt.grid()
>>> plt.axis('tight')
>>> plt.show()
```



`scipy.signal.`**`group_delay`**(*system*, *w=None*, *whole=False*)

Compute the group delay of a digital filter.

The group delay measures by how many samples amplitude envelopes of various spectral components of a signal are delayed by a filter. It is formally defined as the derivative of continuous (unwrapped) phase:

```
          d        jw
D(w) = - -- arg H(e)
         dw
```

Parameters **system** : tuple of array_like (b, a)

Numerator and denominator coefficients of a filter transfer function.

w : {None, int, array-like}, optional

If None (default), then compute at 512 frequencies equally spaced around the unit circle. If a single integer, then compute at that many frequencies. If array, compute the delay at the frequencies given (in radians/sample).

whole : bool, optional

Normally, frequencies are computed from 0 to the Nyquist frequency, pi radians/sample (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to `2*pi` radians/sample.

Returns

w : ndarray

The normalized frequencies at which the group delay was computed, in radians/sample.

gd : ndarray

The group delay.

See also:

freqz	Frequency response of a digital filter

Notes

The similar function in MATLAB is called *grpdelay*.

If the transfer function $H(z)$ has zeros or poles on the unit circle, the group delay at corresponding frequencies is undefined. When such a case arises the warning is raised and the group delay is set to 0 at those frequencies.

For the details of numerical computation of the group delay refer to [R177].

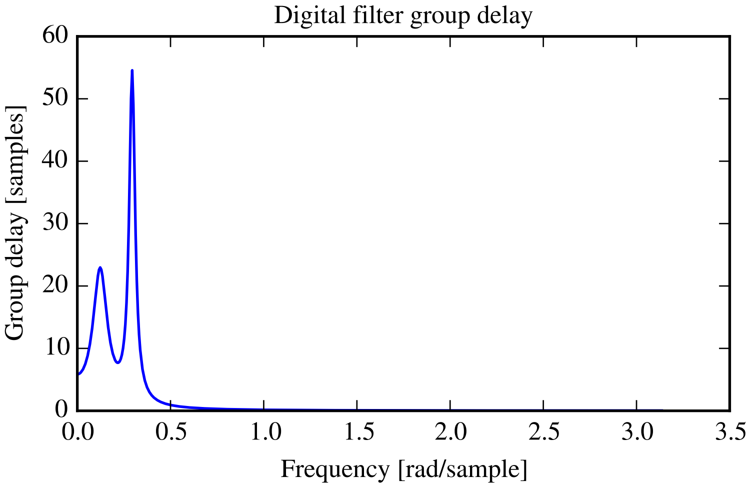
References

[R177]

Examples

```
>>> from scipy import signal
>>> b, a = signal.iirdesign(0.1, 0.3, 5, 50, ftype='cheby1')
>>> w, gd = signal.group_delay((b, a))
```

```
>>> import matplotlib.pyplot as plt
>>> plt.title('Digital filter group delay')
>>> plt.plot(w, gd)
>>> plt.ylabel('Group delay [samples]')
>>> plt.xlabel('Frequency [rad/sample]')
>>> plt.show()
```



`scipy.signal.`**`iirdesign`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *ftype='ellip'*, *output='ba'*)

Complete IIR digital and analog filter design.

Given passband and stopband frequencies and gains, construct an analog or digital IIR filter of minimum order for a given basic type. Return the output in numerator, denominator ('ba'), pole-zero ('zpk') or second order sections ('sos') form.

Parameters **wp, ws** : float

Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g. rad/s).

gpass : float

The maximum loss in the passband (dB).

gstop : float

The minimum attenuation in the stopband (dB).

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

ftype : str, optional

The type of IIR filter to design:

- Butterworth : 'butter'
- Chebyshev I : 'cheby1'
- Chebyshev II : 'cheby2'
- Cauer/elliptic: 'ellip'
- Bessel/Thomson: 'bessel'

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns **b, a** : ndarray, ndarray

Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float

Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray

Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`butter`	Filter design using order and critical points
`cheby1`, `cheby2`, `ellip`, `bessel`	
`buttord`	Find order and critical points from passband and stopband spec
`cheb1ord`, `cheb2ord`, `ellipord`	
`iirfilter`	General filter design using order and critical frequencies

Notes

The `'sos'` output parameter was added in 0.16.0.

`scipy.signal.`**`iirfilter`**(*N*, *Wn*, *rp=None*, *rs=None*, *btype='band'*, *analog=False*, *ftype='butter'*, *output='ba'*)

IIR digital and analog filter design given order and critical points.

Design an Nth order digital or analog filter and return the filter coefficients.

Parameters **N** : int

The order of the filter.

Wn : array_like

A scalar or length-2 sequence giving the critical frequencies. For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

rp : float, optional

For Chebyshev and elliptic filters, provides the maximum ripple in the passband. (dB)

rs : float, optional

For Chebyshev and elliptic filters, provides the minimum attenuation in the stop band. (dB)

btype : {'bandpass', 'lowpass', 'highpass', 'bandstop'}, optional

The type of filter. Default is 'bandpass'.

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

ftype : str, optional

The type of IIR filter to design:

- Butterworth : 'butter'
- Chebyshev I : 'cheby1',
- Chebyshev II : 'cheby2'
- Cauer/elliptic: 'ellip'
- Bessel/Thomson: 'bessel'

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns **b, a** : ndarray, ndarray

Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float

Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray

Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`butter`	Filter design using order and critical points
`cheby1`, `cheby2`, `ellip`, `bessel`	
`buttord`	Find order and critical points from passband and stopband spec
`cheb1ord`, `cheb2ord`, `ellipord`	
`iirdesign`	General filter design using passband and stopband spec

Notes

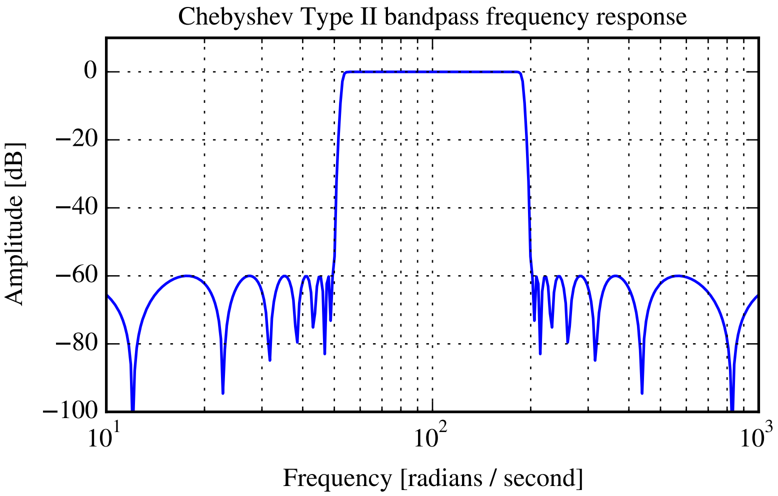
The `'sos'` output parameter was added in 0.16.0.

Examples

Generate a 17th-order Chebyshev II bandpass filter and plot the frequency response:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.iirfilter(17, [50, 200], rs=60, btype='band',
...                         analog=True, ftype='cheby2')
>>> w, h = signal.freqs(b, a, 1000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.semilogx(w, 20 * np.log10(abs(h)))
>>> ax.set_title('Chebyshev Type II bandpass frequency response')
>>> ax.set_xlabel('Frequency [radians / second]')
>>> ax.set_ylabel('Amplitude [dB]')
>>> ax.axis((10, 1000, -100, 10))
>>> ax.grid(which='both', axis='both')
>>> plt.show()
```



`scipy.signal.`**`kaiser_atten`**(*numtaps*, *width*)

Compute the attenuation of a Kaiser FIR filter.

Given the number of taps *N* and the transition width *width*, compute the attenuation *a* in dB, given by Kaiser's formula:

> a = 2.285 * (N - 1) * pi * width + 7.95

Parameters	**numtaps** : int	The number of taps in the FIR filter.
	width : float	The desired width of the transition region between passband and stopband (or, in general, at any discontinuity) for the filter.
Returns	**a** : float	The attenuation of the ripple, in dB.

See also:

`kaiserord`, `kaiser_beta`

`scipy.signal.`**`kaiser_beta`**`(`*a*`)`

Compute the Kaiser parameter *beta*, given the attenuation *a*.

Parameters	**a** : float	The desired attenuation in the stopband and maximum ripple in the passband, in dB. This should be a *positive* number.
Returns	**beta** : float	The *beta* parameter to be used in the formula for a Kaiser window.

References

Oppenheim, Schafer, "Discrete-Time Signal Processing", p.475-476.

`scipy.signal.`**`kaiserord`**`(`*ripple*, *width*`)`

Design a Kaiser window to limit ripple and width of transition region.

Parameters	**ripple** : float	Positive number specifying maximum ripple in passband (dB) and minimum ripple in stopband.
	width : float	Width of transition region (normalized so that 1 corresponds to pi radians / sample).
Returns	**numtaps** : int	The length of the kaiser window.
	beta : float	The beta parameter for the kaiser window.

See also:

`kaiser_beta`, `kaiser_atten`

Notes

There are several ways to obtain the Kaiser window:

- `signal.kaiser(numtaps, beta, sym=0)`
- `signal.get_window(beta, numtaps)`
- `signal.get_window(('kaiser', beta), numtaps)`

The empirical equations discovered by Kaiser are used.

References

Oppenheim, Schafer, "Discrete-Time Signal Processing", p.475-476.

`scipy.signal.`**`savgol_coeffs`**`(`*window_length*, *polyorder*, *deriv=0*, *delta=1.0*, *pos=None*, *use='conv'*`)`

Compute the coefficients for a 1-d Savitzky-Golay FIR filter.

Parameters	**window_length** : int	The length of the filter window (i.e. the number of coefficients). *window_length* must be an odd positive integer.

polyorder : int
The order of the polynomial used to fit the samples. *polyorder* must be less than *window_length*.

deriv : int, optional
The order of the derivative to compute. This must be a nonnegative integer. The default is 0, which means to filter the data without differentiating.

delta : float, optional
The spacing of the samples to which the filter will be applied. This is only used if deriv > 0.

pos : int or None, optional
If pos is not None, it specifies evaluation position within the window. The default is the middle of the window.

use : str, optional
Either 'conv' or 'dot'. This argument chooses the order of the coefficients. The default is 'conv', which means that the coefficients are ordered to be used in a convolution. With use='dot', the order is reversed, so the filter is applied by dotting the coefficients with the data set.

Returns **coeffs** : 1-d ndarray
The filter coefficients.

See also:

`savgol_filter`

Notes

New in version 0.14.0.

References

A. Savitzky, M. J. E. Golay, Smoothing and Differentiation of Data by Simplified Least Squares Procedures. Analytical Chemistry, 1964, 36 (8), pp 1627-1639.

Examples

```
>>> from scipy.signal import savgol_coeffs
>>> savgol_coeffs(5, 2)
array([-0.08571429,  0.34285714,  0.48571429,  0.34285714, -0.08571429])
>>> savgol_coeffs(5, 2, deriv=1)
array([  2.00000000e-01,   1.00000000e-01,   2.00607895e-16,
        -1.00000000e-01,  -2.00000000e-01])
```

Note that use='dot' simply reverses the coefficients.

```
>>> savgol_coeffs(5, 2, pos=3)
array([ 0.25714286,  0.37142857,  0.34285714,  0.17142857, -0.14285714])
>>> savgol_coeffs(5, 2, pos=3, use='dot')
array([-0.14285714,  0.17142857,  0.34285714,  0.37142857,  0.25714286])
```

x contains data from the parabola x = t**2, sampled at t = -1, 0, 1, 2, 3. *c* holds the coefficients that will compute the derivative at the last position. When dotted with *x* the result should be 6.

```
>>> x = np.array([1, 0, 1, 4, 9])
>>> c = savgol_coeffs(5, 2, pos=4, deriv=1, use='dot')
>>> c.dot(x)
6.0000000000000018
```

`scipy.signal.`**`remez`**`(`*numtaps*, *bands*, *desired*, *weight=None*, *Hz=1*, *type='bandpass'*, *maxiter=25*, *grid_density=16*`)`

Calculate the minimax optimal filter using the Remez exchange algorithm.

Calculate the filter-coefficients for the finite impulse response (FIR) filter whose transfer function minimizes the maximum error between the desired gain and the realized gain in the specified frequency bands using the Remez exchange algorithm.

Parameters

numtaps : int

The desired number of taps in the filter. The number of taps is the number of terms in the filter, or the filter order plus one.

bands : array_like

A monotonic sequence containing the band edges in Hz. All elements must be non-negative and less than half the sampling frequency as given by *Hz*.

desired : array_like

A sequence half the size of bands containing the desired gain in each of the specified bands.

weight : array_like, optional

A relative weighting to give to each band region. The length of *weight* has to be half the length of *bands*.

Hz : scalar, optional

The sampling frequency in Hz. Default is 1.

type : {'bandpass', 'differentiator', 'hilbert'}, optional

The type of filter:

'bandpass' : flat response in bands. This is the default.

'differentiator' : frequency proportional response in bands.

'hilbert' [filter with odd symmetry, that is, type III] (for even order) or type IV (for odd order) linear phase filters.

maxiter : int, optional

Maximum number of iterations of the algorithm. Default is 25.

grid_density : int, optional

Grid density. The dense grid used in `remez` is of size `(numtaps + 1) * grid_density`. Default is 16.

Returns

out : ndarray

A rank-1 array containing the coefficients of the optimal (in a minimax sense) filter.

See also:

`freqz` Compute the frequency response of a digital filter.

References

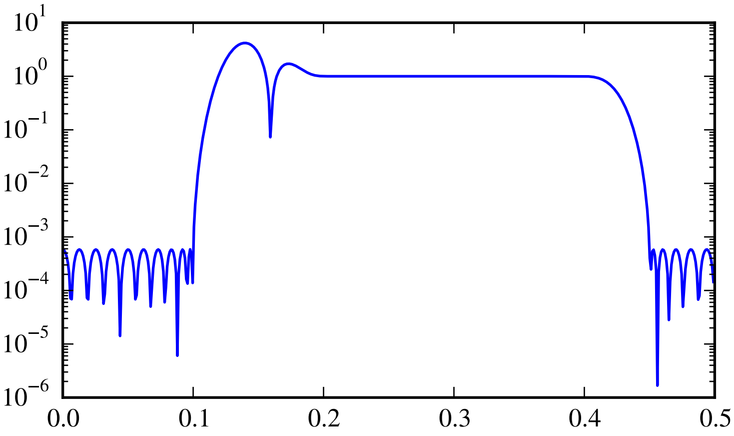
[R196], [R197]

Examples

We want to construct a filter with a passband at 0.2-0.4 Hz, and stop bands at 0-0.1 Hz and 0.45-0.5 Hz. Note that this means that the behavior in the frequency ranges between those bands is unspecified and may overshoot.

```
>>> from scipy import signal
>>> bpass = signal.remez(72, [0, 0.1, 0.2, 0.4, 0.45, 0.5], [0, 1, 0])
>>> freq, response = signal.freqz(bpass)
>>> ampl = np.abs(response)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(111)
>>> ax1.semilogy(freq/(2*np.pi), ampl, 'b-')  # freq in Hz
>>> plt.show()
```



`scipy.signal.`**`unique_roots`**(*p*, *tol=0.001*, *rtype='min'*)

Determine unique roots and their multiplicities from a list of roots.

Parameters **p** : array_like

The list of roots.

tol : float, optional

The tolerance for two roots to be considered equal. Default is 1e-3.

rtype : {‘max’, ‘min, ‘avg’}, optional

How to determine the returned root if multiple roots are within *tol* of each other.

- ‘max’: pick the maximum of those roots.
- ‘min’: pick the minimum of those roots.
- ‘avg’: take the average of those roots.

Returns **pout** : ndarray

The list of unique roots, sorted from low to high.

mult : ndarray

The multiplicity of each root.

Notes

This utility function is not specific to roots but can be used for any sequence of values for which uniqueness and multiplicity has to be determined. For a more general routine, see `numpy.unique`.

Examples

```
>>> from scipy import signal
>>> vals = [0, 1.3, 1.31, 2.8, 1.25, 2.2, 10.3]
>>> uniq, mult = signal.unique_roots(vals, tol=2e-2, rtype='avg')
```

Check which roots have multiplicity larger than 1:

```
>>> uniq[mult > 1]
array([ 1.305])
```

`scipy.signal.`**`residue`**(*b*, *a*, *tol=0.001*, *rtype='avg'*)

Compute partial-fraction expansion of b(s) / a(s).

If `M = len(b)` and `N = len(a)`, then the partial-fraction expansion H(s) is defined as:

```
        b(s)     b[0] s**(M-1) + b[1] s**(M-2) + ... + b[M-1]
H(s) = ------ = ------------------------------------------------
        a(s)     a[0] s**(N-1) + a[1] s**(N-2) + ... + a[N-1]

          r[0]       r[1]             r[-1]
     = -------- + -------- + ... + --------- + k(s)
       (s-p[0])   (s-p[1])         (s-p[-1])
```

If there are any repeated roots (closer together than *tol*), then H(s) has terms like:

```
  r[i]      r[i+1]              r[i+n-1]
-------- + ----------- + ... + -----------
(s-p[i])  (s-p[i])**2          (s-p[i])**n
```

Returns **r** : ndarray

Residues.

p : ndarray

Poles.

k : ndarray

Coefficients of the direct polynomial term.

See also:

`invres`, `numpy.poly`, `unique_roots`

`scipy.signal.`**`residuez`**(*b*, *a*, *tol=0.001*, *rtype='avg'*)

Compute partial-fraction expansion of b(z) / a(z).

If `M = len(b)` and `N = len(a)`:

```
        b(z)     b[0] + b[1] z**(-1) + ... + b[M-1] z**(-M+1)
H(z) = ------ = ------------------------------------------------
        a(z)     a[0] + a[1] z**(-1) + ... + a[N-1] z**(-N+1)

          r[0]                   r[-1]
 = --------------- + ... + ---------------- + k[0] + k[1]z**(-1) ...
   (1-p[0]z**(-1))         (1-p[-1]z**(-1))
```

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like:

```
     r[i]              r[i+1]                    r[i+n-1]
-------------- + ------------------ + ... + ------------------
(1-p[i]z**(-1))  (1-p[i]z**(-1))**2         (1-p[i]z**(-1))**n
```

See also:

`invresz`, `unique_roots`

`scipy.signal.`**`invres`**(*r*, *p*, *k*, *tol=0.001*, *rtype='avg'*)

Compute b(s) and a(s) from partial fraction expansion.

If `M = len(b)` and `N = len(a)`:

```
        b(s)     b[0] x**(M-1) + b[1] x**(M-2) + ... + b[M-1]
H(s) = ------ = ----------------------------------------------
        a(s)     a[0] x**(N-1) + a[1] x**(N-2) + ... + a[N-1]

         r[0]       r[1]             r[-1]
     = -------- + -------- + ... + --------- + k(s)
       (s-p[0])   (s-p[1])         (s-p[-1])
```

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like:

```
  r[i]      r[i+1]              r[i+n-1]
-------- + ----------- + ... + -----------
(s-p[i])  (s-p[i])**2          (s-p[i])**n
```

Parameters

r : ndarray
Residues.

p : ndarray
Poles.

k : ndarray
Coefficients of the direct polynomial term.

tol : float, optional
The tolerance for two roots to be considered equal. Default is 1e-3.

rtype : {'max', 'min, 'avg'}, optional
How to determine the returned root if multiple roots are within *tol* of each other.

'max': pick the maximum of those roots.
'min': pick the minimum of those roots.
'avg': take the average of those roots.

See also:

`residue`, `unique_roots`

`scipy.signal.`**`invresz`**(*r*, *p*, *k*, *tol=0.001*, *rtype='avg'*)

Compute b(z) and a(z) from partial fraction expansion.

If `M = len(b)` and `N = len(a)`:

```
        b(z)     b[0] + b[1] z**(-1) + ... + b[M-1] z**(-M+1)
H(z) = ------ = ----------------------------------------------
        a(z)     a[0] + a[1] z**(-1) + ... + a[N-1] z**(-N+1)

             r[0]                   r[-1]
     = --------------- + ... + ---------------- + k[0] + k[1]z**(-1)...
       (1-p[0]z**(-1))         (1-p[-1]z**(-1))
```

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like:

```
     r[i]              r[i+1]                    r[i+n-1]
-------------- + ------------------ + ... + ------------------
(1-p[i]z**(-1))  (1-p[i]z**(-1))**2         (1-p[i]z**(-1))**n
```

See also:

`residuez`, `unique_roots`, `invres`

Lower-level filter design functions:

`abcd_normalize`([A, B, C, D])	Check state-space matrices and ensure they are two-dimensional.
`band_stop_obj`(wp, ind, passb, stopb, gpass, ...)	Band Stop Objective Function for order minimization.
`besselap`(N)	Return (z,p,k) for analog prototype of an Nth order Bessel filter.
`buttap`(N)	Return (z,p,k) for analog prototype of Nth order Butterworth filter.
`cheb1ap`(N, rp)	Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.
`cheb2ap`(N, rs)	Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.
`cmplx_sort`(p)	Sort roots based on magnitude.
`ellipap`(N, rp, rs)	Return (z,p,k) of Nth order elliptic analog lowpass filter.
`lp2bp`(b, a[, wo, bw])	Transform a lowpass filter prototype to a bandpass filter.
`lp2bs`(b, a[, wo, bw])	Transform a lowpass filter prototype to a bandstop filter.
`lp2hp`(b, a[, wo])	Transform a lowpass filter prototype to a highpass filter.
`lp2lp`(b, a[, wo])	Transform a lowpass filter prototype to a different frequency.
`normalize`(b, a)	Normalize polynomial representation of a transfer function.

`scipy.signal.`**`abcd_normalize`**(*A=None*, *B=None*, *C=None*, *D=None*)

Check state-space matrices and ensure they are two-dimensional.

If enough information on the system is provided, that is, enough properly-shaped arrays are passed to the function, the missing ones are built from this information, ensuring the correct number of rows and columns. Otherwise a ValueError is raised.

Parameters **A, B, C, D** : array_like, optional

State-space matrices. All of them are None (missing) by default.

Returns **A, B, C, D** : array

Properly shaped state-space matrices.

Raises **ValueError**

If not enough information on the system was provided.

`scipy.signal.`**`band_stop_obj`**(*wp*, *ind*, *passb*, *stopb*, *gpass*, *gstop*, *type*)

Band Stop Objective Function for order minimization.

Returns the non-integer order for an analog band stop filter.

Parameters **wp** : scalar

Edge of passband *passb*.

ind : int, {0, 1}

Index specifying which *passb* edge to vary (0 or 1).

passb : ndarray

Two element sequence of fixed passband edges.

stopb : ndarray

Two element sequence of fixed stopband edges.

gstop : float

Amount of attenuation in stopband in dB.

gpass : float

Amount of ripple in the passband in dB.

type : {'butter', 'cheby', 'ellip'}

Type of filter.

Returns **n** : scalar

Filter order (possibly non-integer).

`scipy.signal.`**`besselap`**(*N*)

Return (z,p,k) for analog prototype of an Nth order Bessel filter.

The filter is normalized such that the filter asymptotes are the same as a Butterworth filter of the same order with an angular (e.g. rad/s) cutoff frequency of 1.

Parameters **N** : int

The order of the Bessel filter to return zeros, poles and gain for. Values in the range 0-25 are supported.

Returns **z** : ndarray

Zeros. Is always an empty array.

p : ndarray

Poles.

k : scalar

Gain. Always 1.

`scipy.signal.`**`buttap`**`(`*N*`)`

Return (z,p,k) for analog prototype of Nth order Butterworth filter.

The filter will have an angular (e.g. rad/s) cutoff frequency of 1.

`scipy.signal.`**`cheb1ap`**`(`*N*, *rp*`)`

Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.

The returned filter prototype has *rp* decibels of ripple in the passband.

The filter's angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first drops below `-rp`.

`scipy.signal.`**`cheb2ap`**`(`*N*, *rs*`)`

Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.

The returned filter prototype has *rs* decibels of ripple in the stopband.

The filter's angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first reaches `-rs`.

`scipy.signal.`**`cmplx_sort`**`(`*p*`)`

Sort roots based on magnitude.

Parameters **p** : array_like

The roots to sort, as a 1-D array.

Returns **p_sorted** : ndarray

Sorted roots.

indx : ndarray

Array of indices needed to sort the input *p*.

`scipy.signal.`**`ellipap`**`(`*N*, *rp*, *rs*`)`

Return (z,p,k) of Nth order elliptic analog lowpass filter.

The filter is a normalized prototype that has *rp* decibels of ripple in the passband and a stopband *rs* decibels down.

The filter's angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first drops below `-rp`.

References

Lutova, Tosic, and Evans, "Filter Design for Signal Processing", Chapters 5 and 12.

`scipy.signal.`**`lp2bp`**`(`*b*, *a*, *wo=1.0*, *bw=1.0*`)`

Transform a lowpass filter prototype to a bandpass filter.

Return an analog band-pass filter with center frequency *wo* and bandwidth *bw* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

`scipy.signal.`**`lp2bs`**(*b*, *a*, *wo=1.0*, *bw=1.0*)

Transform a lowpass filter prototype to a bandstop filter.

Return an analog band-stop filter with center frequency *wo* and bandwidth *bw* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

`scipy.signal.`**`lp2hp`**(*b*, *a*, *wo=1.0*)

Transform a lowpass filter prototype to a highpass filter.

Return an analog high-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

`scipy.signal.`**`lp2lp`**(*b*, *a*, *wo=1.0*)

Transform a lowpass filter prototype to a different frequency.

Return an analog low-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

`scipy.signal.`**`normalize`**(*b*, *a*)

Normalize polynomial representation of a transfer function.

If values of *b* are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

5.27.5 Matlab-style IIR filter design

`butter`(N, Wn[, btype, analog, output])	Butterworth digital and analog filter design.
`buttord`(wp, ws, gpass, gstop[, analog])	Butterworth filter order selection.
`cheby1`(N, rp, Wn[, btype, analog, output])	Chebyshev type I digital and analog filter design.
`cheb1ord`(wp, ws, gpass, gstop[, analog])	Chebyshev type I filter order selection.
`cheby2`(N, rs, Wn[, btype, analog, output])	Chebyshev type II digital and analog filter design.
`cheb2ord`(wp, ws, gpass, gstop[, analog])	Chebyshev type II filter order selection.
`ellip`(N, rp, rs, Wn[, btype, analog, output])	Elliptic (Cauer) digital and analog filter design.
`ellipord`(wp, ws, gpass, gstop[, analog])	Elliptic (Cauer) filter order selection.
`bessel`(N, Wn[, btype, analog, output])	Bessel/Thomson digital and analog filter design.

`scipy.signal.`**`butter`**(*N*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*)

Butterworth digital and analog filter design.

Design an Nth order digital or analog Butterworth filter and return the filter coefficients.

Parameters **N** : int

The order of the filter.

Wn : array_like

A scalar or length-2 sequence giving the critical frequencies. For a Butterworth filter, this is the point at which the gain drops to 1/sqrt(2) that of the passband (the "-3 dB point"). For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype : {'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional

The type of filter. Default is 'lowpass'.

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns	**b, a** : ndarray, ndarray Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`. **z, p, k** : ndarray, ndarray, float Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`. **sos** : ndarray Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`buttord`

Notes

The Butterworth filter has maximally flat frequency response in the passband.

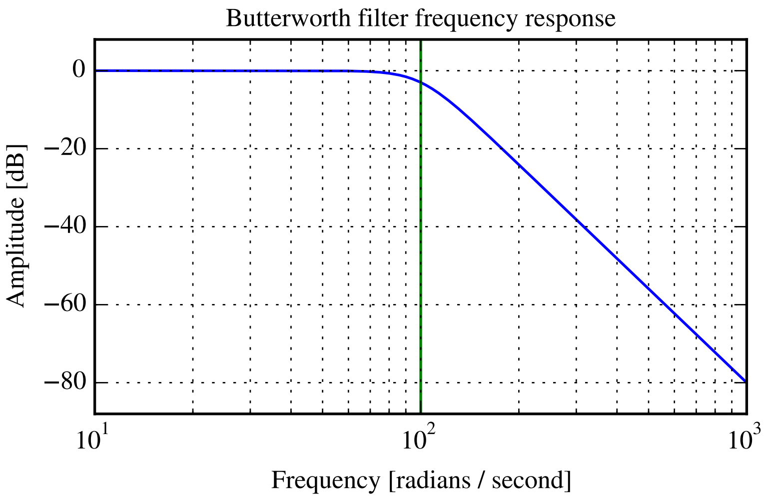
The `'sos'` output parameter was added in 0.16.0.

Examples

Plot the filter's frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth filter frequency response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.show()
```



`scipy.signal.`**`buttord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*)

Butterworth filter order selection.

Return the order of the lowest order digital or analog Butterworth filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters **wp, ws** : float

Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g. rad/s).

gpass : float

The maximum loss in the passband (dB).

gstop : float

The minimum attenuation in the stopband (dB).

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

Returns **ord** : int

The lowest order for a Butterworth filter which meets specs.

wn : ndarray or float

The Butterworth natural frequency (i.e. the “3dB frequency”). Should be used with `butter` to give filter results.

See also:

`butter`	Filter design using order and critical points
`cheb1ord`	Find order and critical points from passband and stopband spec

`cheb2ord`, `ellipord`

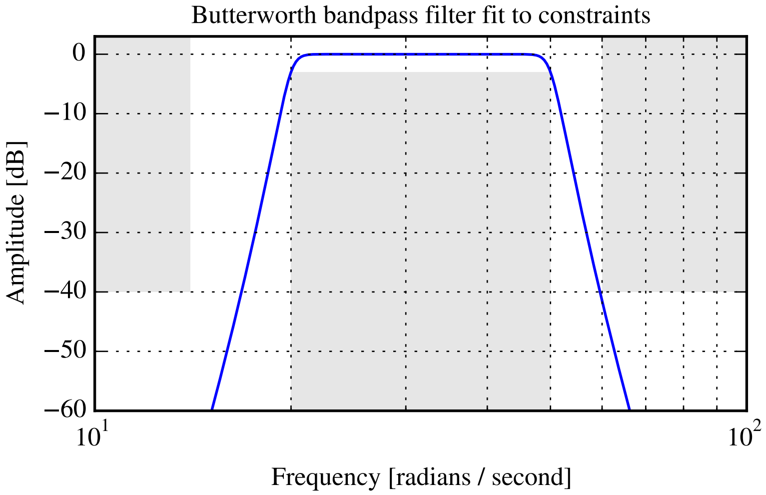
`iirfilter`	General filter design using order and critical frequencies
`iirdesign`	General filter design using passband and stopband spec

Examples

Design an analog bandpass filter with passband within 3 dB from 20 to 50 rad/s, while rejecting at least -40 dB below 14 and above 60 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.buttord([20, 50], [14, 60], 3, 40, True)
>>> b, a = signal.butter(N, Wn, 'band', True)
>>> w, h = signal.freqs(b, a, np.logspace(1, 2, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth bandpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([1,  14,  14,   1], [-40, -40, 99, 99], '0.9', lw=0) # stop
>>> plt.fill([20, 20,  50,  50], [-99, -3, -3, -99], '0.9', lw=0) # pass
>>> plt.fill([60, 60, 1e9, 1e9], [99, -40, -40, 99], '0.9', lw=0) # stop
>>> plt.axis([10, 100, -60, 3])
>>> plt.show()
```



`scipy.signal.`**`cheby1`** (*N*, *rp*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*)

Chebyshev type I digital and analog filter design.

Design an Nth order digital or analog Chebyshev type I filter and return the filter coefficients.

Parameters

N : int

The order of the filter.

rp : float

The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.

Wn : array_like

A scalar or length-2 sequence giving the critical frequencies. For Type I filters, this is the point in the transition band at which the gain first drops below -*rp*. For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype : {'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional

The type of filter. Default is 'lowpass'.

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns

b, a : ndarray, ndarray

Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float

Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray

Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`cheb1ord`

Notes

The Chebyshev type I filter maximizes the rate of cutoff between the frequency response's passband and stopband, at the expense of ripple in the passband and increased ringing in the step response.

Type I filters roll off faster than Type II (`cheby2`), but Type II filters do not have any ripple in the passband.

The equiripple passband has N maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or -rp dB for even-order filters.

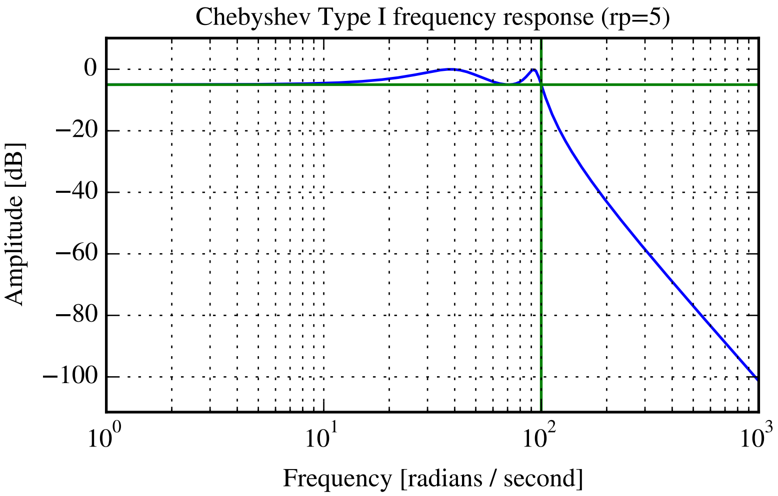
The `'sos'` output parameter was added in 0.16.0.

Examples

Plot the filter's frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.cheby1(4, 5, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev Type I frequency response (rp=5)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-5, color='green') # rp
>>> plt.show()
```



`scipy.signal.`**`cheb1ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*)

Chebyshev type I filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type I filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters **wp, ws** : float

Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g. rad/s).

gpass : float

The maximum loss in the passband (dB).

gstop : float

The minimum attenuation in the stopband (dB).

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

Returns **ord** : int

The lowest order for a Chebyshev type I filter that meets specs.

wn : ndarray or float

The Chebyshev natural frequency (the “3dB frequency”) for use with `cheby1` to give filter results.

See also:

`cheby1`	Filter design using order and critical points
`buttord`	Find order and critical points from passband and stopband spec

`cheb2ord`, `ellipord`

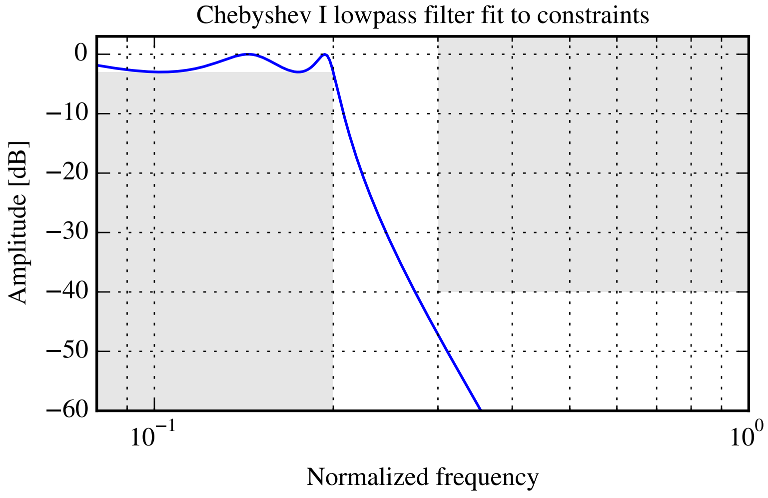
`iirfilter`	General filter design using order and critical frequencies
`iirdesign`	General filter design using passband and stopband spec

Examples

Design a digital lowpass filter such that the passband is within 3 dB up to 0.2*(fs/2), while rejecting at least -40 dB above 0.3*(fs/2). Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.cheb1ord(0.2, 0.3, 3, 40)
>>> b, a = signal.cheby1(N, 3, Wn, 'low')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev I lowpass filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.01, 0.2, 0.2, .01], [-3, -3, -99, -99], '0.9', lw=0) # stop
>>> plt.fill([0.3, 0.3,   2,   2], [ 9, -40, -40,   9], '0.9', lw=0) # pass
>>> plt.axis([0.08, 1, -60, 3])
>>> plt.show()
```



`scipy.signal.`**`cheby2`**(*N*, *rs*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*)

Chebyshev type II digital and analog filter design.

Design an Nth order digital or analog Chebyshev type II filter and return the filter coefficients.

Parameters

N : int
The order of the filter.

rs : float
The minimum attenuation required in the stop band. Specified in decibels, as a positive number.

Wn : array_like
A scalar or length-2 sequence giving the critical frequencies. For Type II filters, this is the point in the transition band at which the gain first reaches -*rs*. For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype : {'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional
The type of filter. Default is 'lowpass'.

analog : bool, optional
When True, return an analog filter, otherwise a digital filter is returned.

output : {'ba', 'zpk', 'sos'}, optional
Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns

b, a : ndarray, ndarray
Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float
Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray
Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`cheb2ord`

Notes

The Chebyshev type II filter maximizes the rate of cutoff between the frequency response's passband and stopband, at the expense of ripple in the stopband and increased ringing in the step response.

Type II filters do not roll off as fast as Type I (`cheby1`).

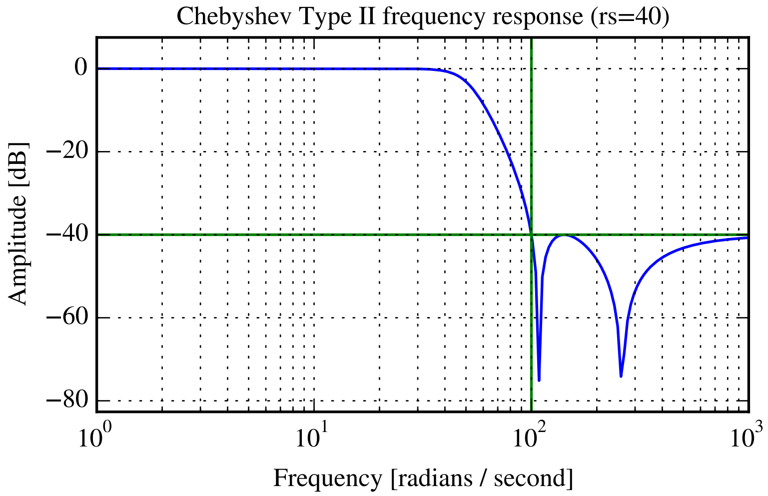
The `'sos'` output parameter was added in 0.16.0.

Examples

Plot the filter's frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.cheby2(4, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev Type II frequency response (rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-40, color='green') # rs
>>> plt.show()
```



`scipy.signal.`**`cheb2ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*)

Chebyshev type II filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type II filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters **wp, ws** : float

Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3

- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g. rad/s).

gpass : float

The maximum loss in the passband (dB).

gstop : float

The minimum attenuation in the stopband (dB).

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

Returns

ord : int

The lowest order for a Chebyshev type II filter that meets specs.

wn : ndarray or float

The Chebyshev natural frequency (the "3dB frequency") for use with `cheby2` to give filter results.

See also:

`cheby2`	Filter design using order and critical points
`buttord`	Find order and critical points from passband and stopband spec

`cheb1ord`, `ellipord`

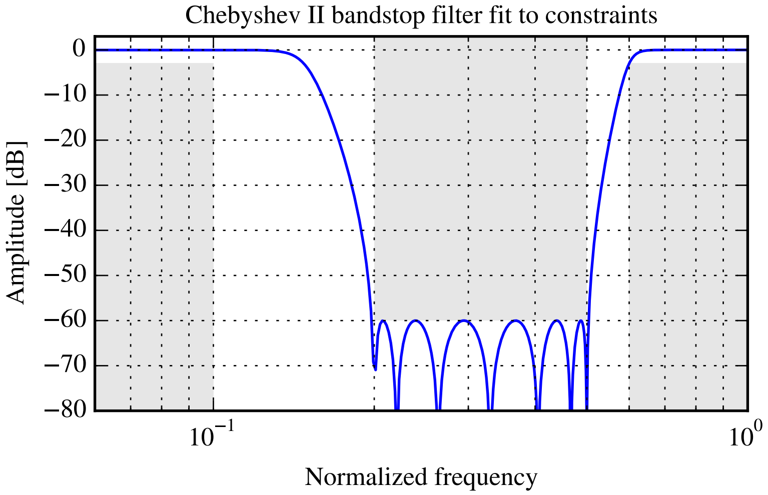
`iirfilter`	General filter design using order and critical frequencies
`iirdesign`	General filter design using passband and stopband spec

Examples

Design a digital bandstop filter which rejects -60 dB from 0.2*(fs/2) to 0.5*(fs/2), while staying within 3 dB below 0.1*(fs/2) or above 0.6*(fs/2). Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.cheb2ord([0.1, 0.6], [0.2, 0.5], 3, 60)
>>> b, a = signal.cheby2(N, 60, Wn, 'stop')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev II bandstop filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.01, .1, .1, .01], [-3,  -3, -99, -99], '0.9', lw=0) # stop
>>> plt.fill([.2,  .2, .5,  .5], [ 9, -60, -60,   9], '0.9', lw=0) # pass
>>> plt.fill([.6,  .6,  2,   2], [-99, -3,  -3, -99], '0.9', lw=0) # stop
>>> plt.axis([0.06, 1, -80, 3])
>>> plt.show()
```



`scipy.signal.`**`ellip`**(*N*, *rp*, *rs*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*)

Elliptic (Cauer) digital and analog filter design.

Design an Nth order digital or analog elliptic filter and return the filter coefficients.

Parameters

N : int

The order of the filter.

rp : float

The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.

rs : float

The minimum attenuation required in the stop band. Specified in decibels, as a positive number.

Wn : array_like

A scalar or length-2 sequence giving the critical frequencies. For elliptic filters, this is the point in the transition band at which the gain first drops below -*rp*. For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype : {'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional

The type of filter. Default is 'lowpass'.

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns

b, a : ndarray, ndarray

Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float

Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray

Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

ellipord

Notes

Also known as Cauer or Zolotarev filters, the elliptical filter maximizes the rate of transition between the frequency response's passband and stopband, at the expense of ripple in both, and increased ringing in the step response.

As *rp* approaches 0, the elliptical filter becomes a Chebyshev type II filter (cheby2). As *rs* approaches 0, it becomes a Chebyshev type I filter (cheby1). As both approach 0, it becomes a Butterworth filter (butter).

The equiripple passband has N maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or -rp dB for even-order filters.

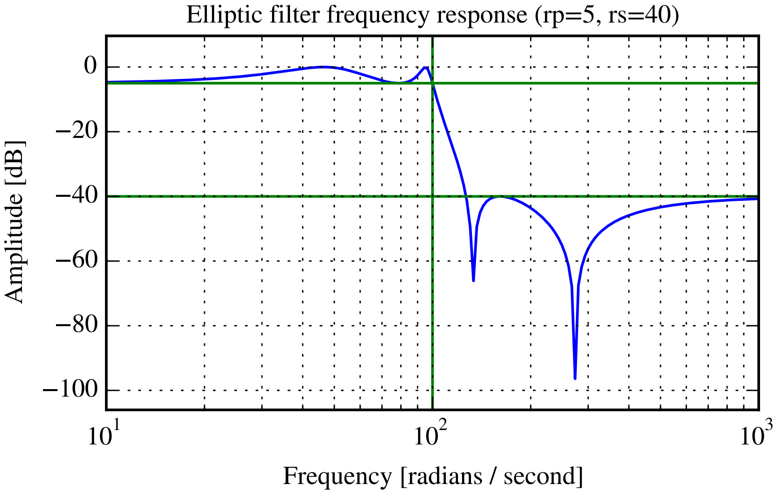
The `'sos'` output parameter was added in 0.16.0.

Examples

Plot the filter's frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.ellip(4, 5, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptic filter frequency response (rp=5, rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-40, color='green') # rs
>>> plt.axhline(-5, color='green') # rp
>>> plt.show()
```



`scipy.signal.`**`ellipord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*)
Elliptic (Cauer) filter order selection.

Return the order of the lowest order digital or analog elliptic filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters **wp, ws** : float

Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g. rad/s).

gpass : float

The maximum loss in the passband (dB).

gstop : float

The minimum attenuation in the stopband (dB).

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

Returns **ord** : int

The lowest order for an Elliptic (Cauer) filter that meets specs.

wn : ndarray or float

The Chebyshev natural frequency (the “3dB frequency”) for use with `ellip` to give filter results.

See also:

ellip	Filter design using order and critical points
buttord	Find order and critical points from passband and stopband spec

`cheb1ord`, `cheb2ord`

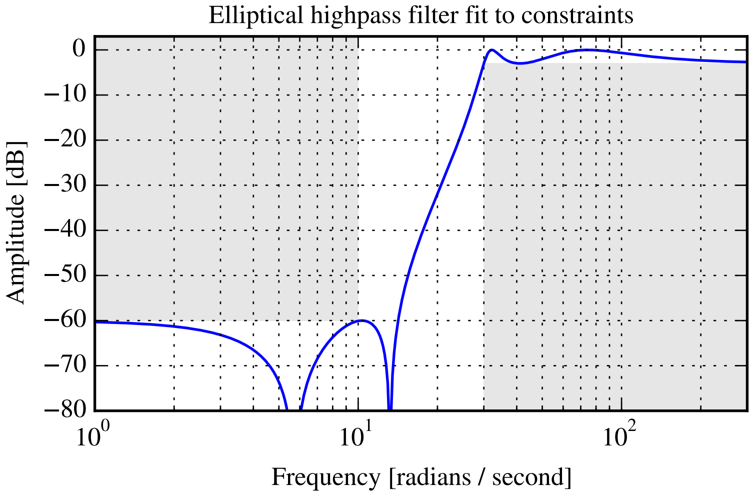
iirfilter	General filter design using order and critical frequencies
iirdesign	General filter design using passband and stopband spec

Examples

Design an analog highpass filter such that the passband is within 3 dB above 30 rad/s, while rejecting -60 dB at 10 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.ellipord(30, 10, 3, 60, True)
>>> b, a = signal.ellip(N, 3, 60, Wn, 'high', True)
>>> w, h = signal.freqs(b, a, np.logspace(0, 3, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptical highpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.1, 10,  10,  .1], [1e4, 1e4, -60, -60], '0.9', lw=0) # stop
>>> plt.fill([30, 30, 1e9, 1e9], [-99,  -3,  -3, -99], '0.9', lw=0) # pass
>>> plt.axis([1, 300, -80, 3])
>>> plt.show()
```



`scipy.signal.`**`bessel`**(*N*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*)

Bessel/Thomson digital and analog filter design.

Design an Nth order digital or analog Bessel filter and return the filter coefficients.

Parameters

N : int

The order of the filter.

Wn : array_like

A scalar or length-2 sequence giving the critical frequencies. For a Bessel filter, this is defined as the point at which the asymptotes of the response are the same as a Butterworth filter of the same order. For digital filters, *Wn* is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype : {'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional

The type of filter. Default is 'lowpass'.

analog : bool, optional

When True, return an analog filter, otherwise a digital filter is returned.

output : {'ba', 'zpk', 'sos'}, optional

Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

Returns

b, a : ndarray, ndarray

Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k : ndarray, ndarray, float

Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos : ndarray

Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

Notes

Also known as a Thomson filter, the analog Bessel filter has maximally flat group delay and maximally linear phase response, with very little ringing in the step response.

As order increases, the Bessel filter approaches a Gaussian filter.

The digital Bessel filter is generated using the bilinear transform, which does not preserve the phase response of the analog filter. As such, it is only approximately correct at frequencies below about fs/4. To get maximally flat group delay at higher frequencies, the analog Bessel filter must be transformed using phase-preserving techniques.

For a given *Wn*, the lowpass and highpass filter have the same phase vs frequency curves; they are "phase-matched".

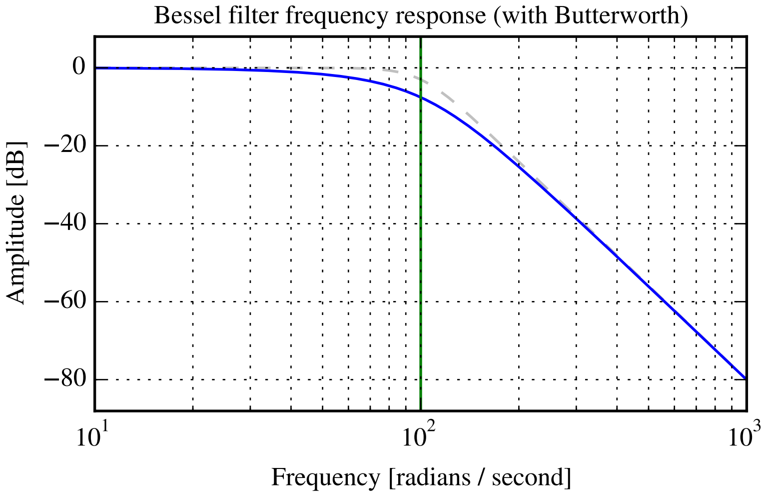
The `'sos'` output parameter was added in 0.16.0.

Examples

Plot the filter's frequency response, showing the flat group delay and the relationship to the Butterworth's cutoff frequency:

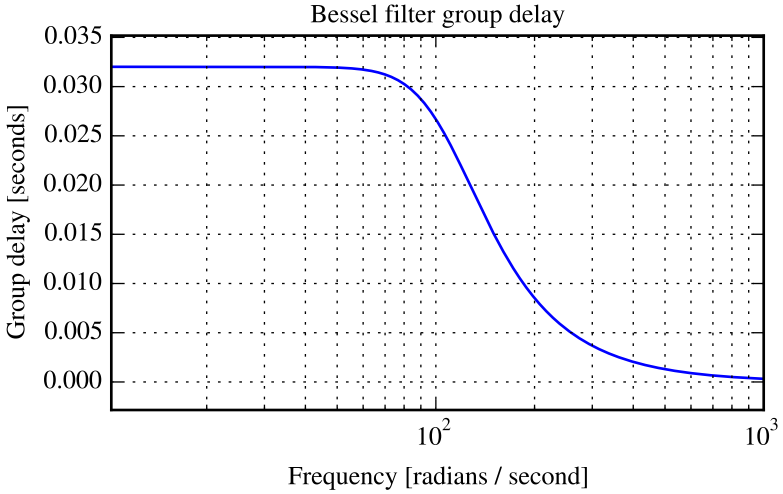
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.plot(w, 20 * np.log10(np.abs(h)), color='silver', ls='dashed')
>>> b, a = signal.bessel(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.title('Bessel filter frequency response (with Butterworth)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.show()
```



```
>>> plt.figure()
>>> plt.semilogx(w[1:], -np.diff(np.unwrap(np.angle(h)))/np.diff(w))
>>> plt.title('Bessel filter group delay')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Group delay [seconds]')
```

```
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.show()
```



5.27.6 Continuous-Time Linear Systems

`freqresp`(system[, w, n])	Calculate the frequency response of a continuous-time system.
`lti`(*system)	Linear Time Invariant system base class.
`StateSpace`(*system)	Linear Time Invariant system class in state-space form.
`TransferFunction`(*system)	Linear Time Invariant system class in transfer function form.
`ZerosPolesGain`(*system)	Linear Time Invariant system class in zeros, poles, gain form.
`lsim`(system, U, T[, X0, interp])	Simulate output of a continuous-time linear system.
`lsim2`(system[, U, T, X0])	Simulate output of a continuous-time linear system, by using the ODE solver `scipy.integra`
`impulse`(system[, X0, T, N])	Impulse response of continuous-time system.
`impulse2`(system[, X0, T, N])	Impulse response of a single-input, continuous-time linear system.
`step`(system[, X0, T, N])	Step response of continuous-time system.
`step2`(system[, X0, T, N])	Step response of continuous-time system.
`bode`(system[, w, n])	Calculate Bode magnitude and phase data of a continuous-time system.

`scipy.signal.`**`freqresp`**(*system*, *w=None*, *n=10000*)

Calculate the frequency response of a continuous-time system.

Parameters **system** : an instance of the LTI class or a tuple describing the system.

The following gives the number of elements in the tuple and the interpretation:

- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

w : array_like, optional

Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n : int, optional

Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns	**w** : 1D ndarray	Frequency array [rad/s]
	H : 1D ndarray	Array of complex magnitude values

Examples

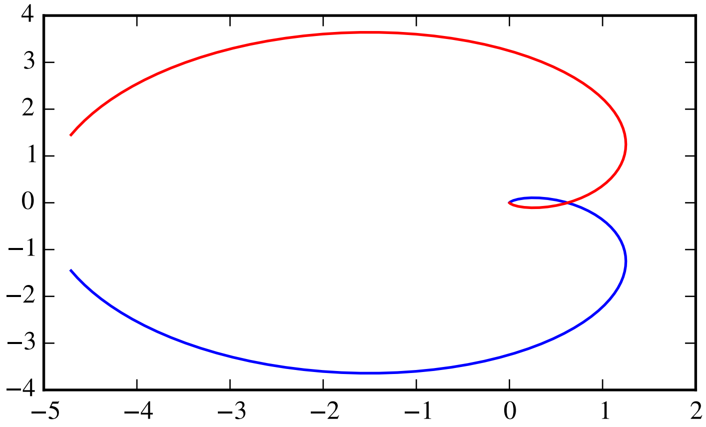
Generating the Nyquist plot of a transfer function

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([], [1, 1, 1], [5])
# transfer function: H(s) = 5 / (s-1)^3
```

```
>>> w, H = signal.freqresp(s1)
```

```
>>> plt.figure()
>>> plt.plot(H.real, H.imag, "b")
>>> plt.plot(H.real, -H.imag, "r")
>>> plt.show()
```



class `scipy.signal.`**`lti`**(**system*)

Linear Time Invariant system base class.

Parameters ***system** : arguments

The `lti` class can be instantiated with either 2, 3 or 4 arguments. The following gives the number of arguments and the corresponding subclass that is created:

- 2: `TransferFunction`: (numerator, denominator)
- 3: `ZerosPolesGain`: (zeros, poles, gain)
- 4: `StateSpace`: (A, B, C, D)

Each argument can be an array or a sequence.

Notes

`lti` instances do not exist directly. Instead, `lti` creates an instance of one of its subclasses: `StateSpace`, `TransferFunction` or `ZerosPolesGain`.

Changing the value of properties that are not directly part of the current system representation (such as the `zeros` of a `StateSpace` system) is very inefficient and may lead to numerical inaccuracies.

Attributes

`A`	A matrix of the `StateSpace` system.
`B`	B matrix of the `StateSpace` system.
`C`	C matrix of the `StateSpace` system.
`D`	D matrix of the `StateSpace` system.
`den`	Denominator of the `TransferFunction` system.
`gain`	Gain of the `ZerosPolesGain` system.
`num`	Numerator of the `TransferFunction` system.
`poles`	Poles of the `ZerosPolesGain` system.
`zeros`	Zeros of the `ZerosPolesGain` system.

`lti.`**`A`**
A matrix of the `StateSpace` system.

`lti.`**`B`**
B matrix of the `StateSpace` system.

`lti.`**`C`**
C matrix of the `StateSpace` system.

`lti.`**`D`**
D matrix of the `StateSpace` system.

`lti.`**`den`**
Denominator of the `TransferFunction` system.

`lti.`**`gain`**
Gain of the `ZerosPolesGain` system.

`lti.`**`num`**
Numerator of the `TransferFunction` system.

`lti.`**`poles`**
Poles of the `ZerosPolesGain` system.

`lti.`**`zeros`**
Zeros of the `ZerosPolesGain` system.

Methods

`bode`([w, n])	Calculate Bode magnitude and phase data of a continuous-time system.
`freqresp`([w, n])	Calculate the frequency response of a continuous-time system.
`impulse`([X0, T, N])	Return the impulse response of a continuous-time system.
`output`(U, T[, X0])	Return the response of a continuous-time system to input *U*.
`step`([X0, T, N])	Return the step response of a continuous-time system.

`lti.`**`bode`**(*w=None*, *n=100*)
Calculate Bode magnitude and phase data of a continuous-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See `scipy.signal.bode` for details.

Notes

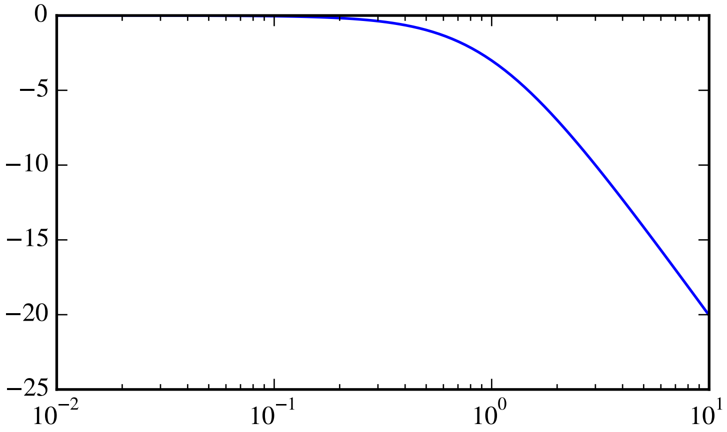
New in version 0.11.0.

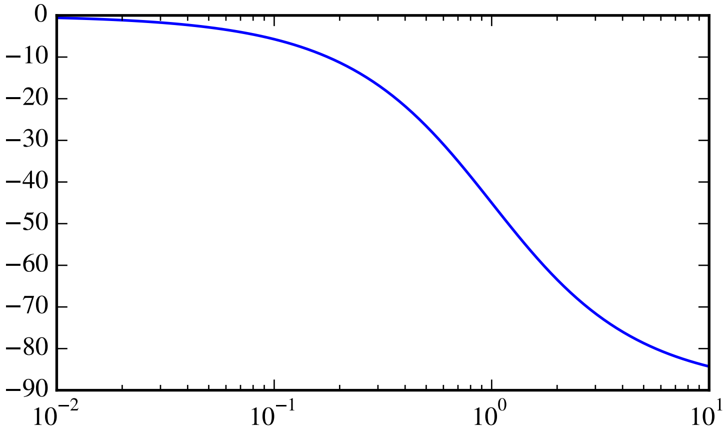
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```





`lti.`**`freqresp`**`(`*w=None*, *n=10000*`)`

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `scipy.signal.freqresp` for details.

`lti.`**`impulse`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the impulse response of a continuous-time system. See `scipy.signal.impulse` for details.

`lti.`**`output`**`(`*U*, *T*, *X0=None*`)`

Return the response of a continuous-time system to input *U*. See `scipy.signal.lsim` for details.

`lti.`**`step`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the step response of a continuous-time system. See `scipy.signal.step` for details.

class `scipy.signal.`**`StateSpace`**`(`**system*`)`

Linear Time Invariant system class in state-space form.

Represents the system as the first order differential equation $\dot{x} = Ax + Bu$.

Parameters ***system** : arguments

The `StateSpace` class can be instantiated with 1 or 4 arguments. The following gives the number of input arguments and their interpretation:

- 1: `lti` system: (`StateSpace`, `TransferFunction` or `ZerosPolesGain`)
- 4: array_like: (A, B, C, D)

Notes

Changing the value of properties that are not part of the `StateSpace` system representation (such as `zeros` or `poles`) is very inefficient and may lead to numerical inaccuracies.

Attributes

`A`
`B`
`C`
`D`

Continued on next page

Table 5.125 – continued from previous page

`den`	Denominator of the `TransferFunction` system.
`gain`	Gain of the `ZerosPolesGain` system.
`num`	Numerator of the `TransferFunction` system.
`poles`	Poles of the `ZerosPolesGain` system.
`zeros`	Zeros of the `ZerosPolesGain` system.

`StateSpace.`**`A`**

`StateSpace.`**`B`**

`StateSpace.`**`C`**

`StateSpace.`**`D`**

`StateSpace.`**`den`**
Denominator of the `TransferFunction` system.

`StateSpace.`**`gain`**
Gain of the `ZerosPolesGain` system.

`StateSpace.`**`num`**
Numerator of the `TransferFunction` system.

`StateSpace.`**`poles`**
Poles of the `ZerosPolesGain` system.

`StateSpace.`**`zeros`**
Zeros of the `ZerosPolesGain` system.

Methods

`bode`([w, n])	Calculate Bode magnitude and phase data of a continuous-time system.
`freqresp`([w, n])	Calculate the frequency response of a continuous-time system.
`impulse`([X0, T, N])	Return the impulse response of a continuous-time system.
`output`(U, T[, X0])	Return the response of a continuous-time system to input *U*.
`step`([X0, T, N])	Return the step response of a continuous-time system.
`to_ss`()	Return a copy of the current `StateSpace` system.
`to_tf`(**kwargs)	Convert system representation to `TransferFunction`.
`to_zpk`(**kwargs)	Convert system representation to `ZerosPolesGain`.

`StateSpace.`**`bode`**(*w=None*, *n=100*)
Calculate Bode magnitude and phase data of a continuous-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See `scipy.signal.bode` for details.

Notes

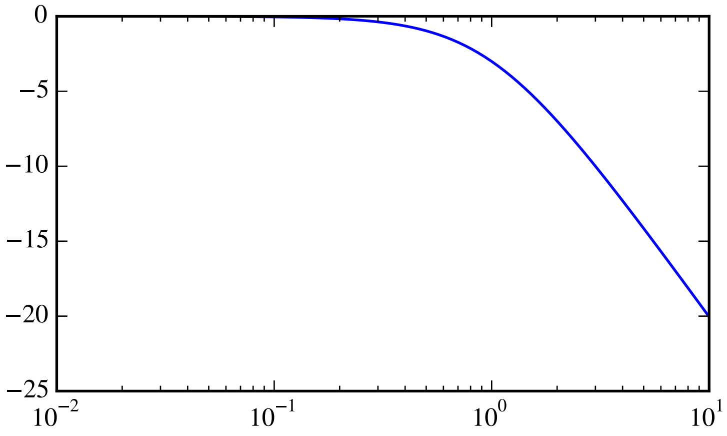
New in version 0.11.0.

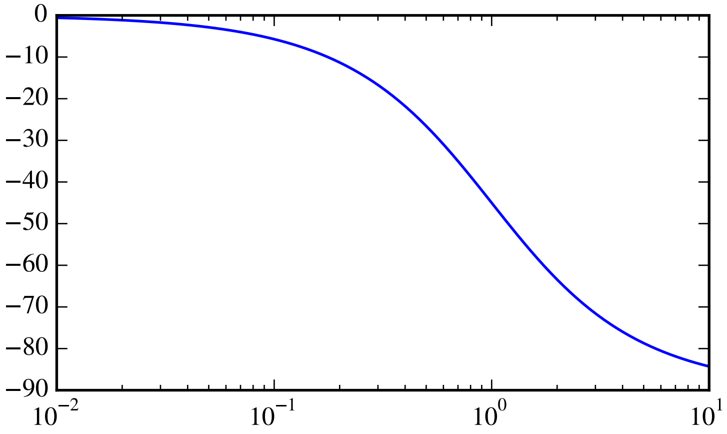
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)     # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)   # Bode phase plot
>>> plt.show()
```





`StateSpace.`**`freqresp`**`(`*w=None*, *n=10000*`)`

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `scipy.signal.freqresp` for details.

`StateSpace.`**`impulse`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the impulse response of a continuous-time system. See `scipy.signal.impulse` for details.

`StateSpace.`**`output`**`(`*U*, *T*, *X0=None*`)`

Return the response of a continuous-time system to input *U*. See `scipy.signal.lsim` for details.

`StateSpace.`**`step`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the step response of a continuous-time system. See `scipy.signal.step` for details.

`StateSpace.`**`to_ss`**`()`

Return a copy of the current `StateSpace` system.

Returns **sys** : instance of `StateSpace`

The current system (copy)

`StateSpace.`**`to_tf`**`(`***kwargs*`)`

Convert system representation to `TransferFunction`.

Parameters **kwargs** : dict, optional

Additional keywords passed to `ss2zpk`

Returns **sys** : instance of `TransferFunction`

Transfer function of the current system

`StateSpace.`**`to_zpk`**`(`***kwargs*`)`

Convert system representation to `ZerosPolesGain`.

Parameters **kwargs** : dict, optional

Additional keywords passed to `ss2zpk`

Returns **sys** : instance of `ZerosPolesGain`

Zeros, poles, gain representation of the current system

class `scipy.signal.`**`TransferFunction`**`(`**system*`)`

Linear Time Invariant system class in transfer function form.

Represents the system as the transfer function $H(s) = \sum_i b[i] s^i / \sum_j a[j] s^i$, where a are elements of the numerator `num` and b are the elements of the denominator `den`.

Parameters ***system** : arguments

The `TransferFunction` class can be instantiated with 1 or 2 arguments. The following gives the number of input arguments and their interpretation:

- 1: `lti` system: (`StateSpace`, `TransferFunction` or `ZerosPolesGain`)
- 2: array_like: (numerator, denominator)

Notes

Changing the value of properties that are not part of the `TransferFunction` system representation (such as the `A`, `B`, `C`, `D` state-space matrices) is very inefficient and may lead to numerical inaccuracies.

Attributes

`A`	A matrix of the `StateSpace` system.
`B`	B matrix of the `StateSpace` system.
`C`	C matrix of the `StateSpace` system.
`D`	D matrix of the `StateSpace` system.
`den`	
`gain`	Gain of the `ZerosPolesGain` system.
`num`	

Continued on next page

Table 5.127 – continued from previous page

`poles`	Poles of the `ZerosPolesGain` system.
`zeros`	Zeros of the `ZerosPolesGain` system.

`TransferFunction.`**`A`**
A matrix of the `StateSpace` system.

`TransferFunction.`**`B`**
B matrix of the `StateSpace` system.

`TransferFunction.`**`C`**
C matrix of the `StateSpace` system.

`TransferFunction.`**`D`**
D matrix of the `StateSpace` system.

`TransferFunction.`**`den`**

`TransferFunction.`**`gain`**
Gain of the `ZerosPolesGain` system.

`TransferFunction.`**`num`**

`TransferFunction.`**`poles`**
Poles of the `ZerosPolesGain` system.

`TransferFunction.`**`zeros`**
Zeros of the `ZerosPolesGain` system.

Methods

`bode`([w, n])	Calculate Bode magnitude and phase data of a continuous-time system.
`freqresp`([w, n])	Calculate the frequency response of a continuous-time system.
`impulse`([X0, T, N])	Return the impulse response of a continuous-time system.
`output`(U, T[, X0])	Return the response of a continuous-time system to input *U*.
`step`([X0, T, N])	Return the step response of a continuous-time system.
`to_ss`()	Convert system representation to `StateSpace`.
`to_tf`()	Return a copy of the current `TransferFunction` system.
`to_zpk`()	Convert system representation to `ZerosPolesGain`.

`TransferFunction.`**`bode`**(*w=None*, *n=100*)
Calculate Bode magnitude and phase data of a continuous-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See `scipy.signal.bode` for details.

Notes

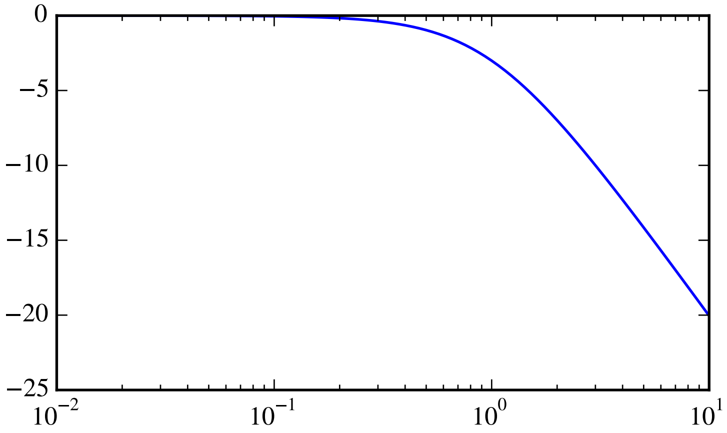
New in version 0.11.0.

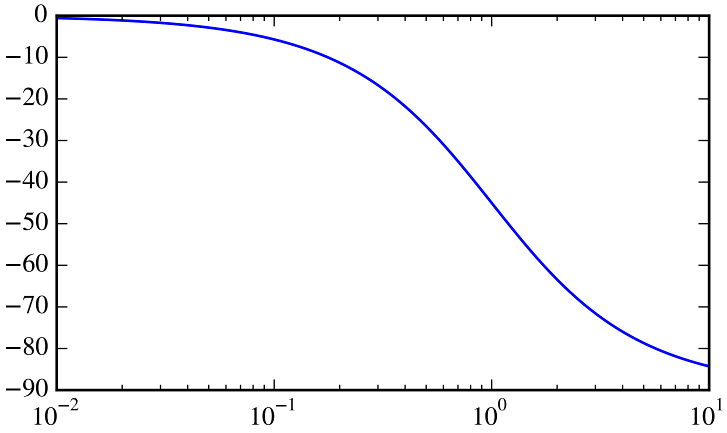
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```





`TransferFunction.`**`freqresp`**(*w=None*, *n=10000*)

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `scipy.signal.freqresp` for details.

`TransferFunction.`**`impulse`**(*X0=None*, *T=None*, *N=None*)

Return the impulse response of a continuous-time system. See `scipy.signal.impulse` for details.

`TransferFunction.`**`output`**`(`*U*, *T*, *X0=None*`)`
Return the response of a continuous-time system to input *U*. See `scipy.signal.lsim` for details.

`TransferFunction.`**`step`**`(`*X0=None*, *T=None*, *N=None*`)`
Return the step response of a continuous-time system. See `scipy.signal.step` for details.

`TransferFunction.`**`to_ss`**`()`
Convert system representation to `StateSpace`.

Returns **sys** : instance of `StateSpace`
State space model of the current system

`TransferFunction.`**`to_tf`**`()`
Return a copy of the current `TransferFunction` system.

Returns **sys** : instance of `TransferFunction`
The current system (copy)

`TransferFunction.`**`to_zpk`**`()`
Convert system representation to `ZerosPolesGain`.

Returns **sys** : instance of `ZerosPolesGain`
Zeros, poles, gain representation of the current system

class `scipy.signal.`**`ZerosPolesGain`**`(`**system*`)`
Linear Time Invariant system class in zeros, poles, gain form.

Represents the system as the transfer function $H(s) = k \prod_i (s - z[i]) / \prod_j (s - p[j])$, where k is the `gain`, z are the `zeros` and p are the `poles`.

Parameters ***system** : arguments
The `ZerosPolesGain` class can be instantiated with 1 or 3 arguments. The following gives the number of input arguments and their interpretation:

- 1: `lti` system: (`StateSpace`, `TransferFunction` or `ZerosPolesGain`)
- 3: array_like: (zeros, poles, gain)

Notes

Changing the value of properties that are not part of the `ZerosPolesGain` system representation (such as the `A`, `B`, `C`, `D` state-space matrices) is very inefficient and may lead to numerical inaccuracies.

Attributes

`A`	A matrix of the `StateSpace` system.
`B`	B matrix of the `StateSpace` system.
`C`	C matrix of the `StateSpace` system.
`D`	D matrix of the `StateSpace` system.
`den`	Denominator of the `TransferFunction` system.
`gain`	
`num`	Numerator of the `TransferFunction` system.
`poles`	
`zeros`	

`ZerosPolesGain.`**`A`**
A matrix of the `StateSpace` system.

`ZerosPolesGain.`**`B`**
B matrix of the `StateSpace` system.

`ZerosPolesGain.`**`C`**

C matrix of the `StateSpace` system.

`ZerosPolesGain.`**`D`**

D matrix of the `StateSpace` system.

`ZerosPolesGain.`**`den`**

Denominator of the `TransferFunction` system.

`ZerosPolesGain.`**`gain`**

`ZerosPolesGain.`**`num`**

Numerator of the `TransferFunction` system.

`ZerosPolesGain.`**`poles`**

`ZerosPolesGain.`**`zeros`**

Methods

`bode`([w, n])	Calculate Bode magnitude and phase data of a continuous-time system.
`freqresp`([w, n])	Calculate the frequency response of a continuous-time system.
`impulse`([X0, T, N])	Return the impulse response of a continuous-time system.
`output`(U, T[, X0])	Return the response of a continuous-time system to input *U*.
`step`([X0, T, N])	Return the step response of a continuous-time system.
`to_ss`()	Convert system representation to `StateSpace`.
`to_tf`()	Convert system representation to `TransferFunction`.
`to_zpk`()	Return a copy of the current ‘ZerosPolesGain’ system.

`ZerosPolesGain.`**`bode`**`(`*w=None*, *n=100*`)`

Calculate Bode magnitude and phase data of a continuous-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See `scipy.signal.bode` for details.

Notes

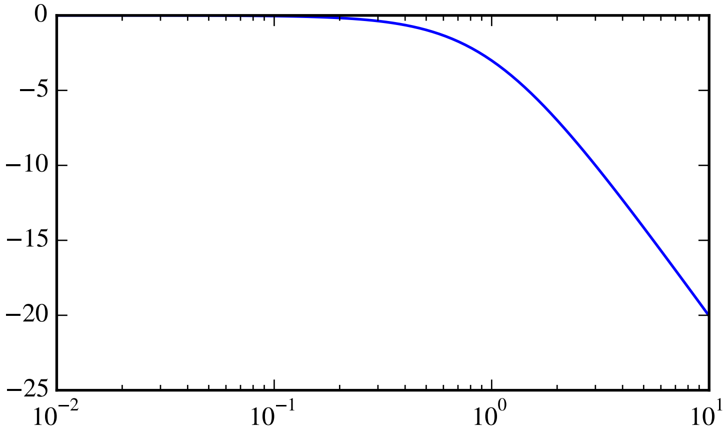
New in version 0.11.0.

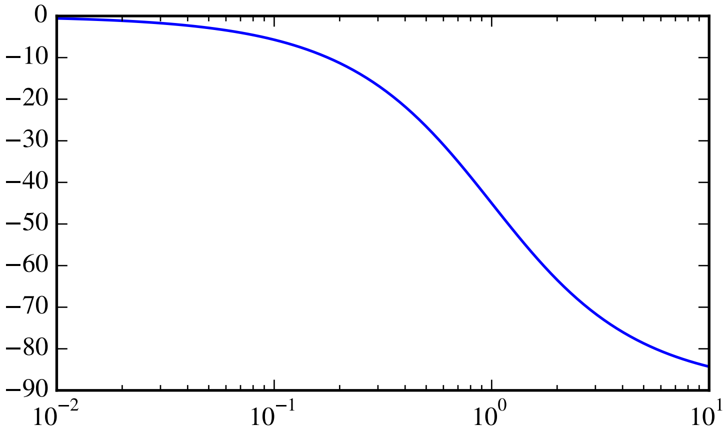
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)     # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)   # Bode phase plot
>>> plt.show()
```





`ZerosPolesGain.`**`freqresp`**`(`*w=None*, *n=10000*`)`

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `scipy.signal.freqresp` for details.

`ZerosPolesGain.`**`impulse`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the impulse response of a continuous-time system. See `scipy.signal.impulse` for details.

`ZerosPolesGain.`**`output`**`(`*U*, *T*, *X0=None*`)`

Return the response of a continuous-time system to input *U*. See `scipy.signal.lsim` for details.

`ZerosPolesGain.`**`step`**`(`*X0=None*, *T=None*, *N=None*`)`

Return the step response of a continuous-time system. See `scipy.signal.step` for details.

`ZerosPolesGain.`**`to_ss`**`()`

Convert system representation to `StateSpace`.

Returns **sys** : instance of `StateSpace`

State space model of the current system

`ZerosPolesGain.`**`to_tf`**`()`

Convert system representation to `TransferFunction`.

Returns **sys** : instance of `TransferFunction`

Transfer function of the current system

`ZerosPolesGain.`**`to_zpk`**`()`

Return a copy of the current 'ZerosPolesGain' system.

Returns **sys** : instance of `ZerosPolesGain`

The current system (copy)

`scipy.signal.`**`lsim`**`(`*system*, *U*, *T*, *X0=None*, *interp=True*`)`

Simulate output of a continuous-time linear system.

Parameters **system** : an instance of the LTI class or a tuple describing the system.

The following gives the number of elements in the tuple and the interpretation:

- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

U : array_like

An input array describing the input at each time *T* (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input. If U = 0 or None, a zero input is used.

T : array_like

The time steps at which the input is defined and at which the output is desired. Must be nonnegative, increasing, and equally spaced.

X0 : array_like, optional

The initial conditions on the state vector (zero by default).

interp : bool, optional

Whether to use linear (True, the default) or zero-order-hold (False) interpolation for the input array.

Returns **T** : 1D ndarray

Time values for the output.

yout : 1D ndarray

System response.

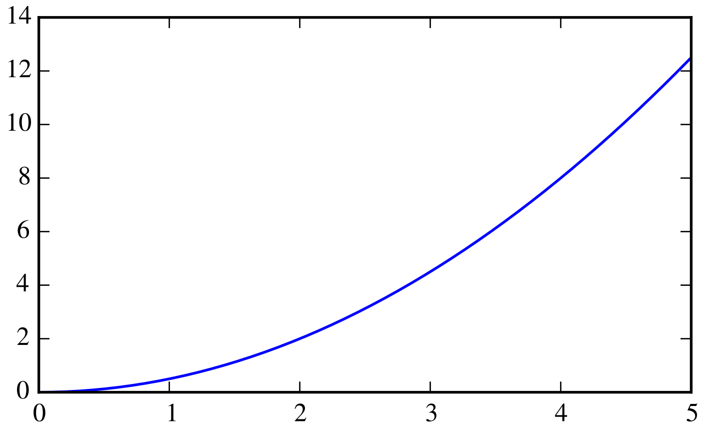
xout : ndarray

Time evolution of the state vector.

Examples

Simulate a double integrator y" = u, with a constant input u = 1

```
>>> from scipy import signal
>>> system = signal.lti([[0., 1.], [0., 0.]], [[0.], [1.]], [[1., 0.]], 0.)
>>> t = np.linspace(0, 5)
>>> u = np.ones_like(t)
>>> tout, y, x = signal.lsim(system, u, t)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, y)
```



`scipy.signal.`**`lsim2`**`(`*system*, *U=None*, *T=None*, *X0=None*, ***kwargs*`)`

Simulate output of a continuous-time linear system, by using the ODE solver `scipy.integrate.odeint`.

Parameters

system : an instance of the LTI class or a tuple describing the system.

The following gives the number of elements in the tuple and the interpretation:

- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

U : array_like (1D or 2D), optional

An input array describing the input at each time T. Linear interpolation is used between given times. If there are multiple inputs, then each column of the rank-2 array represents an input. If U is not given, the input is assumed to be zero.

T : array_like (1D or 2D), optional

The time steps at which the input is defined and at which the output is desired. The default is 101 evenly spaced points on the interval [0,10.0].

X0 : array_like (1D), optional

The initial condition of the state vector. If *X0* is not given, the initial conditions are assumed to be 0.

kwargs : dict

Additional keyword arguments are passed on to the function *odeint*. See the notes below for more details.

Returns

T : 1D ndarray

The time values for the output.

yout : ndarray

The response of the system.

xout : ndarray

The time-evolution of the state-vector.

Notes

This function uses `scipy.integrate.odeint` to solve the system's differential equations. Additional keyword arguments given to `lsim2` are passed on to *odeint*. See the documentation for `scipy.integrate.odeint` for the full list of arguments.

`scipy.signal.`**`impulse`**`(`*system*, *X0=None*, *T=None*, *N=None*`)`

Impulse response of continuous-time system.

Parameters

system : an instance of the LTI class or a tuple of array_like
: describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 2 (num, den)
  - 3 (zeros, poles, gain)
  - 4 (A, B, C, D)

X0 : array_like, optional
: Initial state-vector. Defaults to zero.

T : array_like, optional
: Time points. Computed if not given.

N : int, optional
: The number of time points to compute (if *T* is not given).

Returns

T : ndarray
: A 1-D array of time points.

yout : ndarray
: A 1-D array containing the impulse response of the system (except for singularities at zero).

`scipy.signal.`**`impulse2`**(*system*, *X0=None*, *T=None*, *N=None*, ***kwargs*)

Impulse response of a single-input, continuous-time linear system.

Parameters

system : an instance of the LTI class or a tuple of array_like
: describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 2 (num, den)
  - 3 (zeros, poles, gain)
  - 4 (A, B, C, D)

X0 : 1-D array_like, optional
: The initial condition of the state vector. Default: 0 (the zero vector).

T : 1-D array_like, optional
: The time steps at which the input is defined and at which the output is desired. If *T* is not given, the function will generate a set of time samples automatically.

N : int, optional
: Number of time points to compute. Default: 100.

kwargs : various types
: Additional keyword arguments are passed on to the function `scipy.signal.lsim2`, which in turn passes them on to `scipy.integrate.odeint`; see the latter's documentation for information about these arguments.

Returns

T : ndarray
: The time values for the output.

yout : ndarray
: The output response of the system.

See also:

`impulse`, `lsim2`, `integrate.odeint`

Notes

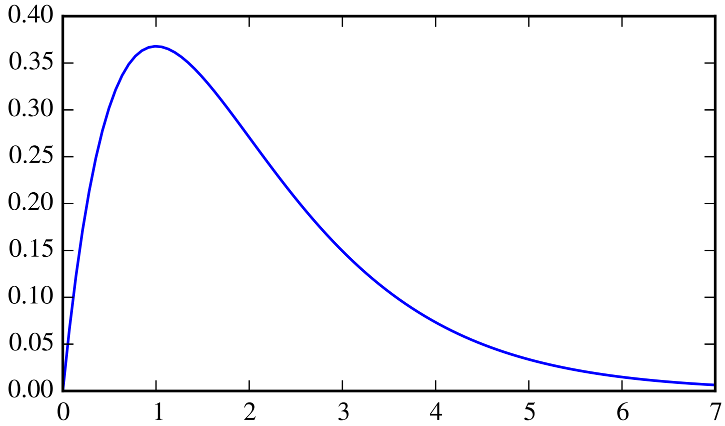
The solution is generated by calling `scipy.signal.lsim2`, which uses the differential equation solver `scipy.integrate.odeint`.

New in version 0.8.0.

Examples

Second order system with a repeated root: x''(t) + 2*x(t) + x(t) = u(t)

```
>>> from scipy import signal
>>> system = ([1.0], [1.0, 2.0, 1.0])
>>> t, y = signal.impulse2(system)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, y)
```



`scipy.signal.`**`step`**(*system*, *X0=None*, *T=None*, *N=None*)

Step response of continuous-time system.

Parameters

system : an instance of the LTI class or a tuple of array_like

describing the system. The following gives the number of elements in the tuple and the interpretation:

- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

X0 : array_like, optional

Initial state-vector (default is zero).

T : array_like, optional

Time points (computed if not given).

N : int, optional

Number of time points to compute if *T* is not given.

Returns

T : 1D ndarray

Output time points.

yout : 1D ndarray

Step response of system.

See also:

`scipy.signal.step2`

`scipy.signal.`**`step2`**(*system*, *X0=None*, *T=None*, *N=None*, ***kwargs*)

Step response of continuous-time system.

This function is functionally the same as `scipy.signal.step`, but it uses the function `scipy.signal.lsim2` to compute the step response.

Parameters

system : an instance of the LTI class or a tuple of array_like

describing the system. The following gives the number of elements in the tuple and the interpretation:

- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

X0 : array_like, optional
Initial state-vector (default is zero).

T : array_like, optional
Time points (computed if not given).

N : int, optional
Number of time points to compute if *T* is not given.

kwargs : various types
Additional keyword arguments are passed on the function `scipy.signal.lsim2`, which in turn passes them on to `scipy.integrate.odeint`. See the documentation for `scipy.integrate.odeint` for information about these arguments.

Returns

T : 1D ndarray
Output time points.

yout : 1D ndarray
Step response of system.

See also:

`scipy.signal.step`

Notes

New in version 0.8.0.

`scipy.signal.`**`bode`**(*system*, *w=None*, *n=100*)

Calculate Bode magnitude and phase data of a continuous-time system.

Parameters

system : an instance of the LTI class or a tuple describing the system.
The following gives the number of elements in the tuple and the interpretation:

- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

w : array_like, optional
Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n : int, optional
Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

w : 1D ndarray
Frequency array [rad/s]

mag : 1D ndarray
Magnitude array [dB]

phase : 1D ndarray
Phase array [deg]

Notes

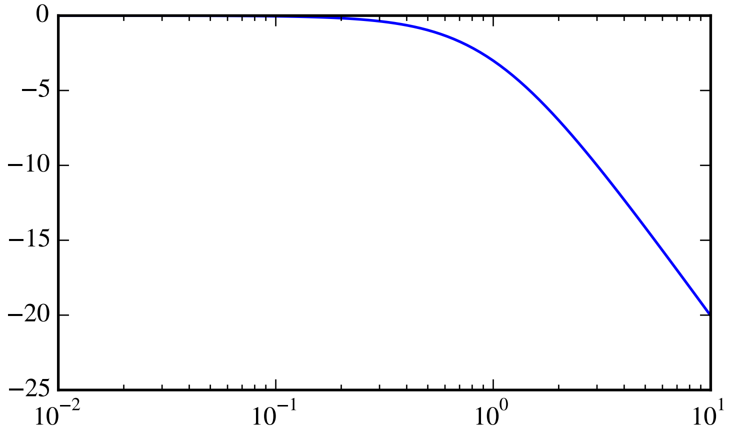
New in version 0.11.0.

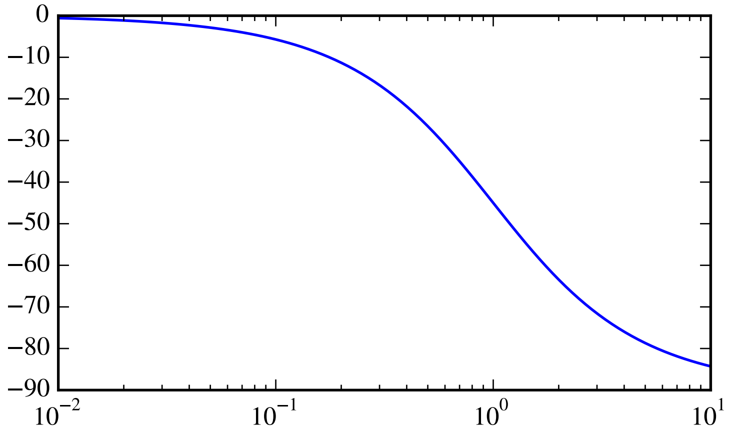
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = signal.bode(s1)
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```





5.27.7 Discrete-Time Linear Systems

`dlsim`(system, u[, t, x0])	Simulate output of a discrete-time linear system.
`dimpulse`(system[, x0, t, n])	Impulse response of discrete-time system.

Continued on next page

Table 5.131 – continued from previous page

dstep(system[, x0, t, n])	Step response of discrete-time system.

scipy.signal.**dlsim**(*system*, *u*, *t=None*, *x0=None*)

Simulate output of a discrete-time linear system.

Parameters **system** : tuple of array_like

A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:

- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

u : array_like

An input array describing the input at each time *t* (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input.

t : array_like, optional

The time steps at which the input is defined. If *t* is given, it must be the same length as *u*, and the final value in *t* determines the number of steps returned in the output.

x0 : array_like, optional

The initial conditions on the state vector (zero by default).

Returns **tout** : ndarray

Time values for the output, as a 1-D array.

yout : ndarray

System response, as a 1-D array.

xout : ndarray, optional

Time-evolution of the state-vector. Only generated if the input is a state-space systems.

See also:

lsim, dstep, dimpulse, cont2discrete

Examples

A simple integrator transfer function with a discrete time step of 1.0 could be implemented as:

```
>>> from scipy import signal
>>> tf = ([1.0,], [1.0, -1.0], 1.0)
>>> t_in = [0.0, 1.0, 2.0, 3.0]
>>> u = np.asarray([0.0, 0.0, 1.0, 1.0])
>>> t_out, y = signal.dlsim(tf, u, t=t_in)
>>> y
array([ 0.,  0.,  0.,  1.])
```

scipy.signal.**dimpulse**(*system*, *x0=None*, *t=None*, *n=None*)

Impulse response of discrete-time system.

Parameters **system** : tuple of array_like

A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:

- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

x0 : array_like, optional

Initial state-vector. Defaults to zero.

t : array_like, optional

Time points. Computed if not given.

n : int, optional

The number of time points to compute (if *t* is not given).

Returns **tout** : ndarray

Time values for the output, as a 1-D array.

yout : ndarray

Impulse response of system. Each element of the tuple represents the output of the system based on an impulse in each input.

See also:

`impulse`, `dstep`, `dlsim`, `cont2discrete`

`scipy.signal.`**`dstep`**(*system*, *x0=None*, *t=None*, *n=None*)

Step response of discrete-time system.

Parameters **system** : tuple of array_like

A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:

- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

x0 : array_like, optional

Initial state-vector. Defaults to zero.

t : array_like, optional

Time points. Computed if not given.

n : int, optional

The number of time points to compute (if *t* is not given).

Returns **tout** : ndarray

Output time points, as a 1-D array.

yout : ndarray

Step response of system. Each element of the tuple represents the output of the system based on a step response to each input.

See also:

`step`, `dimpulse`, `dlsim`, `cont2discrete`

5.27.8 LTI Representations

`tf2zpk`(b, a)	Return zero, pole, gain (z, p, k) representation from a numerator, denominato
`tf2sos`(b, a[, pairing])	Return second-order sections from transfer function representation
`tf2ss`(num, den)	Transfer function to state-space representation.
`zpk2tf`(z, p, k)	Return polynomial transfer function representation from zeros and poles
`zpk2sos`(z, p, k[, pairing])	Return second-order sections from zeros, poles, and gain of a system
`zpk2ss`(z, p, k)	Zero-pole-gain representation to state-space representation
`ss2tf`(A, B, C, D[, input])	State-space to transfer function.
`ss2zpk`(A, B, C, D[, input])	State-space representation to zero-pole-gain representation.
`sos2zpk`(sos)	Return zeros, poles, and gain of a series of second-order sections
`sos2tf`(sos)	Return a single transfer function from a series of second-order sections
`cont2discrete`(sys, dt[, method, alpha])	Transform a continuous to a discrete state-space system.
`place_poles`(A, B, poles[, method, rtol, maxiter])	Compute K such that eigenvalues (A - dot(B, K))=poles.

`scipy.signal.`**`tf2zpk`**(*b*, *a*)

Return zero, pole, gain (z, p, k) representation from a numerator, denominator representation of a linear filter.

Parameters **b** : array_like

Numerator polynomial coefficients.

a : array_like

Denominator polynomial coefficients.

Returns **z** : ndarray

Zeros of the transfer function.

p : ndarray

Poles of the transfer function.

k : float

System gain.

Notes

If some values of *b* are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

The *b* and *a* arrays are interpreted as coefficients for positive, descending powers of the transfer function variable. So the inputs $b = [b_0, b_1, ..., b_M]$ and $a = [a_0, a_1, ..., a_N]$ can represent an analog filter of the form:

$$H(s) = \frac{b_0 s^M + b_1 s^{(M-1)} + \cdots + b_M}{a_0 s^N + a_1 s^{(N-1)} + \cdots + a_N}$$

or a discrete-time filter of the form:

$$H(z) = \frac{b_0 z^M + b_1 z^{(M-1)} + \cdots + b_M}{a_0 z^N + a_1 z^{(N-1)} + \cdots + a_N}$$

This "positive powers" form is found more commonly in controls engineering. If *M* and *N* are equal (which is true for all filters generated by the bilinear transform), then this happens to be equivalent to the "negative powers" discrete-time form preferred in DSP:

$$H(z) = \frac{b_0 + b_1 z^{-1} + \cdots + b_M z^{-M}}{a_0 + a_1 z^{-1} + \cdots + a_N z^{-N}}$$

Although this is true for common filters, remember that this is not true in the general case. If *M* and *N* are not equal, the discrete-time transfer function coefficients must first be converted to the "positive powers" form before finding the poles and zeros.

`scipy.signal.`**`tf2sos`**(*b*, *a*, *pairing='nearest'*)

Return second-order sections from transfer function representation

Parameters **b** : array_like

Numerator polynomial coefficients.

a : array_like

Denominator polynomial coefficients.

pairing : {'nearest', 'keep_odd'}, optional

The method to use to combine pairs of poles and zeros into sections. See `zpk2sos`.

Returns **sos** : ndarray

Array of second-order filter coefficients, with shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

See also:

`zpk2sos`, `sosfilt`

Notes

It is generally discouraged to convert from TF to SOS format, since doing so usually will not improve numerical precision errors. Instead, consider designing filters in ZPK format and converting directly to SOS. TF is converted to SOS by first converting to ZPK format, then converting ZPK to SOS.

New in version 0.16.0.

`scipy.signal.`**`tf2ss`**`(`*num*, *den*`)`

Transfer function to state-space representation.

Parameters	**num, den** : array_like	
		Sequences representing the numerator and denominator polynomials. The denominator needs to be at least as long as the numerator.
Returns	**A, B, C, D** : ndarray	
		State space representation of the system, in controller canonical form.

`scipy.signal.`**`zpk2tf`**`(`*z*, *p*, *k*`)`

Return polynomial transfer function representation from zeros and poles

Parameters	**z** : array_like	
		Zeros of the transfer function.
	p : array_like	
		Poles of the transfer function.
	k : float	
		System gain.
Returns	**b** : ndarray	
		Numerator polynomial coefficients.
	a : ndarray	
		Denominator polynomial coefficients.

`scipy.signal.`**`zpk2sos`**`(`*z*, *p*, *k*, *pairing='nearest'*`)`

Return second-order sections from zeros, poles, and gain of a system

Parameters	**z** : array_like	
		Zeros of the transfer function.
	p : array_like	
		Poles of the transfer function.
	k : float	
		System gain.
	pairing : {'nearest', 'keep_odd'}, optional	
		The method to use to combine pairs of poles and zeros into sections. See Notes below.
Returns	**sos** : ndarray	
		Array of second-order filter coefficients, with shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

See also:

`sosfilt`

Notes

The algorithm used to convert ZPK to SOS format is designed to minimize errors due to numerical precision issues. The pairing algorithm attempts to minimize the peak gain of each biquadratic section. This is done by pairing poles with the nearest zeros, starting with the poles closest to the unit circle.

Algorithms

The current algorithms are designed specifically for use with digital filters. Although they can operate on analog filters, the results may be sub-optimal.

The steps in the `pairing='nearest'` and `pairing='keep_odd'` algorithms are mostly shared. The `nearest` algorithm attempts to minimize the peak gain, while `'keep_odd'` minimizes peak gain under the constraint that odd-order systems should retain one section as first order. The algorithm steps and are as follows:

As a pre-processing step, add poles or zeros to the origin as necessary to obtain the same number of poles and zeros for pairing. If `pairing == 'nearest'` and there are an odd number of poles, add an additional pole and a zero at the origin.

The following steps are then iterated over until no more poles or zeros remain:

1. Take the (next remaining) pole (complex or real) closest to the unit circle to begin a new filter section.
2. If the pole is real and there are no other remaining real poles [4], add the closest real zero to the section and leave it as a first order section. Note that after this step we are guaranteed to be left with an even number of real poles, complex poles, real zeros, and complex zeros for subsequent pairing iterations.
3. Else:
    (a) If the pole is complex and the zero is the only remaining real zero*, then pair the pole with the *next* closest zero (guaranteed to be complex). This is necessary to ensure that there will be a real zero remaining to eventually create a first-order section (thus keeping the odd order).
    (b) Else pair the pole with the closest remaining zero (complex or real).
    (c) Proceed to complete the second-order section by adding another pole and zero to the current pole and zero in the section:
        i. If the current pole and zero are both complex, add their conjugates.
        ii. Else if the pole is complex and the zero is real, add the conjugate pole and the next closest real zero.
        iii. Else if the pole is real and the zero is complex, add the conjugate zero and the real pole closest to those zeros.
        iv. Else (we must have a real pole and real zero) add the next real pole closest to the unit circle, and then add the real zero closest to that pole.

New in version 0.16.0.

Examples

Design a 6th order low-pass elliptic digital filter for a system with a sampling rate of 8000 Hz that has a pass-band corner frequency of 1000 Hz. The ripple in the pass-band should not exceed 0.087 dB, and the attenuation in the stop-band should be at least 90 dB.

In the following call to *signal.ellip*, we could use `output='sos'`, but for this example, we'll use `output='zpk'`, and then convert to SOS format with `zpk2sos`:

```
>>> from scipy import signal
>>> z, p, k = signal.ellip(6, 0.087, 90, 1000/(0.5*8000), output='zpk')
```

Now convert to SOS format.

```
>>> sos = signal.zpk2sos(z, p, k)
```

The coefficents of the numerators of the sections:

```
>>> sos[:, :3]
array([[ 0.0014154 ,  0.00248707,  0.0014154 ],
       [ 1.        ,  0.72965193,  1.        ],
       [ 1.        ,  0.17594966,  1.        ]])
```

The symmetry in the coefficients occurs because all the zeros are on the unit circle.

The coefficients of the denominators of the sections:

```
>>> sos[:, 3:]
array([[ 1.        , -1.32543251,  0.46989499],
       [ 1.        , -1.26117915,  0.6262586 ],
       [ 1.        , -1.25707217,  0.86199667]])
```

---

[4] This conditional can only be met for specific odd-order inputs with the `pairing == 'keep_odd'` method.

The next example shows the effect of the *pairing* option. We have a system with three poles and three zeros, so the SOS array will have shape (2, 6). The means there is, in effect, an extra pole and an extra zero at the origin in the SOS representation.

```
>>> z1 = np.array([-1, -0.5-0.5j, -0.5+0.5j])
>>> p1 = np.array([0.75, 0.8+0.1j, 0.8-0.1j])
```

With `pairing='nearest'` (the default), we obtain

```
>>> signal.zpk2sos(z1, p1, 1)
array([[ 1.  ,  1.  ,  0.5 ,  1.  , -0.75,  0.  ],
       [ 1.  ,  1.  ,  0.  ,  1.  , -1.6 ,  0.65]])
```

The first section has the zeros {-0.5-0.05j, -0.5+0.5j} and the poles {0, 0.75}, and the second section has the zeros {-1, 0} and poles {0.8+0.1j, 0.8-0.1j}. Note that the extra pole and zero at the origin have been assigned to different sections.

With `pairing='keep_odd'`, we obtain:

```
>>> signal.zpk2sos(z1, p1, 1, pairing='keep_odd')
array([[ 1.  ,  1.  ,  0.  ,  1.  , -0.75,  0.  ],
       [ 1.  ,  1.  ,  0.5 ,  1.  , -1.6 ,  0.65]])
```

The extra pole and zero at the origin are in the same section. The first section is, in effect, a first-order section.

`scipy.signal.`**`zpk2ss`**(*z*, *p*, *k*)

Zero-pole-gain representation to state-space representation

Parameters **z, p** : sequence

Zeros and poles.

k : float

System gain.

Returns **A, B, C, D** : ndarray

State space representation of the system, in controller canonical form.

`scipy.signal.`**`ss2tf`**(*A*, *B*, *C*, *D*, *input=0*)

State-space to transfer function.

Parameters **A, B, C, D** : ndarray

State-space representation of linear system.

input : int, optional

For multiple-input systems, the input to use.

Returns **num** : 2-D ndarray

Numerator(s) of the resulting transfer function(s). *num* has one row for each of the system's outputs. Each row is a sequence representation of the numerator polynomial.

den : 1-D ndarray

Denominator of the resulting transfer function(s). *den* is a sequence representation of the denominator polynomial.

`scipy.signal.`**`ss2zpk`**(*A*, *B*, *C*, *D*, *input=0*)

State-space representation to zero-pole-gain representation.

Parameters **A, B, C, D** : ndarray

State-space representation of linear system.

input : int, optional

For multiple-input systems, the input to use.

Returns **z, p** : sequence

Zeros and poles.

k : float

System gain.

`scipy.signal.`**`sos2zpk`**(*sos*)

Return zeros, poles, and gain of a series of second-order sections

Parameters **sos** : array_like

Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

Returns **z** : ndarray

Zeros of the transfer function.

p : ndarray

Poles of the transfer function.

k : float

System gain.

Notes

New in version 0.16.0.

`scipy.signal.`**`sos2tf`**(*sos*)

Return a single transfer function from a series of second-order sections

Parameters **sos** : array_like

Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

Returns **b** : ndarray

Numerator polynomial coefficients.

a : ndarray

Denominator polynomial coefficients.

Notes

New in version 0.16.0.

`scipy.signal.`**`cont2discrete`**(*sys*, *dt*, *method='zoh'*, *alpha=None*)

Transform a continuous to a discrete state-space system.

Parameters **sys** : a tuple describing the system.

The following gives the number of elements in the tuple and the interpretation:

- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

dt : float

The discretization time step.

method : {“gbt”, “bilinear”, “euler”, “backward_diff”, “zoh”}, optional

Which method to use:

- gbt: generalized bilinear transformation
- bilinear: Tustin’s approximation (“gbt” with alpha=0.5)
- euler: Euler (or forward differencing) method (“gbt” with alpha=0)
- backward_diff: Backwards differencing (“gbt” with alpha=1.0)
- zoh: zero-order hold (default)

alpha : float within [0, 1], optional

The generalized bilinear transformation weighting parameter, which should only be specified with method=”gbt”, and is ignored otherwise

Returns **sysd** : tuple containing the discrete system

Based on the input type, the output will be of the form

- (num, den, dt) for transfer function input
- (zeros, poles, gain, dt) for zeros-poles-gain input
- (A, B, C, D, dt) for state-space system input

Notes

By default, the routine uses a Zero-Order Hold (zoh) method to perform the transformation. Alternatively, a generalized bilinear transformation may be used, which includes the common Tustin's bilinear approximation, an Euler's method technique, or a backwards differencing technique.

The Zero-Order Hold (zoh) method is based on [R168], the generalized bilinear approximation is based on [R169] and [R170].

References

[R168], [R169], [R170]

`scipy.signal.`**`place_poles`**(*A*, *B*, *poles*, *method='YT'*, *rtol=0.001*, *maxiter=30*)

Compute K such that eigenvalues (A - dot(B, K))=poles.

K is the gain matrix such as the plant described by the linear system `AX+BU` will have its closed-loop poles, i.e the eigenvalues `A - B*K`, as close as possible to those asked for in poles.

SISO, MISO and MIMO systems are supported.

Parameters

A, B : ndarray

State-space representation of linear system `AX + BU`.

poles : array_like

Desired real poles and/or complex conjugates poles. Complex poles are only supported with `method="YT"` (default).

method: {'YT', 'KNV0'}, optional

Which method to choose to find the gain matrix K. One of:

- 'YT': Yang Tits
- 'KNV0': Kautsky, Nichols, Van Dooren update method 0

See References and Notes for details on the algorithms.

rtol: float, optional

After each iteration the determinant of the eigenvectors of `A - B*K` is compared to its previous value, when the relative error between these two values becomes lower than *rtol* the algorithm stops. Default is 1e-3.

maxiter: int, optional

Maximum number of iterations to compute the gain matrix. Default is 30.

Returns

full_state_feedback : Bunch object

full_state_feedback is composed of:

gain_matrix	[1-D ndarray] The closed loop matrix K such as the eigenvalues of `A-BK` are as close as possible to the requested poles.
computed_poles	[1-D ndarray] The poles corresponding to `A-BK` sorted as first the real poles in increasing order, then the complex congugates in lexicographic order.
requested_poles	[1-D ndarray] The poles the algorithm was asked to place sorted as above, they may differ from what was achieved.
X	[2D ndarray] The transfer matrix such as `X * diag(poles) = (A - B*K)*X` (see Notes)
rtol	[float] The relative tolerance achieved on `det(X)` (see Notes). *rtol* will be NaN if the optimisation algorithms can not run, i.e

when `B.shape[1] == 1`, or 0 when the solution is unique.

nb_iter [int] The number of iterations performed before converging. *nb_iter* will be NaN if the optimisation algorithms can not run, i.e when `B.shape[1] == 1`, or 0 when the solution is unique.

Notes

The Tits and Yang (YT), [R195] paper is an update of the original Kautsky et al. (KNV) paper [R194]. KNV relies on rank-1 updates to find the transfer matrix X such that `X * diag(poles) = (A - B*K)*X`, whereas YT uses rank-2 updates. This yields on average more robust solutions (see [R195] pp 21-22), furthermore the YT algorithm supports complex poles whereas KNV does not in its original version. Only update method 0 proposed by KNV has been implemented here, hence the name `'KNV0'`.

KNV extended to complex poles is used in Matlab's `place` function, YT is distributed under a non-free licence by Slicot under the name `robpole`. It is unclear and undocumented how KNV0 has been extended to complex poles (Tits and Yang claim on page 14 of their paper that their method can not be used to extend KNV to complex poles), therefore only YT supports them in this implementation.

As the solution to the problem of pole placement is not unique for MIMO systems, both methods start with a tentative transfer matrix which is altered in various way to increase its determinant. Both methods have been proven to converge to a stable solution, however depending on the way the initial transfer matrix is chosen they will converge to different solutions and therefore there is absolutely no guarantee that using `'KNV0'` will yield results similar to Matlab's or any other implementation of these algorithms.

Using the default method `'YT'` should be fine in most cases; `'KNV0'` is only provided because it is needed by `'YT'` in some specific cases. Furthermore `'YT'` gives on average more robust results than `'KNV0'` when `abs(det(X))` is used as a robustness indicator.

[R195] is available as a technical report on the following URL: http://drum.lib.umd.edu/handle/1903/5598

References

[R194], [R195]

Examples

A simple example demonstrating real pole placement using both KNV and YT algorithms. This is example number 1 from section 4 of the reference KNV publication ([R194]):

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> A = np.array([[ 1.380,  -0.2077,  6.715, -5.676  ],
...                [-0.5814, -4.290,   0,      0.6750 ],
...                [ 1.067,   4.273,  -6.654,  5.893  ],
...                [ 0.0480,  4.273,   1.343, -2.104  ]])
>>> B = np.array([[ 0,      5.679 ],
...                [ 1.136,  1.136 ],
...                [ 0,      0,     ],
...                [-3.146,  0      ]])
>>> P = np.array([-0.2, -0.5, -5.0566, -8.6659])
```

Now compute K with KNV method 0, with the default YT method and with the YT method while forcing 100 iterations of the algorithm and print some results after each call.

```
>>> fsf1 = signal.place_poles(A, B, P, method='KNV0')
>>> fsf1.gain_matrix
array([[ 0.20071427, -0.96665799,  0.24066128, -0.10279785],
       [ 0.50587268,  0.57779091,  0.51795763, -0.41991442]])
```

```
>>> fsf2 = signal.place_poles(A, B, P)  # uses YT method
>>> fsf2.computed_poles
array([-8.6659, -5.0566, -0.5   , -0.2   ])
```

```
>>> fsf3 = signal.place_poles(A, B, P, rtol=-1, maxiter=100)
>>> fsf3.X
array([[ 0.52072442+0.j, -0.08409372+0.j, -0.56847937+0.j,  0.74823657+0.j],
       [-0.04977751+0.j, -0.80872954+0.j,  0.13566234+0.j, -0.29322906+0.j],
       [-0.82266932+0.j, -0.19168026+0.j, -0.56348322+0.j, -0.43815060+0.j],
       [ 0.22267347+0.j,  0.54967577+0.j, -0.58387806+0.j, -0.40271926+0.j]])
```

The absolute value of the determinant of X is a good indicator to check the robustness of the results, both `'KNV0'` and `'YT'` aim at maximizing it. Below a comparison of the robustness of the results above:

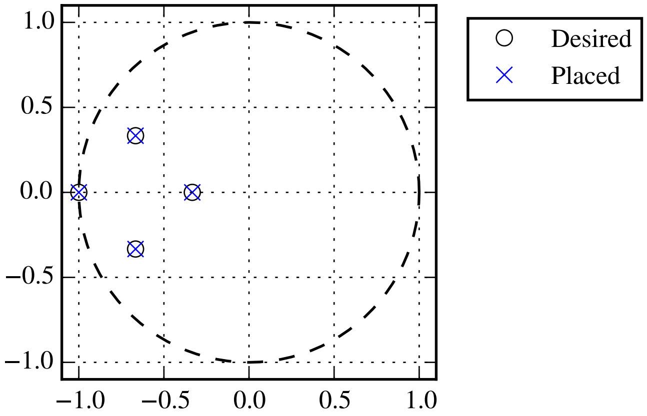
```
>>> abs(np.linalg.det(fsf1.X)) < abs(np.linalg.det(fsf2.X))
True
>>> abs(np.linalg.det(fsf2.X)) < abs(np.linalg.det(fsf3.X))
True
```

Now a simple example for complex poles:

```
>>> A = np.array([[ 0,   7/3.,   0,    0   ],
...               [ 0,    0,     0,   7/9. ],
...               [ 0,    0,     0,    0   ],
...               [ 0,    0,     0,    0   ]])
>>> B = np.array([[ 0,   0 ],
...               [ 0,   0 ],
...               [ 1,   0 ],
...               [ 0,   1 ]])
>>> P = np.array([-3, -1, -2-1j, -2+1j]) / 3.
>>> fsf = signal.place_poles(A, B, P, method='YT')
```

We can plot the desired and computed poles in the complex plane:

```
>>> t = np.linspace(0, 2*np.pi, 401)
>>> plt.plot(np.cos(t), np.sin(t), 'k--')  # unit circle
>>> plt.plot(fsf.requested_poles.real, fsf.requested_poles.imag,
...          'wo', label='Desired')
>>> plt.plot(fsf.computed_poles.real, fsf.computed_poles.imag, 'bx',
...          label='Placed')
>>> plt.grid()
>>> plt.axis('image')
>>> plt.axis([-1.1, 1.1, -1.1, 1.1])
>>> plt.legend(bbox_to_anchor=(1.05, 1), loc=2, numpoints=1)
```



5.27.9 Waveforms

`chirp`(t, f0, t1, f1[, method, phi, vertex_zero])	Frequency-swept cosine generator.
`gausspulse`(t[, fc, bw, bwr, tpr, retquad, ...])	Return a Gaussian modulated sinusoid:
`max_len_seq`(nbits[, state, length, taps])	Maximum Length Sequence (MLS) generator
`sawtooth`(t[, width])	Return a periodic sawtooth or triangle waveform.
`square`(t[, duty])	Return a periodic square-wave waveform.
`sweep_poly`(t, poly[, phi])	Frequency-swept cosine generator, with a time-dependent frequency.

`scipy.signal.`**`chirp`**(*t*, *f0*, *t1*, *f1*, *method='linear'*, *phi=0*, *vertex_zero=True*)

Frequency-swept cosine generator.

In the following, 'Hz' should be interpreted as 'cycles per unit'; there is no requirement here that the unit is one second. The important distinction is that the units of rotation are cycles, not radians. Likewise, *t* could be a measurement of space instead of time.

Parameters

t : array_like
Times at which to evaluate the waveform.

f0 : float
Frequency (e.g. Hz) at time t=0.

t1 : float
Time at which *f1* is specified.

f1 : float
Frequency (e.g. Hz) of the waveform at time *t1*.

method : {'linear', 'quadratic', 'logarithmic', 'hyperbolic'}, optional
Kind of frequency sweep. If not given, *linear* is assumed. See Notes below for more details.

phi : float, optional
Phase offset, in degrees. Default is 0.

vertex_zero : bool, optional
This parameter is only used when *method* is 'quadratic'. It determines whether the vertex of the parabola that is the graph of the frequency is at t=0 or t=t1.

Returns

y : ndarray

A numpy array containing the signal evaluated at *t* with the requested time-varying frequency. More precisely, the function returns `cos(phase + (pi/180)*phi)` where *phase* is the integral (from 0 to *t*) of `2*pi*f(t)`. `f(t)` is defined below.

See also:

`sweep_poly`

Notes

There are four options for the *method*. The following formulas give the instantaneous frequency (in Hz) of the signal generated by *chirp()*. For convenience, the shorter names shown below may also be used.

linear, lin, li:

`f(t) = f0 + (f1 - f0) * t / t1`

quadratic, quad, q:

The graph of the frequency f(t) is a parabola through (0, f0) and (t1, f1). By default, the vertex of the parabola is at (0, f0). If *vertex_zero* is False, then the vertex is at (t1, f1). The formula is:
if vertex_zero is True:
`f(t) = f0 + (f1 - f0) * t**2 / t1**2`
else:
`f(t) = f1 - (f1 - f0) * (t1 - t)**2 / t1**2`
To use a more general quadratic function, or an arbitrary polynomial, use the function `scipy.signal.waveforms.sweep_poly`.

logarithmic, log, lo:

`f(t) = f0 * (f1/f0)**(t/t1)`
f0 and f1 must be nonzero and have the same sign.
This signal is also known as a geometric or exponential chirp.

hyperbolic, hyp:

`f(t) = f0*f1*t1 / ((f0 - f1)*t + f1*t1)`
f0 and f1 must be nonzero.

`scipy.signal.`**`gausspulse`**(*t*, *fc=1000*, *bw=0.5*, *bwr=-6*, *tpr=-60*, *retquad=False*, *retenv=False*)

Return a Gaussian modulated sinusoid:

`exp(-a t^2) exp(1j*2*pi*fc*t).`

If *retquad* is True, then return the real and imaginary parts (in-phase and quadrature). If *retenv* is True, then return the envelope (unmodulated signal). Otherwise, return the real part of the modulated sinusoid.

Parameters

t : ndarray or the string 'cutoff'
Input array.

fc : int, optional
Center frequency (e.g. Hz). Default is 1000.

bw : float, optional
Fractional bandwidth in frequency domain of pulse (e.g. Hz). Default is 0.5.

bwr : float, optional
Reference level at which fractional bandwidth is calculated (dB). Default is -6.

tpr : float, optional
If *t* is 'cutoff', then the function returns the cutoff time for when the pulse amplitude falls below *tpr* (in dB). Default is -60.

retquad : bool, optional
If True, return the quadrature (imaginary) as well as the real part of the signal. Default is False.

retenv : bool, optional
If True, return the envelope of the signal. Default is False.

Returns

yI : ndarray
Real part of signal. Always returned.

yQ : ndarray
Imaginary part of signal. Only returned if *retquad* is True.

yenv : ndarray
Envelope of signal. Only returned if *retenv* is True.

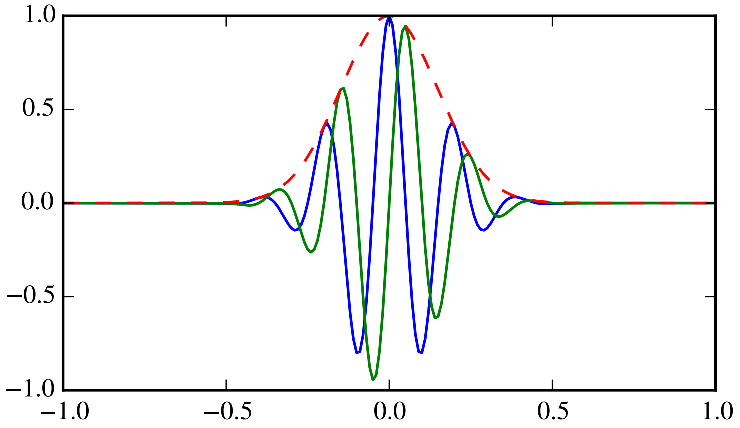
See also:

`scipy.signal.morlet`

Examples

Plot real component, imaginary component, and envelope for a 5 Hz pulse, sampled at 100 Hz for 2 seconds:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 2 * 100, endpoint=False)
>>> i, q, e = signal.gausspulse(t, fc=5, retquad=True, retenv=True)
>>> plt.plot(t, i, t, q, t, e, '--')
```



`scipy.signal.`**`max_len_seq`**(*nbits*, *state=None*, *length=None*, *taps=None*)
Maximum Length Sequence (MLS) generator

Parameters

nbits : int
Number of bits to use. Length of the resulting sequence will be `(2**nbits) - 1`. Note that generating long sequences (e.g., greater than `nbits == 16`) can take a long time.

state : array_like, optional
If array, must be of length `nbits`, and will be cast to binary (bool) representation. If None, a seed of ones will be used, producing a repeatable representation. If `state` is all zeros, an error is raised as this is invalid. Default: None.

length : int | None, optional
Number of samples to compute. If None, the entire length `(2**nbits) - 1` is computed.

taps : array_like, optional
Polynomial taps to use (e.g., `[7, 6, 1]` for an 8-bit sequence). If None, taps will be automatically selected (for up to `nbits == 32`).

Returns **seq** : array
Resulting MLS sequence of 0's and 1's.

state : array
The final state of the shift register.

Notes

The algorithm for MLS generation is generically described in:

> http://en.wikipedia.org/wiki/Maximum_length_sequence

The default values for taps are specifically taken from the first option listed for each value of `nbits` in:

> ***http://www.newwaveinstruments.com/resources/articles/***
> m_sequence_linear_feedback_shift_register_lfsr.htm

New in version 0.15.0.

`scipy.signal.`**`sawtooth`**`(`*t*, *width=1*`)`

Return a periodic sawtooth or triangle waveform.

The sawtooth waveform has a period `2*pi`, rises from -1 to 1 on the interval 0 to `width*2*pi`, then drops from 1 to -1 on the interval `width*2*pi` to `2*pi`. *width* must be in the interval [0, 1].

Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.

Parameters **t** : array_like
Time.

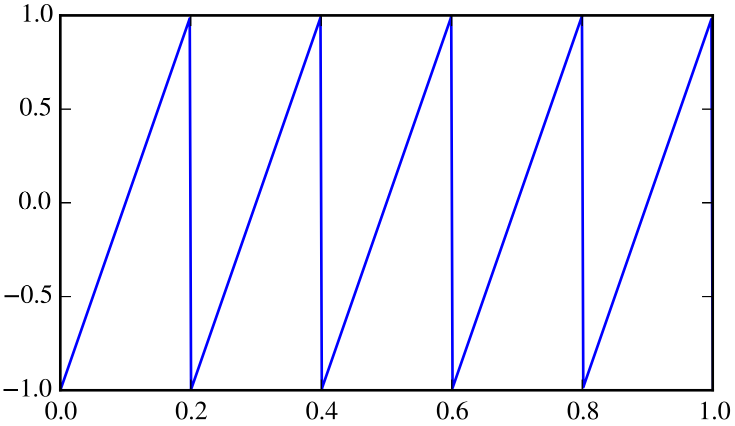
width : array_like, optional
Width of the rising ramp as a proportion of the total cycle. Default is 1, producing a rising ramp, while 0 produces a falling ramp. $t = 0.5$ produces a triangle wave. If an array, causes wave shape to change over time, and must be the same length as t.

Returns **y** : ndarray
Output array containing the sawtooth waveform.

Examples

A 5 Hz waveform sampled at 500 Hz for 1 second:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500)
>>> plt.plot(t, signal.sawtooth(2 * np.pi * 5 * t))
```



`scipy.signal.`**`square`**`(`*t*, *duty=0.5*`)`

Return a periodic square-wave waveform.

The square wave has a period `2*pi`, has value +1 from 0 to `2*pi*duty` and -1 from `2*pi*duty` to `2*pi`. *duty* must be in the interval [0,1].

Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.

Parameters	**t** : array_like	
		The input time array.
	duty : array_like, optional	
		Duty cycle. Default is 0.5 (50% duty cycle). If an array, causes wave shape to change over time, and must be the same length as t.
Returns	**y** : ndarray	
		Output array containing the square waveform.

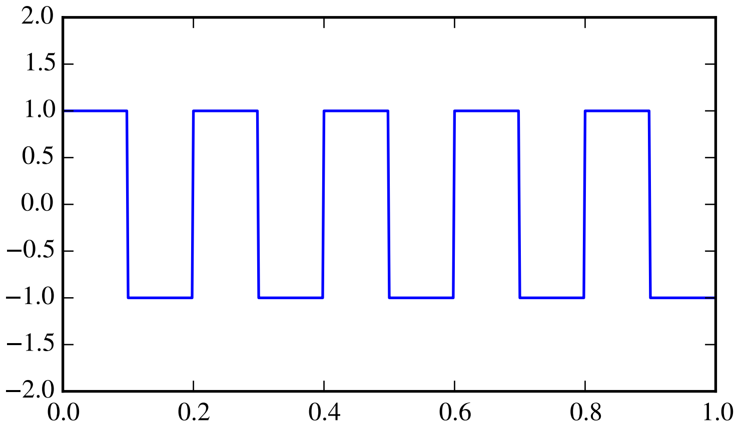
Examples

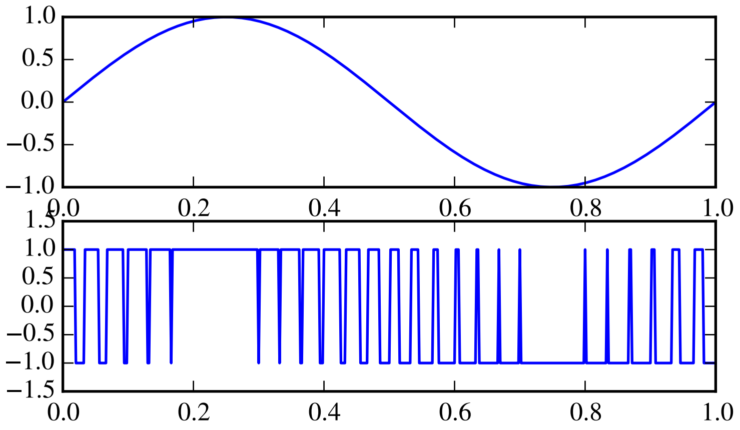
A 5 Hz waveform sampled at 500 Hz for 1 second:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500, endpoint=False)
>>> plt.plot(t, signal.square(2 * np.pi * 5 * t))
>>> plt.ylim(-2, 2)
```

A pulse-width modulated sine wave:

```
>>> plt.figure()
>>> sig = np.sin(2 * np.pi * t)
>>> pwm = signal.square(2 * np.pi * 30 * t, duty=(sig + 1)/2)
>>> plt.subplot(2, 1, 1)
>>> plt.plot(t, sig)
>>> plt.subplot(2, 1, 2)
>>> plt.plot(t, pwm)
>>> plt.ylim(-1.5, 1.5)
```





`scipy.signal.`**`sweep_poly`**(*t*, *poly*, *phi=0*)

Frequency-swept cosine generator, with a time-dependent frequency.

This function generates a sinusoidal function whose instantaneous frequency varies with time. The frequency at time *t* is given by the polynomial *poly*.

Parameters **t** : ndarray

Times at which to evaluate the waveform.

poly : 1-D array_like or instance of numpy.poly1d

The desired frequency expressed as a polynomial. If *poly* is a list or ndarray of length n, then the elements of *poly* are the coefficients of the polynomial, and the instantaneous frequency is

```
f(t) = poly[0]*t**(n-1) +
poly[1]*t**(n-2) + ...  + poly[n-1]
```

If *poly* is an instance of numpy.poly1d, then the instantaneous frequency is

```
f(t) = poly(t)
```

phi : float, optional

Phase offset, in degrees, Default: 0.

Returns **sweep_poly** : ndarray

A numpy array containing the signal evaluated at *t* with the requested time-varying frequency. More precisely, the function returns `cos(phase + (pi/180)*phi)`, where *phase* is the integral (from 0 to t) of `2 * pi * f(t)`; `f(t)` is defined above.

See also:

`chirp`

Notes

New in version 0.8.0.

If *poly* is a list or ndarray of length *n*, then the elements of *poly* are the coefficients of the polynomial, and the instantaneous frequency is:

```
f(t) = poly[0]*t**(n-1) + poly[1]*t**(n-2) + ...  + poly[n-1]
```

If *poly* is an instance of `numpy.poly1d`, then the instantaneous frequency is:

```
f(t) = poly(t)
```

Finally, the output `s` is:

```
cos(phase + (pi/180)*phi)
```

where *phase* is the integral from 0 to *t* of `2 * pi * f(t)`, `f(t)` as defined above.

5.27.10 Window functions

`get_window`(window, Nx[, fftbins])	Return a window.
`barthann`(M[, sym])	Return a modified Bartlett-Hann window.
`bartlett`(M[, sym])	Return a Bartlett window.
`blackman`(M[, sym])	Return a Blackman window.
`blackmanharris`(M[, sym])	Return a minimum 4-term Blackman-Harris window.
`bohman`(M[, sym])	Return a Bohman window.
`boxcar`(M[, sym])	Return a boxcar or rectangular window.
`chebwin`(M, at[, sym])	Return a Dolph-Chebyshev window.
`cosine`(M[, sym])	Return a window with a simple cosine shape.
`exponential`(M[, center, tau, sym])	Return an exponential (or Poisson) window.
`flattop`(M[, sym])	Return a flat top window.
`gaussian`(M, std[, sym])	Return a Gaussian window.
`general_gaussian`(M, p, sig[, sym])	Return a window with a generalized Gaussian shape.
`hamming`(M[, sym])	Return a Hamming window.
`hann`(M[, sym])	Return a Hann window.
`kaiser`(M, beta[, sym])	Return a Kaiser window.
`nuttall`(M[, sym])	Return a minimum 4-term Blackman-Harris window according to Nuttall.
`parzen`(M[, sym])	Return a Parzen window.
`slepian`(M, width[, sym])	Return a digital Slepian (DPSS) window.
`triang`(M[, sym])	Return a triangular window.
`tukey`(M[, alpha, sym])	Return a Tukey window, also known as a tapered cosine window.

`scipy.signal.`**`get_window`**`(`*window*, *Nx*, *fftbins=True*`)`

Return a window.

Parameters	**window** : string, float, or tuple	The type of window to create. See below for more details.
	Nx : int	The number of samples in the window.
	fftbins : bool, optional	If True, create a "periodic" window ready to use with ifftshift and be multiplied by the result of an fft (SEE ALSO fftfreq).
Returns	**get_window** : ndarray	Returns a window of length *Nx* and type *window*

Notes

Window types:

> boxcar, triang, blackman, hamming, hann, bartlett, flattop, parzen, bohman, blackmanharris, nuttall, barthann, kaiser (needs beta), gaussian (needs std), general_gaussian (needs power, width), slepian (needs width), chebwin (needs attenuation) exponential (needs decay scale), tukey (needs taper fraction)

If the window requires no parameters, then *window* can be a string.

If the window requires parameters, then *window* must be a tuple with the first argument the string name of the window, and the next arguments the needed parameters.

If *window* is a floating point number, it is interpreted as the beta parameter of the kaiser window.

Each of the window types listed above is also the name of a function that can be called directly to create a window of that type.

Examples

```
>>> from scipy import signal
>>> signal.get_window('triang', 7)
array([ 0.25,  0.5 ,  0.75,  1.  ,  0.75,  0.5 ,  0.25])
>>> signal.get_window(('kaiser', 4.0), 9)
array([ 0.08848053,  0.32578323,  0.63343178,  0.89640418,  1.        ,
        0.89640418,  0.63343178,  0.32578323,  0.08848053])
>>> signal.get_window(4.0, 9)
array([ 0.08848053,  0.32578323,  0.63343178,  0.89640418,  1.        ,
        0.89640418,  0.63343178,  0.32578323,  0.08848053])
```

`scipy.signal.`**`barthann`**(*M*, *sym=True*)

Return a modified Bartlett-Hann window.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

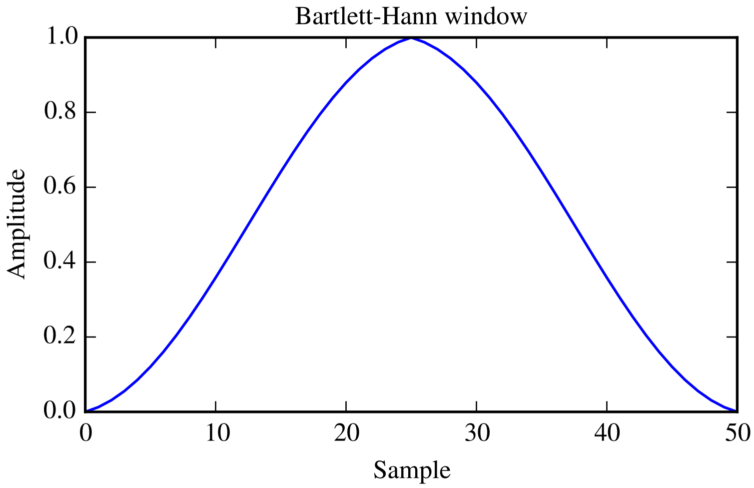
Examples

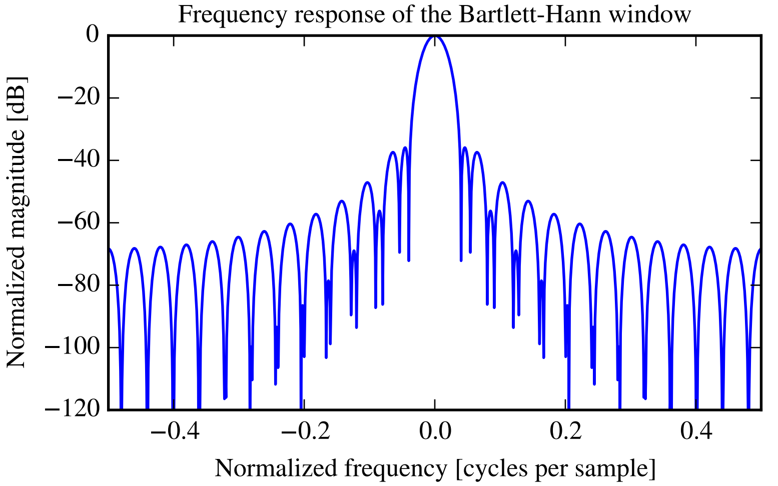
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.barthann(51)
>>> plt.plot(window)
>>> plt.title("Bartlett-Hann window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Bartlett-Hann window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`bartlett`**`(`*M*, *sym=True*`)`

Return a Bartlett window.

The Bartlett window is very similar to a triangular window, except that the end points are at zero. It is often used in signal processing for tapering a signal, without generating too much ripple in the frequency domain.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The triangular window, with the first and last samples equal to zero and the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Bartlett window is defined as

$$w(n) = \frac{2}{M-1}\left(\frac{M-1}{2} - \left|n - \frac{M-1}{2}\right|\right)$$

Most references to the Bartlett window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. Note that convolution with this window produces linear interpolation. It is also known as an apodization (which means"removing the foot", i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function. The Fourier transform of the Bartlett is the product of two sinc functions. Note the excellent discussion in Kanasewich.

References

[R156], [R157], [R158], [R159], [R160]

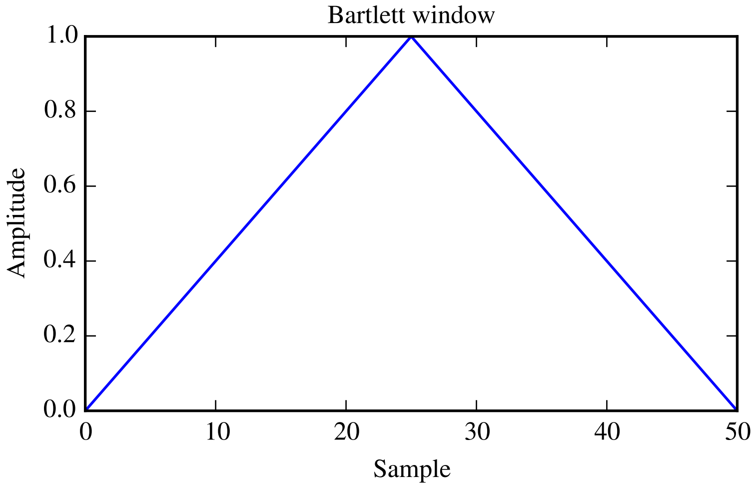
Examples

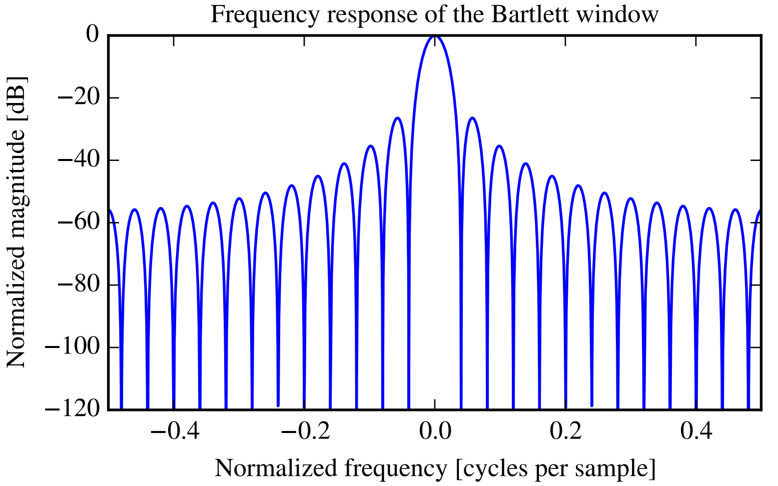
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.bartlett(51)
>>> plt.plot(window)
>>> plt.title("Bartlett window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Bartlett window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`blackman`**(*M*, *sym=True*)

Return a Blackman window.

The Blackman window is a taper formed by using the first three terms of a summation of cosines. It was designed to have close to the minimal leakage possible. It is close to optimal, only slightly worse than a Kaiser window.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Blackman window is defined as

$$w(n) = 0.42 - 0.5 \cos(2\pi n/M) + 0.08 \cos(4\pi n/M)$$

Most references to the Blackman window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means "removing the foot", i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function. It is known as a "near optimal" tapering function, almost as good (by some measures) as the Kaiser window.

References

[R161], [R162]

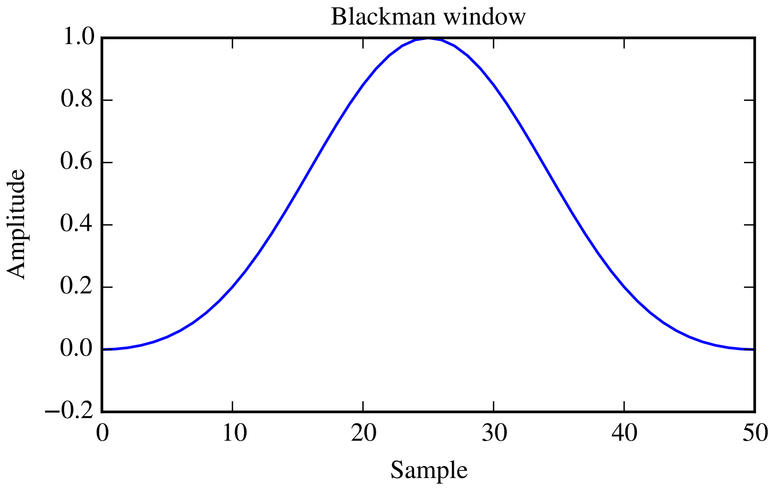
Examples

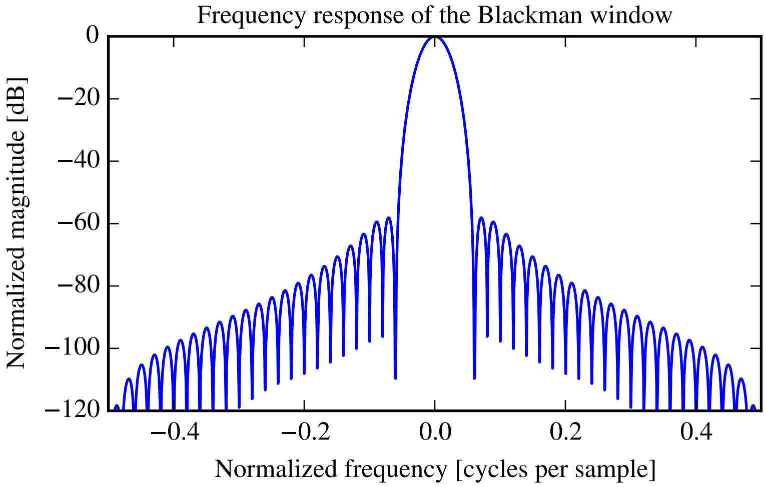
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.blackman(51)
>>> plt.plot(window)
>>> plt.title("Blackman window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Blackman window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`blackmanharris`**(*M*, *sym=True*)

Return a minimum 4-term Blackman-Harris window.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

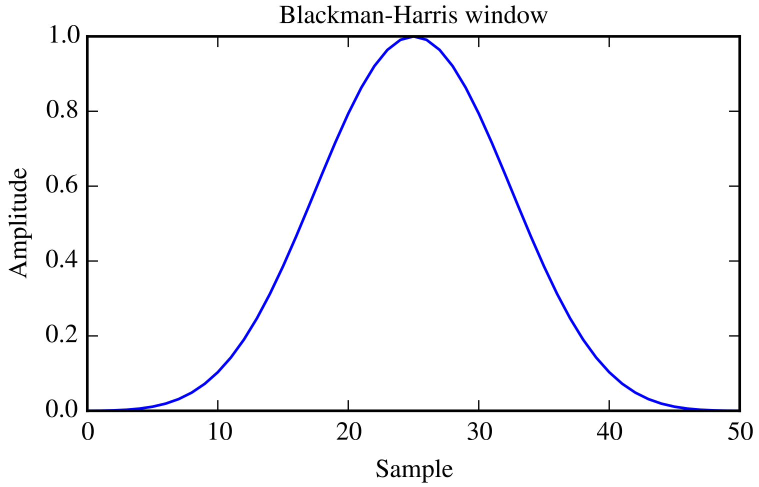
Examples

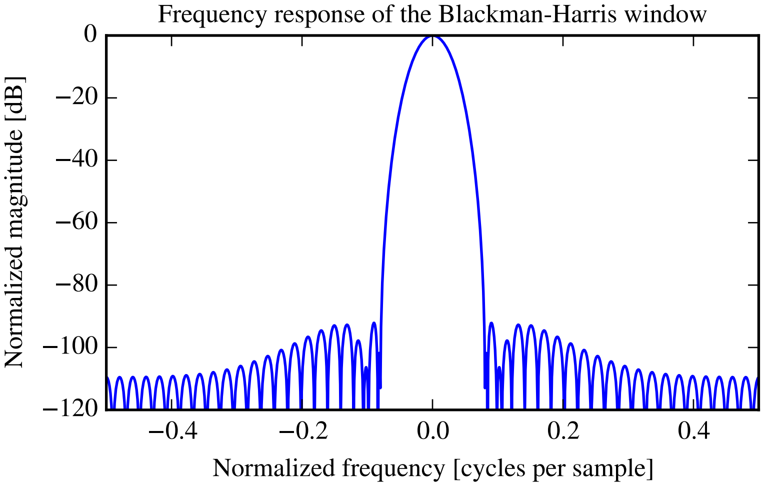
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.blackmanharris(51)
>>> plt.plot(window)
>>> plt.title("Blackman-Harris window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Blackman-Harris window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`bohman`**(*M*, *sym=True*)

Return a Bohman window.

Parameters	**M** : int	
		Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	
		When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	
		The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

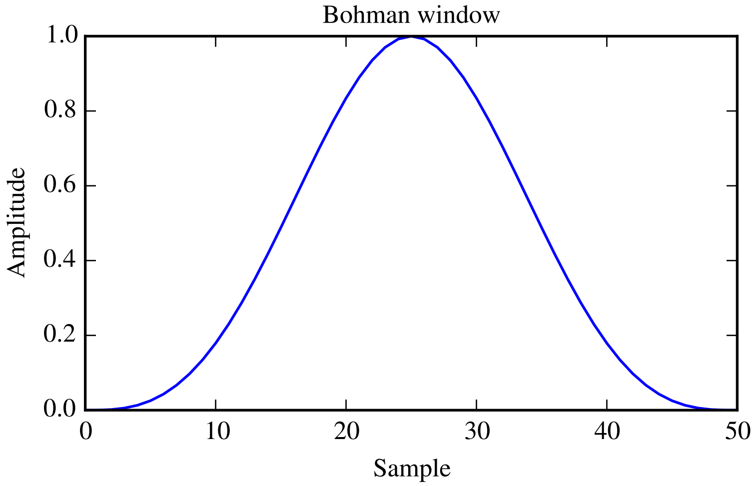
Examples

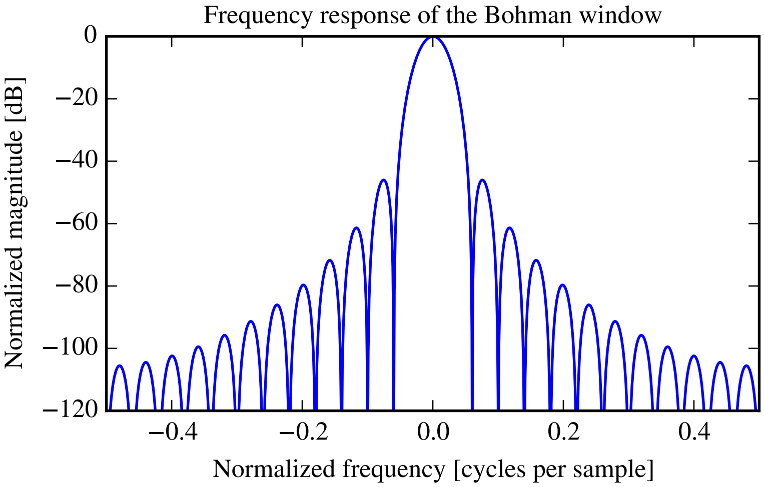
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.bohman(51)
>>> plt.plot(window)
>>> plt.title("Bohman window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Bohman window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`boxcar`**`(`*M*, *sym=True*`)`

Return a boxcar or rectangular window.

Included for completeness, this is equivalent to no window at all.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

sym : bool, optional

Whether the window is symmetric. (Has no effect for boxcar.)

Returns **w** : ndarray

The window, with the maximum value normalized to 1.

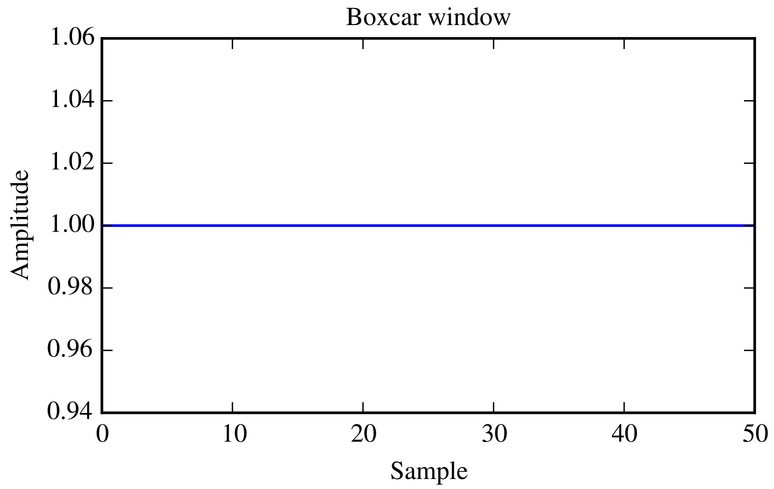
Examples

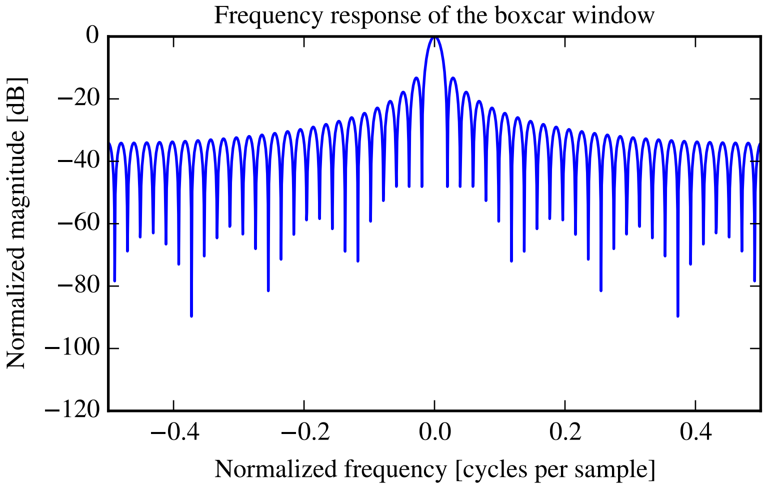
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.boxcar(51)
>>> plt.plot(window)
>>> plt.title("Boxcar window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the boxcar window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





scipy.signal.**chebwin**(*M*, *at*, *sym=True*)

Return a Dolph-Chebyshev window.

Parameters

M : int

Number of points in the output window. If zero or less, an empty array is returned.

at : float

Attenuation (in dB).

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w : ndarray

The window, with the maximum value always normalized to 1

Notes

This window optimizes for the narrowest main lobe width for a given order *M* and sidelobe equiripple attenuation *at*, using Chebyshev polynomials. It was originally developed by Dolph to optimize the directionality of radio antenna arrays.

Unlike most windows, the Dolph-Chebyshev is defined in terms of its frequency response:

$$W(k) = \frac{\cos\{M \cos^{-1}[\beta \cos(\frac{\pi k}{M})]\}}{\cosh[M \cosh^{-1}(\beta)]}$$

where

$$\beta = \cosh \left[\frac{1}{M} \cosh^{-1}(10^{\frac{A}{20}})\right]$$

and 0 <= abs(k) <= M-1. A is the attenuation in decibels (*at*).

The time domain window is then generated using the IFFT, so power-of-two *M* are the fastest to generate, and prime number *M* are the slowest.

The equiripple condition in the frequency domain creates impulses in the time domain, which appear at the ends of the window.

References

[R163], [R164], [R165]

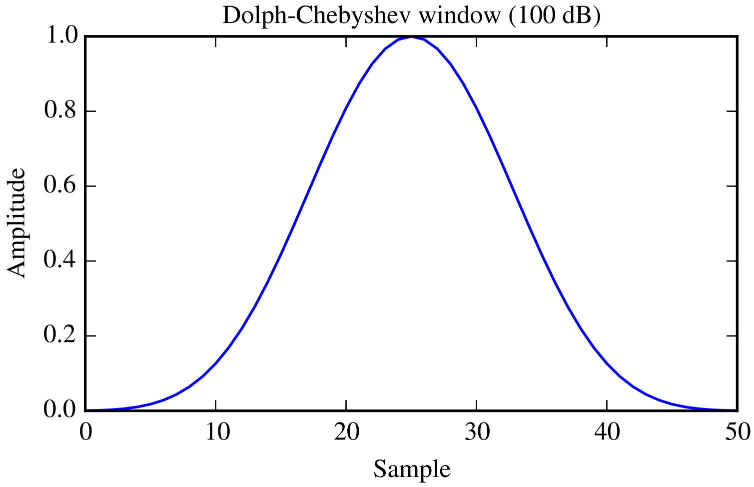
Examples

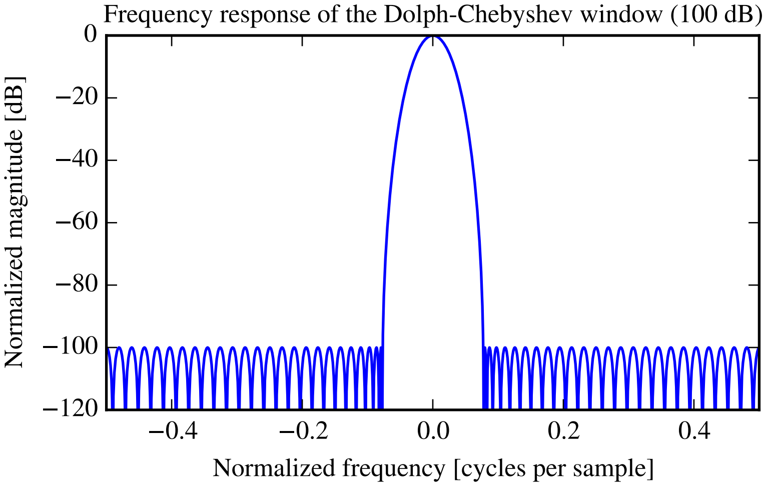
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.chebwin(51, at=100)
>>> plt.plot(window)
>>> plt.title("Dolph-Chebyshev window (100 dB)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Dolph-Chebyshev window (100 dB)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`cosine`**(*M*, *sym=True*)

Return a window with a simple cosine shape.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

New in version 0.13.0.

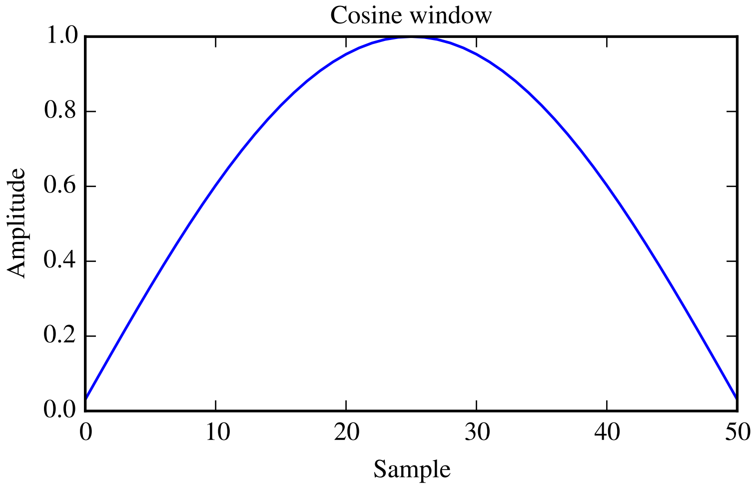
Examples

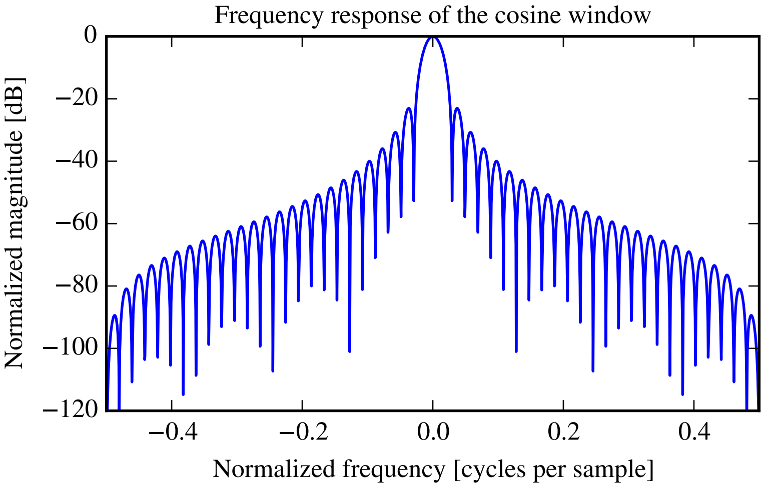
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.cosine(51)
>>> plt.plot(window)
>>> plt.title("Cosine window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the cosine window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
>>> plt.show()
```





`scipy.signal.`**`exponential`**(*M*, *center=None*, *tau=1.0*, *sym=True*)

Return an exponential (or Poisson) window.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

center : float, optional

Parameter defining the center location of the window function. The default value if not given is `center = (M-1) / 2`. This parameter must take its default value for symmetric windows.

tau : float, optional

Parameter defining the decay. For `center = 0` use `tau = -(M-1) / ln(x)` if `x` is the fraction of the window remaining at the end.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Exponential window is defined as

$$w(n) = e^{-|n-center|/\tau}$$

References

S. Gade and H. Herlufsen, "Windows to FFT analysis (Part I)", Technical Review 3, Bruel & Kjaer, 1987.

Examples

Plot the symmetric window and its frequency response:

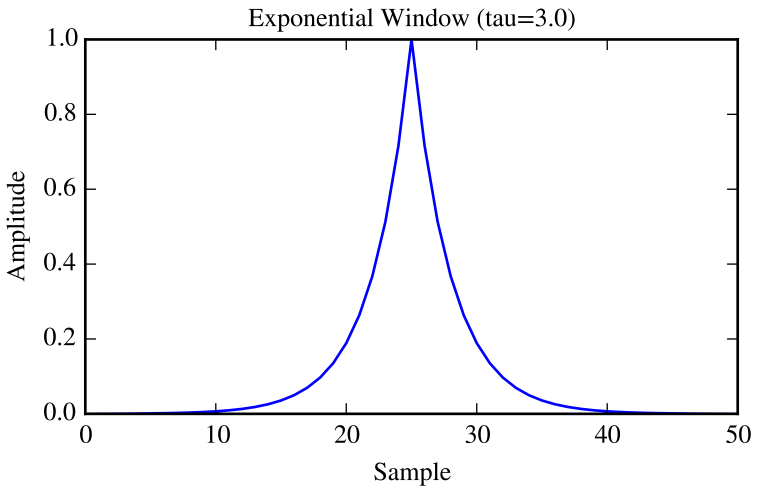
```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

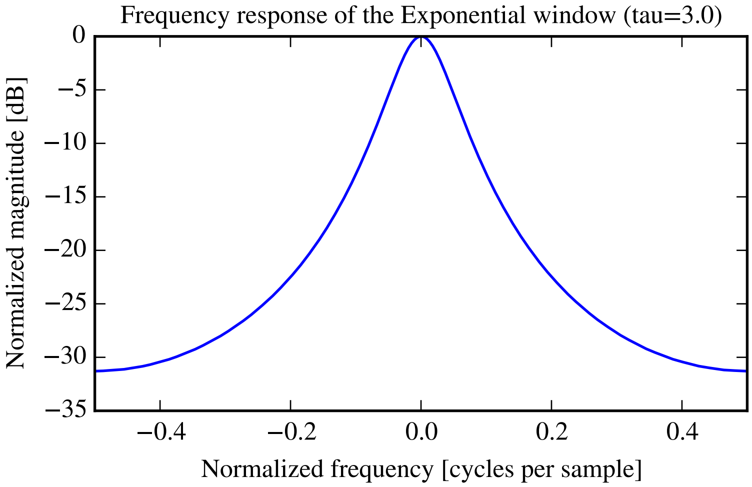
```
>>> M = 51
>>> tau = 3.0
>>> window = signal.exponential(M, tau=tau)
>>> plt.plot(window)
>>> plt.title("Exponential Window (tau=3.0)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

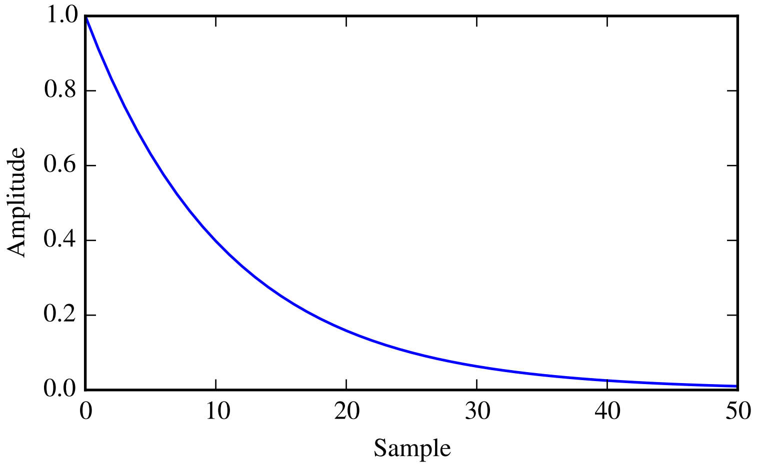
```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -35, 0])
>>> plt.title("Frequency response of the Exponential window (tau=3.0)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

This function can also generate non-symmetric windows:

```
>>> tau2 = -(M-1) / np.log(0.01)
>>> window2 = signal.exponential(M, 0, tau2, False)
>>> plt.figure()
>>> plt.plot(window2)
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```







`scipy.signal.`**`flattop`**`(`*M*, *sym=True*`)`

Return a flat top window.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

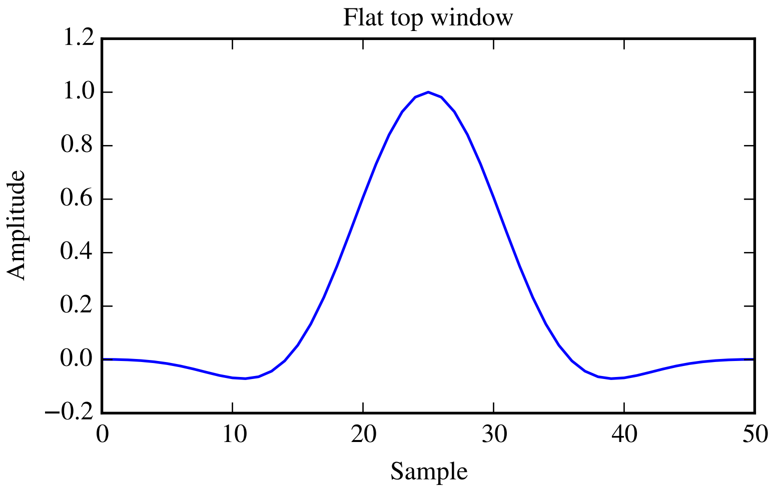
Examples

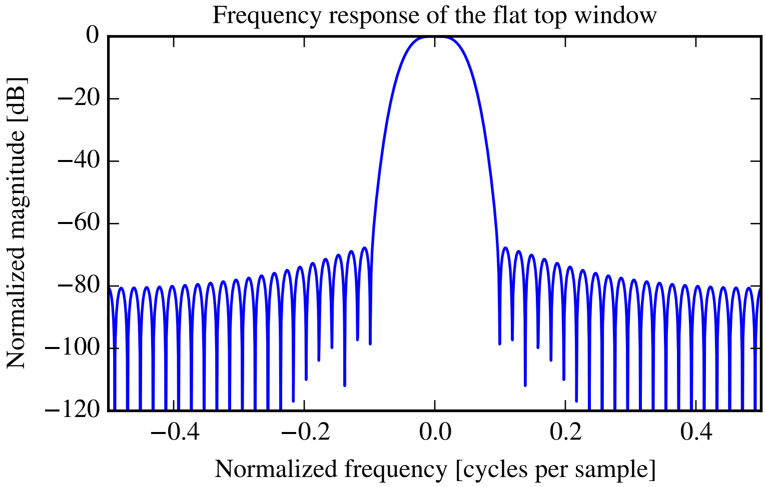
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.flattop(51)
>>> plt.plot(window)
>>> plt.title("Flat top window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the flat top window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`gaussian`**`(`*M*, *std*, *sym=True*`)`

Return a Gaussian window.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

std : float

The standard deviation, sigma.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Gaussian window is defined as

$$w(n) = e^{ -\frac{1}{2}\left(\frac{n}{\sigma}\right)^2 }$$

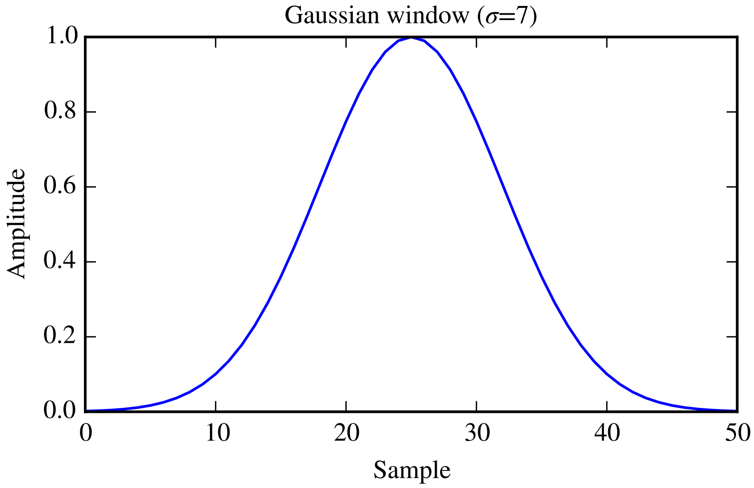
Examples

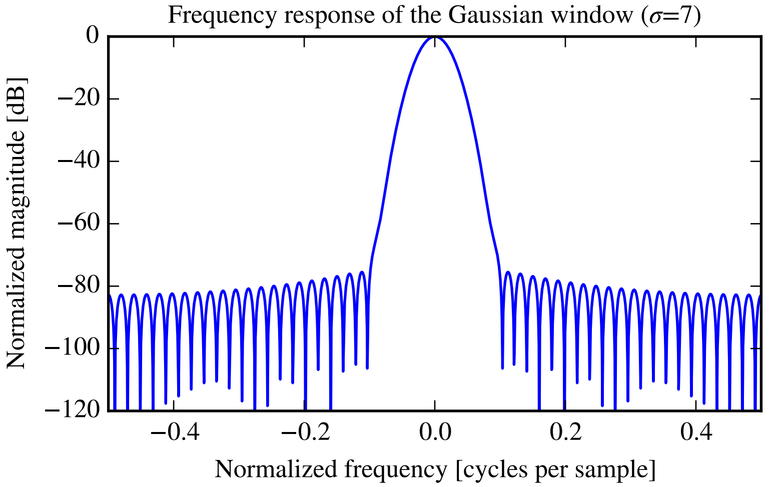
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.gaussian(51, std=7)
>>> plt.plot(window)
>>> plt.title(r"Gaussian window ($\sigma$=7)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title(r"Frequency response of the Gaussian window ($\sigma$=7)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`general_gaussian`**(*M*, *p*, *sig*, *sym=True*)

Return a window with a generalized Gaussian shape.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

p : float

Shape parameter. p = 1 is identical to `gaussian`, p = 0.5 is the same shape as the Laplace distribution.

sig : float

The standard deviation, sigma.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The generalized Gaussian window is defined as

$$w(n) = e^{ -\frac{1}{2}\left|\frac{n}{\sigma}\right|^{2p} }$$

the half-power point is at

$$(2 \log(2))^{1/(2 p)} \sigma$$

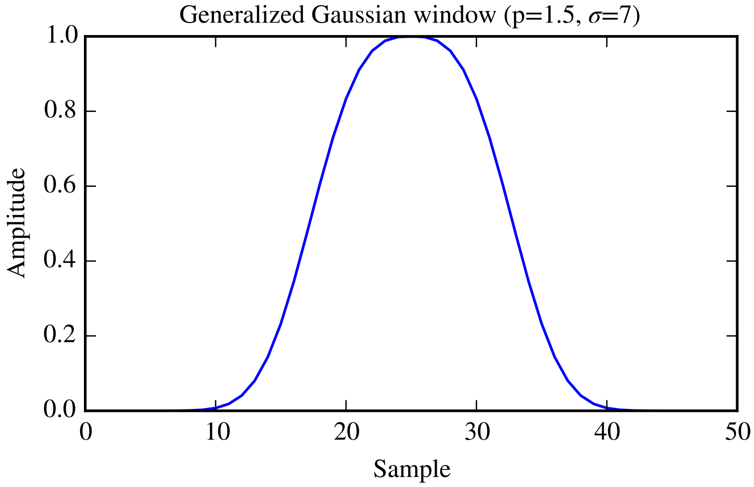
Examples

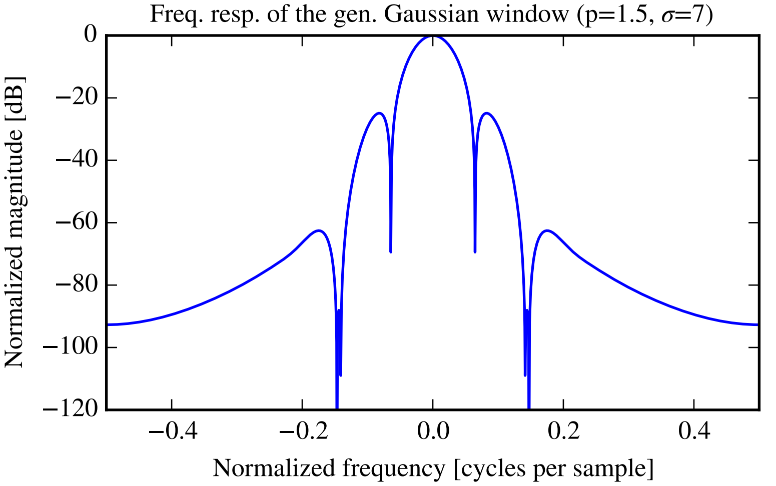
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.general_gaussian(51, p=1.5, sig=7)
>>> plt.plot(window)
>>> plt.title(r"Generalized Gaussian window (p=1.5, $\sigma$=7)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title(r"Freq. resp. of the gen. Gaussian window (p=1.5, $\sigma$=7)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`hamming`**(*M*, *sym=True*)

Return a Hamming window.

The Hamming window is a taper formed by using a raised cosine with non-zero endpoints, optimized to minimize the nearest side lobe.

Parameters

M : int

Number of points in the output window. If zero or less, an empty array is returned.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Hamming window is defined as

$$w(n) = 0.54 - 0.46\cos\left(\frac{2\pi n}{M-1}\right) \qquad 0 \le n \le M-1$$

The Hamming was named for R. W. Hamming, an associate of J. W. Tukey and is described in Blackman and Tukey. It was recommended for smoothing the truncated autocovariance function in the time domain. Most references to the Hamming window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means "removing the foot", i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

References

[R178], [R179], [R180], [R181]

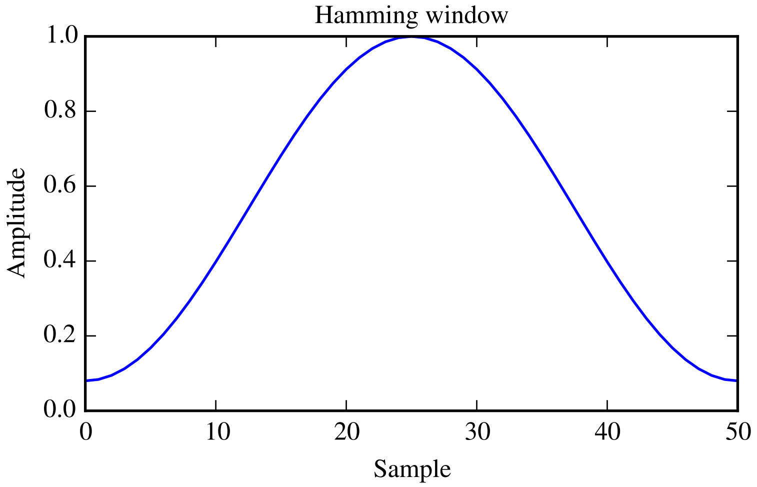
Examples

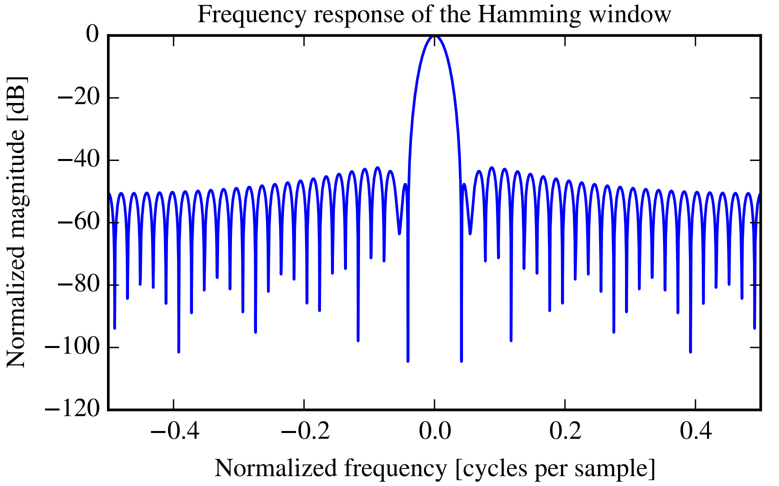
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.hamming(51)
>>> plt.plot(window)
>>> plt.title("Hamming window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Hamming window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`hann`**(*M*, *sym=True*)

Return a Hann window.

The Hann window is a taper formed by using a raised cosine or sine-squared with ends that touch zero.

Parameters **M** : int

Number of points in the output window. If zero or less, an empty array is returned.

sym : bool, optional

When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns **w** : ndarray

The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Hann window is defined as

$$w(n) = 0.5 - 0.5\cos\left(\frac{2\pi n}{M-1}\right) \qquad 0 \leq n \leq M-1$$

The window was named for Julius van Hann, an Austrian meteorologist. It is also known as the Cosine Bell. It is sometimes erroneously referred to as the "Hanning" window, from the use of "hann" as a verb in the original paper and confusion with the very similar Hamming window.

Most references to the Hann window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means "removing the foot", i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

References

[R182], [R183], [R184], [R185]

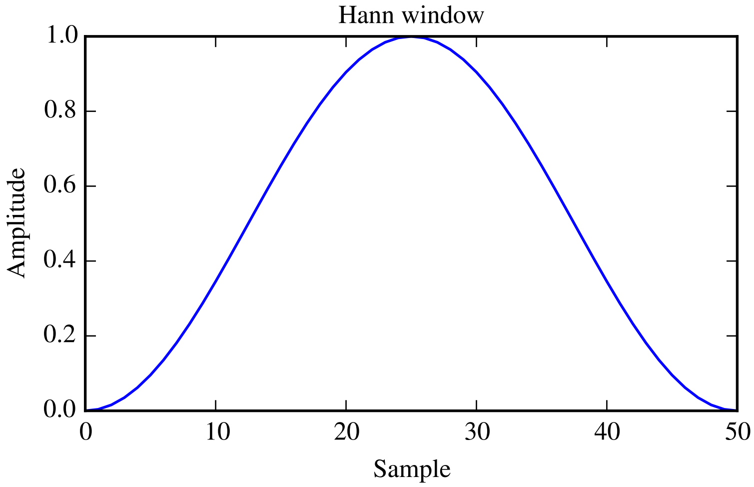
Examples

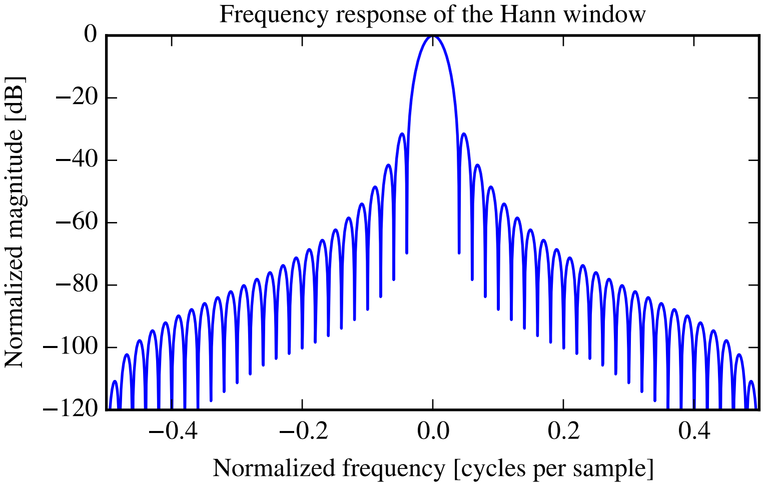
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.hann(51)
>>> plt.plot(window)
>>> plt.title("Hann window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Hann window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`kaiser`**`(`*M*, *beta*, *sym=True*`)`

Return a Kaiser window.

The Kaiser window is a taper formed by using a Bessel function.

Parameters	**M** : int	
		Number of points in the output window. If zero or less, an empty array is returned.
	beta : float	
		Shape parameter, determines trade-off between main-lobe width and side lobe level. As beta gets large, the window narrows.
	sym : bool, optional	
		When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	
		The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

Notes

The Kaiser window is defined as

$$w(n) = I_0\left(\beta\sqrt{1-\frac{4n^2}{(M-1)^2}}\right)/I_0(\beta)$$

with

$$-\frac{M-1}{2} \leq n \leq \frac{M-1}{2},$$

where I_0 is the modified zeroth-order Bessel function.

The Kaiser was named for Jim Kaiser, who discovered a simple approximation to the DPSS window based on Bessel functions. The Kaiser window is a very good approximation to the Digital Prolate Spheroidal Sequence, or Slepian window, which is the transform which maximizes the energy in the main lobe of the window relative to total energy.

The Kaiser can approximate many other windows by varying the beta parameter.

beta	Window shape
0	Rectangular
5	Similar to a Hamming
6	Similar to a Hann
8.6	Similar to a Blackman

A beta value of 14 is probably a good starting point. Note that as beta gets large, the window narrows, and so the number of samples needs to be large enough to sample the increasingly narrow spike, otherwise NaNs will get returned.

Most references to the Kaiser window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means "removing the foot", i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

References

[R188], [R189], [R190]

Examples

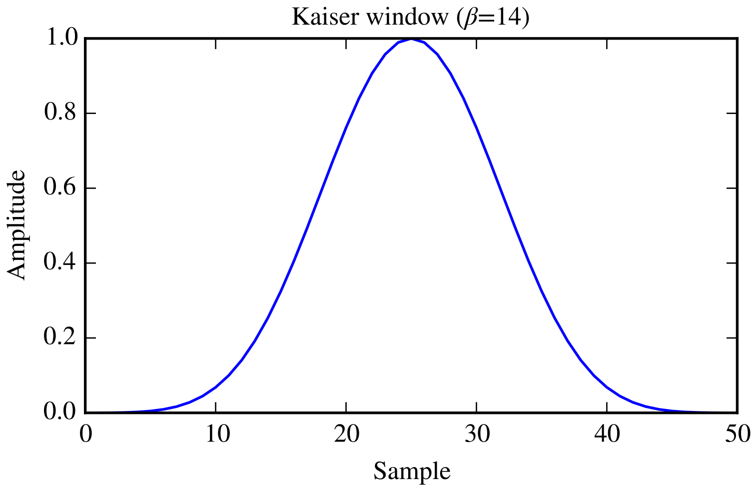
Plot the window and its frequency response:

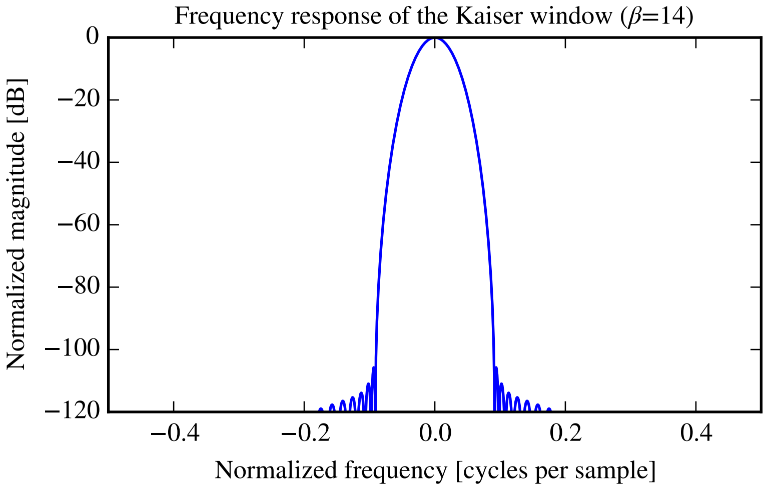
```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.kaiser(51, beta=14)
>>> plt.plot(window)
>>> plt.title(r"Kaiser window ($\beta$=14)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
```

```
>>> plt.title(r"Frequency response of the Kaiser window ($\beta$=14)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`nuttall`**(*M*, *sym=True*)

Return a minimum 4-term Blackman-Harris window according to Nuttall.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

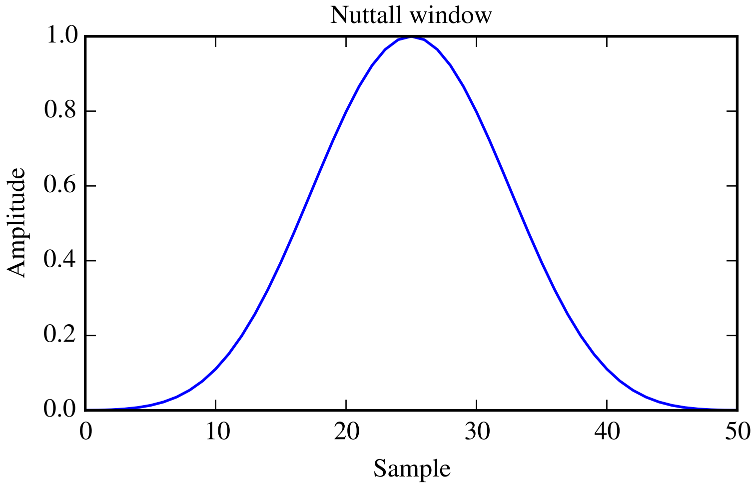
Examples

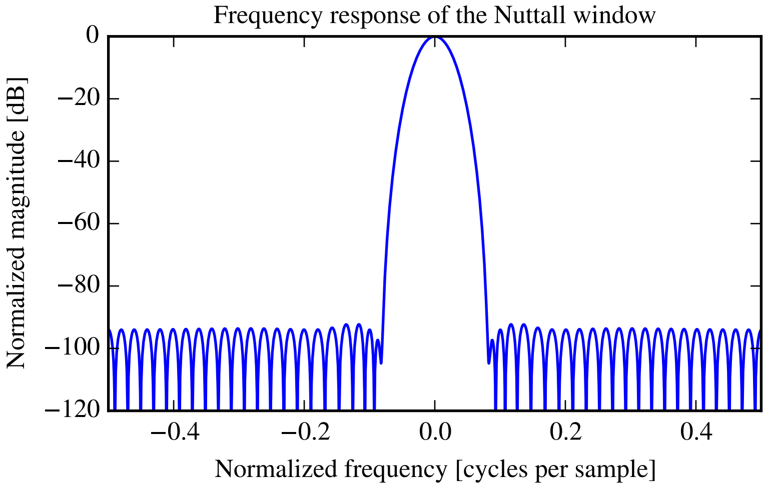
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.nuttall(51)
>>> plt.plot(window)
>>> plt.title("Nuttall window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Nuttall window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`parzen`**`(`*M*, *sym=True*`)`

Return a Parzen window.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

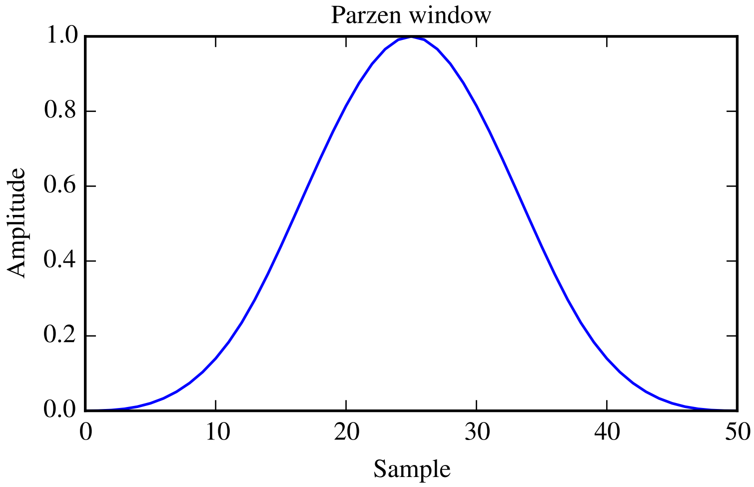
Examples

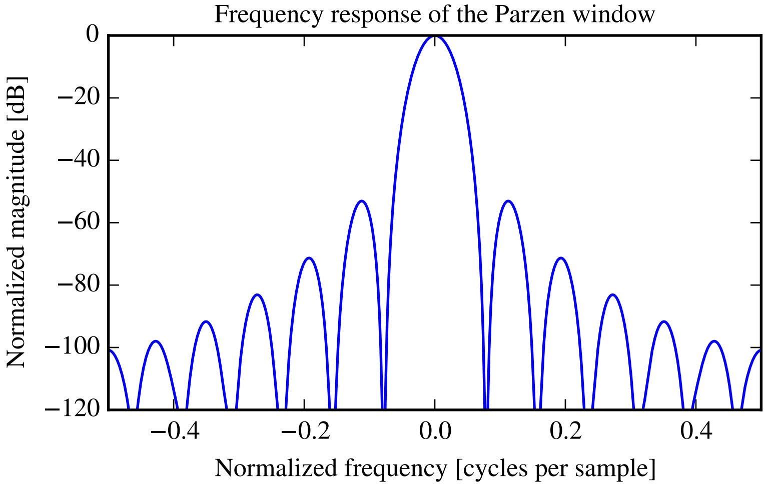
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.parzen(51)
>>> plt.plot(window)
>>> plt.title("Parzen window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Parzen window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`slepian`**(*M*, *width*, *sym=True*)

Return a digital Slepian (DPSS) window.

Used to maximize the energy concentration in the main lobe. Also called the digital prolate spheroidal sequence (DPSS).

Parameters	**M** : int	
		Number of points in the output window. If zero or less, an empty array is returned.
	width : float	
		Bandwidth
	sym : bool, optional	
		When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	
		The window, with the maximum value always normalized to 1

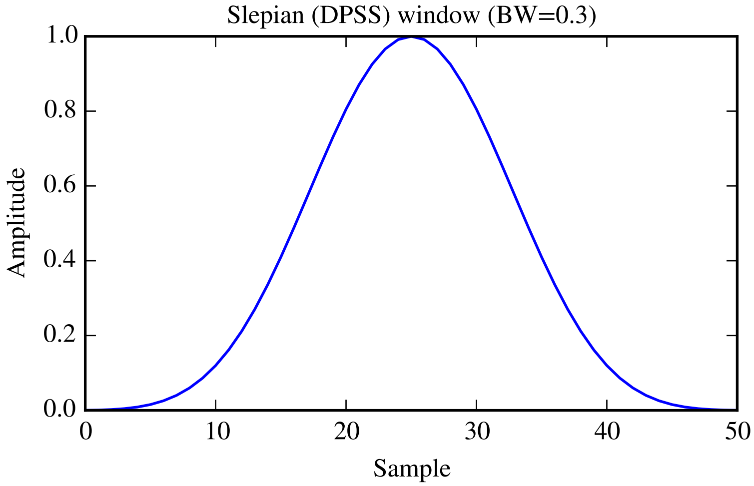
Examples

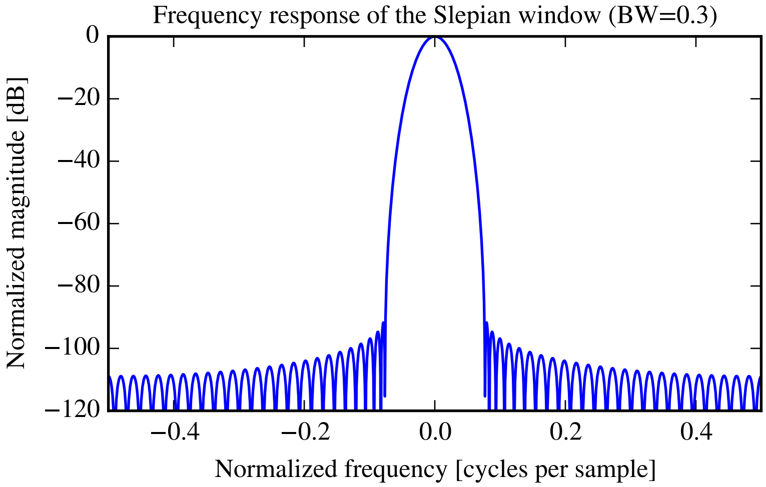
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.slepian(51, width=0.3)
>>> plt.plot(window)
>>> plt.title("Slepian (DPSS) window (BW=0.3)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Slepian window (BW=0.3)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`triang`**(*M*, *sym=True*)

Return a triangular window.

Parameters	**M** : int	Number of points in the output window. If zero or less, an empty array is returned.
	sym : bool, optional	When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray	The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

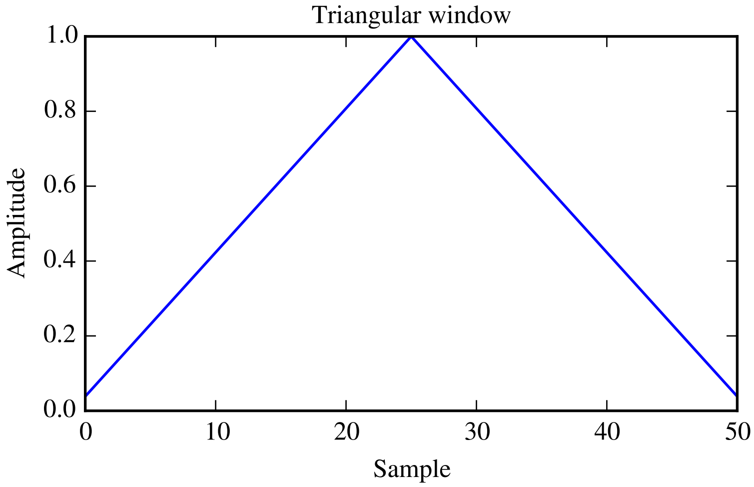
Examples

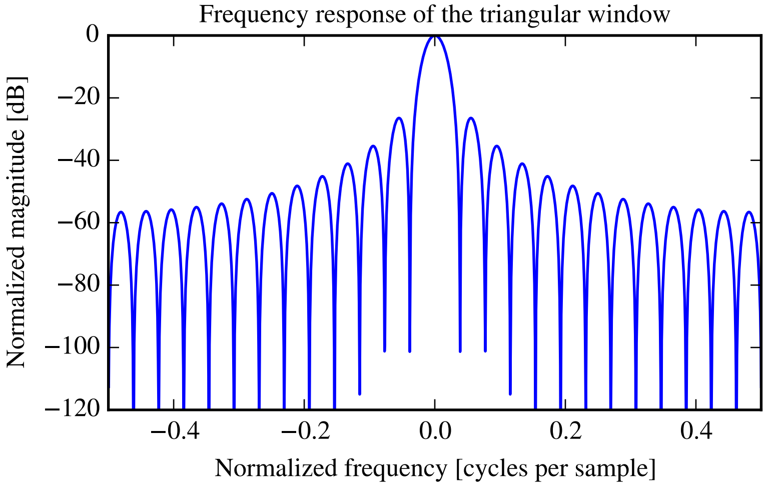
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.triang(51)
>>> plt.plot(window)
>>> plt.title("Triangular window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the triangular window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





`scipy.signal.`**`tukey`**(*M*, *alpha=0.5*, *sym=True*)

Return a Tukey window, also known as a tapered cosine window.

Parameters	**M** : int Number of points in the output window. If zero or less, an empty array is returned. **alpha** : float, optional Shape parameter of the Tukey window, representing the faction of the window inside the cosine tapered region. If zero, the Tukey window is equivalent to a rectangular window. If one, the Tukey window is equivalent to a Hann window. **sym** : bool, optional When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns	**w** : ndarray The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and *sym* is True).

References

[R198], [R199]

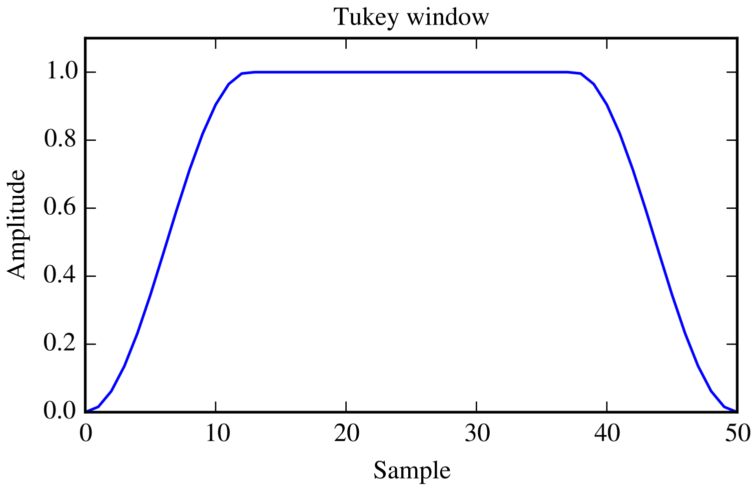
Examples

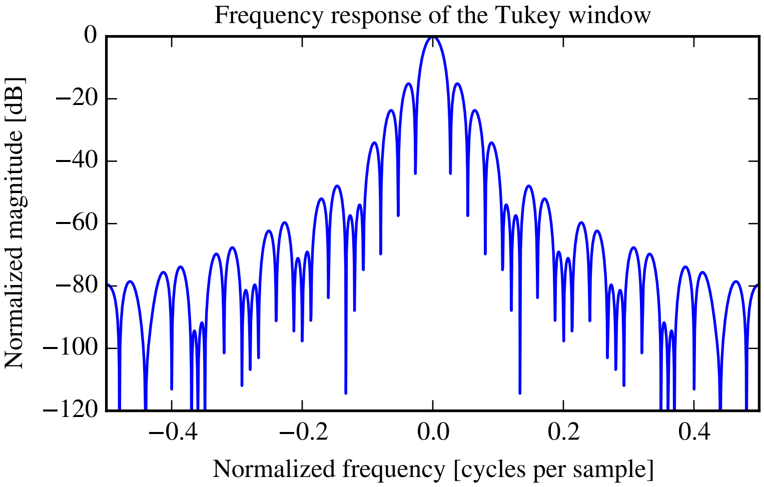
Plot the window and its frequency response:

```
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```

```
>>> window = signal.tukey(51)
>>> plt.plot(window)
>>> plt.title("Tukey window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
>>> plt.ylim([0, 1.1])
```

```
>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Tukey window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```





5.27.11 Wavelets

`cascade`(hk[, J])	Return (x, phi, psi) at dyadic points `K/2**J` from filter coefficients.
`daub`(p)	The coefficients for the FIR low-pass filter producing Daubechies wavelets.
`morlet`(M[, w, s, complete])	Complex Morlet wavelet.
`qmf`(hk)	Return high-pass qmf filter from low-pass
`ricker`(points, a)	Return a Ricker wavelet, also known as the “Mexican hat wavelet”.
`cwt`(data, wavelet, widths)	Continuous wavelet transform.

`scipy.signal.`**`cascade`**`(`*hk*, *J=7*`)`

Return (x, phi, psi) at dyadic points `K/2**J` from filter coefficients.

Parameters **hk** : array_like

Coefficients of low-pass filter.

J : int, optional

Values will be computed at grid points `K/2**J`. Default is 7.

Returns **x** : ndarray

The dyadic points `K/2**J` for `K=0...N * (2**J)-1` where `len(hk) = len(gk) = N+1`.

phi : ndarray

The scaling function `phi(x)` at *x*: `phi(x) = sum(hk * phi(2x-k))`, where k is from 0 to N.

psi : ndarray, optional

The wavelet function `psi(x)` at *x*: `phi(x) = sum(gk * phi(2x-k))`, where k is from 0 to N. *psi* is only returned if *gk* is not None.

Notes

The algorithm uses the vector cascade algorithm described by Strang and Nguyen in “Wavelets and Filter Banks”. It builds a dictionary of values and slices for quick reuse. Then inserts vectors into final vector at the end.

`scipy.signal.`**`daub`**(*p*)

The coefficients for the FIR low-pass filter producing Daubechies wavelets.

p>=1 gives the order of the zero at f=1/2. There are 2p filter coefficients.

Parameters **p** : int

Order of the zero at f=1/2, can have values from 1 to 34.

Returns **daub** : ndarray

Return

`scipy.signal.`**`morlet`**(*M*, *w=5.0*, *s=1.0*, *complete=True*)

Complex Morlet wavelet.

Parameters **M** : int

Length of the wavelet.

w : float, optional

Omega0. Default is 5

s : float, optional

Scaling factor, windowed from `-s*2*pi` to `+s*2*pi`. Default is 1.

complete : bool, optional

Whether to use the complete or the standard version.

Returns **morlet** : (M,) ndarray

See also:

`scipy.signal.gausspulse`

Notes

The standard version:

```
pi**-0.25 * exp(1j*w*x) * exp(-0.5*(x**2))
```

This commonly used wavelet is often referred to simply as the Morlet wavelet. Note that this simplified version can cause admissibility problems at low values of w.

The complete version:

```
pi**-0.25 * (exp(1j*w*x) - exp(-0.5*(w**2))) * exp(-0.5*(x**2))
```

The complete version of the Morlet wavelet, with a correction term to improve admissibility. For w greater than 5, the correction term is negligible.

Note that the energy of the return wavelet is not normalised according to s.

The fundamental frequency of this wavelet in Hz is given by `f = 2*s*w*r / M` where r is the sampling rate.

`scipy.signal.`**`qmf`**(*hk*)

Return high-pass qmf filter from low-pass

Parameters **hk** : array_like

Coefficients of high-pass filter.

`scipy.signal.`**`ricker`**(*points*, *a*)

Return a Ricker wavelet, also known as the "Mexican hat wavelet".

It models the function:

```
A (1 - x^2/a^2) exp(-x^2/2 a^2),
```

where `A = 2/sqrt(3a)pi^1/4`.

Parameters **points** : int

Number of points in *vector*. Will be centered around 0.

a : scalar

Width parameter of the wavelet.

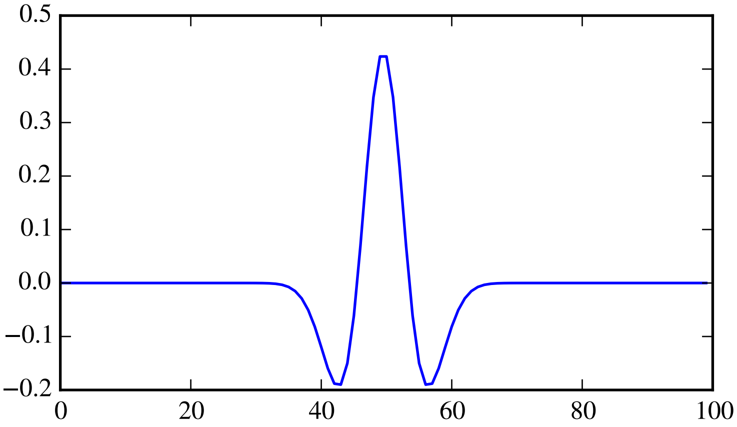
Returns **vector** : (N,) ndarray

Array of length *points* in shape of ricker curve.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> points = 100
>>> a = 4.0
>>> vec2 = signal.ricker(points, a)
>>> print(len(vec2))
100
>>> plt.plot(vec2)
>>> plt.show()
```



`scipy.signal.`**`cwt`**(*data*, *wavelet*, *widths*)

Continuous wavelet transform.

Performs a continuous wavelet transform on *data*, using the *wavelet* function. A CWT performs a convolution with *data* using the *wavelet* function, which is characterized by a width parameter and length parameter.

Parameters **data** : (N,) ndarray

data on which to perform the transform.

wavelet : function

Wavelet function, which should take 2 arguments. The first argument is the number of points that the returned vector will have (len(wavelet(width,length)) == length). The second is a width parameter, defining the size of the wavelet (e.g. standard deviation of a gaussian). See `ricker`, which satisfies these requirements.

widths : (M,) sequence

Widths to use for transform.

Returns cwt: (M, N) ndarray

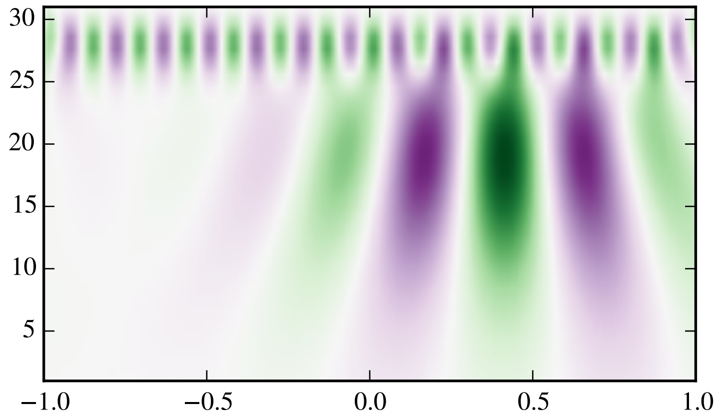
Will have shape of (len(widths), len(data)).

Notes

```
>>> length = min(10 * width[ii], len(data))
>>> cwt[ii,:] = scipy.signal.convolve(data, wavelet(length,
...                                     width[ii]), mode='same')
```

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 200, endpoint=False)
>>> sig  = np.cos(2 * np.pi * 7 * t) + signal.gausspulse(t - 0.4, fc=2)
>>> widths = np.arange(1, 31)
>>> cwtmatr = signal.cwt(sig, signal.ricker, widths)
>>> plt.imshow(cwtmatr, extent=[-1, 1, 1, 31], cmap='PRGn', aspect='auto',
...            vmax=abs(cwtmatr).max(), vmin=-abs(cwtmatr).max())
>>> plt.show()
```



5.27.12 Peak finding

`find_peaks_cwt`(vector, widths[, wavelet, ...])	Attempt to find the peaks in a 1-D array.
`argrelmin`(data[, axis, order, mode])	Calculate the relative minima of *data*.
`argrelmax`(data[, axis, order, mode])	Calculate the relative maxima of *data*.
`argrelextrema`(data, comparator[, axis, ...])	Calculate the relative extrema of *data*.

`scipy.signal.`**`find_peaks_cwt`**(*vector*, *widths*, *wavelet=None*, *max_distances=None*, *gap_thresh=None*, *min_length=None*, *min_snr=1*, *noise_perc=10*)

Attempt to find the peaks in a 1-D array.

The general approach is to smooth *vector* by convolving it with *wavelet(width)* for each width in *widths*. Relative maxima which appear at enough length scales, and with sufficiently high SNR, are accepted.

Parameters **vector** : ndarray

1-D array in which to find the peaks.

widths : sequence
1-D array of widths to use for calculating the CWT matrix. In general, this range should cover the expected width of peaks of interest.

wavelet : callable, optional
Should take a single variable and return a 1-D array to convolve with *vector*. Should be normalized to unit area. Default is the ricker wavelet.

max_distances : ndarray, optional
At each row, a ridge line is only connected if the relative max at row[n] is within `max_distances[n]` from the relative max at `row[n+1]`. Default value is `widths/4`.

gap_thresh : float, optional
If a relative maximum is not found within *max_distances*, there will be a gap. A ridge line is discontinued if there are more than *gap_thresh* points without connecting a new relative maximum. Default is 2.

min_length : int, optional
Minimum length a ridge line needs to be acceptable. Default is `cwt.shape[0] / 4`, ie 1/4-th the number of widths.

min_snr : float, optional
Minimum SNR ratio. Default 1. The signal is the value of the cwt matrix at the shortest length scale (`cwt[0, loc]`), the noise is the *noise_perc'th percentile of datapoints contained within a window of 'window_size* around `cwt[0, loc]`.

noise_perc : float, optional
When calculating the noise floor, percentile of data points examined below which to consider noise. Calculated using *stats.scoreatpercentile*. Default is 10.

Returns

peaks_indices : list
Indices of the locations in the *vector* where peaks were found. The list is sorted.

See also:

`cwt`

Notes

This approach was designed for finding sharp peaks among noisy data, however with proper parameter selection it should function well for different peak shapes.

The algorithm is as follows:

1. Perform a continuous wavelet transform on *vector*, for the supplied *widths*. This is a convolution of *vector* with *wavelet(width)* for each width in *widths*. See `cwt`
2. Identify "ridge lines" in the cwt matrix. These are relative maxima at each row, connected across adjacent rows. See identify_ridge_lines
3. Filter the ridge_lines using filter_ridge_lines.

New in version 0.11.0.

References

[R174]

Examples

```
>>> from scipy import signal
>>> xs = np.arange(0, np.pi, 0.05)
>>> data = np.sin(xs)
>>> peakind = signal.find_peaks_cwt(data, np.arange(1,10))
```

```
>>> peakind, xs[peakind], data[peakind]
([32], array([ 1.6]), array([ 0.9995736]))
```

`scipy.signal.`**`argrelmin`**(*data*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative minima of *data*.

Parameters **data** : ndarray

Array in which to find the relative minima.

axis : int, optional

Axis over which to select from *data*. Default is 0.

order : int, optional

How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.

mode : str, optional

How the edges of the vector are treated. Available options are 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default 'clip'. See numpy.take

Returns **extrema** : tuple of ndarrays

Indices of the minima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is one-dimensional.

See also:

`argrelextrema`, `argrelmax`

Notes

This function uses `argrelextrema` with np.less as comparator.

New in version 0.11.0.

Examples

```
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmin(x)
(array([1, 5]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
>>> argrelmin(y, axis=1)
(array([0, 2]), array([2, 1]))
```

`scipy.signal.`**`argrelmax`**(*data*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative maxima of *data*.

Parameters **data** : ndarray

Array in which to find the relative maxima.

axis : int, optional

Axis over which to select from *data*. Default is 0.

order : int, optional

How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.

mode : str, optional

How the edges of the vector are treated. Available options are 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default 'clip'. See `numpy.take`.

Returns **extrema** : tuple of ndarrays

Indices of the maxima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is one-dimensional.

See also:

`argrelextrema`, `argrelmin`

Notes

This function uses `argrelextrema` with np.greater as comparator.

New in version 0.11.0.

Examples

```
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmax(x)
(array([3, 6]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
>>> argrelmax(y, axis=1)
(array([0]), array([1]))
```

`scipy.signal.`**`argrelextrema`**(*data*, *comparator*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative extrema of *data*.

Parameters **data** : ndarray

Array in which to find the relative extrema.

comparator : callable

Function to use to compare two data points. Should take 2 numbers as arguments.

axis : int, optional

Axis over which to select from *data*. Default is 0.

order : int, optional

How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.

mode : str, optional

How the edges of the vector are treated. 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default is 'clip'. See `numpy.take`.

Returns **extrema** : tuple of ndarrays

Indices of the maxima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is one-dimensional.

See also:

`argrelmin`, `argrelmax`

Notes

New in version 0.11.0.

Examples

```
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelextrema(x, np.greater)
(array([3, 6]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
>>> argrelextrema(y, np.less, axis=1)
(array([0, 2]), array([2, 1]))
```

5.27.13 Spectral Analysis

`periodogram`(x[, fs, window, nfft, detrend, ...])	Estimate power spectral density using a periodogram.
`welch`(x[, fs, window, nperseg, noverlap, ...])	Estimate power spectral density using Welch's method.
`csd`(x, y[, fs, window, nperseg, noverlap, ...])	Estimate the cross power spectral density, Pxy, using Welch's method.
`coherence`(x, y[, fs, window, nperseg, ...])	Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals
`spectrogram`(x[, fs, window, nperseg, ...])	Compute a spectrogram with consecutive Fourier transforms.
`lombscargle`(x, y, freqs)	Computes the Lomb-Scargle periodogram.
`vectorstrength`(events, period)	Determine the vector strength of the events corresponding to the given period.

`scipy.signal.`**`periodogram`**(*x*, *fs=1.0*, *window=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=-1*)

Estimate power spectral density using a periodogram.

Parameters

x : array_like

Time series of measurement values

fs : float, optional

Sampling frequency of the *x* time series. Defaults to 1.0.

window : str or tuple or array_like, optional

Desired window to use. See `get_window` for a list of windows and required parameters. If *window* is an array it will be used directly as the window. Defaults to None; equivalent to 'boxcar'.

nfft : int, optional

Length of the FFT used. If None the length of *x* will be used.

detrend : str or function or False, optional

Specifies how to detrend *x* prior to computing the spectrum. If `detrend` is a string, it is passed as the `type` argument to `detrend`. If it is a function, it should return a detrended array. If `detrend` is False, no detrending is done. Defaults to 'constant'.

return_onesided : bool, optional

If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.

scaling : { 'density', 'spectrum' }, optional

Selects between computing the power spectral density ('density') where *Pxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Pxx* has units of V**2, if *x* is measured in V and fs is measured in Hz. Defaults to 'density'

axis : int, optional

Axis along which the periodogram is computed; the default is over the last axis (i.e. `axis=-1`).

Returns

f : ndarray

Array of sample frequencies.

Pxx : ndarray
Power spectral density or power spectrum of *x*.

See also:

`welch`	Estimate power spectral density using Welch's method
`lombscargle`	Lomb-Scargle periodogram for unevenly sampled data

Notes

New in version 0.12.0.

Examples

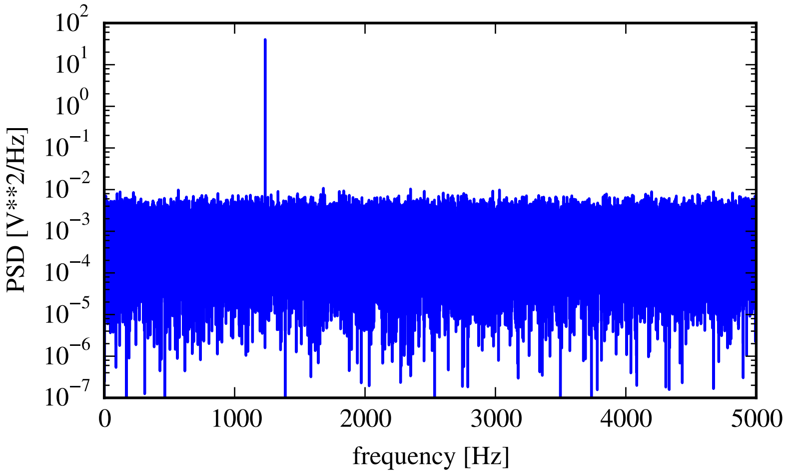
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the power spectral density.

```
>>> f, Pxx_den = signal.periodogram(x, fs)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([1e-7, 1e2])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

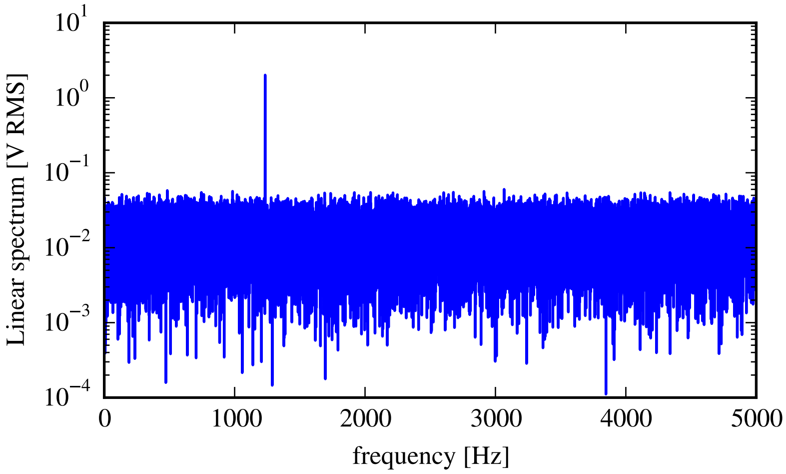


If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.

```
>>> np.mean(Pxx_den[256:])
0.0009924865443739191
```

Now compute and plot the power spectrum.

```
>>> f, Pxx_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.ylim([1e-4, 1e1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```



The peak height in the power spectrum is an estimate of the RMS amplitude.

```
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

`scipy.signal.`**`welch`**(*x*, *fs=1.0*, *window='hanning'*, *nperseg=256*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=-1*)

Estimate power spectral density using Welch's method.

Welch's method [R200] computes an estimate of the power spectral density by dividing the data into overlapping segments, computing a modified periodogram for each segment and averaging the periodograms.

Parameters

x : array_like

Time series of measurement values

fs : float, optional

Sampling frequency of the *x* time series. Defaults to 1.0.

window : str or tuple or array_like, optional

Desired window to use. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length will be used for nperseg. Defaults to 'hanning'.

nperseg : int, optional

Length of each segment. Defaults to 256.

noverlap : int, optional
Number of points to overlap between segments. If None, `noverlap = nperseg // 2`. Defaults to None.

nfft : int, optional
Length of the FFT used, if a zero padded FFT is desired. If None, the FFT length is *nperseg*. Defaults to None.

detrend : str or function or False, optional
Specifies how to detrend each segment. If `detrend` is a string, it is passed as the `type` argument to `detrend`. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is False, no detrending is done. Defaults to 'constant'.

return_onesided : bool, optional
If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.

scaling : { 'density', 'spectrum' }, optional
Selects between computing the power spectral density ('density') where *Pxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Pxx* has units of V**2, if *x* is measured in V and fs is measured in Hz. Defaults to 'density'

axis : int, optional
Axis along which the periodogram is computed; the default is over the last axis (i.e. `axis=-1`).

Returns

f : ndarray
Array of sample frequencies.

Pxx : ndarray
Power spectral density or power spectrum of x.

See also:

`periodogram`
Simple, optionally modified periodogram

`lombscargle`
Lomb-Scargle periodogram for unevenly sampled data

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default 'hanning' window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

If *noverlap* is 0, this method is equivalent to Bartlett's method [R201].

New in version 0.12.0.

References

[R200], [R201]

Examples

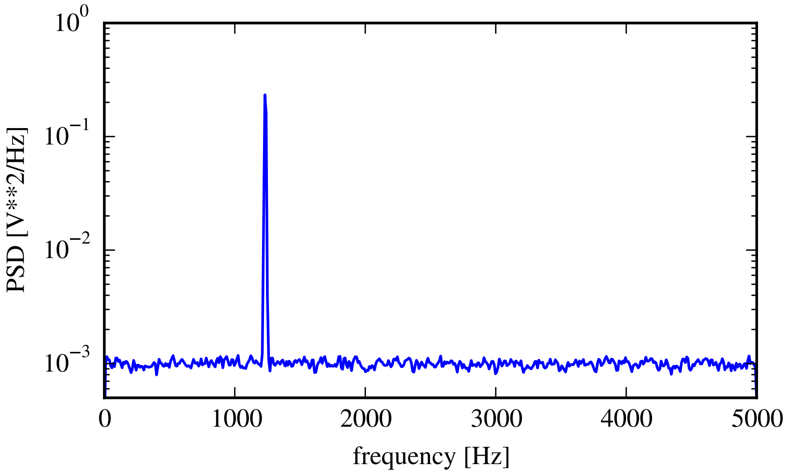
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the power spectral density.

```
>>> f, Pxx_den = signal.welch(x, fs, nperseg=1024)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([0.5e-3, 1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

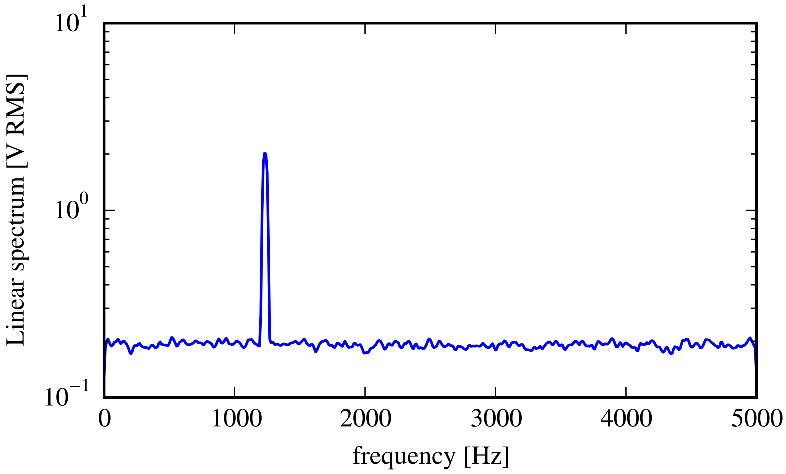


If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.

```
>>> np.mean(Pxx_den[256:])
0.0009924865443739191
```

Now compute and plot the power spectrum.

```
>>> f, Pxx_spec = signal.welch(x, fs, 'flattop', 1024, scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```



The peak height in the power spectrum is an estimate of the RMS amplitude.

```
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

`scipy.signal.csd`(*x*, *y*, *fs=1.0*, *window='hanning'*, *nperseg=256*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=-1*)

Estimate the cross power spectral density, Pxy, using Welch's method.

Parameters

x : array_like

Time series of measurement values

y : array_like

Time series of measurement values

fs : float, optional

Sampling frequency of the *x* and *y* time series. Defaults to 1.0.

window : str or tuple or array_like, optional

Desired window to use. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length will be used for nperseg. Defaults to 'hanning'.

nperseg : int, optional

Length of each segment. Defaults to 256.

noverlap: int, optional

Number of points to overlap between segments. If None, `noverlap = nperseg // 2`. Defaults to None.

nfft : int, optional

Length of the FFT used, if a zero padded FFT is desired. If None, the FFT length is *nperseg*. Defaults to None.

detrend : str or function or False, optional

Specifies how to detrend each segment. If `detrend` is a string, it is passed as the `type` argument to `detrend`. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is False, no detrending is done. Defaults to 'constant'.

return_onesided : bool, optional

If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.

scaling : { 'density', 'spectrum' }, optional

Selects between computing the cross spectral density ('density') where *Pxy* has units of V**2/Hz and computing the cross spectrum ('spectrum') where *Pxy* has units of V**2, if *x* and *y* are measured in V and fs is measured in Hz. Defaults to 'density'

axis : int, optional

Axis along which the CSD is computed for both inputs; the default is over the last axis (i.e. `axis=-1`).

Returns

f : ndarray

Array of sample frequencies.

Pxy : ndarray

Cross spectral density or cross power spectrum of x,y.

See also:

`periodogram`	Simple, optionally modified periodogram
`lombscargle`	Lomb-Scargle periodogram for unevenly sampled data
`welch`	Power spectral density by Welch's method. [Equivalent to csd(x,x)]
`coherence`	Magnitude squared coherence by Welch's method.

Notes

By convention, Pxy is computed with the conjugate FFT of X multiplied by the FFT of Y.

If the input series differ in length, the shorter series will be zero-padded to match.

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default 'hanning' window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References

[R171], [R172]

Examples

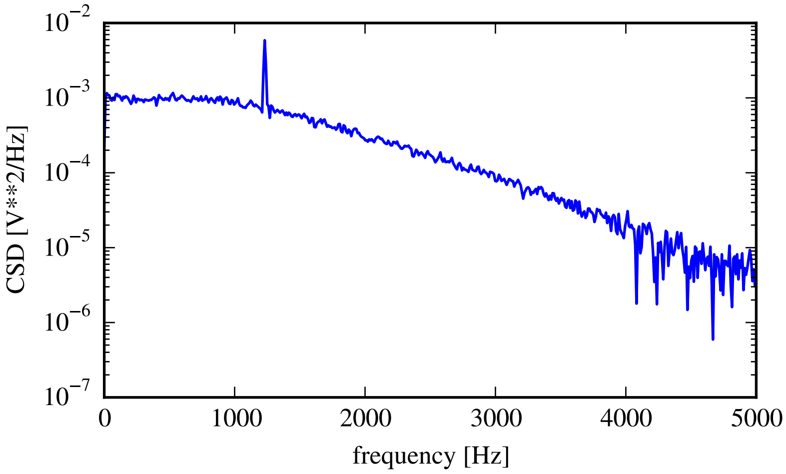
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate two test signals with some common features.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += np.random.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)
```

Compute and plot the magnitude of the cross spectral density.

```
>>> f, Pxy = signal.csd(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, np.abs(Pxy))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('CSD [V**2/Hz]')
>>> plt.show()
```



`scipy.signal.`**`coherence`**(*x*, *y*, *fs=1.0*, *window='hanning'*, *nperseg=256*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *axis=-1*)

Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals X and Y using Welch's method.

Cxy = abs(Pxy)**2/(Pxx*Pyy), where Pxx and Pyy are power spectral density estimates of X and Y, and Pxy is the cross spectral density estimate of X and Y.

Parameters

x : array_like
  Time series of measurement values

y : array_like
  Time series of measurement values

fs : float, optional
  Sampling frequency of the *x* and *y* time series. Defaults to 1.0.

window : str or tuple or array_like, optional
  Desired window to use. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length will be used for nperseg. Defaults to 'hanning'.

nperseg : int, optional
  Length of each segment. Defaults to 256.

noverlap: int, optional
  Number of points to overlap between segments. If None, `noverlap = nperseg // 2`. Defaults to None.

nfft : int, optional
  Length of the FFT used, if a zero padded FFT is desired. If None, the FFT length is *nperseg*. Defaults to None.

detrend : str or function or False, optional
  Specifies how to detrend each segment. If `detrend` is a string, it is passed as the `type` argument to `detrend`. If it is a function, it takes a segment

and returns a detrended segment. If `detrend` is False, no detrending is done. Defaults to 'constant'.

axis : int, optional

Axis along which the coherence is computed for both inputs; the default is over the last axis (i.e. `axis=-1`).

Returns

f : ndarray

Array of sample frequencies.

Cxy : ndarray

Magnitude squared coherence of x and y.

See also:

`periodogram`	Simple, optionally modified periodogram
`lombscargle`	Lomb-Scargle periodogram for unevenly sampled data
`welch`	Power spectral density by Welch's method.
`csd`	Cross spectral density by Welch's method.

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default 'hanning' window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References

[R166], [R167]

Examples

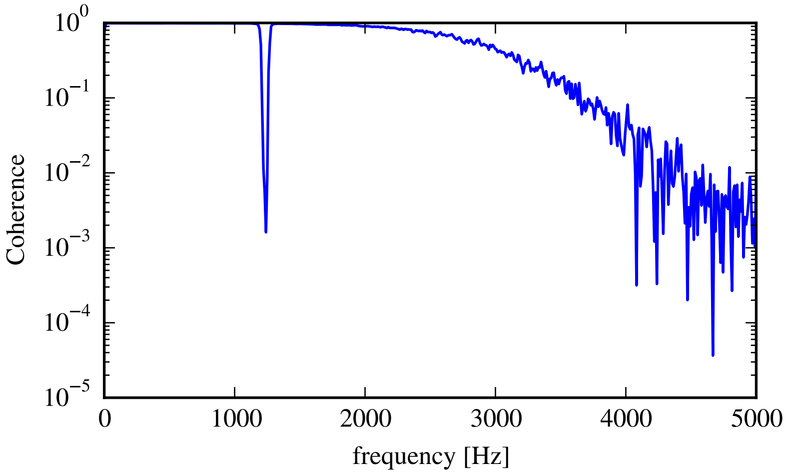
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate two test signals with some common features.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += np.random.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)
```

Compute and plot the coherence.

```
>>> f, Cxy = signal.coherence(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, Cxy)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Coherence')
>>> plt.show()
```



`scipy.signal.`**`spectrogram`**(*x*, *fs=1.0*, *window=('tukey', 0.25)*, *nperseg=256*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=-1*)

Compute a spectrogram with consecutive Fourier transforms.

Spectrograms can be used as a way of visualizing the change of a nonstationary signal's frequency content over time.

Parameters

x : array_like
  Time series of measurement values

fs : float, optional
  Sampling frequency of the *x* time series. Defaults to 1.0.

window : str or tuple or array_like, optional
  Desired window to use. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length will be used for nperseg. Defaults to a Tukey window with shape parameter of 0.25.

nperseg : int, optional
  Length of each segment. Defaults to 256.

noverlap : int, optional
  Number of points to overlap between segments. If None, `noverlap = nperseg // 8`. Defaults to None.

nfft : int, optional
  Length of the FFT used, if a zero padded FFT is desired. If None, the FFT length is *nperseg*. Defaults to None.

detrend : str or function or False, optional
  Specifies how to detrend each segment. If `detrend` is a string, it is passed as the `type` argument to `detrend`. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is False, no detrending is done. Defaults to 'constant'.

return_onesided : bool, optional
  If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.

scaling : { 'density', 'spectrum' }, optional

Selects between computing the power spectral density ('density') where *Pxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Pxx* has units of V**2, if *x* is measured in V and fs is measured in Hz. Defaults to 'density'

axis : int, optional

Axis along which the spectrogram is computed; the default is over the last axis (i.e. `axis=-1`).

Returns **f** : ndarray

Array of sample frequencies.

t : ndarray

Array of segment times.

Sxx : ndarray

Spectrogram of x. By default, the last axis of Sxx corresponds to the segment times.

See also:

`periodogram`	Simple, optionally modified periodogram
`lombscargle`	Lomb-Scargle periodogram for unevenly sampled data
`welch`	Power spectral density by Welch's method.
`csd`	Cross spectral density by Welch's method.

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. In contrast to welch's method, where the entire data stream is averaged over, one may wish to use a smaller overlap (or perhaps none at all) when computing a spectrogram, to maintain some statistical independence between individual segments.

New in version 0.16.0.

References

...[1] Oppenheim, Alan V., Ronald W. Schafer, John R. Buck "Discrete-Time

Signal Processing", Prentice Hall, 1999.

Examples

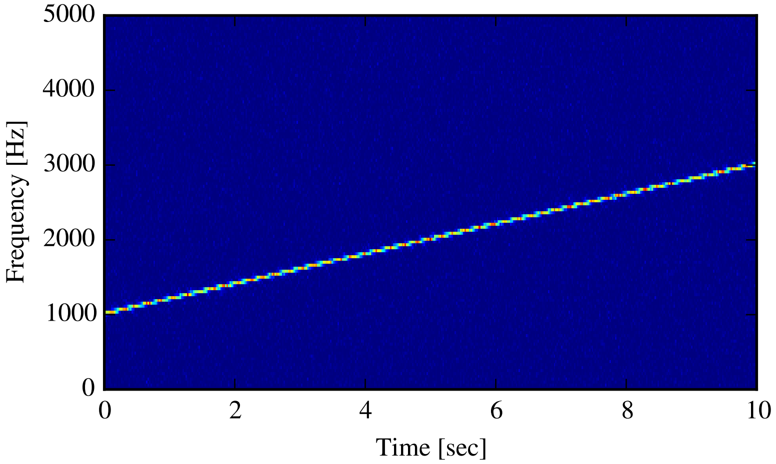
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate a test signal, a 2 Vrms sine wave whose frequency linearly changes with time from 1kHz to 2kHz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> freq = np.linspace(1e3, 2e3, N)
>>> x = amp * np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the spectrogram.

```
>>> f, t, Sxx = signal.spectrogram(x, fs)
>>> plt.pcolormesh(t, f, Sxx)
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```



`scipy.signal.`**`lombscargle`**(*x*, *y*, *freqs*)

Computes the Lomb-Scargle periodogram.

The Lomb-Scargle periodogram was developed by Lomb [R191] and further extended by Scargle [R192] to find, and test the significance of weak periodic signals with uneven temporal sampling.

The computed periodogram is unnormalized, it takes the value `(A**2) * N/4` for a harmonic signal with amplitude A for sufficiently large N.

Parameters

x : array_like

Sample times.

y : array_like

Measurement values.

freqs : array_like

Angular frequencies for output periodogram.

Returns

pgram : array_like

Lomb-Scargle periodogram.

Raises

ValueError

If the input arrays *x* and *y* do not have the same shape.

Notes

This subroutine calculates the periodogram using a slightly modified algorithm due to Townsend [R193] which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The algorithm running time scales roughly as O(x * freqs) or O(N^2) for a large number of samples and frequencies.

References

[R191], [R192], [R193]

Examples

```
>>> import scipy.signal
>>> import matplotlib.pyplot as plt
```

First define some input parameters for the signal:

```
>>> A = 2.
>>> w = 1.
>>> phi = 0.5 * np.pi
>>> nin = 1000
>>> nout = 100000
>>> frac_points = 0.9 # Fraction of points to select
```

Randomly select a fraction of an array with timesteps:

```
>>> r = np.random.rand(nin)
>>> x = np.linspace(0.01, 10*np.pi, nin)
>>> x = x[r >= frac_points]
>>> normval = x.shape[0] # For normalization of the periodogram
```

Plot a sine wave for the selected times:

```
>>> y = A * np.sin(w*x+phi)
```

Define the array of frequencies for which to compute the periodogram:

```
>>> f = np.linspace(0.01, 10, nout)
```

Calculate Lomb-Scargle periodogram:

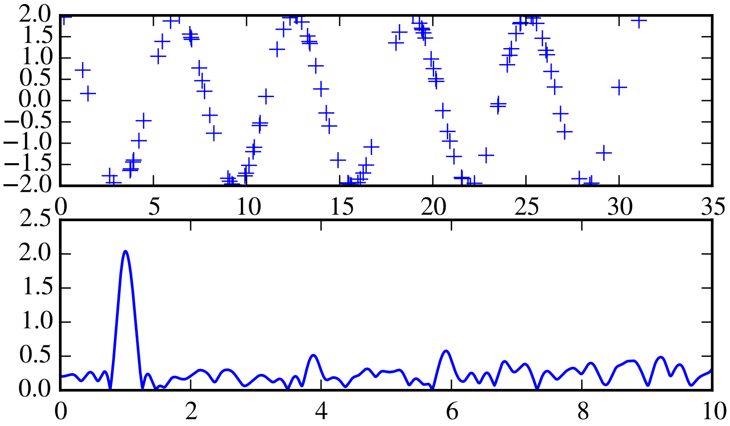
```
>>> import scipy.signal as signal
>>> pgram = signal.lombscargle(x, y, f)
```

Now make a plot of the input data:

```
>>> plt.subplot(2, 1, 1)
<matplotlib.axes.AxesSubplot object at 0x102154f50>
>>> plt.plot(x, y, 'b+')
[<matplotlib.lines.Line2D object at 0x102154a10>]
```

Then plot the normalized periodogram:

```
>>> plt.subplot(2, 1, 2)
<matplotlib.axes.AxesSubplot object at 0x104b0a990>
>>> plt.plot(f, np.sqrt(4*(pgram/normval)))
[<matplotlib.lines.Line2D object at 0x104b2f910>]
>>> plt.show()
```



`scipy.signal.`**`vectorstrength`**(*events*, *period*)

Determine the vector strength of the events corresponding to the given period.

The vector strength is a measure of phase synchrony, how well the timing of the events is synchronized to a single period of a periodic signal.

If multiple periods are used, calculate the vector strength of each. This is called the “resonating vector strength”.

Parameters

events : 1D array_like

An array of time points containing the timing of the events.

period : float or array_like

The period of the signal that the events should synchronize to. The period is in the same units as *events*. It can also be an array of periods, in which case the outputs are arrays of the same length.

Returns

strength : float or 1D array

The strength of the synchronization. 1.0 is perfect synchronization and 0.0 is no synchronization. If *period* is an array, this is also an array with each element containing the vector strength at the corresponding period.

phase : float or array

The phase that the events are most strongly synchronized to in radians. If *period* is an array, this is also an array with each element containing the phase for the corresponding period.

References

van Hemmen, JL, Longtin, A, and Vollmayr, AN. Testing resonating vector strength: Auditory system, electric fish, and noise. Chaos 21, 047508 (2011); doi: 10.1063/1.3670512

van Hemmen, JL. Vector strength after Goldberg, Brown, and von Mises: biological and mathematical perspectives. Biol Cybern. 2013 Aug;107(4):385-96. doi: 10.1007/s00422-013-0561-7.

van Hemmen, JL and Vollmayr, AN. Resonating vector strength: what happens when we vary the “probing” frequency while keeping the spike times fixed. Biol Cybern. 2013 Aug;107(4):491-94. doi: 10.1007/s00422-013-0560-8

5.28 Sparse matrices (`scipy.sparse`)

SciPy 2-D sparse matrix package for numeric data.

5.28.1 Contents

Sparse matrix classes

`bsr_matrix`(arg1[, shape, dtype, copy, blocksize])	Block Sparse Row matrix
`coo_matrix`(arg1[, shape, dtype, copy])	A sparse matrix in COOrdinate format.
`csc_matrix`(arg1[, shape, dtype, copy])	Compressed Sparse Column matrix
`csr_matrix`(arg1[, shape, dtype, copy])	Compressed Sparse Row matrix
`dia_matrix`(arg1[, shape, dtype, copy])	Sparse matrix with DIAgonal storage
`dok_matrix`(arg1[, shape, dtype, copy])	Dictionary Of Keys based sparse matrix.
`lil_matrix`(arg1[, shape, dtype, copy])	Row-based linked list sparse matrix

class `scipy.sparse.`**`bsr_matrix`**(*arg1*, *shape=None*, *dtype=None*, *copy=False*, *blocksize=None*)

Block Sparse Row matrix

This can be instantiated in several ways:

bsr_matrix(D, [blocksize=(R,C)])
where D is a dense matrix or 2-D ndarray.

bsr_matrix(S, [blocksize=(R,C)])
with another sparse matrix S (equivalent to S.tobsr())

bsr_matrix((M, N), [blocksize=(R,C), dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

bsr_matrix((data, ij), [blocksize=(R,C), shape=(M, N)])
where `data` and `ij` satisfy `a[ij[0, k], ij[1, k]] = data[k]`

bsr_matrix((data, indices, indptr), [shape=(M, N)])
is the standard BSR representation where the block column indices for row i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding block values are stored in `data[ indptr[i]: indptr[i+1] ]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Summary of BSR format

The Block Compressed Row (BSR) format is very similar to the Compressed Sparse Row (CSR) format. BSR is appropriate for sparse matrices with dense sub matrices like the last example below. Block matrices often arise in vector-valued finite element discretizations. In such cases, BSR is considerably more efficient than CSR and CSC for many sparse arithmetic operations.

Blocksize

The blocksize (R,C) must evenly divide the shape of the matrix (M,N). That is, R and C must satisfy the relationship `M % R = 0` and `N % C = 0`.

If no blocksize is specified, a simple heuristic is applied to determine an appropriate blocksize.

Examples

```
>>> from scipy.sparse import bsr_matrix
>>> bsr_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 0, 1, 2, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3 ,4, 5, 6])
>>> bsr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6]).repeat(4).reshape(6, 2, 2)
>>> bsr_matrix((data,indices,indptr), shape=(6, 6)).toarray()
array([[1, 1, 0, 0, 2, 2],
       [1, 1, 0, 0, 2, 2],
       [0, 0, 0, 0, 3, 3],
       [0, 0, 0, 0, 3, 3],
       [4, 4, 5, 5, 6, 6],
       [4, 4, 5, 5, 6, 6]])
```

Attributes

`has_sorted_indices`	Determine whether the matrix has sorted indices

`bsr_matrix.`**`has_sorted_indices`**

Determine whether the matrix has sorted indices

Returns

- True: if the indices of the matrix are in sorted order
- False: otherwise

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
nnz	Number of nonzero elements
data	Data array of the matrix
indices	BSR format index array
indptr	BSR format index pointer array
blocksize	Block size of the matrix

Methods

`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`asformat`(format)	Return this matrix in a given sparse format

Continued on next page

Table 5.140 – continued from previous page

`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`ceil`()	Element-wise ceil.
`check_format`([full_check])	check whether the matrix format is valid
`conj`()	
`conjugate`()	
`copy`()	
`deg2rad`()	Element-wise deg2rad.
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`eliminate_zeros`()	
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	
`get_shape`()	
`getcol`(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
`getdata`(ind)	
`getformat`()	
`getmaxprint`()	
`getnnz`()	
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
`log1p`()	Element-wise log1p.
`matmat`(other)	
`matvec`(other)	
`max`([axis])	Maximum of the elements of this matrix.
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`min`([axis])	Minimum of the elements of this matrix.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix, vector, or scalar.
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`prune`()	Remove empty space after all non-zero elements.
`rad2deg`()	Element-wise rad2deg.
`reshape`(shape)	
`rint`()	Element-wise rint.
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sign`()	Element-wise sign.
`sin`()	Element-wise sin.
`sinh`()	Element-wise sinh.
`sort_indices`()	Sort the indices of this matrix *in place*
`sorted_indices`()	Return a copy of this matrix with sorted indices
`sqrt`()	Element-wise sqrt.
`sum`([axis])	Sum the matrix over the given axis.
`sum_duplicates`()	
`tan`()	Element-wise tan.
`tanh`()	Element-wise tanh.
`toarray`([order, out])	See the docstring for `spmatrix.toarray`.
`tobsr`([blocksize, copy])	

Continued on next page

Table 5.140 – continued from previous page

tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc()	
tocsr()	
todense([order, out])	Return a dense matrix representation of this matrix.
todia()	
todok()	
tolil()	
transpose()	
trunc()	Element-wise trunc.

`bsr_matrix.`**`arcsin`**`()`

Element-wise arcsin.

See numpy.arcsin for more information.

`bsr_matrix.`**`arcsinh`**`()`

Element-wise arcsinh.

See numpy.arcsinh for more information.

`bsr_matrix.`**`arctan`**`()`

Element-wise arctan.

See numpy.arctan for more information.

`bsr_matrix.`**`arctanh`**`()`

Element-wise arctanh.

See numpy.arctanh for more information.

`bsr_matrix.`**`asformat`**`(`*format*`)`

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- None for no format conversion
- "csr" for csr_matrix format
- "csc" for csc_matrix format
- "lil" for lil_matrix format
- "dok" for dok_matrix format and so on

`bsr_matrix.`**`asfptype`**`()`

Upcast matrix to a floating point format (if necessary)

`bsr_matrix.`**`astype`**`(`*t*`)`

`bsr_matrix.`**`ceil`**`()`

Element-wise ceil.

See numpy.ceil for more information.

`bsr_matrix.`**`check_format`**`(`*full_check=True*`)`

check whether the matrix format is valid

Parameters*:*

full_check: True - rigorous check, O(N) operations : default False - basic check, O(1) operations `bsr_matrix.`**`conj`**`()`

`bsr_matrix.`**`conjugate`**`()`

`bsr_matrix.`**`copy`**`()`

`bsr_matrix.`**`deg2rad`**`()`

Element-wise deg2rad.

See numpy.deg2rad for more information.

`bsr_matrix.`**`diagonal`**`()`

Returns the main diagonal of the matrix

`bsr_matrix.`**`dot`**`(`*other*`)`

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

`bsr_matrix.`**`eliminate_zeros`**`()`

`bsr_matrix.`**`expm1`**`()`

Element-wise expm1.

See numpy.expm1 for more information.

`bsr_matrix.`**`floor`**`()`

Element-wise floor.

See numpy.floor for more information.

`bsr_matrix.`**`getH`**`()`

`bsr_matrix.`**`get_shape`**`()`

`bsr_matrix.`**`getcol`**`(`*j*`)`

Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

`bsr_matrix.`**`getdata`**`(`*ind*`)`

`bsr_matrix.`**`getformat`**`()`

`bsr_matrix.`**`getmaxprint`**`()`

`bsr_matrix.`**`getnnz`**`()`

`bsr_matrix.`**`getrow`**`(`*i*`)`

Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

`bsr_matrix.`**`log1p`**`()`

Element-wise log1p.

See numpy.log1p for more information.

`bsr_matrix.`**`matmat`**`(`*other*`)`

`bsr_matrix.`**`matvec`**`(`*other*`)`

`bsr_matrix.`**`max`**`(`*axis=None*`)`

Maximum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns **amax** : self.dtype

Maximum element.

`bsr_matrix.`**`maximum`**`(`*other*`)`

`bsr_matrix.`**`mean`**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`bsr_matrix.`**`min`**`(`*axis=None*`)`

Minimum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns **amin** : self.dtype

Minimum element.

`bsr_matrix.`**`minimum`**`(`*other*`)`

`bsr_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix, vector, or scalar.

`bsr_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`bsr_matrix.`**`power`**`(`*n*, *dtype=None*`)`

This function performs element-wise power.

Parameters **n** : n is a scalar

dtype : If dtype is not specified, the current dtype will be preserved.

`bsr_matrix.`**`prune`**`()`

Remove empty space after all non-zero elements.

`bsr_matrix.`**`rad2deg`**`()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

`bsr_matrix.`**`reshape`**`(`*shape*`)`

`bsr_matrix.`**`rint`**`()`

Element-wise rint.

See numpy.rint for more information.

`bsr_matrix.`**`set_shape`**`(`*shape*`)`

`bsr_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters	**values** : array_like New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.
	k : int, optional Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`bsr_matrix.`**`sign`**`()`

Element-wise sign.

See numpy.sign for more information.

`bsr_matrix.`**`sin`**`()`

Element-wise sin.

See numpy.sin for more information.

`bsr_matrix.`**`sinh`**`()`

Element-wise sinh.

See numpy.sinh for more information.

`bsr_matrix.`**`sort_indices`**`()`

Sort the indices of this matrix *in place*

`bsr_matrix.`**`sorted_indices`**`()`

Return a copy of this matrix with sorted indices

`bsr_matrix.`**`sqrt`**`()`

Element-wise sqrt.

See numpy.sqrt for more information.

`bsr_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`bsr_matrix.`**`sum_duplicates`**`()`

`bsr_matrix.`**`tan`**`()`

Element-wise tan.

See numpy.tan for more information.

`bsr_matrix.`**`tanh`**`()`

Element-wise tanh.

See numpy.tanh for more information.

`bsr_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

See the docstring for `spmatrix.toarray`.

`bsr_matrix.`**`tobsr`**`(`*blocksize=None*, *copy=False*`)`

`bsr_matrix.`**`tocoo`**`(`*copy=True*`)`

Convert this matrix to COOrdinate format.

When copy=False the data array will be shared between this matrix and the resultant coo_matrix.

`bsr_matrix.`**`tocsc`**`()`

`bsr_matrix.`**`tocsr`**`()`

`bsr_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters	**order** : {'C', 'F'}, optional Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument. **out** : ndarray, 2-dimensional, optional If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.
Returns	**arr** : numpy.matrix, 2-dimensional A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`bsr_matrix.`**`todia`**`()`

`bsr_matrix.`**`todok`**`()`

`bsr_matrix.`**`tolil`**`()`

`bsr_matrix.`**`transpose`**`()`

`bsr_matrix.`**`trunc`**`()`

Element-wise trunc.

See numpy.trunc for more information.

class `scipy.sparse.`**`coo_matrix`**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

A sparse matrix in COOrdinate format.

Also known as the 'ijv' or 'triplet' format.

This can be instantiated in several ways:

coo_matrix(D)
with a dense matrix D

coo_matrix(S) with another sparse matrix S (equivalent to S.tocoo())

coo_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

coo_matrix((data, (i, j)), [shape=(M, N)])

to construct from three arrays:

1. data[:] the entries of the matrix, in any order
2. i[:] the row indices of the matrix entries
3. j[:] the column indices of the matrix entries

Where `A[i[k], j[k]] = data[k]`. When shape is not specified, it is inferred from the index arrays

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the COO format

- facilitates fast conversion among sparse formats
- permits duplicate entries (see example)
- very fast conversion to and from CSR/CSC formats

Disadvantages of the COO format

- ***does not directly support:***
  - arithmetic operations
  - slicing

Intended Usage

- COO is a fast format for constructing sparse matrices
- Once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and matrix vector operations
- By default when converting to CSR or CSC format, duplicate (i,j) entries will be summed together. This facilitates efficient construction of finite element matrices and the like. (see example)

Examples

```
>>> from scipy.sparse import coo_matrix
>>> coo_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row  = np.array([0, 3, 1, 0])
>>> col  = np.array([0, 3, 1, 2])
>>> data = np.array([4, 5, 7, 9])
>>> coo_matrix((data, (row, col)), shape=(4, 4)).toarray()
array([[4, 0, 9, 0],
       [0, 7, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 5]])
```

```
>>> # example with duplicates
>>> row  = np.array([0, 0, 1, 3, 1, 0, 0])
>>> col  = np.array([0, 2, 1, 3, 1, 0, 0])
>>> data = np.array([1, 1, 1, 1, 1, 1, 1])
>>> coo_matrix((data, (row, col)), shape=(4, 4)).toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

Attributes

`nnz`	Get the count of explicitly-stored values (nonzeros)

`coo_matrix.`**`nnz`**

Get the count of explicitly-stored values (nonzeros)

Parameters **axis** : None, 0, or 1

Select between the number of values across the whole matrix, in each column, or in each row.

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
data	COO format data array of the matrix
row	COO format row index array of the matrix
col	COO format column index array of the matrix

Methods

`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`ceil`()	Element-wise ceil.
`conj`()	
`conjugate`()	
`copy`()	
`deg2rad`()	Element-wise deg2rad.
`diagonal`()	Returns the main diagonal of the matrix

Continued on next page

Table 5.142 – continued from previous page

`dot`(other)	Ordinary dot product
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	
`get_shape`()	
`getcol`(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
`getformat`()	
`getmaxprint`()	
`getnnz`([axis])	Get the count of explicitly-stored values (nonzeros)
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
`log1p`()	Element-wise log1p.
`max`([axis])	Maximum of the elements of this matrix.
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`min`([axis])	Minimum of the elements of this matrix.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`rad2deg`()	Element-wise rad2deg.
`reshape`(shape)	
`rint`()	Element-wise rint.
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sign`()	Element-wise sign.
`sin`()	Element-wise sin.
`sinh`()	Element-wise sinh.
`sqrt`()	Element-wise sqrt.
`sum`([axis])	Sum the matrix over the given axis.
`sum_duplicates`()	Eliminate duplicate matrix entries by adding them together
`tan`()	Element-wise tan.
`tanh`()	Element-wise tanh.
`toarray`([order, out])	See the docstring for `spmatrix.toarray`.
`tobsr`([blocksize])	
`tocoo`([copy])	
`tocsc`()	Return a copy of this matrix in Compressed Sparse Column format
`tocsr`()	Return a copy of this matrix in Compressed Sparse Row format
`todense`([order, out])	Return a dense matrix representation of this matrix.
`todia`()	
`todok`()	
`tolil`()	
`transpose`([copy])	
`trunc`()	Element-wise trunc.

`coo_matrix.`**`arcsin`**`()`

Element-wise arcsin.

See numpy.arcsin for more information.

`coo_matrix.`**`arcsinh`**`()`

Element-wise arcsinh.

See numpy.arcsinh for more information.

`coo_matrix.`**`arctan`**`()`

Element-wise arctan.

See numpy.arctan for more information.

`coo_matrix.`**`arctanh`**`()`

Element-wise arctanh.

See numpy.arctanh for more information.

`coo_matrix.`**`asformat`**`(`*format*`)`

Return this matrix in a given sparse format

Parameters	**format** : {string, None} ***desired sparse matrix format*** •None for no format conversion •“csr” for csr_matrix format •“csc” for csc_matrix format •“lil” for lil_matrix format •“dok” for dok_matrix format and so on

`coo_matrix.`**`asfptype`**`()`

Upcast matrix to a floating point format (if necessary)

`coo_matrix.`**`astype`**`(`*t*`)`

`coo_matrix.`**`ceil`**`()`

Element-wise ceil.

See numpy.ceil for more information.

`coo_matrix.`**`conj`**`()`

`coo_matrix.`**`conjugate`**`()`

`coo_matrix.`**`copy`**`()`

`coo_matrix.`**`deg2rad`**`()`

Element-wise deg2rad.

See numpy.deg2rad for more information.

`coo_matrix.`**`diagonal`**`()`

Returns the main diagonal of the matrix

`coo_matrix.`**`dot`**`(`*other*`)`

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

`coo_matrix.`**`expm1`**`()`

Element-wise expm1.

See numpy.expm1 for more information.

`coo_matrix.`**`floor`**`()`

Element-wise floor.

See numpy.floor for more information.

`coo_matrix.`**`getH`**`()`

`coo_matrix.`**`get_shape`**`()`

`coo_matrix.`**`getcol`**`(`*j*`)`

Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

`coo_matrix.`**`getformat`**`()`

`coo_matrix.`**`getmaxprint`**`()`

`coo_matrix.`**`getnnz`**`(`*axis=None*`)`

Get the count of explicitly-stored values (nonzeros)

Parameters	**axis** : None, 0, or 1 Select between the number of values across the whole matrix, in each column, or in each row.

`coo_matrix.`**`getrow`**`(`*i*`)`

Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

`coo_matrix.`**`log1p`**`()`

Element-wise log1p.

See numpy.log1p for more information.

`coo_matrix.`**`max`**`(`*axis=None*`)`

Maximum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns	**amax** : self.dtype Maximum element.

`coo_matrix.`**`maximum`**`(`*other*`)`

`coo_matrix.`**`mean`**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`coo_matrix.`**`min`**`(`*axis=None*`)`

Minimum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns	**amin** : self.dtype Minimum element.

`coo_matrix.`**`minimum`**`(`*other*`)`

`coo_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix

`coo_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`coo_matrix.`**`power`**`(`*n*, *dtype=None*`)`

This function performs element-wise power.

Parameters

n : n is a scalar

dtype : If dtype is not specified, the current dtype will be preserved.

`coo_matrix.`**`rad2deg`**`()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

`coo_matrix.`**`reshape`**`(`*shape*`)`

`coo_matrix.`**`rint`**`()`

Element-wise rint.

See numpy.rint for more information.

`coo_matrix.`**`set_shape`**`(`*shape*`)`

`coo_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters

values : array_like

New values of the diagonal elements.

Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.

If a scalar value is given, all of the diagonal is set to it.

k : int, optional

Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`coo_matrix.`**`sign`**`()`

Element-wise sign.

See numpy.sign for more information.

`coo_matrix.`**`sin`**`()`

Element-wise sin.

See numpy.sin for more information.

`coo_matrix.`**`sinh`**`()`

Element-wise sinh.

See numpy.sinh for more information.

`coo_matrix.`**`sqrt`**`()`

Element-wise sqrt.

See numpy.sqrt for more information.

`coo_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`coo_matrix.`**`sum_duplicates`**`()`

Eliminate duplicate matrix entries by adding them together

This is an *in place* operation

`coo_matrix.`**`tan`**`()`

Element-wise tan.

See numpy.tan for more information.

`coo_matrix.`**`tanh`**`()`

Element-wise tanh.

See numpy.tanh for more information.

`coo_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

See the docstring for `spmatrix.toarray`.

`coo_matrix.`**`tobsr`**`(`*blocksize=None*`)`

`coo_matrix.`**`tocoo`**`(`*copy=False*`)`

`coo_matrix.`**`tocsc`**`()`

Return a copy of this matrix in Compressed Sparse Column format

Duplicate entries will be summed together.

Examples

```
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row  = array([0, 0, 1, 3, 1, 0, 0])
>>> col  = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsc()
>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

`coo_matrix.`**`tocsr`**`()`

Return a copy of this matrix in Compressed Sparse Row format

Duplicate entries will be summed together.

Examples

```
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row  = array([0, 0, 1, 3, 1, 0, 0])
>>> col  = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsr()
>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

`coo_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters **order** : {'C', 'F'}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns **arr** : numpy.matrix, 2-dimensional

A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`coo_matrix.`**`todia`**`()`

`coo_matrix.`**`todok`**`()`

`coo_matrix.`**`tolil`**`()`

`coo_matrix.`**`transpose`**`(`*copy=False*`)`

`coo_matrix.`**`trunc`**`()`

Element-wise trunc.

See numpy.trunc for more information.

class `scipy.sparse.`**`csc_matrix`**`(`*arg1*, *shape=None*, *dtype=None*, *copy=False*`)`

Compressed Sparse Column matrix

This can be instantiated in several ways:

csc_matrix(D) with a dense matrix or rank-2 ndarray D

csc_matrix(S) with another sparse matrix S (equivalent to S.tocsc())

csc_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

csc_matrix((data, (row_ind, col_ind)), [shape=(M, N)])

where `data`, `row_ind` and `col_ind` satisfy the relationship `a[row_ind[k], col_ind[k]] = data[k]`.

csc_matrix((data, indices, indptr), [shape=(M, N)])
is the standard CSC representation where the row indices for column i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding values are stored in `data[indptr[i]:indptr[i+1]]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the CSC format

- efficient arithmetic operations CSC + CSC, CSC * CSC, etc.
- efficient column slicing
- fast matrix vector products (CSR, BSR may be faster)

Disadvantages of the CSC format

- slow row slicing operations (consider CSR)
- changes to the sparsity structure are expensive (consider LIL or DOK)

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix
>>> csc_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 2, 2, 0, 1, 2])
>>> col = np.array([0, 0, 1, 2, 2, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 4],
       [0, 0, 5],
       [2, 3, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 4],
       [0, 0, 5],
       [2, 3, 6]])
```

Attributes

`nnz`	Get the count of explicitly-stored values (nonzeros)
`has_sorted_indices`	Determine whether the matrix has sorted indices

`csc_matrix.`**`nnz`**
Get the count of explicitly-stored values (nonzeros)

Parameters **axis** : {None, 0, 1}, optional

Select between the number of values across the whole matrix, in each column, or in each row.

`csc_matrix.`**`has_sorted_indices`**

Determine whether the matrix has sorted indices

Returns

- True: if the indices of the matrix are in sorted order
- False: otherwise

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
data	Data array of the matrix
indices	CSC format index array
indptr	CSC format index pointer array

Methods

`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`ceil`()	Element-wise ceil.
`check_format`([full_check])	check whether the matrix format is valid
`conj`()	
`conjugate`()	
`copy`()	
`deg2rad`()	Element-wise deg2rad.
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`eliminate_zeros`()	Remove zero entries from the matrix
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	
`get_shape`()	
`getcol`(i)	Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).
`getformat`()	
`getmaxprint`()	
`getnnz`([axis])	Get the count of explicitly-stored values (nonzeros)
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
`log1p`()	Element-wise log1p.
`max`([axis])	Maximum of the elements of this matrix.
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`min`([axis])	Minimum of the elements of this matrix.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix, vector, or scalar.
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`prune`()	Remove empty space after all non-zero elements.

Continued on next page

Table 5.144 – continued from previous page

`rad2deg`()	Element-wise rad2deg.
`reshape`(shape)	
`rint`()	Element-wise rint.
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sign`()	Element-wise sign.
`sin`()	Element-wise sin.
`sinh`()	Element-wise sinh.
`sort_indices`()	Sort the indices of this matrix *in place*
`sorted_indices`()	Return a copy of this matrix with sorted indices
`sqrt`()	Element-wise sqrt.
`sum`([axis])	Sum the matrix over the given axis.
`sum_duplicates`()	Eliminate duplicate matrix entries by adding them together
`tan`()	Element-wise tan.
`tanh`()	Element-wise tanh.
`toarray`([order, out])	See the docstring for `spmatrix.toarray`.
`tobsr`([blocksize])	
`tocoo`([copy])	Return a COOrdinate representation of this matrix
`tocsc`([copy])	
`tocsr`()	
`todense`([order, out])	Return a dense matrix representation of this matrix.
`todia`()	
`todok`()	
`tolil`()	
`transpose`([copy])	
`trunc`()	Element-wise trunc.

`csc_matrix.`**`arcsin`**`()`

Element-wise arcsin.

See numpy.arcsin for more information.

`csc_matrix.`**`arcsinh`**`()`

Element-wise arcsinh.

See numpy.arcsinh for more information.

`csc_matrix.`**`arctan`**`()`

Element-wise arctan.

See numpy.arctan for more information.

`csc_matrix.`**`arctanh`**`()`

Element-wise arctanh.

See numpy.arctanh for more information.

`csc_matrix.`**`asformat`**`(`*format*`)`

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- None for no format conversion
- "csr" for csr_matrix format
- "csc" for csc_matrix format

- “lil” for lil_matrix format
- “dok” for dok_matrix format and so on

`csc_matrix.`**`asfptype`**`()`

Upcast matrix to a floating point format (if necessary)

`csc_matrix.`**`astype`**`(`*t*`)`

`csc_matrix.`**`ceil`**`()`

Element-wise ceil.

See numpy.ceil for more information.

`csc_matrix.`**`check_format`**`(`*full_check=True*`)`

check whether the matrix format is valid

Parameters **full_check** : bool, optional

If *True*, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).

`csc_matrix.`**`conj`**`()`

`csc_matrix.`**`conjugate`**`()`

`csc_matrix.`**`copy`**`()`

`csc_matrix.`**`deg2rad`**`()`

Element-wise deg2rad.

See numpy.deg2rad for more information.

`csc_matrix.`**`diagonal`**`()`

Returns the main diagonal of the matrix

`csc_matrix.`**`dot`**`(`*other*`)`

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

`csc_matrix.`**`eliminate_zeros`**`()`

Remove zero entries from the matrix

This is an *in place* operation

`csc_matrix.`**`expm1`**`()`

Element-wise expm1.

See numpy.expm1 for more information.

`csc_matrix.`**`floor`**`()`

Element-wise floor.

See numpy.floor for more information.

`csc_matrix.`**getH**`()`

`csc_matrix.`**get_shape**`()`

`csc_matrix.`**getcol**`(`*i*`)`

Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).

`csc_matrix.`**getformat**`()`

`csc_matrix.`**getmaxprint**`()`

`csc_matrix.`**getnnz**`(`*axis=None*`)`

Get the count of explicitly-stored values (nonzeros)

Parameters	**axis** : {None, 0, 1}, optional Select between the number of values across the whole matrix, in each column, or in each row.

`csc_matrix.`**getrow**`(`*i*`)`

Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

`csc_matrix.`**log1p**`()`

Element-wise log1p.

See numpy.log1p for more information.

`csc_matrix.`**max**`(`*axis=None*`)`

Maximum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns	**amax** : self.dtype Maximum element.

`csc_matrix.`**maximum**`(`*other*`)`

`csc_matrix.`**mean**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`csc_matrix.`**min**`(`*axis=None*`)`

Minimum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns	**amin** : self.dtype Minimum element.

`csc_matrix.`**minimum**`(`*other*`)`

`csc_matrix.`**multiply**`(`*other*`)`

Point-wise multiplication by another matrix, vector, or scalar.

`csc_matrix.`**nonzero**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`csc_matrix.`**`power`**`(`*n*, *dtype=None*`)`

This function performs element-wise power.

Parameters **n** : n is a scalar

dtype : If dtype is not specified, the current dtype will be preserved.

`csc_matrix.`**`prune`**`()`

Remove empty space after all non-zero elements.

`csc_matrix.`**`rad2deg`**`()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

`csc_matrix.`**`reshape`**`(`*shape*`)`

`csc_matrix.`**`rint`**`()`

Element-wise rint.

See numpy.rint for more information.

`csc_matrix.`**`set_shape`**`(`*shape*`)`

`csc_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters **values** : array_like

New values of the diagonal elements.

Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.

If a scalar value is given, all of the diagonal is set to it.

k : int, optional

Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`csc_matrix.`**`sign`**`()`

Element-wise sign.

See numpy.sign for more information.

`csc_matrix.`**`sin`**`()`

Element-wise sin.

See numpy.sin for more information.

`csc_matrix.`**`sinh`**`()`

Element-wise sinh.

See numpy.sinh for more information.

`csc_matrix.`**`sort_indices`**`()`

Sort the indices of this matrix *in place* `csc_matrix.`**`sorted_indices`**`()`

Return a copy of this matrix with sorted indices

`csc_matrix.`**`sqrt`**`()`

Element-wise sqrt.

See numpy.sqrt for more information.

`csc_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`csc_matrix.`**`sum_duplicates`**`()`

Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

`csc_matrix.`**`tan`**`()`

Element-wise tan.

See numpy.tan for more information.

`csc_matrix.`**`tanh`**`()`

Element-wise tanh.

See numpy.tanh for more information.

`csc_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

See the docstring for `spmatrix.toarray`.

`csc_matrix.`**`tobsr`**`(`*blocksize=None*`)`

`csc_matrix.`**`tocoo`**`(`*copy=True*`)`

Return a COOrdinate representation of this matrix

When copy=False the index and data arrays are not copied.

`csc_matrix.`**`tocsc`**`(`*copy=False*`)`

`csc_matrix.`**`tocsr`**`()`

`csc_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters **order** : {‘C’, ‘F’}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns **arr** : numpy.matrix, 2-dimensional

A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`csc_matrix.`**`todia`**`()`

`csc_matrix.`**`todok`**`()`

`csc_matrix.`**`tolil`**`()`

`csc_matrix.`**`transpose`**`(`*copy=False*`)`

`csc_matrix.`**`trunc`**`()`

Element-wise trunc.

See numpy.trunc for more information.

class `scipy.sparse.`**`csr_matrix`**`(`*arg1*, *shape=None*, *dtype=None*, *copy=False*`)`

Compressed Sparse Row matrix

This can be instantiated in several ways:

csr_matrix(D) with a dense matrix or rank-2 ndarray D

csr_matrix(S) with another sparse matrix S (equivalent to S.tocsr())

csr_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

csr_matrix((data, (row_ind, col_ind)), [shape=(M, N)])
where `data`, `row_ind` and `col_ind` satisfy the relationship `a[row_ind[k], col_ind[k]] = data[k]`.

csr_matrix((data, indices, indptr), [shape=(M, N)])
is the standard CSR representation where the column indices for row i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding values are stored in `data[indptr[i]:indptr[i+1]]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the CSR format

- efficient arithmetic operations CSR + CSR, CSR * CSR, etc.
- efficient row slicing
- fast matrix vector products

Disadvantages of the CSR format

- slow column slicing operations (consider CSC)
- changes to the sparsity structure are expensive (consider LIL or DOK)

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> csr_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
```

```
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 0, 1, 2, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

As an example of how to construct a CSR matrix incrementally, the following snippet builds a term-document matrix from texts:

```
>>> docs = [["hello", "world", "hello"], ["goodbye", "cruel", "world"]]
>>> indptr = [0]
>>> indices = []
>>> data = []
>>> vocabulary = {}
>>> for d in docs:
...     for term in d:
...         index = vocabulary.setdefault(term, len(vocabulary))
...         indices.append(index)
...         data.append(1)
...     indptr.append(len(indices))
...
>>> csr_matrix((data, indices, indptr), dtype=int).toarray()
array([[2, 1, 0, 0],
       [0, 1, 1, 1]])
```

Attributes

`nnz`	Get the count of explicitly-stored values (nonzeros)
`has_sorted_indices`	Determine whether the matrix has sorted indices

`csr_matrix.`**`nnz`**

Get the count of explicitly-stored values (nonzeros)

Parameters **axis** : {None, 0, 1}, optional

Select between the number of values across the whole matrix, in each column, or in each row.

`csr_matrix.`**`has_sorted_indices`**

Determine whether the matrix has sorted indices

Returns

- True: if the indices of the matrix are in sorted order
- False: otherwise

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
data	CSR format data array of the matrix
indices	CSR format index array of the matrix
indptr	CSR format index pointer array of the matrix

Methods

`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`ceil`()	Element-wise ceil.
`check_format`([full_check])	check whether the matrix format is valid
`conj`()	
`conjugate`()	
`copy`()	
`deg2rad`()	Element-wise deg2rad.
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`eliminate_zeros`()	Remove zero entries from the matrix
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	
`get_shape`()	
`getcol`(i)	Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).
`getformat`()	
`getmaxprint`()	
`getnnz`([axis])	Get the count of explicitly-stored values (nonzeros)
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
`log1p`()	Element-wise log1p.
`max`([axis])	Maximum of the elements of this matrix.
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`min`([axis])	Minimum of the elements of this matrix.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix, vector, or scalar.
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`prune`()	Remove empty space after all non-zero elements.
`rad2deg`()	Element-wise rad2deg.
`reshape`(shape)	
`rint`()	Element-wise rint.
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sign`()	Element-wise sign.
`sin`()	Element-wise sin.

Continued on next page

Table 5.146 – continued from previous page

sinh()	Element-wise sinh.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sqrt()	Element-wise sqrt.
sum([axis])	Sum the matrix over the given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	See the docstring for `spmatrix.toarray`.
tobsr([blocksize, copy])	
tocoo([copy])	Return a COOrdinate representation of this matrix
tocsc()	
tocsr([copy])	
todense([order, out])	Return a dense matrix representation of this matrix.
todia()	
todok()	
tolil()	
transpose([copy])	
trunc()	Element-wise trunc.

`csr_matrix.`**`arcsin`**`()`

Element-wise arcsin.

See numpy.arcsin for more information.

`csr_matrix.`**`arcsinh`**`()`

Element-wise arcsinh.

See numpy.arcsinh for more information.

`csr_matrix.`**`arctan`**`()`

Element-wise arctan.

See numpy.arctan for more information.

`csr_matrix.`**`arctanh`**`()`

Element-wise arctanh.

See numpy.arctanh for more information.

`csr_matrix.`**`asformat`**`(`*format*`)`

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- None for no format conversion
- “csr” for csr_matrix format
- “csc” for csc_matrix format
- “lil” for lil_matrix format
- “dok” for dok_matrix format and so on

`csr_matrix.`**`asfptype`**`()`

Upcast matrix to a floating point format (if necessary)

`csr_matrix.`**`astype`**`(`*t*`)`

`csr_matrix.`**`ceil`**`()`

Element-wise ceil.

See numpy.ceil for more information.

`csr_matrix.`**`check_format`**`(`*full_check=True*`)`

check whether the matrix format is valid

Parameters	**full_check** : bool, optional If *True*, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).

`csr_matrix.`**`conj`**`()`

`csr_matrix.`**`conjugate`**`()`

`csr_matrix.`**`copy`**`()`

`csr_matrix.`**`deg2rad`**`()`

Element-wise deg2rad.

See numpy.deg2rad for more information.

`csr_matrix.`**`diagonal`**`()`

Returns the main diagonal of the matrix

`csr_matrix.`**`dot`**`(`*other*`)`

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

`csr_matrix.`**`eliminate_zeros`**`()`

Remove zero entries from the matrix

This is an *in place* operation

`csr_matrix.`**`expm1`**`()`

Element-wise expm1.

See numpy.expm1 for more information.

`csr_matrix.`**`floor`**`()`

Element-wise floor.

See numpy.floor for more information.

`csr_matrix.`**`getH`**`()`

`csr_matrix.`**`get_shape`**`()`

`csr_matrix.`**`getcol`**`(`*i*`)`

Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).

`csr_matrix.`**`getformat`**`()`

`csr_matrix.`**`getmaxprint`**`()`

`csr_matrix.`**`getnnz`**`(`*axis=None*`)`

Get the count of explicitly-stored values (nonzeros)

Parameters **axis** : {None, 0, 1}, optional

Select between the number of values across the whole matrix, in each column, or in each row.

`csr_matrix.`**`getrow`**`(`*i*`)`

Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

`csr_matrix.`**`log1p`**`()`

Element-wise log1p.

See numpy.log1p for more information.

`csr_matrix.`**`max`**`(`*axis=None*`)`

Maximum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns **amax** : self.dtype

Maximum element.

`csr_matrix.`**`maximum`**`(`*other*`)`

`csr_matrix.`**`mean`**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`csr_matrix.`**`min`**`(`*axis=None*`)`

Minimum of the elements of this matrix.

This takes all elements into account, not just the non-zero ones.

Returns **amin** : self.dtype

Minimum element.

`csr_matrix.`**`minimum`**`(`*other*`)`

`csr_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix, vector, or scalar.

`csr_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`csr_matrix.`**`power`**`(`*n*, *dtype=None*`)`

This function performs element-wise power.

Parameters	**n** : n is a scalar **dtype** : If dtype is not specified, the current dtype will be preserved.

`csr_matrix.`**`prune`**`()`

Remove empty space after all non-zero elements.

`csr_matrix.`**`rad2deg`**`()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

`csr_matrix.`**`reshape`**`(`*shape*`)`

`csr_matrix.`**`rint`**`()`

Element-wise rint.

See numpy.rint for more information.

`csr_matrix.`**`set_shape`**`(`*shape*`)`

`csr_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters	**values** : array_like New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it. **k** : int, optional Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`csr_matrix.`**`sign`**`()`

Element-wise sign.

See numpy.sign for more information.

`csr_matrix.`**`sin`**`()`

Element-wise sin.

See numpy.sin for more information.

`csr_matrix.`**`sinh`**`()`

Element-wise sinh.

See numpy.sinh for more information.

`csr_matrix.`**`sort_indices`**`()`

Sort the indices of this matrix *in place*

`csr_matrix.`**`sorted_indices`**`()`

Return a copy of this matrix with sorted indices

`csr_matrix.`**`sqrt`**`()`

Element-wise sqrt.

See numpy.sqrt for more information.

`csr_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`csr_matrix.`**`sum_duplicates`**`()`

Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

`csr_matrix.`**`tan`**`()`

Element-wise tan.

See numpy.tan for more information.

`csr_matrix.`**`tanh`**`()`

Element-wise tanh.

See numpy.tanh for more information.

`csr_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

See the docstring for `spmatrix.toarray`.

`csr_matrix.`**`tobsr`**`(`*blocksize=None*, *copy=True*`)`

`csr_matrix.`**`tocoo`**`(`*copy=True*`)`

Return a COOrdinate representation of this matrix

When copy=False the index and data arrays are not copied.

`csr_matrix.`**`tocsc`**`()`

`csr_matrix.`**`tocsr`**`(`*copy=False*`)`

`csr_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters	**order** : {'C', 'F'}, optional	
		Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.
	out : ndarray, 2-dimensional, optional	
		If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.
Returns	**arr** : numpy.matrix, 2-dimensional	
		A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`csr_matrix.`**`todia`**`()`

`csr_matrix.`**`todok`**`()`

`csr_matrix.`**`tolil`**`()`

`csr_matrix.`**`transpose`**`(`*copy=False*`)`

`csr_matrix.`**`trunc`**`()`

Element-wise trunc.

See numpy.trunc for more information.

class `scipy.sparse.`**`dia_matrix`**`(`*arg1*, *shape=None*, *dtype=None*, *copy=False*`)`

Sparse matrix with DIAgonal storage

This can be instantiated in several ways:

dia_matrix(D) with a dense matrix

dia_matrix(S) with another sparse matrix S (equivalent to S.todia())

dia_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N), dtype is optional, defaulting to dtype='d'.

dia_matrix((data, offsets), shape=(M, N))

where the `data[k,:]` stores the diagonal entries for diagonal `offsets[k]` (See example below)

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Examples

```
>>> import numpy as np
>>> from scipy.sparse import dia_matrix
>>> dia_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> data = np.array([[1, 2, 3, 4]]).repeat(3, axis=0)
>>> offsets = np.array([0, -1, 2])
>>> dia_matrix((data, offsets), shape=(4, 4)).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

Attributes

`nnz`	number of nonzero values

`dia_matrix.`**`nnz`**

number of nonzero values

explicit zero values are included in this number

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
data	DIA format data array of the matrix
offsets	DIA format offset array of the matrix

Methods

`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`ceil`()	Element-wise ceil.
`conj`()	
`conjugate`()	
`copy`()	
`deg2rad`()	Element-wise deg2rad.
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	
`get_shape`()	
`getcol`(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
`getformat`()	
`getmaxprint`()	
`getnnz`()	number of nonzero values
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
`log1p`()	Element-wise log1p.
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`rad2deg`()	Element-wise rad2deg.
`reshape`(shape)	
`rint`()	Element-wise rint.
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sign`()	Element-wise sign.
`sin`()	Element-wise sin.
`sinh`()	Element-wise sinh.
`sqrt`()	Element-wise sqrt.
`sum`([axis])	Sum the matrix over the given axis.
`tan`()	Element-wise tan.
`tanh`()	Element-wise tanh.
`toarray`([order, out])	Return a dense ndarray representation of this matrix.

Continued on next page

Table 5.148 – continued from previous page

`tobsr`([blocksize])	
`tocoo`()	
`tocsc`()	
`tocsr`()	
`todense`([order, out])	Return a dense matrix representation of this matrix.
`todia`([copy])	
`todok`()	
`tolil`()	
`transpose`()	
`trunc`()	Element-wise trunc.

`dia_matrix.`**`arcsin`**`()`

Element-wise arcsin.

See numpy.arcsin for more information.

`dia_matrix.`**`arcsinh`**`()`

Element-wise arcsinh.

See numpy.arcsinh for more information.

`dia_matrix.`**`arctan`**`()`

Element-wise arctan.

See numpy.arctan for more information.

`dia_matrix.`**`arctanh`**`()`

Element-wise arctanh.

See numpy.arctanh for more information.

`dia_matrix.`**`asformat`**`(`*format*`)`

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- •None for no format conversion
- •“csr” for csr_matrix format
- •“csc” for csc_matrix format
- •“lil” for lil_matrix format
- •“dok” for dok_matrix format and so on

`dia_matrix.`**`asfptype`**`()`

Upcast matrix to a floating point format (if necessary)

`dia_matrix.`**`astype`**`(`*t*`)`

`dia_matrix.`**`ceil`**`()`

Element-wise ceil.

See numpy.ceil for more information.

`dia_matrix.`**`conj`**`()`

`dia_matrix.`**`conjugate`**`()`

dia_matrix.**copy**()

dia_matrix.**deg2rad**()
Element-wise deg2rad.

See numpy.deg2rad for more information.

dia_matrix.**diagonal**()
Returns the main diagonal of the matrix

dia_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

dia_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

dia_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

dia_matrix.**getH**()

dia_matrix.**get_shape**()

dia_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

dia_matrix.**getformat**()

dia_matrix.**getmaxprint**()

dia_matrix.**getnnz**()
number of nonzero values

explicit zero values are included in this number

dia_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

dia_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

dia_matrix.**maximum**(*other*)

`dia_matrix.`**`mean`**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`dia_matrix.`**`minimum`**`(`*other*`)`

`dia_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix

`dia_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`dia_matrix.`**`power`**`(`*n*, *dtype=None*`)`

This function performs element-wise power.

Parameters **n** : n is a scalar

dtype : If dtype is not specified, the current dtype will be preserved.

`dia_matrix.`**`rad2deg`**`()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

`dia_matrix.`**`reshape`**`(`*shape*`)`

`dia_matrix.`**`rint`**`()`

Element-wise rint.

See numpy.rint for more information.

`dia_matrix.`**`set_shape`**`(`*shape*`)`

`dia_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters **values** : array_like

New values of the diagonal elements.

Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.

If a scalar value is given, all of the diagonal is set to it.

k : int, optional

Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`dia_matrix.`**`sign`**`()`

Element-wise sign.

See numpy.sign for more information.

`dia_matrix.`**`sin`**`()`

Element-wise sin.

See numpy.sin for more information.

`dia_matrix.`**`sinh`**`()`

Element-wise sinh.

See numpy.sinh for more information.

`dia_matrix.`**`sqrt`**`()`

Element-wise sqrt.

See numpy.sqrt for more information.

`dia_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`dia_matrix.`**`tan`**`()`

Element-wise tan.

See numpy.tan for more information.

`dia_matrix.`**`tanh`**`()`

Element-wise tanh.

See numpy.tanh for more information.

`dia_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

Return a dense ndarray representation of this matrix.

Parameters **order** : {'C', 'F'}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns **arr** : ndarray, 2-dimensional

An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

`dia_matrix.`**`tobsr`**`(`*blocksize=None*`)`

`dia_matrix.`**`tocoo`**`()`

`dia_matrix.`**`tocsc`**`()`

`dia_matrix.`**`tocsr`**`()`

`dia_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters **order** : {‘C’, ‘F’}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns **arr** : numpy.matrix, 2-dimensional

A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`dia_matrix.`**`todia`**(*copy=False*)

`dia_matrix.`**`todok`**()

`dia_matrix.`**`tolil`**()

`dia_matrix.`**`transpose`**()

`dia_matrix.`**`trunc`**()

Element-wise trunc.

See numpy.trunc for more information.

class `scipy.sparse.`**`dok_matrix`**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

Dictionary Of Keys based sparse matrix.

This is an efficient structure for constructing sparse matrices incrementally.

This can be instantiated in several ways:

dok_matrix(D) with a dense matrix, D

dok_matrix(S) with a sparse matrix, S

dok_matrix((M,N), [dtype]) create the matrix with initial shape (M,N) dtype is optional, defaulting to dtype=’d’

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Allows for efficient O(1) access of individual elements. Duplicates are not allowed. Can be efficiently converted to a coo_matrix once constructed.

Examples

```
>>> import numpy as np
>>> from scipy.sparse import dok_matrix
>>> S = dok_matrix((5, 5), dtype=np.float32)
>>> for i in range(5):
...     for j in range(5):
...         S[i, j] = i + j    # Update element
```

Attributes

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
nnz	Number of nonzero elements

Methods

`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`clear`(() -> None. Remove all items from D.)	
`conj`()	
`conjtransp`()	Return the conjugate transpose
`conjugate`()	
`copy`()	
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`fromkeys`(...)	v defaults to None.
`get`(key[, default])	This overrides the dict.get method, providing type checking but otherwise equiva
`getH`()	
`get_shape`()	
`getcol`(j)	Returns a copy of column j of the matrix as a (m x 1) DOK matrix.
`getformat`()	
`getmaxprint`()	
`getnnz`()	
`getrow`(i)	Returns a copy of row i of the matrix as a (1 x n) DOK matrix.
`has_key`((k) -> True if D has a key k, else False)	
`items`(() -> list of D's (key, value) pairs, ...)	
`iteritems`(() -> an iterator over the (key, ...)	
`iterkeys`(() -> an iterator over the keys of D)	
`itervalues`(...)	
`keys`(() -> list of D's keys)	
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix
`nonzero`()	nonzero indices
`pop`((k[,d]) -> v, ...)	If key is not found, d is returned if given, otherwise KeyError is raised
`popitem`(() -> (k, v), ...)	2-tuple; but raise KeyError if D is empty.
`power`(n[, dtype])	
`reshape`(shape)	
`resize`(shape)	Resize the matrix in-place to dimensions given by 'shape'.
`set_shape`(shape)	

Continu

Table 5.149 – continued from previous page

`setdefault`((k[,d]) -> D.get(k,d), ...)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sum`([axis])	Sum the matrix over the given axis.
`toarray`([order, out])	Return a dense ndarray representation of this matrix.
`tobsr`([blocksize])	
`tocoo`()	Return a copy of this matrix in COOrdinate format
`tocsc`()	Return a copy of this matrix in Compressed Sparse Column format
`tocsr`()	Return a copy of this matrix in Compressed Sparse Row format
`todense`([order, out])	Return a dense matrix representation of this matrix.
`todia`()	
`todok`([copy])	
`tolil`()	
`transpose`()	Return the transpose
`update`(([E, ...)	If E present and has a .keys() method, does: for k in E: D[k] = E[k]
`values`(() -> list of D's values)	
`viewitems`(...)	
`viewkeys`(...)	
`viewvalues`(...)	

`dok_matrix.`**`asformat`**(*format*)

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- None for no format conversion
- "csr" for csr_matrix format
- "csc" for csc_matrix format
- "lil" for lil_matrix format
- "dok" for dok_matrix format and so on

`dok_matrix.`**`asfptype`**()

Upcast matrix to a floating point format (if necessary)

`dok_matrix.`**`astype`**(*t*)

`dok_matrix.`**`clear`**() → None. Remove all items from D.

`dok_matrix.`**`conj`**()

`dok_matrix.`**`conjtransp`**()

Return the conjugate transpose

`dok_matrix.`**`conjugate`**()

`dok_matrix.`**`copy`**()

`dok_matrix.`**`diagonal`**()

Returns the main diagonal of the matrix

`dok_matrix.`**`dot`**(*other*)

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

static `dok_matrix.`**`fromkeys`**(*S*[, *v*]) → New dict with keys from S and values equal to v.
v defaults to None.

`dok_matrix.`**`get`**(*key*, *default=0.0*)
This overrides the dict.get method, providing type checking but otherwise equivalent functionality.

`dok_matrix.`**`getH`**()

`dok_matrix.`**`get_shape`**()

`dok_matrix.`**`getcol`**(*j*)
Returns a copy of column j of the matrix as a (m x 1) DOK matrix.

`dok_matrix.`**`getformat`**()

`dok_matrix.`**`getmaxprint`**()

`dok_matrix.`**`getnnz`**()

`dok_matrix.`**`getrow`**(*i*)
Returns a copy of row i of the matrix as a (1 x n) DOK matrix.

`dok_matrix.`**`has_key`**(*k*) → True if D has a key k, else False

`dok_matrix.`**`items`**() → list of D's (key, value) pairs, as 2-tuples

`dok_matrix.`**`iteritems`**() → an iterator over the (key, value) items of D

`dok_matrix.`**`iterkeys`**() → an iterator over the keys of D

`dok_matrix.`**`itervalues`**() → an iterator over the values of D

`dok_matrix.`**`keys`**() → list of D's keys

`dok_matrix.`**`maximum`**(*other*)

`dok_matrix.`**`mean`**(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`dok_matrix.`**`minimum`**(*other*)

`dok_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix

`dok_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`dok_matrix.`**`pop`**`(`*k*[, *d*]`)` → v, remove specified key and return the corresponding value.

If key is not found, d is returned if given, otherwise KeyError is raised

`dok_matrix.`**`popitem`**`()` → (k, v), remove and return some (key, value) pair as a

2-tuple; but raise KeyError if D is empty.

`dok_matrix.`**`power`**`(`*n*, *dtype=None*`)`

`dok_matrix.`**`reshape`**`(`*shape*`)`

`dok_matrix.`**`resize`**`(`*shape*`)`

Resize the matrix in-place to dimensions given by ‘shape’.

Any non-zero elements that lie outside the new shape are removed.

`dok_matrix.`**`set_shape`**`(`*shape*`)`

`dok_matrix.`**`setdefault`**`(`*k*[, *d*]`)` → D.get(k,d), also set D[k]=d if k not in D

`dok_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters **values** : array_like

New values of the diagonal elements.

Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.

If a scalar value is given, all of the diagonal is set to it.

k : int, optional

Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`dok_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`dok_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

Return a dense ndarray representation of this matrix.

Parameters **order** : {‘C’, ‘F’}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns **arr** : ndarray, 2-dimensional

An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

`dok_matrix.`**`tobsr`**`(`*blocksize=None*`)`

`dok_matrix.`**`tocoo`**`()`

Return a copy of this matrix in COOrdinate format

`dok_matrix.`**`tocsc`**`()`

Return a copy of this matrix in Compressed Sparse Column format

`dok_matrix.`**`tocsr`**`()`

Return a copy of this matrix in Compressed Sparse Row format

`dok_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters **order** : {‘C’, ‘F’}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns **arr** : numpy.matrix, 2-dimensional

A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`dok_matrix.`**`todia`**`()`

`dok_matrix.`**`todok`**`(`*copy=False*`)`

`dok_matrix.`**`tolil`**`()`

`dok_matrix.`**`transpose`**`()`

Return the transpose

`dok_matrix.`**`update`**`(`$[E]$, ***F*`)` → None. Update D from dict/iterable E and F.

If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

`dok_matrix.`**`values`**`()` → list of D's values

`dok_matrix.`**`viewitems`**`()` → a set-like object providing a view on D's items

`dok_matrix.`**`viewkeys`**`()` → a set-like object providing a view on D's keys

`dok_matrix.`**`viewvalues`**`()` → an object providing a view on D's values

class `scipy.sparse.`**`lil_matrix`**`(`*arg1*, *shape=None*, *dtype=None*, *copy=False*`)`

Row-based linked list sparse matrix

This is a structure for constructing sparse matrices incrementally. Note that inserting a single item can take linear time in the worst case; to construct a matrix efficiently, make sure the items are pre-sorted by index, per row.

This can be instantiated in several ways:

lil_matrix(D)	with a dense matrix or rank-2 ndarray D
lil_matrix(S)	with another sparse matrix S (equivalent to S.tolil())
lil_matrix((M, N), [dtype])	to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the LIL format

- supports flexible slicing
- changes to the matrix sparsity structure are efficient

Disadvantages of the LIL format

- arithmetic operations LIL + LIL are slow (consider CSR or CSC)
- slow column slicing (consider CSC)
- slow matrix vector products (consider CSR or CSC)

Intended Usage

- LIL is a convenient format for constructing sparse matrices
- once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and matrix vector operations
- consider using the COO format when constructing large matrices

Data Structure

- An array (`self.rows`) of rows, each of which is a sorted list of column indices of non-zero elements.
- The corresponding nonzero values are stored in similar fashion in `self.data`.

Attributes

nnz	Get the count of explicitly-stored values (nonzeros)

`lil_matrix.`**`nnz`**

Get the count of explicitly-stored values (nonzeros)

Parameters **axis** : None, 0, or 1

Select between the number of values across the whole matrix, in each column, or in each row.

dtype	(dtype) Data type of the matrix
shape	(2-tuple) Shape of the matrix
ndim	(int) Number of dimensions (this is always 2)
data	LIL format data array of the matrix
rows	LIL format row index array of the matrix

Methods

`asformat`(format)	Return this matrix in a given sparse format
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(t)	
`conj`()	
`conjugate`()	
`copy`()	
`diagonal`()	Returns the main diagonal of the matrix
`dot`(other)	Ordinary dot product
`getH`()	
`get_shape`()	
`getcol`(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
`getformat`()	
`getmaxprint`()	
`getnnz`([axis])	Get the count of explicitly-stored values (nonzeros)
`getrow`(i)	Returns a copy of the 'i'th row.
`getrowview`(i)	Returns a view of the 'i'th row (without copying).
`maximum`(other)	
`mean`([axis])	Average the matrix over the given axis.
`minimum`(other)	
`multiply`(other)	Point-wise multiplication by another matrix
`nonzero`()	nonzero indices
`power`(n[, dtype])	
`reshape`(shape)	
`set_shape`(shape)	
`setdiag`(values[, k])	Set diagonal or off-diagonal elements of the array.
`sum`([axis])	Sum the matrix over the given axis.
`toarray`([order, out])	See the docstring for `spmatrix.toarray`.
`tobsr`([blocksize])	
`tocoo`()	
`tocsc`()	Return Compressed Sparse Column format arrays for this matrix.
`tocsr`()	Return Compressed Sparse Row format arrays for this matrix.
`todense`([order, out])	Return a dense matrix representation of this matrix.
`todia`()	
`todok`()	

Continued on next page

Table 5.151 – continued from previous page

`tolil`([copy])
`transpose`()

`lil_matrix.`**`asformat`**(*format*)

Return this matrix in a given sparse format

Parameters **format** : {string, None}

desired sparse matrix format

- None for no format conversion
- "csr" for csr_matrix format
- "csc" for csc_matrix format
- "lil" for lil_matrix format
- "dok" for dok_matrix format and so on

`lil_matrix.`**`asfptype`**()

Upcast matrix to a floating point format (if necessary)

`lil_matrix.`**`astype`**(*t*)

`lil_matrix.`**`conj`**()

`lil_matrix.`**`conjugate`**()

`lil_matrix.`**`copy`**()

`lil_matrix.`**`diagonal`**()

Returns the main diagonal of the matrix

`lil_matrix.`**`dot`**(*other*)

Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

`lil_matrix.`**`getH`**()

`lil_matrix.`**`get_shape`**()

`lil_matrix.`**`getcol`**(*j*)

Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

`lil_matrix.`**`getformat`**()

`lil_matrix.`**`getmaxprint`**()

`lil_matrix.`**`getnnz`**`(`*axis=None*`)`

Get the count of explicitly-stored values (nonzeros)

Parameters	**axis** : None, 0, or 1 Select between the number of values across the whole matrix, in each column, or in each row.

`lil_matrix.`**`getrow`**`(`*i*`)`

Returns a copy of the 'i'th row.

`lil_matrix.`**`getrowview`**`(`*i*`)`

Returns a view of the 'i'th row (without copying).

`lil_matrix.`**`maximum`**`(`*other*`)`

`lil_matrix.`**`mean`**`(`*axis=None*`)`

Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

`lil_matrix.`**`minimum`**`(`*other*`)`

`lil_matrix.`**`multiply`**`(`*other*`)`

Point-wise multiplication by another matrix

`lil_matrix.`**`nonzero`**`()`

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

`lil_matrix.`**`power`**`(`*n*, *dtype=None*`)`

`lil_matrix.`**`reshape`**`(`*shape*`)`

`lil_matrix.`**`set_shape`**`(`*shape*`)`

`lil_matrix.`**`setdiag`**`(`*values*, *k=0*`)`

Set diagonal or off-diagonal elements of the array.

Parameters	**values** : array_like New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.
	k : int, optional Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

`lil_matrix.`**`sum`**`(`*axis=None*`)`

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

`lil_matrix.`**`toarray`**`(`*order=None*, *out=None*`)`

See the docstring for `spmatrix.toarray`.

`lil_matrix.`**`tobsr`**`(`*blocksize=None*`)`

`lil_matrix.`**`tocoo`**`()`

`lil_matrix.`**`tocsc`**`()`

Return Compressed Sparse Column format arrays for this matrix.

`lil_matrix.`**`tocsr`**`()`

Return Compressed Sparse Row format arrays for this matrix.

`lil_matrix.`**`todense`**`(`*order=None*, *out=None*`)`

Return a dense matrix representation of this matrix.

Parameters **order** : {'C', 'F'}, optional

Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out : ndarray, 2-dimensional, optional

If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns **arr** : numpy.matrix, 2-dimensional

A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

`lil_matrix.`**`todia`**`()`

`lil_matrix.`**`todok`**`()`

`lil_matrix.`**`tolil`**`(`*copy=False*`)`

`lil_matrix.`**`transpose`**`()`

Functions

Building sparse matrices:

`eye`(m[, n, k, dtype, format])	Sparse matrix with ones on diagonal
`identity`(n[, dtype, format])	Identity matrix in sparse format

Continued on ne

Table 5.152 – continued from previous page

`kron`(A, B[, format])	kronecker product of sparse matrices A and B
`kronsum`(A, B[, format])	kronecker sum of sparse matrices A and B
`diags`(diagonals, offsets[, shape, format, dtype])	Construct a sparse matrix from diagonals.
`spdiags`(data, diags, m, n[, format])	Return a sparse matrix from diagonals.
`block_diag`(mats[, format, dtype])	Build a block diagonal sparse matrix from provided matrices.
`tril`(A[, k, format])	Return the lower triangular portion of a matrix in sparse format
`triu`(A[, k, format])	Return the upper triangular portion of a matrix in sparse format
`bmat`(blocks[, format, dtype])	Build a sparse matrix from sparse sub-blocks
`hstack`(blocks[, format, dtype])	Stack sparse matrices horizontally (column wise)
`vstack`(blocks[, format, dtype])	Stack sparse matrices vertically (row wise)
`rand`(m, n[, density, format, dtype, ...])	Generate a sparse matrix of the given shape and density with uniformly distribute
`norm`	

`scipy.sparse.`**`eye`**(*m*, *n=None*, *k=0*, *dtype=<type 'float'>*, *format=None*)

Sparse matrix with ones on diagonal

Returns a sparse (m x n) matrix where the k-th diagonal is all ones and everything else is zeros.

Parameters **n** : int

Number of rows in the matrix.

m : int, optional

Number of columns. Default: n

k : int, optional

Diagonal to place ones on. Default: 0 (main diagonal)

dtype : dtype, optional

Data type of the matrix

format : str, optional

Sparse format of the result, e.g. format="csr", etc.

Examples

```
>>> from scipy import sparse
>>> sparse.eye(3).toarray()
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> sparse.eye(3, dtype=np.int8)
<3x3 sparse matrix of type '<type 'numpy.int8'>'
    with 3 stored elements (1 diagonals) in DIAgonal format>
```

`scipy.sparse.`**`identity`**(*n*, *dtype='d'*, *format=None*)

Identity matrix in sparse format

Returns an identity matrix with shape (n,n) using a given sparse format and dtype.

Parameters **n** : int

Shape of the identity matrix.

dtype : dtype, optional

Data type of the matrix

format : str, optional

Sparse format of the result, e.g. format="csr", etc.

Examples

```
>>> identity(3).toarray()
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> identity(3, dtype='int8', format='dia')
<3x3 sparse matrix of type '<type 'numpy.int8'>'
        with 3 stored elements (1 diagonals) in DIAgonal format>
```

`scipy.sparse.`**`kron`**(*A*, *B*, *format=None*)

kronecker product of sparse matrices A and B

Parameters **A** : sparse or dense matrix

first matrix of the product

B : sparse or dense matrix

second matrix of the product

format : str, optional

format of the result (e.g. "csr")

Returns kronecker product in a sparse matrix format

Examples

```
>>> from scipy import sparse
>>> A = sparse.csr_matrix(np.array([[0, 2], [5, 0]]))
>>> B = sparse.csr_matrix(np.array([[1, 2], [3, 4]]))
>>> sparse.kron(A, B).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

```
>>> sparse.kron(A, [[1, 2], [3, 4]]).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

`scipy.sparse.`**`kronsum`**(*A*, *B*, *format=None*)

kronecker sum of sparse matrices A and B

Kronecker sum of two sparse matrices is a sum of two Kronecker products kron(I_n,A) + kron(B,I_m) where A has shape (m,m) and B has shape (n,n) and I_m and I_n are identity matrices of shape (m,m) and (n,n) respectively.

Parameters **A**

square matrix

B

square matrix

format : str

format of the result (e.g. "csr")

Returns kronecker sum in a sparse matrix format

`scipy.sparse.`**`diags`**(*diagonals*, *offsets*, *shape=None*, *format=None*, *dtype=None*)

Construct a sparse matrix from diagonals.

Parameters **diagonals** : sequence of array_like

Sequence of arrays containing the matrix diagonals, corresponding to *offsets*.

offsets : sequence of int

Diagonals to set:

- k = 0 the main diagonal
- k > 0 the k-th upper diagonal
- k < 0 the k-th lower diagonal

shape : tuple of int, optional

Shape of the result. If omitted, a square matrix large enough to contain the diagonals is returned.

format : {"dia", "csr", "csc", "lil", ...}, optional

Matrix format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

dtype : dtype, optional

Data type of the matrix.

See also:

`spdiags`	construct matrix from diagonals

Notes

This function differs from `spdiags` in the way it handles off-diagonals.

The result from `diags` is the sparse equivalent of:

```
np.diag(diagonals[0], offsets[0])
+ ...
+ np.diag(diagonals[k], offsets[k])
```

Repeated diagonal offsets are disallowed.

New in version 0.11.

Examples

```
>>> diagonals = [[1, 2, 3, 4], [1, 2, 3], [1, 2]]
>>> diags(diagonals, [0, -1, 2]).toarray()
array([[1, 0, 1, 0],
       [1, 2, 0, 2],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

Broadcasting of scalars is supported (but shape needs to be specified):

```
>>> diags([1, -2, 1], [-1, 0, 1], shape=(4, 4)).toarray()
array([[-2.,  1.,  0.,  0.],
       [ 1., -2.,  1.,  0.],
       [ 0.,  1., -2.,  1.],
       [ 0.,  0.,  1., -2.]])
```

If only one diagonal is wanted (as in `numpy.diag`), the following works as well:

```
>>> diags([1, 2, 3], 1).toarray()
array([[ 0.,  1.,  0.,  0.],
       [ 0.,  0.,  2.,  0.],
       [ 0.,  0.,  0.,  3.],
       [ 0.,  0.,  0.,  0.]])
```

`scipy.sparse.`**`spdiags`**(*data*, *diags*, *m*, *n*, *format=None*)

Return a sparse matrix from diagonals.

Parameters **data** : array_like

matrix diagonals stored row-wise

diags : diagonals to set

- k = 0 the main diagonal
- k > 0 the k-th upper diagonal
- k < 0 the k-th lower diagonal

m, n : int

shape of the result

format : str, optional

Format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

See also:

`diags`	more convenient form of this function
`dia_matrix`	the sparse DIAgonal format.

Examples

```
>>> data = np.array([[1, 2, 3, 4], [1, 2, 3, 4], [1, 2, 3, 4]])
>>> diags = np.array([0, -1, 2])
>>> spdiags(data, diags, 4, 4).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

`scipy.sparse.`**`block_diag`**(*mats*, *format=None*, *dtype=None*)

Build a block diagonal sparse matrix from provided matrices.

Parameters **mats** : sequence of matrices

Input matrices.

format : str, optional

The sparse format of the result (e.g. "csr"). If not given, the matrix is returned in "coo" format.

dtype : dtype specifier, optional

The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

Returns **res** : sparse matrix

See also:

`bmat`, `diags`

Notes

New in version 0.11.0.

Examples

```
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> C = coo_matrix([[7]])
>>> block_diag((A, B, C)).toarray()
array([[1, 2, 0, 0],
       [3, 4, 0, 0],
       [0, 0, 5, 0],
```

```
       [0, 0, 6, 0],
       [0, 0, 0, 7]])
```

`scipy.sparse.`**`tril`**(*A*, *k=0*, *format=None*)

Return the lower triangular portion of a matrix in sparse format

Returns the elements on or below the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters	**A** : dense or sparse matrix Matrix whose lower trianglar portion is desired. **k** : integer The top-most diagonal of the lower triangle. **format** : string Sparse format of the result, e.g. format="csr", etc.
Returns	**L** : sparse matrix Lower triangular portion of A in sparse format.

See also:

`triu`	upper triangle in sparse format

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7], [0, 0, 8, 9, 0]],
...                dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> tril(A).toarray()
array([[1, 0, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 8, 0, 0]])
>>> tril(A).nnz
4
>>> tril(A, k=1).toarray()
array([[1, 2, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 8, 9, 0]])
>>> tril(A, k=-1).toarray()
array([[0, 0, 0, 0, 0],
       [4, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> tril(A, format='csc')
<3x5 sparse matrix of type '<type 'numpy.int32'>'
        with 4 stored elements in Compressed Sparse Column format>
```

`scipy.sparse.`**`triu`**(*A*, *k=0*, *format=None*)

Return the upper triangular portion of a matrix in sparse format

Returns the elements on or above the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal

- k < 0 is below the main diagonal

Parameters

A : dense or sparse matrix
Matrix whose upper trianglar portion is desired.

k : integer
The bottom-most diagonal of the upper triangle.

format : string
Sparse format of the result, e.g. format="csr", etc.

Returns

L : sparse matrix
Upper triangular portion of A in sparse format.

See also:

`tril`	lower triangle in sparse format

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7], [0, 0, 8, 9, 0]],
...                dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).toarray()
array([[1, 2, 0, 0, 3],
       [0, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).nnz
8
>>> triu(A, k=1).toarray()
array([[0, 2, 0, 0, 3],
       [0, 0, 0, 6, 7],
       [0, 0, 0, 9, 0]])
>>> triu(A, k=-1).toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A, format='csc')
<3x5 sparse matrix of type '<type 'numpy.int32'>'
        with 8 stored elements in Compressed Sparse Column format>
```

`scipy.sparse.`**`bmat`**(*blocks*, *format=None*, *dtype=None*)

Build a sparse matrix from sparse sub-blocks

Parameters

blocks : array_like
Grid of sparse matrices with compatible shapes. An entry of None implies an all-zero matrix.

format : {'bsr', 'coo', 'csc', 'csr', 'dia', 'dok', 'lil'}, optional
The sparse format of the result (e.g. "csr"). By default an appropriate sparse matrix format is returned. This choice is subject to change.

dtype : dtype, optional
The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

Returns

bmat : sparse matrix

See also:

`block_diag`, `diags`

Examples

```
>>> from scipy.sparse import coo_matrix, bmat
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> C = coo_matrix([[7]])
>>> bmat([[A, B], [None, C]]).toarray()
array([[1, 2, 5],
       [3, 4, 6],
       [0, 0, 7]])
```

```
>>> bmat([[A, None], [None, C]]).toarray()
array([[1, 2, 0],
       [3, 4, 0],
       [0, 0, 7]])
```

`scipy.sparse.`**`hstack`**(*blocks*, *format=None*, *dtype=None*)

Stack sparse matrices horizontally (column wise)

Parameters **blocks**

sequence of sparse matrices with compatible shapes

format : str

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

dtype : dtype, optional

The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

See also:

`vstack`	stack sparse matrices vertically (row wise)

Examples

```
>>> from scipy.sparse import coo_matrix, hstack
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> hstack([A,B]).toarray()
array([[1, 2, 5],
       [3, 4, 6]])
```

`scipy.sparse.`**`vstack`**(*blocks*, *format=None*, *dtype=None*)

Stack sparse matrices vertically (row wise)

Parameters **blocks**

sequence of sparse matrices with compatible shapes

format : str, optional

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

dtype : dtype, optional

The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

See also:

`hstack`	stack sparse matrices horizontally (column wise)

Examples

```
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5, 6]])
>>> vstack([A, B]).toarray()
array([[1, 2],
       [3, 4],
       [5, 6]])
```

`scipy.sparse.`**`rand`**(*m*, *n*, *density=0.01*, *format='coo'*, *dtype=None*, *random_state=None*)

Generate a sparse matrix of the given shape and density with uniformly distributed values.

Parameters **m, n** : int
shape of the matrix
density : real, optional
density of the generated matrix: density equal to one means a full matrix, density of 0 means a matrix with no non-zero items.
format : str, optional
sparse matrix format.
dtype : dtype, optional
type of the returned matrix values.
random_state : {numpy.random.RandomState, int}, optional
Random number generator or random seed. If not given, the singleton numpy.random will be used.

Notes

Only float types are supported for now.

Sparse matrix tools:

`find`(A)	Return the indices and values of the nonzero elements of a matrix

`scipy.sparse.`**`find`**(*A*)

Return the indices and values of the nonzero elements of a matrix

Parameters **A** : dense or sparse matrix
Matrix whose nonzero elements are desired.

Returns **(I,J,V)** : tuple of arrays
I,J, and V contain the row indices, column indices, and values of the nonzero matrix entries.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[7.0, 8.0, 0],[0, 0, 9.0]])
>>> find(A)
(array([0, 0, 1], dtype=int32), array([0, 1, 2], dtype=int32), array([ 7.,  8.,  9.]))
```

Identifying sparse matrices:

`issparse`(x)
`isspmatrix`(x)
`isspmatrix_csc`(x)
`isspmatrix_csr`(x)

Continued on next page

Table 5.154 – continued from previous page

`isspmatrix_bsr`(x)
`isspmatrix_lil`(x)
`isspmatrix_dok`(x)
`isspmatrix_coo`(x)
`isspmatrix_dia`(x)

`scipy.sparse.`**`issparse`**(*x*)

`scipy.sparse.`**`isspmatrix`**(*x*)

`scipy.sparse.`**`isspmatrix_csc`**(*x*)

`scipy.sparse.`**`isspmatrix_csr`**(*x*)

`scipy.sparse.`**`isspmatrix_bsr`**(*x*)

`scipy.sparse.`**`isspmatrix_lil`**(*x*)

`scipy.sparse.`**`isspmatrix_dok`**(*x*)

`scipy.sparse.`**`isspmatrix_coo`**(*x*)

`scipy.sparse.`**`isspmatrix_dia`**(*x*)

Submodules

`csgraph`
`linalg`

Compressed Sparse Graph Routines (`scipy.sparse.csgraph`) Fast graph algorithms based on sparse matrix representations.

`connected_components`(csgraph[, directed, ...])	Analyze the connected components of a sparse graph
`laplacian`(csgraph[, normed, return_diag, ...])	Return the Laplacian matrix of a directed graph.
`shortest_path`(csgraph[, method, directed, ...])	Perform a shortest-path graph search on a positive directed or undirected gra
`dijkstra`(csgraph[, directed, indices, ...])	Dijkstra algorithm using Fibonacci Heaps
`floyd_warshall`(csgraph[, directed, ...])	Compute the shortest path lengths using the Floyd-Warshall algorithm
`bellman_ford`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using the Bellman-Ford algorithm.
`johnson`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using Johnson's algorithm.
`breadth_first_order`(csgraph, i_start[, ...])	Return a breadth-first ordering starting with specified node.
`depth_first_order`(csgraph, i_start[, ...])	Return a depth-first ordering starting with specified node.
`breadth_first_tree`(csgraph, i_start[, directed])	Return the tree generated by a breadth-first search

Table 5.156 – continued from previous page

`depth_first_tree`(csgraph, i_start[, directed])	Return a tree generated by a depth-first search.
`minimum_spanning_tree`(csgraph[, overwrite])	Return a minimum spanning tree of an undirected graph
`reverse_cuthill_mckee`	Returns the permutation array that orders a sparse CSR or CSC matrix in Re
`maximum_bipartite_matching`	Returns an array of row or column permutations that makes the diagonal of

Contents

`scipy.sparse.csgraph.`**`connected_components`**(*csgraph*, *directed=True*, *connection='weak'*, *return_labels=True*)

Analyze the connected components of a sparse graph

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

connection : str, optional

['weak'|'strong']. For directed graphs, the type of connection to use. Nodes i and j are strongly connected if a path exists both from i to j and from j to i. Nodes i and j are weakly connected if only one of these paths exists. If directed == False, this keyword is not referenced.

return_labels : str, optional

If True (default), then return the labels for each of the connected components.

Returns

n_components: int

The number of connected components.

labels: ndarray

The length-N array of labels of the connected components.

References

[R13]

`scipy.sparse.csgraph.`**`laplacian`**(*csgraph*, *normed=False*, *return_diag=False*, *use_out_degree=False*)

Return the Laplacian matrix of a directed graph.

Parameters

csgraph : array_like or sparse matrix, 2 dimensions

compressed-sparse graph, with shape (N, N).

normed : bool, optional

If True, then compute normalized Laplacian.

return_diag : bool, optional

If True, then also return an array related to vertex degrees.

use_out_degree : bool, optional

If True, then use out-degree instead of in-degree. This distinction matters only if the graph is asymmetric. Default: False.

Returns

lap : ndarray

The N x N laplacian matrix of graph.

diag : ndarray, optional

The length-N diagonal of the Laplacian matrix. For the normalized Laplacian, this is the array of square roots of vertex degrees or 1 if the degree is zero.

Notes

The Laplacian matrix of a graph is sometimes referred to as the “Kirchoff matrix” or the “admittance matrix”, and is useful in many parts of spectral graph theory. In particular, the eigen-decomposition of the laplacian matrix can give insight into many properties of the graph.

Examples

```
>>> from scipy.sparse import csgraph
>>> G = np.arange(5) * np.arange(5)[:, np.newaxis]
>>> G
array([[ 0,  0,  0,  0,  0],
       [ 0,  1,  2,  3,  4],
       [ 0,  2,  4,  6,  8],
       [ 0,  3,  6,  9, 12],
       [ 0,  4,  8, 12, 16]])
>>> csgraph.laplacian(G, normed=False)
array([[  0,   0,   0,   0,   0],
       [  0,   9,  -2,  -3,  -4],
       [  0,  -2,  16,  -6,  -8],
       [  0,  -3,  -6,  21, -12],
       [  0,  -4,  -8, -12,  24]])
```

`scipy.sparse.csgraph.`**`shortest_path`**`(`*csgraph, method='auto', directed=True, return_predecessors=False, unweighted=False, overwrite=False*`)`

Perform a shortest-path graph search on a positive directed or undirected graph.

New in version 0.11.0.

Parameters **csgraph** : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

method : string ['auto'|'FW'|'D'], optional

Algorithm to use for shortest paths. Options are:

'auto' – (default) select the best among 'FW', 'D', 'BF', or 'J'

based on the input data.

'FW' – Floyd-Warshall algorithm. Computational cost is

approximately `O[N^3]`. The input csgraph will be converted to a dense representation.

'D' – Dijkstra's algorithm with Fibonacci heaps. Computational

cost is approximately `O[N(N*k + N*log(N))]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'BF' – Bellman-Ford algorithm. This algorithm can be used when

weights are negative. If a negative cycle is encountered, an error will be raised. Computational cost is approximately `O[N(N^2 k)]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'J' – Johnson's algorithm. Like the Bellman-Ford algorithm,

Johnson's algorithm is designed for use when the weights are negative. It combines the Bellman-Ford algorithm with Dijkstra's algorithm for faster computation.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite : bool, optional

If True, overwrite csgraph with the result. This applies only if method == 'FW' and csgraph is a dense, c-ordered array with dtype=float64.

Returns

dist_matrix : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:

if there are negative cycles in the graph

Notes

As currently implemented, Dijkstra's algorithm and Johnson's algorithm do not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are non-equal edges, method='D' may yield an incorrect result.

`scipy.sparse.csgraph.`**`dijkstra`**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Dijkstra algorithm using Fibonacci Heaps

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of non-negative distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

limit : float, optional

The maximum distance to calculate, must be >= 0. Using a smaller limit will decrease computation time by aborting calculations between pairs that are separated by a distance > limit. For such pairs, the distance will be equal to np.inf (i.e., not connected). .. versionadded:: 0.14.0

Returns **dist_matrix** : ndarray

The matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Notes

As currently implemented, Dijkstra's algorithm does not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are not equal and both are nonzero, setting directed=False will not yield the correct result.

Also, this routine does not work for graphs with negative distances. Negative distances can lead to infinite cycles that must be handled by specialized algorithms such as Bellman-Ford's algorithm or Johnson's algorithm.

`scipy.sparse.csgraph.`**`floyd_warshall`**(*csgraph*, *directed=True*, *return_predecessors=False*, *unweighted=False*, *overwrite=False*)

Compute the shortest path lengths using the Floyd-Warshall algorithm

New in version 0.11.0.

Parameters **csgraph** : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite : bool, optional

If True, overwrite csgraph with the result. This applies only if csgraph is a dense, c-ordered array with dtype=float64.

Returns **dist_matrix** : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

`scipy.sparse.csgraph.`**`bellman_ford`**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Compute the shortest path lengths using the Bellman-Ford algorithm.

The Bellman-ford algorithm can robustly deal with graphs with negative weights. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra's algorithm may be faster.

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

dist_matrix : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

`scipy.sparse.csgraph.`**`johnson`**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Compute the shortest path lengths using Johnson's algorithm.

Johnson's algorithm combines the Bellman-Ford algorithm and Dijkstra's algorithm to quickly find shortest paths in a way that is robust to the presence of negative cycles. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra() may be faster.

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns **dist_matrix** : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

`scipy.sparse.csgraph.`**`breadth_first_order`**(*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*)

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique, but the tree which it generates is unique.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix

The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors : bool, optional

If True (default), then return the predecesor array (see below).

Returns **node_array** : ndarray, one dimension

The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors : ndarray, one dimension

Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

`scipy.sparse.csgraph.`**`depth_first_order`**(*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*)

Return a depth-first ordering starting with specified node.

Note that a depth-first order is not unique. Furthermore, for graphs with cycles, the tree generated by a depth-first search is not unique either.

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix

The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors : bool, optional

If True (default), then return the predecesor array (see below).

Returns

node_array : ndarray, one dimension

The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors : ndarray, one dimension

Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

`scipy.sparse.csgraph.`**`breadth_first_tree`**(*csgraph*, *i_start*, *directed=True*)

Return the tree generated by a breadth-first search

Note that a breadth-first tree from a specified node is unique.

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns

cstree : csr matrix

The N x N directed compressed-sparse representation of the breadth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
input graph          breadth first tree from (0)

    (0)                         (0)
```

```
    /   \                       /   \
   3     8                     3     8
  /       \                   /       \
(3)---5---(1)               (3)       (1)
  \       /                           /
   6     2                           2
    \   /                           /
     (2)                         (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = breadth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 3],
       [0, 0, 2, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. A breadth-first tree from a given node is unique.

`scipy.sparse.csgraph.`**`depth_first_tree`**(*csgraph*, *i_start*, *directed=True*)

Return a tree generated by a depth-first search.

Note that a tree generated by a depth-first search is not unique: it depends on the order that the children of each node are searched.

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns

cstree : csr matrix

The N x N directed compressed-sparse representation of the depth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
 input graph           depth first tree from (0)

     (0)                         (0)
    /   \                           \
   3     8                           8
```

```
  /       \                           \
(3)---5---(1)               (3)       (1)
  \       /                   \       /
   6     2                     6     2
    \   /                       \   /
     (2)                         (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = depth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 0],
       [0, 0, 2, 0],
       [0, 0, 0, 6],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. Unlike a breadth-first tree, a depth-first tree of a given graph is not unique if the graph contains cycles. If the above solution had begun with the edge connecting nodes 0 and 3, the result would have been different.

`scipy.sparse.csgraph.`**`minimum_spanning_tree`**(*csgraph*, *overwrite=False*)

Return a minimum spanning tree of an undirected graph

A minimum spanning tree is a graph consisting of the subset of edges which together connect all connected nodes, while minimizing the total sum of weights on the edges. This is computed using the Kruskal algorithm.

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix, 2 dimensions

The N x N matrix representing an undirected graph over N nodes (see notes below).

overwrite : bool, optional

if true, then parts of the input graph will be overwritten for efficiency.

Returns

span_tree : csr matrix

The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).

Notes

This routine uses undirected graphs as input and output. That is, if graph[i, j] and graph[j, i] are both zero, then nodes i and j do not have an edge connecting them. If either is nonzero, then the two are connected by the minimum nonzero value of the two.

Examples

The following example shows the computation of a minimum spanning tree over a simple four-component graph:

```
 input graph             minimum spanning tree

     (0)                         (0)
    /   \                       /
   3     8                     3
```

```
  /       \                   /
(3)---5---(1)               (3)---5---(1)
  \       /                           /
   6     2                           2
    \   /                           /
     (2)                         (2)
```

It is easy to see from inspection that the minimum spanning tree involves removing the edges with weights 8 and 6. In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import minimum_spanning_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = minimum_spanning_tree(X)
>>> Tcsr.toarray().astype(int)
array([[0, 0, 0, 3],
       [0, 0, 2, 5],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

`scipy.sparse.csgraph.`**`reverse_cuthill_mckee`**`()`

Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.

It is assumed by default, `symmetric_mode=False`, that the input matrix is not symmetric and works on the matrix `A+A.T`. If you are guaranteed that the matrix is symmetric in structure (values of matrix elements do not matter) then set `symmetric_mode=True`.

Parameters

graph : sparse matrix

Input sparse in CSC or CSR sparse matrix format.

symmetric_mode : bool, optional

Is input matrix guaranteed to be symmetric.

Returns

perm : ndarray

Array of permuted row and column indices.

Notes

New in version 0.15.0.

References

E. Cuthill and J. McKee, "Reducing the Bandwidth of Sparse Symmetric Matrices", ACM '69 Proceedings of the 1969 24th national conference, (1969).

`scipy.sparse.csgraph.`**`maximum_bipartite_matching`**`()`

Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.

Such a permutation is always possible provided that the matrix is nonsingular. This function looks at the structure of the matrix only. The input matrix will be converted to CSC matrix format if necessary.

Parameters

graph : sparse matrix

Input sparse in CSC format

perm_type : str, {'row', 'column'}

Type of permutation to generate.

Returns

perm : ndarray

Array of row or column permutations.

Notes

This function relies on a maximum cardinality bipartite matching algorithm based on a breadth-first search (BFS) of the underlying graph.

New in version 0.15.0.

References

I. S. Duff, K. Kaya, and B. Ucar, “Design, Implementation, and Analysis of Maximum Transversal Algorithms”, ACM Trans. Math. Softw. 38, no. 2, (2011).

Graph Representations This module uses graphs which are stored in a matrix format. A graph with N nodes can be represented by an (N x N) adjacency matrix G. If there is a connection from node i to node j, then G[i, j] = w, where w is the weight of the connection. For nodes i and j which are not connected, the value depends on the representation:

- for dense array representations, non-edges are represented by G[i, j] = 0, infinity, or NaN.
- for dense masked representations (of type np.ma.MaskedArray), non-edges are represented by masked values. This can be useful when graphs with zero-weight edges are desired.
- for sparse array representations, non-edges are represented by non-entries in the matrix. This sort of sparse representation also allows for edges with zero weights.

As a concrete example, imagine that you would like to represent the following undirected graph:

```
      G

     (0)
    /   \
   1     2
  /       \
(2)       (1)
```

This graph has three nodes, where node 0 and 1 are connected by an edge of weight 2, and nodes 0 and 2 are connected by an edge of weight 1. We can construct the dense, masked, and sparse representations as follows, keeping in mind that an undirected graph is represented by a symmetric matrix:

```
>>> G_dense = np.array([[0, 2, 1],
...                     [2, 0, 0],
...                     [1, 0, 0]])
>>> G_masked = np.ma.masked_values(G_dense, 0)
>>> from scipy.sparse import csr_matrix
>>> G_sparse = csr_matrix(G_dense)
```

This becomes more difficult when zero edges are significant. For example, consider the situation when we slightly modify the above graph:

```
     G2

     (0)
    /   \
   0     2
  /       \
(2)       (1)
```

This is identical to the previous graph, except nodes 0 and 2 are connected by an edge of zero weight. In this case, the dense representation above leads to ambiguities: how can non-edges be represented if zero is a meaningful value? In this case, either a masked or sparse representation must be used to eliminate the ambiguity:

```
>>> G2_data = np.array([[np.inf, 2,      0     ],
...                     [2,      np.inf, np.inf],
...                     [0,      np.inf, np.inf]])
>>> G2_masked = np.ma.masked_invalid(G2_data)
>>> from scipy.sparse.csgraph import csgraph_from_dense
>>> # G2_sparse = csr_matrix(G2_data) would give the wrong result
>>> G2_sparse = csgraph_from_dense(G2_data, null_value=np.inf)
>>> G2_sparse.data
array([ 2.,  0.,  2.,  0.])
```

Here we have used a utility routine from the csgraph submodule in order to convert the dense representation to a sparse representation which can be understood by the algorithms in submodule. By viewing the data array, we can see that the zero values are explicitly encoded in the graph.

Directed vs. Undirected Matrices may represent either directed or undirected graphs. This is specified throughout the csgraph module by a boolean keyword. Graphs are assumed to be directed by default. In a directed graph, traversal from node i to node j can be accomplished over the edge G[i, j], but not the edge G[j, i]. In a non-directed graph, traversal from node i to node j can be accomplished over either G[i, j] or G[j, i]. If both edges are not null, and the two have unequal weights, then the smaller of the two is used. Note that a symmetric matrix will represent an undirected graph, regardless of whether the 'directed' keyword is set to True or False. In this case, using `directed=True` generally leads to more efficient computation.

The routines in this module accept as input either scipy.sparse representations (csr, csc, or lil format), masked representations, or dense representations with non-edges indicated by zeros, infinities, and NaN entries.

Functions

`bellman_ford`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using the Bellman-Ford algorithm.
`breadth_first_order`(csgraph, i_start[, ...])	Return a breadth-first ordering starting with specified node.
`breadth_first_tree`(csgraph, i_start[, directed])	Return the tree generated by a breadth-first search
`connected_components`(csgraph[, directed, ...])	Analyze the connected components of a sparse graph
`construct_dist_matrix`(graph, predecessors[, ...])	Construct distance matrix from a predecessor matrix
`cs_graph_components`(*args, **kwds)	`cs_graph_components` is deprecated!
`csgraph_from_dense`(graph[, null_value, ...])	Construct a CSR-format sparse graph from a dense matrix.
`csgraph_from_masked`(graph)	Construct a CSR-format graph from a masked array.
`csgraph_masked_from_dense`(graph[, ...])	Construct a masked array graph representation from a dense matrix.
`csgraph_to_dense`(csgraph[, null_value])	Convert a sparse graph representation to a dense representation
`depth_first_order`(csgraph, i_start[, ...])	Return a depth-first ordering starting with specified node.
`depth_first_tree`(csgraph, i_start[, directed])	Return a tree generated by a depth-first search.
`dijkstra`(csgraph[, directed, indices, ...])	Dijkstra algorithm using Fibonacci Heaps
`floyd_warshall`(csgraph[, directed, ...])	Compute the shortest path lengths using the Floyd-Warshall algorithm
`johnson`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using Johnson's algorithm.
`laplacian`(csgraph[, normed, return_diag, ...])	Return the Laplacian matrix of a directed graph.
`maximum_bipartite_matching`	Returns an array of row or column permutations that makes the diagonal
`minimum_spanning_tree`(csgraph[, overwrite])	Return a minimum spanning tree of an undirected graph
`reconstruct_path`(csgraph, predecessors[, ...])	Construct a tree from a graph and a predecessor list.
`reverse_cuthill_mckee`	Returns the permutation array that orders a sparse CSR or CSC matrix in
`shortest_path`(csgraph[, method, directed, ...])	Perform a shortest-path graph search on a positive directed or undirected

Classes

`Tester`	alias of `NoseTester`

Exceptions

`NegativeCycleError`

Sparse linear algebra (`scipy.sparse.linalg`)

`LinearOperator`(dtype, shape)	Common interface for performing matrix vector products
`aslinearoperator`(A)	Return A as a LinearOperator.

Abstract linear operators

class `scipy.sparse.linalg.`**`LinearOperator`**(*dtype*, *shape*)

Common interface for performing matrix vector products

Many iterative methods (e.g. cg, gmres) do not need to know the individual entries of a matrix to solve a linear system A*x=b. Such solvers only require the computation of matrix vector products, A*v where v is a dense vector. This class serves as an abstract interface between iterative solvers and matrix-like objects.

To construct a concrete LinearOperator, either pass appropriate callables to the constructor of this class, or subclass it.

A subclass must implement either one of the methods `_matvec` and `_matmat`, and the attributes/properties `shape` (pair of integers) and `dtype` (may be None). It may call the `__init__` on this class to have these attributes validated. Implementing `_matvec` automatically implements `_matmat` (using a naive algorithm) and vice-versa.

Optionally, a subclass may implement `_rmatvec` or `_adjoint` to implement the Hermitian adjoint (conjugate transpose). As with `_matvec` and `_matmat`, implementing either `_rmatvec` or `_adjoint` implements the other automatically. Implementing `_adjoint` is preferable; `_rmatvec` is mostly there for backwards compatibility.

Parameters

shape : tuple

Matrix dimensions (M,N).

matvec : callable f(v)

Returns returns A * v.

rmatvec : callable f(v)

Returns A^H * v, where A^H is the conjugate transpose of A.

matmat : callable f(V)

Returns A * V, where V is a dense matrix with dimensions (N,K).

dtype : dtype

Data type of the matrix.

See also:

`aslinearoperator`

Construct LinearOperators

Notes

The user-defined matvec() function must properly handle the case where v has shape (N,) as well as the (N,1) case. The shape of the return type is handled internally by LinearOperator.

LinearOperator instances can also be multiplied, added with each other and exponentiated, all lazily: the result of these operations is always a new, composite LinearOperator, that defers linear operations to the original operators and combines the results.

Examples

```
>>> import numpy as np
>>> from scipy.sparse.linalg import LinearOperator
>>> def mv(v):
...     return np.array([2*v[0], 3*v[1]])
...
>>> A = LinearOperator((2,2), matvec=mv)
>>> A
<2x2 LinearOperator with unspecified dtype>
>>> A.matvec(np.ones(2))
array([ 2.,  3.])
>>> A * np.ones(2)
array([ 2.,  3.])
```

Attributes

args	(tuple) For linear operators describing products etc. of other linear operators, the operands of the binary operation.

Methods

`__call__`(x)	
`adjoint`()	Hermitian adjoint.
`dot`(x)	Matrix-matrix or matrix-vector multiplication.
`matmat`(X)	Matrix-matrix multiplication.
`matvec`(x)	Matrix-vector multiplication.
`rmatvec`(x)	Adjoint matrix-vector multiplication.
`transpose`()	Transpose this linear operator.

`LinearOperator.`**`__call__`**`(x)`

`LinearOperator.`**`adjoint`**`()`

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** : LinearOperator

Hermitian adjoint of self.

`LinearOperator.`**`dot`**`(x)`

Matrix-matrix or matrix-vector multiplication.

Parameters **x** : array_like

1-d or 2-d array, representing a vector or matrix.

Returns **Ax** : array

1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

`LinearOperator.`**`matmat`**`(X)`

Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** : {matrix, ndarray}

An array with shape (N,K).

Returns **Y** : {matrix, ndarray}

A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

`LinearOperator.`**`matvec`**`(x)`

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** : {matrix, ndarray}

An array with shape (N,) or (N,1).

Returns **y** : {matrix, ndarray}

A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

`LinearOperator.`**`rmatvec`**`(x)`

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** : {matrix, ndarray}

An array with shape (M,) or (M,1).

Returns **y** : {matrix, ndarray}

A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

`LinearOperator.`**`transpose`**`()`

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

`scipy.sparse.linalg.`**`aslinearoperator`**`(A)`

Return A as a LinearOperator.

'A' may be any of the following types:

- ndarray
- matrix
- sparse matrix (e.g. csr_matrix, lil_matrix, etc.)
- LinearOperator
- An object with .shape and .matvec attributes

See the LinearOperator documentation for additional information.

Examples

```
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```

`inv`(A)	Compute the inverse of a sparse matrix
`expm`(A)	Compute the matrix exponential using Pade approximation.
`expm_multiply`(A, B[, start, stop, num, endpoint])	Compute the action of the matrix exponential of A on B.

Matrix Operations

`scipy.sparse.linalg.`**`inv`**(*A*)

Compute the inverse of a sparse matrix

Parameters **A** : (M,M) ndarray or sparse matrix

square matrix to be inverted

Returns **Ainv** : (M,M) ndarray or sparse matrix

inverse of *A*

Notes

This computes the sparse inverse of *A*. If the inverse of *A* is expected to be non-sparse, it will likely be faster to convert *A* to dense and use scipy.linalg.inv.

New in version 0.12.0.

`scipy.sparse.linalg.`**`expm`**(*A*)

Compute the matrix exponential using Pade approximation.

Parameters **A** : (M,M) array_like or sparse matrix

2D Array or Matrix (sparse or dense) to be exponentiated

Returns **expA** : (M,M) ndarray

Matrix exponential of *A*

Notes

This is algorithm (6.1) which is a simplification of algorithm (5.1).

New in version 0.12.0.

References

[R18]

`scipy.sparse.linalg.`**`expm_multiply`**(*A*, *B*, *start=None*, *stop=None*, *num=None*, *endpoint=None*)

Compute the action of the matrix exponential of A on B.

Parameters **A** : transposable linear operator

The operator whose exponential is of interest.

B : ndarray

The matrix or vector to be multiplied by the matrix exponential of A.

start : scalar, optional

The starting time point of the sequence.

stop : scalar, optional

The end time point of the sequence, unless *endpoint* is set to False. In that case, the sequence consists of all but the last of `num + 1` evenly spaced time points, so that *stop* is excluded. Note that the step size changes when *endpoint* is False.

num : int, optional
Number of time points to use.

endpoint : bool, optional
If True, *stop* is the last time point. Otherwise, it is not included.

Returns **expm_A_B** : ndarray
The result of the action $e^{t_k A} B$.

Notes

The optional arguments defining the sequence of evenly spaced time points are compatible with the arguments of `numpy.linspace`.

The output ndarray shape is somewhat complicated so I explain it here. The ndim of the output could be either 1, 2, or 3. It would be 1 if you are computing the expm action on a single vector at a single time point. It would be 2 if you are computing the expm action on a vector at multiple time points, or if you are computing the expm action on a matrix at a single time point. It would be 3 if you want the action on a matrix with multiple columns at multiple time points. If multiple time points are requested, expm_A_B[0] will always be the action of the expm at the first time point, regardless of whether the action is on a vector or a matrix.

References

[R19], [R20]

`onenormest`(A[, t, itmax, compute_v, compute_w])	Compute a lower bound of the 1-norm of a sparse matrix.

Matrix norms

`scipy.sparse.linalg.`**`onenormest`**(*A*, *t=2*, *itmax=5*, *compute_v=False*, *compute_w=False*)

Compute a lower bound of the 1-norm of a sparse matrix.

Parameters **A** : ndarray or other linear operator
A linear operator that can be transposed and that can produce matrix products.

t : int, optional
A positive parameter controlling the tradeoff between accuracy versus time and memory usage. Larger values take longer and use more memory but give more accurate output.

itmax : int, optional
Use at most this many iterations.

compute_v : bool, optional
Request a norm-maximizing linear operator input vector if True.

compute_w : bool, optional
Request a norm-maximizing linear operator output vector if True.

Returns **est** : float
An underestimate of the 1-norm of the sparse matrix.

v : ndarray, optional
The vector such that ||Av||_1 == est*||v||_1. It can be thought of as an input to the linear operator that gives an output with particularly large norm.

w : ndarray, optional
The vector Av which has relatively large 1-norm. It can be thought of as an output of the linear operator that is relatively large in norm compared to the input.

Notes

This is algorithm 2.4 of [1].

In [2] it is described as follows. “This algorithm typically requires the evaluation of about 4t matrix-vector products and almost invariably produces a norm estimate (which is, in fact, a lower bound on the norm) correct to within a factor 3.”

New in version 0.13.0.

References

[R31], [R32]

Solving linear problems Direct methods for linear equation systems:

`spsolve`(A, b[, permc_spec, use_umfpack])	Solve the sparse linear system Ax=b, where b may be a vector or a matrix.
`factorized`(A)	Return a fuction for solving a sparse linear system, with A pre-factorized.

`scipy.sparse.linalg.`**`spsolve`**(*A*, *b*, *permc_spec=None*, *use_umfpack=True*)

Solve the sparse linear system Ax=b, where b may be a vector or a matrix.

Parameters

A : ndarray or sparse matrix

The square matrix A will be converted into CSC or CSR form

b : ndarray or sparse matrix

The matrix or vector representing the right hand side of the equation. If a vector, b.size must be (n,) or (n, 1)

permc_spec : str, optional

How to permute the columns of the matrix for sparsity preservation. (default: ‘COLAMD’)

- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering

use_umfpack : bool, optional

if True (default) then use umfpack for the solution. This is only referenced if b is a vector and `scikit-umfpack` is installed.

Returns

x : ndarray or sparse matrix

the solution of the sparse linear equation. If b is a vector, then x is a vector of size A.shape[1] If b is a matrix, then x is a matrix of size (A.shape[1], b.shape[1])

Notes

For solving the matrix expression AX = B, this solver assumes the resulting matrix X is sparse, as is often the case for very sparse inputs. If the resulting X is dense, the construction of this sparse result will be relatively expensive. In that case, consider converting A to a dense matrix and using scipy.linalg.solve or its variants.

`scipy.sparse.linalg.`**`factorized`**(*A*)

Return a fuction for solving a sparse linear system, with A pre-factorized.

Parameters

A : (N, N) array_like

Input.

Returns

solve : callable

To solve the linear system of equations given in *A*, the *solve* callable should be passed an ndarray of shape (N,).

Examples

```
>>> A = np.array([[ 3. ,  2. , -1. ],
                  [ 2. , -2. ,  4. ],
                  [-1. ,  0.5, -1. ]])
```

```
>>> solve = factorized( A ) # Makes LU decomposition.
```

```
>>> rhs1 = np.array([1,-2,0])
>>> x1 = solve( rhs1 ) # Uses the LU factors.
array([ 1., -2., -2.])
```

Iterative methods for linear equation systems:

`bicg`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient iteration to solve A x = b
`bicgstab`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient STABilized iteration to solve A x = b
`cg`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient iteration to solve A x = b
`cgs`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient Squared iteration to solve A x = b
`gmres`(A, b[, x0, tol, restart, maxiter, ...])	Use Generalized Minimal RESidual iteration to solve A x = b.
`lgmres`(A, b[, x0, tol, maxiter, M, ...])	Solve a matrix equation using the LGMRES algorithm.
`minres`(A, b[, x0, shift, tol, maxiter, ...])	Use MINimum RESidual iteration to solve Ax=b
`qmr`(A, b[, x0, tol, maxiter, xtype, M1, M2, ...])	Use Quasi-Minimal Residual iteration to solve A x = b

`scipy.sparse.linalg.`**`bicg`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use BIConjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system It is required that the linear operator can produce `Ax` and `A^T x`.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {‘f’,’d’,’F’,’D’}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’f’,’d’,’F’,or ‘D’. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`bicgstab`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use BIConjugate Gradient STABilized iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system `A` must represent a hermitian, positive definite matrix

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {‘f’,’d’,’F’,’D’}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’f’,’d’,’F’,or ‘D’. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`cg`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use Conjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system `A` must represent a hermitian, positive definite matrix

b : {array, matrix}
Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}
The converged solution.

info : integer
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}
Starting guess for the solution.

tol : float
Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer
Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}
Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function
User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}
This parameter is deprecated – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`cgs`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use Conjugate Gradient Squared iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}
The real-valued N-by-N matrix of the linear system

b : {array, matrix}
Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}
The converged solution.

info : integer
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}
Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`gmres`**(*A*, *b*, *x0=None*, *tol=1e-05*, *restart=None*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*, *restrt=None*)

Use Generalized Minimal RESidual iteration to solve A x = b.

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : int

Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution (a vector of zeros by default).

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

restart : int, optional

Number of iterations between restarts. Larger values increase iteration cost, but may be necessary for convergence. Default is 20.

maxiter : int, optional

Maximum number of iterations (restart cycles). Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

xtype : {'f','d','F','D'}

This parameter is DEPRECATED — avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

M : {sparse matrix, dense matrix, LinearOperator}

Inverse of the preconditioner of A. M should approximate the inverse of A and be easy to solve for (see Notes). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance. By default, no preconditioner is used.

callback : function

User-supplied function to call after each iteration. It is called as callback(rk), where rk is the current residual vector.

restrt : int, optional

DEPRECATED - use *restart* instead.

See also:

`LinearOperator`

Notes

A preconditioner, P, is chosen such that P is close to A but easy to solve for. The preconditioner parameter required by this routine is `M = P^-1`. The inverse should preferably not be calculated explicitly. Rather, use the following template to produce M:

```
# Construct a linear operator that computes P^-1 * x.
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

`scipy.sparse.linalg.`**`lgmres`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=1000*, *M=None*, *callback=None*, *inner_m=30*, *outer_k=3*, *outer_v=None*, *store_outer_Av=True*)

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm [R21] [R22] is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

x0 : {array, matrix}

Starting guess for the solution.

tol : float, optional

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : int, optional

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}, optional

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function, optional

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

inner_m : int, optional

Number of inner GMRES iterations per each outer iteration.

outer_k : int, optional

Number of vectors to carry between inner GMRES iterations. According to [R21], good values are in the range of 1...3. However, note that if you want to use the additional vectors to accelerate solving multiple similar problems, larger values may be beneficial.

outer_v : list of tuples, optional

List containing tuples `(v, Av)` of vectors and corresponding matrix-vector products, used to augment the Krylov subspace, and carried between inner GMRES iterations. The element `Av` can be *None* if the matrix-vector product should be re-evaluated. This parameter is modified in-place by `lgmres`, and can be used to pass "guess" vectors in and out of the algorithm when solving similar problems.

store_outer_Av : bool, optional

Whether LGMRES should store also A*v in addition to vectors *v* in the *outer_v* list. Default is True.

Returns **x** : array or matrix

The converged solution.

info : int

Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Notes

The LGMRES algorithm [R21] [R22] is designed to avoid the slowing of convergence in restarted GMRES, due to alternating residual vectors. Typically, it often outperforms GMRES(m) of comparable memory requirements by some measure, or at least is not much worse.

Another advantage in this algorithm is that you can supply it with 'guess' vectors in the *outer_v* argument that augment the Krylov subspace. If the solution lies close to the span of these vectors, the algorithm converges faster. This can be useful if several very similar matrices need to be inverted one after another, such as in Newton-Krylov iteration where the Jacobian matrix often changes little in the nonlinear steps.

References

[R21], [R22]

`scipy.sparse.linalg.`**`minres`**(*A*, *b*, *x0=None*, *shift=0.0*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*, *show=False*, *check=False*)

Use MINimum RESidual iteration to solve Ax=b

MINRES minimizes norm(A*x - b) for a real symmetric matrix A. Unlike the Conjugate Gradient method, A can be indefinite or singular.

If shift != 0 then the method solves (A - shift*I)x = b

Parameters **A** : {sparse matrix, dense matrix, LinearOperator}

The real symmetric N-by-N matrix of the linear system

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns **x** : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not

achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}
Starting guess for the solution.

tol : float
Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer
Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}
Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function
User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}
This parameter is deprecated – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

Notes

THIS FUNCTION IS EXPERIMENTAL AND SUBJECT TO CHANGE!

References

Solution of sparse indefinite systems of linear equations,
C. C. Paige and M. A. Saunders (1975), SIAM J. Numer. Anal. 12(4), pp. 617-629. http://www.stanford.edu/group/SOL/software/minres.html

This file is a translation of the following MATLAB implementation:
http://www.stanford.edu/group/SOL/software/minres/matlab/

`scipy.sparse.linalg.`**`qmr`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M1=None*, *M2=None*, *callback=None*)

Use Quasi-Minimal Residual iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}
The real-valued N-by-N matrix of the linear system. It is required that the linear operator can produce `Ax` and `A^T x`.

b : {array, matrix}
Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}
The converged solution.

info : integer
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M1 : {sparse matrix, dense matrix, LinearOperator}

Left preconditioner for A.

M2 : {sparse matrix, dense matrix, LinearOperator}

Right preconditioner for A. Used together with the left preconditioner M1. The matrix M1*A*M2 should have better conditioned than A alone.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is DEPRECATED – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

See also:

`LinearOperator`

Iterative methods for least-squares problems:

`lsqr`(A, b[, damp, atol, btol, conlim, ...])	Find the least-squares solution to a large, sparse, linear system of equations.
`lsmr`(A, b[, damp, atol, btol, conlim, ...])	Iterative solver for least-squares problems.

`scipy.sparse.linalg.`**`lsqr`**(*A*, *b*, *damp=0.0*, *atol=1e-08*, *btol=1e-08*, *conlim=100000000.0*, *iter_lim=None*, *show=False*, *calc_var=False*)

Find the least-squares solution to a large, sparse, linear system of equations.

The function solves `Ax = b` or `min ||b - Ax||^2` or `min ||Ax - b||^2 + d^2 ||x||^2`.

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

```
1. Unsymmetric equations --    solve  A*x = b

2. Linear least squares  --    solve  A*x = b
                               in the least-squares sense

3. Damped least squares  --    solve  (   A    )*x = ( b )
                                      ( damp*I )     ( 0 )
                               in the least-squares sense
```

Parameters

A : {sparse matrix, ndarray, LinearOperator}

Representation of an m-by-n matrix. It is required that the linear operator can produce `Ax` and `A^T x`.

b : (m,) ndarray

Right-hand side vector `b`.

damp : float

Damping coefficient.

atol, btol : float, optional

Stopping tolerances. If both are 1.0e-9 (say), the final residual norm should be accurate to about 9 digits. (The final x will usually have fewer correct digits, depending on cond(A) and the size of damp.)

conlim : float, optional

Another stopping tolerance. lsqr terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, *conlim* could be as large as 1.0e+12 (say). For least-squares problems, conlim should be less than 1.0e+8. Maximum precision can be obtained by setting `atol = btol = conlim = zero`, but the number of iterations may then be excessive.

iter_lim : int, optional

Explicit limitation on number of iterations (for safety).

show : bool, optional

Display an iteration log.

calc_var : bool, optional

Whether to estimate diagonals of `(A'A + damp^2*I)^{-1}`.

Returns **x** : ndarray of float

The final solution.

istop : int

Gives the reason for termination. 1 means x is an approximate solution to Ax = b. 2 means x approximately solves the least-squares problem.

itn : int

Iteration number upon termination.

r1norm : float

`norm(r)`, where `r = b - Ax`.

r2norm : float

`sqrt( norm(r)^2 + damp^2 * norm(x)^2 )`. Equal to *r1norm* if `damp == 0`.

anorm : float

Estimate of Frobenius norm of `Abar = [[A]; [damp*I]]`.

acond : float

Estimate of `cond(Abar)`.

arnorm : float

Estimate of `norm(A'*r - damp^2*x)`.

xnorm : float

`norm(x)`

var : ndarray of float

If `calc_var` is True, estimates all diagonals of `(A'A)^{-1}` (if `damp == 0`) or more generally `(A'A + damp^2*I)^{-1}`. This is well defined if A has full column rank or `damp > 0`. (Not sure what var means if `rank(A) < n` and `damp = 0.`)

Notes

LSQR uses an iterative method to approximate the solution. The number of iterations required to reach a certain accuracy depends strongly on the scaling of the problem. Poor scaling of the rows or columns of A should therefore be avoided where possible.

For example, in problem 1 the solution is unaltered by row-scaling. If a row of A is very small or large compared to the other rows of A, the corresponding row of (A b) should be scaled up or down.

In problems 1 and 2, the solution x is easily recovered following column-scaling. Unless better information is known, the nonzero columns of A should be scaled so that they all have the same Euclidean norm (e.g., 1.0).

In problem 3, there is no freedom to re-scale if damp is nonzero. However, the value of damp should be assigned only after attention has been paid to the scaling of A.

The parameter damp is intended to help regularize ill-conditioned systems, by preventing the true solution from being very large. Another aid to regularization is provided by the parameter acond, which may be used to terminate iterations before the computed solution becomes very large.

If some initial estimate `x0` is known and if `damp == 0`, one could proceed as follows:

1. Compute a residual vector `r0 = b - A*x0`.
2. Use LSQR to solve the system `A*dx = r0`.
3. Add the correction dx to obtain a final solution `x = x0 + dx`.

This requires that `x0` be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes k1 iterations to solve A*x = b and k2 iterations to solve A*dx = r0. If x0 is "good", norm(r0) will be smaller than norm(b). If the same stopping tolerances atol and btol are used for each system, k1 and k2 will be similar, but the final solution x0 + dx should be more accurate. The only way to reduce the total work is to use a larger stopping tolerance for the second system. If some value btol is suitable for A*x = b, the larger value btol*norm(b)/norm(r0) should be suitable for A*dx = r0.

Preconditioning is another way to reduce the number of iterations. If it is possible to solve a related system `M*x = b` efficiently, where M approximates A in some helpful way (e.g. M - A has low rank or its elements are small relative to those of A), LSQR may converge more rapidly on the system `A*M(inverse)*z = b`, after which x can be recovered by solving M*x = z.

If A is symmetric, LSQR should not be used!

Alternatives are the symmetric conjugate-gradient method (cg) and/or SYMMLQ. SYMMLQ is an implementation of symmetric cg that applies to any symmetric A and will converge more rapidly than LSQR. If A is positive definite, there are other implementations of symmetric cg that require slightly less work per iteration than SYMMLQ (but will take the same number of iterations).

References

[R28], [R29], [R30]

`scipy.sparse.linalg.`**`lsmr`**(*A*, *b*, *damp=0.0*, *atol=1e-06*, *btol=1e-06*, *conlim=100000000.0*, *maxiter=None*, *show=False*)

Iterative solver for least-squares problems.

lsmr solves the system of linear equations `Ax = b`. If the system is inconsistent, it solves the least-squares problem `min ||b - Ax||_2`. A is a rectangular matrix of dimension m-by-n, where all cases are allowed: m = n, m > n, or m < n. B is a vector of length m. The matrix A may be dense or sparse (usually sparse).

Parameters

A : {matrix, sparse matrix, ndarray, LinearOperator}

Matrix A in the linear system.

b : (m,) ndarray

Vector b in the linear system.

damp : float

Damping factor for regularized least-squares. `lsmr` solves the regularized least-squares problem:

```
min ||(b) - (   A    )x||
    ||(0)    (damp*I) ||_2
```

where damp is a scalar. If damp is None or 0, the system is solved without regularization.

atol, btol : float, optional

Stopping tolerances. `lsmr` continues iterations until a certain backward error estimate is smaller than some quantity depending on atol and btol. Let `r = b - Ax` be the residual vector for the current approximate solution

x. If `Ax = b` seems to be consistent, `lsmr` terminates when `norm(r) <= atol * norm(A) * norm(x) + btol * norm(b)`. Otherwise, lsmr terminates when `norm(A^{T} r) <= atol * norm(A) * norm(r)`. If both tolerances are 1.0e-6 (say), the final `norm(r)` should be accurate to about 6 digits. (The final x will usually have fewer correct digits, depending on `cond(A)` and the size of LAMBDA.) If *atol* or *btol* is None, a default value of 1.0e-6 will be used. Ideally, they should be estimates of the relative error in the entries of A and B respectively. For example, if the entries of *A* have 7 correct digits, set atol = 1e-7. This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

conlim : float, optional

`lsmr` terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, conlim could be as large as 1.0e+12 (say). For least-squares problems, *conlim* should be less than 1.0e+8. If *conlim* is None, the default value is 1e+8. Maximum precision can be obtained by setting `atol = btol = conlim = 0`, but the number of iterations may then be excessive.

maxiter : int, optional

`lsmr` terminates if the number of iterations reaches *maxiter*. The default is `maxiter = min(m, n)`. For ill-conditioned systems, a larger value of *maxiter* may be needed.

show : bool, optional

Print iterations logs if `show=True`.

Returns **x** : ndarray of float

Least-square solution returned.

istop : int

istop gives the reason for stopping:

```
istop   = 0 means x=0 is a solution.
        = 1 means x is an approximate solution to A*x = B,
            according to atol and btol.
        = 2 means x approximately solves the least-squares problem
            according to atol.
        = 3 means COND(A) seems to be greater than CONLIM.
        = 4 is the same as 1 with atol = btol = eps (machine
            precision)
        = 5 is the same as 2 with atol = eps.
        = 6 is the same as 3 with CONLIM = 1/eps.
        = 7 means ITN reached maxiter before the other stopping
            conditions were satisfied.
```

itn : int

Number of iterations used.

normr : float

`norm(b-Ax)`

normar : float

`norm(A^T (b - Ax))`

norma : float

`norm(A)`

conda : float

Condition number of A.

normx : float

`norm(x)`

Notes

New in version 0.11.0.

References

[R26], [R27]

Matrix factorizations Eigenvalue problems:

`eigs`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the square matrix A.
`eigsh`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex h
`lobpcg`(A, X[, B, M, Y, tol, maxiter, ...])	Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

`scipy.sparse.linalg.`**`eigs`**(*A*, *k=6*, *M=None*, *sigma=None*, *which='LM'*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *OPpart=None*)

Find k eigenvalues and eigenvectors of the square matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i]

Parameters

A : ndarray, sparse matrix or LinearOperator

An array, sparse matrix, or LinearOperator representing the operation `A * x`, where A is a real or complex square matrix.

k : int, optional

The number of eigenvalues and eigenvectors desired. *k* must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

M : ndarray, sparse matrix or LinearOperator, optional

An array, sparse matrix, or LinearOperator representing the operation M*x for the generalized eigenvalue problem

A * x = w * M * x.

M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If *sigma* is None, M is positive definite
If sigma is specified, M is positive semi-definite

If sigma is None, eigs requires an operator to compute the solution of the linear equation `M * x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv * b = M^-1 * b`.

sigma : real or complex, optional

Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system `[A - sigma * M] * x = b`, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv * b = [A - sigma * M]^-1 * b`. For a real matrix A, shift-invert can either be done in imaginary mode or real mode, specified by the parameter OPpart ('r' or 'i'). Note that when sigma is specified, the keyword 'which' (below) refers to the shifted eigenvalues `w'[i]` where:

If A is real and OPpart == 'r' (default),

`w'[i] = 1/2 * [1/(w[i]-sigma) + 1/(w[i]-conj(sigma))].`

If A is real and OPpart == 'i',

`w'[i] = 1/2i * [1/(w[i]-sigma) - 1/(w[i]-conj(sigma))].`

If A is complex, `w'[i] = 1/(w[i]-sigma).`

v0 : ndarray, optional

Starting vector for iteration. Default: random

ncv : int, optional

The number of Lanczos vectors generated *ncv* must be greater than *k*; it is recommended that `ncv > 2*k`. Default: `min(n, 2*k + 1)`

which : str, ['LM' | 'SM' | 'LR' | 'SR' | 'LI' | 'SI'], optional

Which *k* eigenvectors and eigenvalues to find:

'LM' : largest magnitude
'SM' : smallest magnitude
'LR' : largest real part
'SR' : smallest real part
'LI' : largest imaginary part
'SI' : smallest imaginary part

When sigma != None, 'which' refers to the shifted eigenvalues w'[i] (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter : int, optional

Maximum number of Arnoldi update iterations allowed Default: `n*10`

tol : float, optional

Relative accuracy for eigenvalues (stopping criterion) The default value of 0 implies machine precision.

return_eigenvectors : bool, optional

Return eigenvectors (True) in addition to eigenvalues

Minv : ndarray, sparse matrix or LinearOperator, optional

See notes in M, above.

OPinv : ndarray, sparse matrix or LinearOperator, optional

See notes in sigma, above.

OPpart : {'r' or 'i'}, optional

See notes in sigma, above

Returns

w : ndarray

Array of k eigenvalues.

v : ndarray

An array of *k* eigenvectors. `v[:, i]` is the eigenvector corresponding to the eigenvalue w[i].

Raises

ArpackNoConvergence

When the requested convergence is not obtained. The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

eigsh	eigenvalues and eigenvectors for symmetric matrix A
svds	singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [R14] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [R15].

References

[R14], [R15]

Examples

Find 6 eigenvectors of the identity matrix:

```
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigs(id, k=6)
>>> vals
array([ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j])
>>> vecs.shape
(13, 6)
```

`scipy.sparse.linalg.`**`eigsh`**(*A*, *k=6*, *M=None*, *sigma=None*, *which='LM'*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *mode='normal'*)

Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i]

Parameters **A** : An N x N matrix, array, sparse matrix, or LinearOperator representing

the operation A * x, where A is a real symmetric matrix For buckling mode (see below) A must additionally be positive-definite

k : int, optional

The number of eigenvalues and eigenvectors desired. *k* must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

Returns **w** : array

Array of k eigenvalues

v : array

An array representing the *k* eigenvectors. The column `v[:, i]` is the eigenvector corresponding to the eigenvalue `w[i]`.

Other Parameters

M : An N x N matrix, array, sparse matrix, or linear operator representing

the operation M * x for the generalized eigenvalue problem

A * x = w * M * x.

M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If sigma is None, M is symmetric positive definite
If sigma is specified, M is symmetric positive semi-definite
In buckling mode, M is symmetric indefinite.

If sigma is None, eigsh requires an operator to compute the solution of the linear equation `M * x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv * b = M^-1 * b`.

sigma : real

Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system *[A - sigma * M] x = b*, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv * b = [A - sigma * M]^-1 * b`. Note that when sigma is specified, the keyword 'which' refers to the shifted eigenvalues `w'[i]` where:

if mode == 'normal', `w'[i] = 1 / (w[i] - sigma)`.
if mode == 'cayley', `w'[i] = (w[i] + sigma) / (w[i] - sigma)`.
if mode == 'buckling', `w'[i] = w[i] / (w[i] - sigma)`.

(see further discussion in 'mode' below)

v0 : ndarray, optional

Starting vector for iteration. Default: random

ncv : int, optional

The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that `ncv > 2*k`. Default: `min(n, 2*k + 1)`

which : str ['LM' | 'SM' | 'LA' | 'SA' | 'BE']

If A is a complex hermitian matrix, 'BE' is invalid. Which *k* eigenvectors and eigenvalues to find:

'LM' : Largest (in magnitude) eigenvalues
'SM' : Smallest (in magnitude) eigenvalues
'LA' : Largest (algebraic) eigenvalues
'SA' : Smallest (algebraic) eigenvalues
'BE' : Half (k/2) from each end of the spectrum

When k is odd, return one more (k/2+1) from the high end. When sigma != None, 'which' refers to the shifted eigenvalues `w'[i]` (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter : int, optional

Maximum number of Arnoldi update iterations allowed Default: `n*10`

tol : float

Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Minv : N x N matrix, array, sparse matrix, or LinearOperator

See notes in M, above

OPinv : N x N matrix, array, sparse matrix, or LinearOperator

See notes in sigma, above.

return_eigenvectors : bool

Return eigenvectors (True) in addition to eigenvalues

mode : string ['normal' | 'buckling' | 'cayley']

Specify strategy to use for shift-invert mode. This argument applies only for real-valued A and sigma != None. For shift-invert mode, ARPACK internally solves the eigenvalue problem `OP * x'[i] = w'[i] * B * x'[i]` and transforms the resulting Ritz vectors x'[i] and Ritz values w'[i] into the desired eigenvectors and eigenvalues of the problem `A * x[i] = w[i] * M * x[i]`. The modes are as follows:

***'normal'* :** OP = [A - sigma * M]^-1 * M, B = M, w'[i] = 1 / (w[i] - sigma)

'buckling' : OP = [A - sigma * M]^-1 * A, B = A, w'[i] = w[i] / (w[i] - sigma)

'cayley' : OP = [A - sigma * M]^-1 * [A + sigma * M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma)

The choice of mode will affect which eigenvalues are selected by the keyword 'which', and can also impact the stability of convergence (see [2] for a discussion)

Raises **ArpackNoConvergence**

When the requested convergence is not obtained.

The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

`eigs`	eigenvalues and eigenvectors for a general (nonsymmetric) matrix A
`svds`	singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [R16] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [R17].

References

[R16], [R17]

Examples

```
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigsh(id, k=6)
>>> vals
array([ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j])
>>> vecs.shape
(13, 6)
```

`scipy.sparse.linalg.`**`lobpcg`**(*A*, *X*, *B=None*, *M=None*, *Y=None*, *tol=None*, *maxiter=20*, *largest=True*, *verbosityLevel=0*, *retLambdaHistory=False*, *retResidualNormsHistory=False*)

Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

LOBPCG is a preconditioned eigensolver for large symmetric positive definite (SPD) generalized eigenproblems.

Parameters **A** : {sparse matrix, dense matrix, LinearOperator}

The symmetric linear operator of the problem, usually a sparse matrix. Often called the "stiffness matrix".

X : array_like

Initial approximation to the k eigenvectors. If A has shape=(n,n) then X should have shape shape=(n,k).

B : {dense matrix, sparse matrix, LinearOperator}, optional

the right hand side operator in a generalized eigenproblem. by default, B = Identity often called the "mass matrix"

M : {dense matrix, sparse matrix, LinearOperator}, optional

preconditioner to A; by default M = Identity M should approximate the inverse of A

Y : array_like, optional

n-by-sizeY matrix of constraints, sizeY < n The iterations will be performed in the B-orthogonal complement of the column-space of Y. Y must be full rank.

Returns **w** : array

Array of k eigenvalues

v : array

An array of k eigenvectors. V has the same shape as X.

Other Parameters

tol : scalar, optional

Solver tolerance (stopping criterion) by default: tol=n*sqrt(eps)

maxiter : integer, optional

maximum number of iterations by default: maxiter=min(n,20)

largest : bool, optional

when True, solve for the largest eigenvalues, otherwise the smallest

verbosityLevel : integer, optional

controls solver output. default: verbosityLevel = 0.

retLambdaHistory : boolean, optional

whether to return eigenvalue history

retResidualNormsHistory : boolean, optional

whether to return history of residual norms

Notes

If both retLambdaHistory and retResidualNormsHistory are True, the return tuple has the following format (lambda, V, lambda history, residual norms history).

In the following `n` denotes the matrix size and `m` the number of required eigenvalues (smallest or largest).

The LOBPCG code internally solves eigenproblems of the size 3‘‘m‘‘ on every iteration by calling the “standard” dense eigensolver, so if `m` is not small enough compared to `n`, it does not make sense to call the LOBPCG code, but rather one should use the “standard” eigensolver, e.g. numpy or scipy function in this case. If one calls the LOBPCG algorithm for 5‘‘m‘‘>‘‘n‘‘, it will most likely break internally, so the code tries to call the standard function instead.

It is not that n should be large for the LOBPCG to work, but rather the ratio `n/m` should be large. It you call the LOBPCG code with `m``=1 and ``n``=10, it should work, though ``n` is small. The method is intended for extremely large `n/m`, see e.g., reference [28] in http://arxiv.org/abs/0705.2626

The convergence speed depends basically on two factors:

1. How well relatively separated the seeking eigenvalues are from the rest of the eigenvalues. One can try to vary `m` to make this better.
2. How well conditioned the problem is. This can be changed by using proper preconditioning. For example, a rod vibration test problem (under tests directory) is ill-conditioned for large `n`, so convergence will be slow, unless efficient preconditioning is used. For this specific problem, a good simple preconditioner function would be a linear solve for A, which is easy to code since A is tridiagonal.

Acknowledgements

lobpcg.py code was written by Robert Cimrman. Many thanks belong to Andrew Knyazev, the author of the algorithm, for lots of advice and support.

References

[R23], [R24], [R25]

Examples

```
>>> # Solve A x = lambda B x with constraints and preconditioning.
>>> n = 100
>>> vals = [nm.arange( n, dtype = nm.float64 ) + 1]
```

```
>>> # Matrix A.
>>> operatorA = spdiags( vals, 0, n, n )
>>> # Matrix B
>>> operatorB = nm.eye( n, n )
>>> # Constraints.
>>> Y = nm.eye( n, 3 )
>>> # Initial guess for eigenvectors, should have linearly independent
>>> # columns. Column dimension = number of requested eigenvalues.
>>> X = sc.rand( n, 3 )
>>> # Preconditioner - inverse of A.
>>> ivals = [1./vals[0]]
>>> def precond( x ):
    invA = spdiags( ivals, 0, n, n )
    y = invA  * x
    if sp.issparse( y ):
        y = y.toarray()
```

return as2d(y)

```
>>> # Alternative way of providing the same preconditioner.
>>> #precond = spdiags( ivals, 0, n, n )
```

```
>>> tt = time.clock()
>>> eigs, vecs = lobpcg(X, operatorA, operatorB, blockVectorY=Y,
>>>                     operatorT=precond,
>>>                     residualTolerance=1e-4, maxIterations=40,
>>>                     largest=False, verbosityLevel=1)
>>> print 'solution time:', time.clock() - tt
>>> print eigs
```

Singular values problems:

`svds`(A[, k, ncv, tol, which, v0, maxiter, ...])	Compute the largest k singular values/vectors for a sparse matrix.

`scipy.sparse.linalg.`**`svds`**(*A*, *k=6*, *ncv=None*, *tol=0*, *which='LM'*, *v0=None*, *maxiter=None*, *return_singular_vectors=True*)

Compute the largest k singular values/vectors for a sparse matrix.

Parameters

A : {sparse matrix, LinearOperator}

Array to compute the SVD on, of shape (M, N)

k : int, optional

Number of singular values and vectors to compute.

ncv : int, optional

The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2*k Default: `min(n, 2*k + 1)`

tol : float, optional

Tolerance for singular values. Zero (default) means machine precision.

which : str, ['LM' | 'SM'], optional

Which *k* singular values to find:

- 'LM' : largest singular values
- 'SM' : smallest singular values

New in version 0.12.0.

v0 : ndarray, optional

Starting vector for iteration, of length min(A.shape). Should be an (approximate) right singular vector if N > M and a right singular vector otherwise. Default: random

New in version 0.12.0.

maxiter : int, optional

Maximum number of iterations.

New in version 0.12.0.

return_singular_vectors : bool or str, optional

- True: return singular vectors (True) in addition to singular values.

New in version 0.12.0.

- "u": only return the u matrix, without computing vh (if N > M).
- "vh": only return the vh matrix, without computing u (if N <= M).

New in version 0.16.0.

Returns **u** : ndarray, shape=(M, k)

Unitary matrix having left singular vectors as columns. If *return_singular_vectors* is "vh", this variable is not computed, and None is returned instead.

s : ndarray, shape=(k,)

The singular values.

vt : ndarray, shape=(k, N)

Unitary matrix having right singular vectors as rows. If *return_singular_vectors* is "u", this variable is not computed, and None is returned instead.

Notes

This is a naive implementation using ARPACK as an eigensolver on A.H * A or A * A.H, depending on which one is more efficient.

Complete or incomplete LU factorizations

`splu`(A[, permc_spec, diag_pivot_thresh, ...])	Compute the LU decomposition of a sparse, square matrix.
`spilu`(A[, drop_tol, fill_factor, drop_rule, ...])	Compute an incomplete LU decomposition for a sparse, square matrix.
`SuperLU`	LU factorization of a sparse matrix.

`scipy.sparse.linalg.`**`splu`**(*A*, *permc_spec=None*, *diag_pivot_thresh=None*, *drop_tol=None*, *relax=None*, *panel_size=None*, *options={}*)

Compute the LU decomposition of a sparse, square matrix.

Parameters **A** : sparse matrix

Sparse matrix to factorize. Should be in CSR or CSC format.

permc_spec : str, optional

How to permute the columns of the matrix for sparsity preservation. (default: 'COLAMD')

- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering

diag_pivot_thresh : float, optional

Threshold used for a diagonal entry to be an acceptable pivot. See SuperLU user's guide for details [R35]

drop_tol : float, optional

(deprecated) No effect.

relax : int, optional

Expert option for customizing the degree of relaxing supernodes. See SuperLU user's guide for details [R35]

panel_size : int, optional

Expert option for customizing the panel size. See SuperLU user's guide for details [R35]

options : dict, optional

Dictionary containing additional expert options to SuperLU. See SuperLU user guide [R35] (section 2.4 on the 'Options' argument) for more details. For example, you can specify `options=dict(Equil=False, IterRefine='SINGLE'))` to turn equilibration off and perform a single iterative refinement.

Returns **invA** : scipy.sparse.linalg.SuperLU

Object, which has a `solve` method.

See also:

`spilu`	incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[R35]

`scipy.sparse.linalg.`**`spilu`**(*A*, *drop_tol=None*, *fill_factor=None*, *drop_rule=None*, *permc_spec=None*, *diag_pivot_thresh=None*, *relax=None*, *panel_size=None*, *options=None*)

Compute an incomplete LU decomposition for a sparse, square matrix.

The resulting object is an approximation to the inverse of *A*.

Parameters **A** : (N, N) array_like

Sparse matrix to factorize

drop_tol : float, optional

Drop tolerance (0 <= tol <= 1) for an incomplete LU decomposition. (default: 1e-4)

fill_factor : float, optional

Specifies the fill ratio upper bound (>= 1.0) for ILU. (default: 10)

drop_rule : str, optional

Comma-separated string of drop rules to use. Available rules: `basic`, `prows`, `column`, `area`, `secondary`, `dynamic`, `interp`. (Default: `basic,area`)

See SuperLU documentation for details.

Remaining other options

Same as for `splu`

Returns **invA_approx** : scipy.sparse.linalg.SuperLU

Object, which has a `solve` method.

See also:

`splu`	complete LU decomposition

Notes

To improve the better approximation to the inverse, you may need to increase *fill_factor* AND decrease *drop_tol*.

This function uses the SuperLU library.

class `scipy.sparse.linalg.`**`SuperLU`**

LU factorization of a sparse matrix.

Factorization is represented as:

```
Pr * A * Pc = L * U
```

To construct these `SuperLU` objects, call the `splu` and `spilu` functions.

Notes

New in version 0.14.0.

Examples

The LU decomposition can be used to solve matrix equations. Consider:

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix, linalg as sla
>>> A = csc_matrix([[1,2,0,4],[1,0,0,1],[1,0,2,1],[2,2,1,0.]])
```

This can be solved for a given right-hand side:

```
>>> lu = sla.splu(A)
>>> b = np.array([1, 2, 3, 4])
>>> x = lu.solve(b)
>>> A.dot(x)
array([ 1.,  2.,  3.,  4.])
```

The `lu` object also contains an explicit representation of the decomposition. The permutations are represented as mappings of indices:

```
>>> lu.perm_r
array([0, 2, 1, 3], dtype=int32)
>>> lu.perm_c
array([2, 0, 1, 3], dtype=int32)
```

The L and U factors are sparse matrices in CSC format:

```
>>> lu.L.A
array([[ 1. ,  0. ,  0. ,  0. ],
       [ 0. ,  1. ,  0. ,  0. ],
       [ 0. ,  0. ,  1. ,  0. ],
       [ 1. ,  0.5,  0.5,  1. ]])
>>> lu.U.A
array([[ 2.,  0.,  1.,  4.],
       [ 0.,  2.,  1.,  1.],
       [ 0.,  0.,  1.,  1.],
       [ 0.,  0.,  0., -5.]])
```

The permutation matrices can be constructed:

```
>>> Pr = csc_matrix((4, 4))
>>> Pr[lu.perm_r, np.arange(4)] = 1
>>> Pc = csc_matrix((4, 4))
>>> Pc[np.arange(4), lu.perm_c] = 1
```

We can reassemble the original matrix:

```
>>> (Pr.T * (lu.L * lu.U) * Pc.T).A
array([[ 1.,  2.,  0.,  4.],
       [ 1.,  0.,  0.,  1.],
       [ 1.,  0.,  2.,  1.],
       [ 2.,  2.,  1.,  0.]])
```

Attributes

`shape`	Shape of the original matrix as a tuple of ints.
`nnz`	Number of nonzero elements in the matrix.
`perm_c`	Permutation Pc represented as an array of indices.
`perm_r`	Permutation Pr represented as an array of indices.
`L`	Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`.
`U`	Upper triangular factor as a `scipy.sparse.csc_matrix`.

`SuperLU.`**`shape`**

Shape of the original matrix as a tuple of ints.

`SuperLU.`**`nnz`**

Number of nonzero elements in the matrix.

`SuperLU.`**`perm_c`**

Permutation Pc represented as an array of indices.

The column permutation matrix can be reconstructed via:

```
>>> Pc = np.zeros((n, n))
>>> Pc[np.arange(n), perm_c] = 1
```

`SuperLU.`**`perm_r`**

Permutation Pr represented as an array of indices.

The row permutation matrix can be reconstructed via:

```
>>> Pr = np.zeros((n, n))
>>> Pr[perm_r, np.arange(n)] = 1
```

`SuperLU.`**`L`**

Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

`SuperLU.`**`U`**

Upper triangular factor as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

Methods

`solve`(rhs[, trans])	Solves linear system of equations with one or several right-hand sides.

`SuperLU.`**`solve`**`(`*rhs*[, *trans*]`)`

Solves linear system of equations with one or several right-hand sides.

Parameters **rhs** : ndarray, shape (n,) or (n, k)

Right hand side(s) of equation

trans : {‘N’, ‘T’, ‘H’}, optional

Type of system to solve:

```
'N':   A   * x == rhs  (default)
'T':   A^T * x == rhs
'H':   A^H * x == rhs
```

i.e., normal, transposed, and hermitian conjugate.

Returns **x** : ndarray, shape `rhs.shape`

Solution vector(s)

`ArpackNoConvergence`(msg, eigenvalues, ...)	ARPACK iteration did not converge
`ArpackError`(info[, infodict])	ARPACK error

Exceptions

exception `scipy.sparse.linalg.`**`ArpackNoConvergence`**(*msg*, *eigenvalues*, *eigenvectors*)

ARPACK iteration did not converge

Attributes

eigenvalues	(ndarray) Partial result. Converged eigenvalues.
eigenvectors	(ndarray) Partial result. Converged eigenvectors.

exception scipy.sparse.linalg.**ArpackError**(*info*, *infodict={‘c’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -1: ‘N must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation;’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: “BMAT must be one of ‘I’ or ‘G’.”, -5: ” WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI”’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘s’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3, 4.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation;’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: “BMAT must be one of ‘I’ or ‘G’.”, -5: ” WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI”’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -1: ‘N must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘z’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size*

ARPACK error

Functions

`all`(a[, axis, out, keepdims])	Test whether all array elements along a given axis evaluate to True.
`amax`(a[, axis, out, keepdims])	Return the maximum of an array or maximum along an axis.
`amin`(a[, axis, out, keepdims])	Return the minimum of an array or minimum along an axis.
`array`(object[, dtype, copy, order, subok, ndmin])	Create an array.
`asarray`(a[, dtype, order])	Convert the input to an array.
`aslinearoperator`(A)	Return A as a LinearOperator.
`bicg`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient iteration to solve A x = b
`bicgstab`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient STABilized iteration to solve A x = b
`cg`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient iteration to solve A x = b
`cgs`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient Squared iteration to solve A x = b
`dot`(a, b[, out])	Dot product of two arrays.
`eigs`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the square matrix A.
`eigsh`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the real symmetric square matrix or c
`empty`(shape[, dtype, order])	Return a new array of given shape and type, without initializing entries.
`empty_like`(a[, dtype, order, subok])	Return a new array with the same shape and type as a given array.
`expm`(A)	Compute the matrix exponential using Pade approximation.
`expm_multiply`(A, B[, start, stop, num, endpoint])	Compute the action of the matrix exponential of A on B.
`factorized`(A)	Return a fuction for solving a sparse linear system, with A pre-factorized.
`fastCopyAndTranspose`(a)	
`geterrobj`()	Return the current object that defines floating-point error handling.
`gmres`(A, b[, x0, tol, restart, maxiter, ...])	Use Generalized Minimal RESidual iteration to solve A x = b.
`inv`(A)	Compute the inverse of a sparse matrix
`issparse`(x)	
`lgmres`(A, b[, x0, tol, maxiter, M, ...])	Solve a matrix equation using the LGMRES algorithm.
`lobpcg`(A, X[, B, M, Y, tol, maxiter, ...])	Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPC
`lsmr`(A, b[, damp, atol, btol, conlim, ...])	Iterative solver for least-squares problems.
`lsqr`(A, b[, damp, atol, btol, conlim, ...])	Find the least-squares solution to a large, sparse, linear system of equations.
`minres`(A, b[, x0, shift, tol, maxiter, ...])	Use MINimum RESidual iteration to solve Ax=b
`norm`(x[, ord])	Norm of a sparse matrix
`onenormest`(A[, t, itmax, compute_v, compute_w])	Compute a lower bound of the 1-norm of a sparse matrix.
`product`(a[, axis, dtype, out, keepdims])	Return the product of array elements over a given axis.
`qmr`(A, b[, x0, tol, maxiter, xtype, M1, M2, ...])	Use Quasi-Minimal Residual iteration to solve A x = b
`ravel`(a[, order])	Return a flattened array.
`rollaxis`(a, axis[, start])	Roll the specified axis backwards, until it lies in a given position.
`size`(a[, axis])	Return the number of elements along a given axis.
`spilu`(A[, drop_tol, fill_factor, drop_rule, ...])	Compute an incomplete LU decomposition for a sparse, square matrix.
`splu`(A[, permc_spec, diag_pivot_thresh, ...])	Compute the LU decomposition of a sparse, square matrix.
`spsolve`(A, b[, permc_spec, use_umfpack])	Solve the sparse linear system Ax=b, where b may be a vector or a matrix.
`sum`(a[, axis, dtype, out, keepdims])	Sum of array elements over a given axis.
`svds`(A[, k, ncv, tol, which, v0, maxiter, ...])	Compute the largest k singular values/vectors for a sparse matrix.
`transpose`(a[, axes])	Permute the dimensions of an array.
`use_solver`(**kwargs)	Valid keyword arguments with defaults (other ignored):
`zeros`(shape[, dtype, order])	Return a new array of given shape and type, filled with zeros.

Classes

`LinearOperator`(dtype, shape)	Common interface for performing matrix vector products

Continued on next page

Table 5.174 – continued from previous page

`SuperLU`	LU factorization of a sparse matrix.
`Tester`	alias of `NoseTester`
`broadcast`	Produce an object that mimics broadcasting.
`cdouble`	alias of `complex128`
`complexfloating`	***Attributes***
`csingle`	alias of `complex64`
`double`	alias of `float64`
`errstate`(**kwargs)	Context manager for floating-point error handling.
`finfo`	Machine limits for floating point types.
`inexact`	***Attributes***
`intc`	alias of `int32`
`longdouble`	alias of `float128`
`single`	alias of `float32`

Exceptions

`ArpackError`(info[, infodict])	ARPACK error
`ArpackNoConvergence`(msg, eigenvalues, ...)	ARPACK iteration did not converge
`MatrixRankWarning`	

Exceptions

`SparseEfficiencyWarning`
`SparseWarning`

exception `scipy.sparse.`**`SparseEfficiencyWarning`**

exception `scipy.sparse.`**`SparseWarning`**

5.28.2 Usage information

There are seven available sparse matrix types:

1. csc_matrix: Compressed Sparse Column format
2. csr_matrix: Compressed Sparse Row format
3. bsr_matrix: Block Sparse Row format
4. lil_matrix: List of Lists format
5. dok_matrix: Dictionary of Keys format
6. coo_matrix: COOrdinate format (aka IJV, triplet format)
7. dia_matrix: DIAgonal format

To construct a matrix efficiently, use either dok_matrix or lil_matrix. The lil_matrix class supports basic slicing and fancy indexing with a similar syntax to NumPy arrays. As illustrated below, the COO format may also be used to efficiently construct matrices.

To perform manipulations such as multiplication or inversion, first convert the matrix to either CSC or CSR format. The lil_matrix format is row-based, so conversion to CSR is efficient, whereas conversion to CSC is less so.

All conversions among the CSR, CSC, and COO formats are efficient, linear-time operations.

Matrix vector product

To do a vector product between a sparse matrix and a vector simply use the matrix *dot* method, as described in its docstring:

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

Warning: As of NumPy 1.7, *np.dot* is not aware of sparse matrices, therefore using it will result on unexpected results or errors. The corresponding dense array should be obtained first instead:

```
>>> np.dot(A.toarray(), v)
array([ 1, -3, -1], dtype=int64)
```

but then all the performance advantages would be lost.

The CSR format is specially suitable for fast matrix vector products.

Example 1

Construct a 1000x1000 lil_matrix and add some values to it:

```
>>> from scipy.sparse import lil_matrix
>>> from scipy.sparse.linalg import spsolve
>>> from numpy.linalg import solve, norm
>>> from numpy.random import rand
```

```
>>> A = lil_matrix((1000, 1000))
>>> A[0, :100] = rand(100)
>>> A[1, 100:200] = A[0, :100]
>>> A.setdiag(rand(1000))
```

Now convert it to CSR format and solve A x = b for x:

```
>>> A = A.tocsr()
>>> b = rand(1000)
>>> x = spsolve(A, b)
```

Convert it to a dense matrix and solve, and check that the result is the same:

```
>>> x_ = solve(A.toarray(), b)
```

Now we can compute norm of the error with:

```
>>> err = norm(x-x_)
>>> err < 1e-10
True
```

It should be small :)

Example 2

Construct a matrix in COO format:

```
>>> from scipy import sparse
>>> from numpy import array
>>> I = array([0,3,1,0])
>>> J = array([0,3,1,2])
>>> V = array([4,5,7,9])
>>> A = sparse.coo_matrix((V,(I,J)),shape=(4,4))
```

Notice that the indices do not need to be sorted.

Duplicate (i,j) entries are summed when converting to CSR or CSC.

```
>>> I = array([0,0,1,3,1,0,0])
>>> J = array([0,2,1,3,1,0,0])
>>> V = array([1,1,1,1,1,1,1])
>>> B = sparse.coo_matrix((V,(I,J)),shape=(4,4)).tocsr()
```

This is useful for constructing finite-element stiffness and mass matrices.

Further Details

CSR column indices are not necessarily sorted. Likewise for CSC row indices. Use the .sorted_indices() and .sort_indices() methods when sorted indices are required (e.g. when passing data to other libraries).

5.29 Sparse linear algebra (`scipy.sparse.linalg`)

5.29.1 Abstract linear operators

`LinearOperator`(dtype, shape)	Common interface for performing matrix vector products
`aslinearoperator`(A)	Return A as a LinearOperator.

class `scipy.sparse.linalg.`**`LinearOperator`**(*dtype*, *shape*)

Common interface for performing matrix vector products

Many iterative methods (e.g. cg, gmres) do not need to know the individual entries of a matrix to solve a linear system A*x=b. Such solvers only require the computation of matrix vector products, A*v where v is a dense vector. This class serves as an abstract interface between iterative solvers and matrix-like objects.

To construct a concrete LinearOperator, either pass appropriate callables to the constructor of this class, or subclass it.

A subclass must implement either one of the methods `_matvec` and `_matmat`, and the attributes/properties `shape` (pair of integers) and `dtype` (may be None). It may call the `__init__` on this class to have these attributes validated. Implementing `_matvec` automatically implements `_matmat` (using a naive algorithm) and vice-versa.

Optionally, a subclass may implement `_rmatvec` or `_adjoint` to implement the Hermitian adjoint (conjugate transpose). As with `_matvec` and `_matmat`, implementing either `_rmatvec` or `_adjoint` implements the other automatically. Implementing `_adjoint` is preferable; `_rmatvec` is mostly there for backwards compatibility.

Parameters

shape : tuple
Matrix dimensions (M,N).

matvec : callable f(v)
Returns returns A * v.

rmatvec : callable f(v)
Returns A^H * v, where A^H is the conjugate transpose of A.

matmat : callable f(V)
Returns A * V, where V is a dense matrix with dimensions (N,K).

dtype : dtype
Data type of the matrix.

See also:

`aslinearoperator`
Construct LinearOperators

Notes

The user-defined matvec() function must properly handle the case where v has shape (N,) as well as the (N,1) case. The shape of the return type is handled internally by LinearOperator.

LinearOperator instances can also be multiplied, added with each other and exponentiated, all lazily: the result of these operations is always a new, composite LinearOperator, that defers linear operations to the original operators and combines the results.

Examples

```
>>> import numpy as np
>>> from scipy.sparse.linalg import LinearOperator
>>> def mv(v):
...     return np.array([2*v[0], 3*v[1]])
...
>>> A = LinearOperator((2,2), matvec=mv)
>>> A
<2x2 LinearOperator with unspecified dtype>
>>> A.matvec(np.ones(2))
array([ 2.,  3.])
>>> A * np.ones(2)
array([ 2.,  3.])
```

Attributes

args	(tuple) For linear operators describing products etc. of other linear operators, the operands of the binary operation.

Methods

`__call__`(x)	
`adjoint`()	Hermitian adjoint.

Continued on next page

Table 5.178 – continued from previous page

`dot`(x)	Matrix-matrix or matrix-vector multiplication.
`matmat`(X)	Matrix-matrix multiplication.
`matvec`(x)	Matrix-vector multiplication.
`rmatvec`(x)	Adjoint matrix-vector multiplication.
`transpose`()	Transpose this linear operator.

`LinearOperator.`**`__call__`**`(`*x*`)`

`LinearOperator.`**`adjoint`**`()`

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** : LinearOperator

Hermitian adjoint of self.

`LinearOperator.`**`dot`**`(`*x*`)`

Matrix-matrix or matrix-vector multiplication.

Parameters **x** : array_like

1-d or 2-d array, representing a vector or matrix.

Returns **Ax** : array

1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

`LinearOperator.`**`matmat`**`(`*X*`)`

Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** : {matrix, ndarray}

An array with shape (N,K).

Returns **Y** : {matrix, ndarray}

A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

`LinearOperator.`**`matvec`**`(`*x*`)`

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** : {matrix, ndarray}

An array with shape (N,) or (N,1).

Returns **y** : {matrix, ndarray}

A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

`LinearOperator.`**`rmatvec`**`(`*x*`)`

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** : {matrix, ndarray}

An array with shape (M,) or (M,1).

Returns **y** : {matrix, ndarray}

A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

`LinearOperator.`**`transpose`**`()`

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

`scipy.sparse.linalg.`**`aslinearoperator`**`(`*A*`)`

Return A as a LinearOperator.

'A' may be any of the following types:

- ndarray
- matrix
- sparse matrix (e.g. csr_matrix, lil_matrix, etc.)
- LinearOperator
- An object with .shape and .matvec attributes

See the LinearOperator documentation for additional information.

Examples

```
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```

5.29.2 Matrix Operations

`inv`(A)	Compute the inverse of a sparse matrix
`expm`(A)	Compute the matrix exponential using Pade approximation.
`expm_multiply`(A, B[, start, stop, num, endpoint])	Compute the action of the matrix exponential of A on B.

`scipy.sparse.linalg.`**`inv`**`(`*A*`)`

Compute the inverse of a sparse matrix

Parameters **A** : (M,M) ndarray or sparse matrix

square matrix to be inverted

Returns **Ainv** : (M,M) ndarray or sparse matrix

inverse of *A*

Notes

This computes the sparse inverse of *A*. If the inverse of *A* is expected to be non-sparse, it will likely be faster to convert *A* to dense and use scipy.linalg.inv.

New in version 0.12.0.

`scipy.sparse.linalg.`**`expm`**`(`*A*`)`

Compute the matrix exponential using Pade approximation.

Parameters **A** : (M,M) array_like or sparse matrix

2D Array or Matrix (sparse or dense) to be exponentiated

Returns **expA** : (M,M) ndarray

Matrix exponential of *A*

Notes

This is algorithm (6.1) which is a simplification of algorithm (5.1).

New in version 0.12.0.

References

[R254]

`scipy.sparse.linalg.`**`expm_multiply`**`(`*A*, *B*, *start=None*, *stop=None*, *num=None*, *endpoint=None*`)`

Compute the action of the matrix exponential of A on B.

Parameters **A** : transposable linear operator

The operator whose exponential is of interest.

B : ndarray

The matrix or vector to be multiplied by the matrix exponential of A.

start : scalar, optional

The starting time point of the sequence.

stop : scalar, optional

The end time point of the sequence, unless *endpoint* is set to False. In that case, the sequence consists of all but the last of `num + 1` evenly spaced time points, so that *stop* is excluded. Note that the step size changes when *endpoint* is False.

num : int, optional

Number of time points to use.

endpoint : bool, optional

If True, *stop* is the last time point. Otherwise, it is not included.

Returns **expm_A_B** : ndarray

The result of the action $e^{t_k A} B$.

Notes

The optional arguments defining the sequence of evenly spaced time points are compatible with the arguments of `numpy.linspace`.

The output ndarray shape is somewhat complicated so I explain it here. The ndim of the output could be either 1, 2, or 3. It would be 1 if you are computing the expm action on a single vector at a single time point. It would be 2 if you are computing the expm action on a vector at multiple time points, or if you are computing the expm action on a matrix at a single time point. It would be 3 if you want the action on a matrix with multiple columns at multiple time points. If multiple time points are requested, expm_A_B[0] will always be the action of the expm at the first time point, regardless of whether the action is on a vector or a matrix.

References

[R255], [R256]

5.29.3 Matrix norms

`onenormest`(A[, t, itmax, compute_v, compute_w])	Compute a lower bound of the 1-norm of a sparse matrix.

`scipy.sparse.linalg.`**`onenormest`**(*A*, *t=2*, *itmax=5*, *compute_v=False*, *compute_w=False*)

Compute a lower bound of the 1-norm of a sparse matrix.

Parameters

A : ndarray or other linear operator

A linear operator that can be transposed and that can produce matrix products.

t : int, optional

A positive parameter controlling the tradeoff between accuracy versus time and memory usage. Larger values take longer and use more memory but give more accurate output.

itmax : int, optional

Use at most this many iterations.

compute_v : bool, optional

Request a norm-maximizing linear operator input vector if True.

compute_w : bool, optional

Request a norm-maximizing linear operator output vector if True.

Returns

est : float

An underestimate of the 1-norm of the sparse matrix.

v : ndarray, optional

The vector such that ||Av||_1 == est*||v||_1. It can be thought of as an input to the linear operator that gives an output with particularly large norm.

w : ndarray, optional

The vector Av which has relatively large 1-norm. It can be thought of as an output of the linear operator that is relatively large in norm compared to the input.

Notes

This is algorithm 2.4 of [1].

In [2] it is described as follows. “This algorithm typically requires the evaluation of about 4t matrix-vector products and almost invariably produces a norm estimate (which is, in fact, a lower bound on the norm) correct to within a factor 3.”

New in version 0.13.0.

References

[R267], [R268]

5.29.4 Solving linear problems

Direct methods for linear equation systems:

`spsolve`(A, b[, permc_spec, use_umfpack])	Solve the sparse linear system Ax=b, where b may be a vector or a matrix.
`factorized`(A)	Return a fuction for solving a sparse linear system, with A pre-factorized.

`scipy.sparse.linalg.`**`spsolve`**(*A*, *b*, *permc_spec=None*, *use_umfpack=True*)

Solve the sparse linear system Ax=b, where b may be a vector or a matrix.

Parameters

A : ndarray or sparse matrix

The square matrix A will be converted into CSC or CSR form

b : ndarray or sparse matrix

The matrix or vector representing the right hand side of the equation. If a vector, b.size must be (n,) or (n, 1)

permc_spec : str, optional

How to permute the columns of the matrix for sparsity preservation. (default: 'COLAMD')

- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering

use_umfpack : bool, optional

if True (default) then use umfpack for the solution. This is only referenced if b is a vector and `scikit-umfpack` is installed.

Returns **x** : ndarray or sparse matrix

the solution of the sparse linear equation. If b is a vector, then x is a vector of size A.shape[1] If b is a matrix, then x is a matrix of size (A.shape[1], b.shape[1])

Notes

For solving the matrix expression AX = B, this solver assumes the resulting matrix X is sparse, as is often the case for very sparse inputs. If the resulting X is dense, the construction of this sparse result will be relatively expensive. In that case, consider converting A to a dense matrix and using scipy.linalg.solve or its variants.

`scipy.sparse.linalg.`**`factorized`**(*A*)

Return a fuction for solving a sparse linear system, with A pre-factorized.

Parameters **A** : (N, N) array_like

Input.

Returns **solve** : callable

To solve the linear system of equations given in *A*, the *solve* callable should be passed an ndarray of shape (N,).

Examples

```
>>> A = np.array([[ 3. ,  2. , -1. ],
                  [ 2. , -2. ,  4. ],
                  [-1. ,  0.5, -1. ]])
```

```
>>> solve = factorized( A ) # Makes LU decomposition.
```

```
>>> rhs1 = np.array([1,-2,0])
>>> x1 = solve( rhs1 ) # Uses the LU factors.
array([ 1., -2., -2.])
```

Iterative methods for linear equation systems:

`bicg`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient iteration to solve A x = b
`bicgstab`(A, b[, x0, tol, maxiter, xtype, M, ...])	Use BIConjugate Gradient STABilized iteration to solve A x = b
`cg`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient iteration to solve A x = b
`cgs`(A, b[, x0, tol, maxiter, xtype, M, callback])	Use Conjugate Gradient Squared iteration to solve A x = b
`gmres`(A, b[, x0, tol, restart, maxiter, ...])	Use Generalized Minimal RESidual iteration to solve A x = b.
`lgmres`(A, b[, x0, tol, maxiter, M, ...])	Solve a matrix equation using the LGMRES algorithm.

Continued on next page

Table 5.182 – continued from previous page

`minres`(A, b[, x0, shift, tol, maxiter, ...])	Use MINimum RESidual iteration to solve Ax=b
`qmr`(A, b[, x0, tol, maxiter, xtype, M1, M2, ...])	Use Quasi-Minimal Residual iteration to solve A x = b

`scipy.sparse.linalg.`**`bicg`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use BIConjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system It is required that the linear operator can produce `Ax` and `A^T x`.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {‘f’,’d’,’F’,’D’}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’f’,’d’,’F’,or ‘D’. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`bicgstab`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use BIConjugate Gradient STABilized iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system `A` must represent a hermitian, positive definite matrix

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`cg`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use Conjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system `A` must represent a hermitian, positive definite matrix

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`cgs`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*)

Use Conjugate Gradient Squared iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real-valued N-by-N matrix of the linear system

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

`scipy.sparse.linalg.`**`gmres`**(*A*, *b*, *x0=None*, *tol=1e-05*, *restart=None*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*, *restrt=None*)

Use Generalized Minimal RESidual iteration to solve A x = b.

Parameters

A : {sparse matrix, dense matrix, LinearOperator}
The real or complex N-by-N matrix of the linear system.

b : {array, matrix}
Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}
The converged solution.

info : int
Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}
Starting guess for the solution (a vector of zeros by default).

tol : float
Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

restart : int, optional
Number of iterations between restarts. Larger values increase iteration cost, but may be necessary for convergence. Default is 20.

maxiter : int, optional
Maximum number of iterations (restart cycles). Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

xtype : {‘f’,’d’,’F’,’D’}
This parameter is DEPRECATED — avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’f’,’d’,’F’,or ‘D’. This parameter has been superseded by LinearOperator.

M : {sparse matrix, dense matrix, LinearOperator}
Inverse of the preconditioner of A. M should approximate the inverse of A and be easy to solve for (see Notes). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance. By default, no preconditioner is used.

callback : function
User-supplied function to call after each iteration. It is called as callback(rk), where rk is the current residual vector.

restrt : int, optional
DEPRECATED - use *restart* instead.

See also:

`LinearOperator`

Notes

A preconditioner, P, is chosen such that P is close to A but easy to solve for. The preconditioner parameter required by this routine is `M = P^-1`. The inverse should preferably not be calculated explicitly. Rather, use the following template to produce M:

```
# Construct a linear operator that computes P^-1 * x.
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

`scipy.sparse.linalg.`**`lgmres`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=1000*, *M=None*, *callback=None*, *inner_m=30*, *outer_k=3*, *outer_v=None*, *store_outer_Av=True*)

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm [R257] [R258] is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real or complex N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

x0 : {array, matrix}

Starting guess for the solution.

tol : float, optional

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : int, optional

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}, optional

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function, optional

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

inner_m : int, optional

Number of inner GMRES iterations per each outer iteration.

outer_k : int, optional

Number of vectors to carry between inner GMRES iterations. According to [R257], good values are in the range of 1...3. However, note that if you want to use the additional vectors to accelerate solving multiple similar problems, larger values may be beneficial.

outer_v : list of tuples, optional

List containing tuples `(v, Av)` of vectors and corresponding matrix-vector products, used to augment the Krylov subspace, and carried between inner GMRES iterations. The element `Av` can be *None* if the matrix-vector product should be re-evaluated. This parameter is modified in-place by `lgmres`, and can be used to pass "guess" vectors in and out of the algorithm when solving similar problems.

store_outer_Av : bool, optional

Whether LGMRES should store also A*v in addition to vectors *v* in the *outer_v* list. Default is True.

Returns

x : array or matrix

The converged solution.

info : int

Provides convergence information:

- 0 : successful exit

- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Notes

The LGMRES algorithm [R257] [R258] is designed to avoid the slowing of convergence in restarted GMRES, due to alternating residual vectors. Typically, it often outperforms GMRES(m) of comparable memory requirements by some measure, or at least is not much worse.

Another advantage in this algorithm is that you can supply it with 'guess' vectors in the *outer_v* argument that augment the Krylov subspace. If the solution lies close to the span of these vectors, the algorithm converges faster. This can be useful if several very similar matrices need to be inverted one after another, such as in Newton-Krylov iteration where the Jacobian matrix often changes little in the nonlinear steps.

References

[R257], [R258]

`scipy.sparse.linalg.`**`minres`**(*A*, *b*, *x0=None*, *shift=0.0*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M=None*, *callback=None*, *show=False*, *check=False*)

Use MINimum RESidual iteration to solve Ax=b

MINRES minimizes norm(A*x - b) for a real symmetric matrix A. Unlike the Conjugate Gradient method, A can be indefinite or singular.

If shift != 0 then the method solves (A - shift*I)x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The real symmetric N-by-N matrix of the linear system

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}

The converged solution.

info : integer

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}

Starting guess for the solution.

tol : float

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M : {sparse matrix, dense matrix, LinearOperator}

Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback : function

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

Notes

THIS FUNCTION IS EXPERIMENTAL AND SUBJECT TO CHANGE!

References

Solution of sparse indefinite systems of linear equations,
C. C. Paige and M. A. Saunders (1975), SIAM J. Numer. Anal. 12(4), pp. 617-629. http://www.stanford.edu/group/SOL/software/minres.html

This file is a translation of the following MATLAB implementation:
http://www.stanford.edu/group/SOL/software/minres/matlab/

`scipy.sparse.linalg.`**`qmr`**`(`*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *xtype=None*, *M1=None*, *M2=None*, *callback=None*`)`

Use Quasi-Minimal Residual iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}
The real-valued N-by-N matrix of the linear system. It is required that the linear operator can produce `Ax` and `A^T x`.

b : {array, matrix}
Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x : {array, matrix}
The converged solution.

info : integer
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 : {array, matrix}
Starting guess for the solution.

tol : float
Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below *tol*.

maxiter : integer
Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M1 : {sparse matrix, dense matrix, LinearOperator}
Left preconditioner for A.

M2 : {sparse matrix, dense matrix, LinearOperator}
Right preconditioner for A. Used together with the left preconditioner M1. The matrix M1*A*M2 should have better conditioned than A alone.

callback : function
User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}
This parameter is DEPRECATED – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A

does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

See also:

`LinearOperator`

Iterative methods for least-squares problems:

`lsqr`(A, b[, damp, atol, btol, conlim, ...])	Find the least-squares solution to a large, sparse, linear system of equations.
`lsmr`(A, b[, damp, atol, btol, conlim, ...])	Iterative solver for least-squares problems.

`scipy.sparse.linalg.`**`lsqr`**(*A*, *b*, *damp=0.0*, *atol=1e-08*, *btol=1e-08*, *conlim=100000000.0*, *iter_lim=None*, *show=False*, *calc_var=False*)

Find the least-squares solution to a large, sparse, linear system of equations.

The function solves `Ax = b` or `min ||b - Ax||^2` or `min ||Ax - b||^2 + d^2 ||x||^2`.

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

```
1. Unsymmetric equations --    solve  A*x = b

2. Linear least squares  --    solve  A*x = b
                               in the least-squares sense

3. Damped least squares  --    solve  (   A    )*x = ( b )
                                      ( damp*I )     ( 0 )
                               in the least-squares sense
```

Parameters

A : {sparse matrix, ndarray, LinearOperator}
Representation of an m-by-n matrix. It is required that the linear operator can produce `Ax` and `A^T x`.

b : (m,) ndarray
Right-hand side vector `b`.

damp : float
Damping coefficient.

atol, btol : float, optional
Stopping tolerances. If both are 1.0e-9 (say), the final residual norm should be accurate to about 9 digits. (The final x will usually have fewer correct digits, depending on cond(A) and the size of damp.)

conlim : float, optional
Another stopping tolerance. lsqr terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, *conlim* could be as large as 1.0e+12 (say). For least-squares problems, conlim should be less than 1.0e+8. Maximum precision can be obtained by setting `atol = btol = conlim = zero`, but the number of iterations may then be excessive.

iter_lim : int, optional
Explicit limitation on number of iterations (for safety).

show : bool, optional
Display an iteration log.

calc_var : bool, optional
Whether to estimate diagonals of `(A'A + damp^2*I)^{-1}`.

Returns

x : ndarray of float
The final solution.

istop : int

Gives the reason for termination. 1 means x is an approximate solution to Ax = b. 2 means x approximately solves the least-squares problem.

itn : int

Iteration number upon termination.

r1norm : float

`norm(r)`, where `r = b - Ax`.

r2norm : float

`sqrt( norm(r)^2 + damp^2 * norm(x)^2 )`. Equal to *r1norm* if `damp == 0`.

anorm : float

Estimate of Frobenius norm of `Abar = [[A]; [damp*I]]`.

acond : float

Estimate of `cond(Abar)`.

arnorm : float

Estimate of `norm(A'*r - damp^2*x)`.

xnorm : float

`norm(x)`

var : ndarray of float

If `calc_var` is True, estimates all diagonals of `(A'A)^{-1}` (if `damp == 0`) or more generally `(A'A + damp^2*I)^{-1}`. This is well defined if A has full column rank or `damp > 0`. (Not sure what var means if `rank(A) < n` and `damp = 0.`)

Notes

LSQR uses an iterative method to approximate the solution. The number of iterations required to reach a certain accuracy depends strongly on the scaling of the problem. Poor scaling of the rows or columns of A should therefore be avoided where possible.

For example, in problem 1 the solution is unaltered by row-scaling. If a row of A is very small or large compared to the other rows of A, the corresponding row of (A b) should be scaled up or down.

In problems 1 and 2, the solution x is easily recovered following column-scaling. Unless better information is known, the nonzero columns of A should be scaled so that they all have the same Euclidean norm (e.g., 1.0).

In problem 3, there is no freedom to re-scale if damp is nonzero. However, the value of damp should be assigned only after attention has been paid to the scaling of A.

The parameter damp is intended to help regularize ill-conditioned systems, by preventing the true solution from being very large. Another aid to regularization is provided by the parameter acond, which may be used to terminate iterations before the computed solution becomes very large.

If some initial estimate `x0` is known and if `damp == 0`, one could proceed as follows:

1. Compute a residual vector `r0 = b - A*x0`.
2. Use LSQR to solve the system `A*dx = r0`.
3. Add the correction dx to obtain a final solution `x = x0 + dx`.

This requires that `x0` be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes k1 iterations to solve A*x = b and k2 iterations to solve A*dx = r0. If x0 is “good”, norm(r0) will be smaller than norm(b). If the same stopping tolerances atol and btol are used for each system, k1 and k2 will be similar, but the final solution x0 + dx should be more accurate. The only way to reduce the total work is to use a larger stopping tolerance for the second system. If some value btol is suitable for A*x = b, the larger value btol*norm(b)/norm(r0) should be suitable for A*dx = r0.

Preconditioning is another way to reduce the number of iterations. If it is possible to solve a related system `M*x = b` efficiently, where M approximates A in some helpful way (e.g. M - A has low rank or its elements are small relative to those of A), LSQR may converge more rapidly on the system `A*M(inverse)*z = b`, after which x can be recovered by solving M*x = z.

If A is symmetric, LSQR should not be used!

Alternatives are the symmetric conjugate-gradient method (cg) and/or SYMMLQ. SYMMLQ is an implementation of symmetric cg that applies to any symmetric A and will converge more rapidly than LSQR. If A is positive definite, there are other implementations of symmetric cg that require slightly less work per iteration than SYMMLQ (but will take the same number of iterations).

References

[R264], [R265], [R266]

`scipy.sparse.linalg.`**`lsmr`**`(`*A*, *b*, *damp=0.0*, *atol=1e-06*, *btol=1e-06*, *conlim=100000000.0*, *maxiter=None*, *show=False*`)`

Iterative solver for least-squares problems.

lsmr solves the system of linear equations `Ax = b`. If the system is inconsistent, it solves the least-squares problem `min ||b - Ax||_2`. A is a rectangular matrix of dimension m-by-n, where all cases are allowed: m = n, m > n, or m < n. B is a vector of length m. The matrix A may be dense or sparse (usually sparse).

Parameters

A : {matrix, sparse matrix, ndarray, LinearOperator}

Matrix A in the linear system.

b : (m,) ndarray

Vector b in the linear system.

damp : float

Damping factor for regularized least-squares. `lsmr` solves the regularized least-squares problem:

```
min ||(b) - (   A   )x||
    ||(0)   (damp*I) ||_2
```

where damp is a scalar. If damp is None or 0, the system is solved without regularization.

atol, btol : float, optional

Stopping tolerances. `lsmr` continues iterations until a certain backward error estimate is smaller than some quantity depending on atol and btol. Let `r = b - Ax` be the residual vector for the current approximate solution `x`. If `Ax = b` seems to be consistent, `lsmr` terminates when `norm(r) <= atol * norm(A) * norm(x) + btol * norm(b)`. Otherwise, lsmr terminates when `norm(A^{T} r) <= atol * norm(A) * norm(r)`. If both tolerances are 1.0e-6 (say), the final `norm(r)` should be accurate to about 6 digits. (The final x will usually have fewer correct digits, depending on `cond(A)` and the size of LAMBDA.) If *atol* or *btol* is None, a default value of 1.0e-6 will be used. Ideally, they should be estimates of the relative error in the entries of A and B respectively. For example, if the entries of *A* have 7 correct digits, set atol = 1e-7. This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

conlim : float, optional

`lsmr` terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, conlim could be as large as 1.0e+12 (say). For least-squares problems, *conlim* should be less than 1.0e+8. If *conlim* is None, the default value is 1e+8. Maximum precision can be obtained by setting `atol = btol = conlim = 0`, but the number of iterations may then be excessive.

maxiter : int, optional

`lsmr` terminates if the number of iterations reaches *maxiter*. The default is `maxiter = min(m, n)`. For ill-conditioned systems, a larger value of *maxiter* may be needed.

show : bool, optional

Print iterations logs if `show=True`.

Returns

x : ndarray of float

Least-square solution returned.

istop : int

istop gives the reason for stopping:

```
istop   = 0 means x=0 is a solution.
        = 1 means x is an approximate solution to A*x = B,
            according to atol and btol.
        = 2 means x approximately solves the least-squares problem
            according to atol.
        = 3 means COND(A) seems to be greater than CONLIM.
        = 4 is the same as 1 with atol = btol = eps (machine
            precision)
        = 5 is the same as 2 with atol = eps.
        = 6 is the same as 3 with CONLIM = 1/eps.
        = 7 means ITN reached maxiter before the other stopping
            conditions were satisfied.
```

itn : int

Number of iterations used.

normr : float

`norm(b-Ax)`

normar : float

`norm(A^T (b - Ax))`

norma : float

`norm(A)`

conda : float

Condition number of A.

normx : float

`norm(x)`

Notes

New in version 0.11.0.

References

[R262], [R263]

5.29.5 Matrix factorizations

Eigenvalue problems:

`eigs`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the square matrix A.
`eigsh`(A[, k, M, sigma, which, v0, ncv, ...])	Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex h
`lobpcg`(A, X[, B, M, Y, tol, maxiter, ...])	Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

`scipy.sparse.linalg.`**`eigs`**(*A*, *k=6*, *M=None*, *sigma=None*, *which='LM'*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *OPpart=None*)

Find k eigenvalues and eigenvectors of the square matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i]

Parameters

A : ndarray, sparse matrix or LinearOperator

An array, sparse matrix, or LinearOperator representing the operation `A * x`, where A is a real or complex square matrix.

k : int, optional

The number of eigenvalues and eigenvectors desired. *k* must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

M : ndarray, sparse matrix or LinearOperator, optional

An array, sparse matrix, or LinearOperator representing the operation M*x for the generalized eigenvalue problem

A * x = w * M * x.

M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If *sigma* is None, M is positive definite

If sigma is specified, M is positive semi-definite

If sigma is None, eigs requires an operator to compute the solution of the linear equation `M * x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv * b = M^-1 * b`.

sigma : real or complex, optional

Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system `[A - sigma * M] * x = b`, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv * b = [A - sigma * M]^-1 * b`. For a real matrix A, shift-invert can either be done in imaginary mode or real mode, specified by the parameter OPpart (‘r’ or ‘i’). Note that when sigma is specified, the keyword ‘which’ (below) refers to the shifted eigenvalues `w'[i]` where:

If A is real and OPpart == ‘r’ (default),

`w'[i] = 1/2 * [1/(w[i]-sigma) + 1/(w[i]-conj(sigma))]`.

If A is real and OPpart == ‘i’,

`w'[i] = 1/2i * [1/(w[i]-sigma) - 1/(w[i]-conj(sigma))]`.

If A is complex, `w'[i] = 1/(w[i]-sigma)`.

v0 : ndarray, optional

Starting vector for iteration. Default: random

ncv : int, optional

The number of Lanczos vectors generated *ncv* must be greater than *k*; it is recommended that `ncv > 2*k`. Default: `min(n, 2*k + 1)`

which : str, [’LM’ | ‘SM’ | ‘LR’ | ‘SR’ | ‘LI’ | ‘SI’], optional

Which *k* eigenvectors and eigenvalues to find:

‘LM’ : largest magnitude

‘SM’ : smallest magnitude

‘LR’ : largest real part

‘SR’ : smallest real part

‘LI’ : largest imaginary part

‘SI’ : smallest imaginary part

When sigma != None, ‘which’ refers to the shifted eigenvalues w’[i] (see discussion in ‘sigma’, above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter : int, optional

Maximum number of Arnoldi update iterations allowed Default: `n*10`

tol : float, optional

Relative accuracy for eigenvalues (stopping criterion) The default value of 0 implies machine precision.

return_eigenvectors : bool, optional

Return eigenvectors (True) in addition to eigenvalues

Minv : ndarray, sparse matrix or LinearOperator, optional

See notes in M, above.

OPinv : ndarray, sparse matrix or LinearOperator, optional

See notes in sigma, above.

OPpart : {‘r’ or ‘i’}, optional

See notes in sigma, above

Returns **w** : ndarray

Array of k eigenvalues.

v : ndarray

An array of *k* eigenvectors. `v[:, i]` is the eigenvector corresponding to the eigenvalue w[i].

Raises **ArpackNoConvergence**

When the requested convergence is not obtained. The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

`eigsh`	eigenvalues and eigenvectors for symmetric matrix A
`svds`	singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [R250] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [R251].

References

[R250], [R251]

Examples

Find 6 eigenvectors of the identity matrix:

```
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigs(id, k=6)
>>> vals
array([ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j])
>>> vecs.shape
(13, 6)
```

`scipy.sparse.linalg.`**`eigsh`**(*A*, *k=6*, *M=None*, *sigma=None*, *which=’LM’*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *mode=’normal’*)

Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i]

Parameters

A : An N x N matrix, array, sparse matrix, or LinearOperator representing

the operation A * x, where A is a real symmetric matrix For buckling mode (see below) A must additionally be positive-definite

k : int, optional

The number of eigenvalues and eigenvectors desired. *k* must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

Returns

w : array

Array of k eigenvalues

v : array

An array representing the *k* eigenvectors. The column `v[:, i]` is the eigenvector corresponding to the eigenvalue `w[i]`.

Other Parameters

M : An N x N matrix, array, sparse matrix, or linear operator representing

the operation M * x for the generalized eigenvalue problem

A * x = w * M * x.

M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If sigma is None, M is symmetric positive definite
If sigma is specified, M is symmetric positive semi-definite
In buckling mode, M is symmetric indefinite.

If sigma is None, eigsh requires an operator to compute the solution of the linear equation `M * x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv * b = M^-1 * b`.

sigma : real

Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system *[A - sigma * M] x = b*, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv * b = [A - sigma * M]^-1 * b`. Note that when sigma is specified, the keyword 'which' refers to the shifted eigenvalues `w'[i]` where:

if mode == 'normal', `w'[i] = 1 / (w[i] - sigma)`.
if mode == 'cayley', `w'[i] = (w[i] + sigma) / (w[i] - sigma)`.
if mode == 'buckling', `w'[i] = w[i] / (w[i] - sigma)`.

(see further discussion in 'mode' below)

v0 : ndarray, optional

Starting vector for iteration. Default: random

ncv : int, optional

The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that `ncv > 2*k`. Default: `min(n, 2*k + 1)`

which : str ['LM' | 'SM' | 'LA' | 'SA' | 'BE']

If A is a complex hermitian matrix, 'BE' is invalid. Which *k* eigenvectors and eigenvalues to find:

'LM' : Largest (in magnitude) eigenvalues
'SM' : Smallest (in magnitude) eigenvalues
'LA' : Largest (algebraic) eigenvalues
'SA' : Smallest (algebraic) eigenvalues
'BE' : Half (k/2) from each end of the spectrum

When k is odd, return one more (k/2+1) from the high end. When sigma != None, 'which' refers to the shifted eigenvalues `w'[i]` (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter : int, optional

Maximum number of Arnoldi update iterations allowed Default: `n*10`

tol : float

Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Minv : N x N matrix, array, sparse matrix, or LinearOperator

See notes in M, above

OPinv : N x N matrix, array, sparse matrix, or LinearOperator

See notes in sigma, above.

return_eigenvectors : bool

Return eigenvectors (True) in addition to eigenvalues

mode : string ['normal' | 'buckling' | 'cayley']

Specify strategy to use for shift-invert mode. This argument applies only for real-valued A and sigma != None. For shift-invert mode, ARPACK internally solves the eigenvalue problem `OP * x'[i] = w'[i] * B * x'[i]` and transforms the resulting Ritz vectors x'[i] and Ritz values w'[i] into the desired eigenvectors and eigenvalues of the problem `A * x[i] = w[i] * M * x[i]`. The modes are as follows:

'normal' :	OP = [A - sigma * M]^-1 * M, B = M, w'[i] = 1 / (w[i] - sigma)
'buckling' :	OP = [A - sigma * M]^-1 * A, B = A, w'[i] = w[i] / (w[i] - sigma)
'cayley' :	OP = [A - sigma * M]^-1 * [A + sigma * M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma)

The choice of mode will affect which eigenvalues are selected by the keyword 'which', and can also impact the stability of convergence (see [2] for a discussion)

Raises **ArpackNoConvergence**

When the requested convergence is not obtained.

The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

eigs	eigenvalues and eigenvectors for a general (nonsymmetric) matrix A
svds	singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [R252] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [R253].

References

[R252], [R253]

Examples

```
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigsh(id, k=6)
>>> vals
array([ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j])
>>> vecs.shape
(13, 6)
```

`scipy.sparse.linalg.`**`lobpcg`**`(`*A, X, B=None, M=None, Y=None, tol=None, maxiter=20, largest=True, verbosityLevel=0, retLambdaHistory=False, retResidualNormsHistory=False*`)`

Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

LOBPCG is a preconditioned eigensolver for large symmetric positive definite (SPD) generalized eigenproblems.

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The symmetric linear operator of the problem, usually a sparse matrix. Often called the “stiffness matrix”.

X : array_like

Initial approximation to the k eigenvectors. If A has shape=(n,n) then X should have shape shape=(n,k).

B : {dense matrix, sparse matrix, LinearOperator}, optional

the right hand side operator in a generalized eigenproblem. by default, B = Identity often called the “mass matrix”

M : {dense matrix, sparse matrix, LinearOperator}, optional

preconditioner to A; by default M = Identity M should approximate the inverse of A

Y : array_like, optional

n-by-sizeY matrix of constraints, sizeY < n The iterations will be performed in the B-orthogonal complement of the column-space of Y. Y must be full rank.

Returns

w : array

Array of k eigenvalues

v : array

An array of k eigenvectors. V has the same shape as X.

Other Parameters

tol : scalar, optional

Solver tolerance (stopping criterion) by default: tol=n*sqrt(eps)

maxiter : integer, optional

maximum number of iterations by default: maxiter=min(n,20)

largest : bool, optional

when True, solve for the largest eigenvalues, otherwise the smallest

verbosityLevel : integer, optional

controls solver output. default: verbosityLevel = 0.

retLambdaHistory : boolean, optional

whether to return eigenvalue history

retResidualNormsHistory : boolean, optional

whether to return history of residual norms

Notes

If both retLambdaHistory and retResidualNormsHistory are True, the return tuple has the following format (lambda, V, lambda history, residual norms history).

In the following `n` denotes the matrix size and `m` the number of required eigenvalues (smallest or largest).

The LOBPCG code internally solves eigenproblems of the size 3‘‘m‘‘ on every iteration by calling the “standard” dense eigensolver, so if `m` is not small enough compared to `n`, it does not make sense to call the LOBPCG code, but rather one should use the “standard” eigensolver, e.g. numpy or scipy function in this case. If one calls the LOBPCG algorithm for 5‘‘m‘‘>‘‘n‘‘, it will most likely break internally, so the code tries to call the standard function instead.

It is not that n should be large for the LOBPCG to work, but rather the ratio `n/m` should be large. It you call the LOBPCG code with `m``=1 and ``n``=10, it should work, though ``n` is small. The method is intended for extremely large `n/m`, see e.g., reference [28] in http://arxiv.org/abs/0705.2626

The convergence speed depends basically on two factors:

1. How well relatively separated the seeking eigenvalues are from the rest of the eigenvalues. One can try to vary `m` to make this better.
2. How well conditioned the problem is. This can be changed by using proper preconditioning. For example, a rod vibration test problem (under tests directory) is ill-conditioned for large `n`, so convergence will be slow, unless efficient preconditioning is used. For this specific problem, a good simple preconditioner function would be a linear solve for A, which is easy to code since A is tridiagonal.

Acknowledgements

lobpcg.py code was written by Robert Cimrman. Many thanks belong to Andrew Knyazev, the author of the algorithm, for lots of advice and support.

References

[R259], [R260], [R261]

Examples

```
>>> # Solve A x = lambda B x with constraints and preconditioning.
>>> n = 100
>>> vals = [nm.arange( n, dtype = nm.float64 ) + 1]
>>> # Matrix A.
>>> operatorA = spdiags( vals, 0, n, n )
>>> # Matrix B
>>> operatorB = nm.eye( n, n )
>>> # Constraints.
>>> Y = nm.eye( n, 3 )
>>> # Initial guess for eigenvectors, should have linearly independent
>>> # columns. Column dimension = number of requested eigenvalues.
>>> X = sc.rand( n, 3 )
>>> # Preconditioner - inverse of A.
>>> ivals = [1./vals[0]]
>>> def precond( x ):
    invA = spdiags( ivals, 0, n, n )
    y = invA  * x
    if sp.issparse( y ):
        y = y.toarray()
```

return as2d(y)

```
>>> # Alternative way of providing the same preconditioner.
>>> #precond = spdiags( ivals, 0, n, n )
```

```
>>> tt = time.clock()
>>> eigs, vecs = lobpcg(X, operatorA, operatorB, blockVectorY=Y,
>>>                     operatorT=precond,
```

```
>>>                          residualTolerance=1e-4, maxIterations=40,
>>>                          largest=False, verbosityLevel=1)
>>> print 'solution time:', time.clock() - tt
>>> print eigs
```

Singular values problems:

`svds`(A[, k, ncv, tol, which, v0, maxiter, ...])	Compute the largest k singular values/vectors for a sparse matrix.

`scipy.sparse.linalg.`**`svds`**(*A*, *k=6*, *ncv=None*, *tol=0*, *which='LM'*, *v0=None*, *maxiter=None*, *return_singular_vectors=True*)

Compute the largest k singular values/vectors for a sparse matrix.

Parameters

A : {sparse matrix, LinearOperator}

Array to compute the SVD on, of shape (M, N)

k : int, optional

Number of singular values and vectors to compute.

ncv : int, optional

The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2*k Default: `min(n, 2*k + 1)`

tol : float, optional

Tolerance for singular values. Zero (default) means machine precision.

which : str, ['LM' | 'SM'], optional

Which *k* singular values to find:

- 'LM' : largest singular values
- 'SM' : smallest singular values

New in version 0.12.0.

v0 : ndarray, optional

Starting vector for iteration, of length min(A.shape). Should be an (approximate) right singular vector if N > M and a right singular vector otherwise. Default: random

New in version 0.12.0.

maxiter : int, optional

Maximum number of iterations.

New in version 0.12.0.

return_singular_vectors : bool or str, optional

- True: return singular vectors (True) in addition to singular values.

New in version 0.12.0.

- "u": only return the u matrix, without computing vh (if N > M).
- "vh": only return the vh matrix, without computing u (if N <= M).

New in version 0.16.0.

Returns

u : ndarray, shape=(M, k)

Unitary matrix having left singular vectors as columns. If *return_singular_vectors* is "vh", this variable is not computed, and None is returned instead.

s : ndarray, shape=(k,)

The singular values.

vt : ndarray, shape=(k, N)

Unitary matrix having right singular vectors as rows. If *return_singular_vectors* is "u", this variable is not computed, and None is returned instead.

Notes

This is a naive implementation using ARPACK as an eigensolver on A.H * A or A * A.H, depending on which one is more efficient.

Complete or incomplete LU factorizations

`splu`(A[, permc_spec, diag_pivot_thresh, ...])	Compute the LU decomposition of a sparse, square matrix.
`spilu`(A[, drop_tol, fill_factor, drop_rule, ...])	Compute an incomplete LU decomposition for a sparse, square matrix.
`SuperLU`	LU factorization of a sparse matrix.

`scipy.sparse.linalg.`**`splu`**(*A*, *permc_spec=None*, *diag_pivot_thresh=None*, *drop_tol=None*, *relax=None*, *panel_size=None*, *options={}*)

Compute the LU decomposition of a sparse, square matrix.

Parameters **A** : sparse matrix

Sparse matrix to factorize. Should be in CSR or CSC format.

permc_spec : str, optional

How to permute the columns of the matrix for sparsity preservation. (default: 'COLAMD')

- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering

diag_pivot_thresh : float, optional

Threshold used for a diagonal entry to be an acceptable pivot. See SuperLU user's guide for details [R271]

drop_tol : float, optional

(deprecated) No effect.

relax : int, optional

Expert option for customizing the degree of relaxing supernodes. See SuperLU user's guide for details [R271]

panel_size : int, optional

Expert option for customizing the panel size. See SuperLU user's guide for details [R271]

options : dict, optional

Dictionary containing additional expert options to SuperLU. See SuperLU user guide [R271] (section 2.4 on the 'Options' argument) for more details. For example, you can specify `options=dict(Equil=False, IterRefine='SINGLE'))` to turn equilibration off and perform a single iterative refinement.

Returns **invA** : scipy.sparse.linalg.SuperLU

Object, which has a `solve` method.

See also:

`spilu` incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[R271]

`scipy.sparse.linalg.`**`spilu`**`(`*A, drop_tol=None, fill_factor=None, drop_rule=None, permc_spec=None, diag_pivot_thresh=None, relax=None, panel_size=None, options=None*`)`

Compute an incomplete LU decomposition for a sparse, square matrix.

The resulting object is an approximation to the inverse of *A*.

Parameters

A : (N, N) array_like
  Sparse matrix to factorize

drop_tol : float, optional
  Drop tolerance (0 <= tol <= 1) for an incomplete LU decomposition. (default: 1e-4)

fill_factor : float, optional
  Specifies the fill ratio upper bound (>= 1.0) for ILU. (default: 10)

drop_rule : str, optional
  Comma-separated string of drop rules to use. Available rules: `basic`, `prows`, `column`, `area`, `secondary`, `dynamic`, `interp`. (Default: `basic,area`)
  See SuperLU documentation for details.

Remaining other options
  Same as for `splu`

Returns

invA_approx : scipy.sparse.linalg.SuperLU
  Object, which has a `solve` method.

See also:

`splu`	complete LU decomposition

Notes

To improve the better approximation to the inverse, you may need to increase *fill_factor* AND decrease *drop_tol*.

This function uses the SuperLU library.

class `scipy.sparse.linalg.`**`SuperLU`**

LU factorization of a sparse matrix.

Factorization is represented as:

```
Pr * A * Pc = L * U
```

To construct these `SuperLU` objects, call the `splu` and `spilu` functions.

Notes

New in version 0.14.0.

Examples

The LU decomposition can be used to solve matrix equations. Consider:

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix, linalg as sla
>>> A = csc_matrix([[1,2,0,4],[1,0,0,1],[1,0,2,1],[2,2,1,0.]])
```

This can be solved for a given right-hand side:

```
>>> lu = sla.splu(A)
>>> b = np.array([1, 2, 3, 4])
>>> x = lu.solve(b)
```

```
>>> A.dot(x)
array([ 1.,  2.,  3.,  4.])
```

The `lu` object also contains an explicit representation of the decomposition. The permutations are represented as mappings of indices:

```
>>> lu.perm_r
array([0, 2, 1, 3], dtype=int32)
>>> lu.perm_c
array([2, 0, 1, 3], dtype=int32)
```

The L and U factors are sparse matrices in CSC format:

```
>>> lu.L.A
array([[ 1. ,  0. ,  0. ,  0. ],
       [ 0. ,  1. ,  0. ,  0. ],
       [ 0. ,  0. ,  1. ,  0. ],
       [ 1. ,  0.5,  0.5,  1. ]])
>>> lu.U.A
array([[ 2.,  0.,  1.,  4.],
       [ 0.,  2.,  1.,  1.],
       [ 0.,  0.,  1.,  1.],
       [ 0.,  0.,  0., -5.]])
```

The permutation matrices can be constructed:

```
>>> Pr = csc_matrix((4, 4))
>>> Pr[lu.perm_r, np.arange(4)] = 1
>>> Pc = csc_matrix((4, 4))
>>> Pc[np.arange(4), lu.perm_c] = 1
```

We can reassemble the original matrix:

```
>>> (Pr.T * (lu.L * lu.U) * Pc.T).A
array([[ 1.,  2.,  0.,  4.],
       [ 1.,  0.,  0.,  1.],
       [ 1.,  0.,  2.,  1.],
       [ 2.,  2.,  1.,  0.]])
```

Attributes

`shape`	Shape of the original matrix as a tuple of ints.
`nnz`	Number of nonzero elements in the matrix.
`perm_c`	Permutation Pc represented as an array of indices.
`perm_r`	Permutation Pr represented as an array of indices.
`L`	Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`.
`U`	Upper triangular factor as a `scipy.sparse.csc_matrix`.

`SuperLU.`**`shape`**
Shape of the original matrix as a tuple of ints.

`SuperLU.`**`nnz`**
Number of nonzero elements in the matrix.

`SuperLU.`**`perm_c`**
Permutation Pc represented as an array of indices.

The column permutation matrix can be reconstructed via:

```
>>> Pc = np.zeros((n, n))
>>> Pc[np.arange(n), perm_c] = 1
```

SuperLU.**perm_r**

Permutation Pr represented as an array of indices.

The row permutation matrix can be reconstructed via:

```
>>> Pr = np.zeros((n, n))
>>> Pr[perm_r, np.arange(n)] = 1
```

SuperLU.**L**

Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

SuperLU.**U**

Upper triangular factor as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

Methods

`solve`(rhs[, trans])	Solves linear system of equations with one or several right-hand sides.

SuperLU.**solve**(*rhs*[, *trans*])

Solves linear system of equations with one or several right-hand sides.

Parameters **rhs** : ndarray, shape (n,) or (n, k)

Right hand side(s) of equation

trans : {‘N’, ‘T’, ‘H’}, optional

Type of system to solve:

```
'N':   A   * x == rhs  (default)
'T':   A^T * x == rhs
'H':   A^H * x == rhs
```

i.e., normal, transposed, and hermitian conjugate.

Returns **x** : ndarray, shape `rhs.shape`

Solution vector(s)

5.29.6 Exceptions

`ArpackNoConvergence`(msg, eigenvalues, ...)	ARPACK iteration did not converge
`ArpackError`(info[, infodict])	ARPACK error

exception scipy.sparse.linalg.**ArpackNoConvergence**(*msg*, *eigenvalues*, *eigenvectors*)

ARPACK iteration did not converge

Attributes

eigenvalues	(ndarray) Partial result. Converged eigenvalues.
eigenvectors	(ndarray) Partial result. Converged eigenvectors.

exception `scipy.sparse.linalg.`**`ArpackError`**(*info, infodict={‘c’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -1: ‘N must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation;’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: “BMAT must be one of ‘I’ or ‘G’.”, -5: ” WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI”’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘s’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3, 4.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation;’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: “BMAT must be one of ‘I’ or ‘G’.”, -5: ” WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI”’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -1: ‘N must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘z’: {0: ‘Normal exit.’, 1: ‘Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.’, 2: ‘No longer an informational error. Deprecated starting with release 2 of ARPACK.’, 3: ‘No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ‘, -9999: ‘Could not build an Arnoldi factorization. IPARAM(5) returns the size*

ARPACK error

5.30 Compressed Sparse Graph Routines (`scipy.sparse.csgraph`)

Fast graph algorithms based on sparse matrix representations.

5.30.1 Contents

`connected_components`(csgraph[, directed, ...])	Analyze the connected components of a sparse graph
`laplacian`(csgraph[, normed, return_diag, ...])	Return the Laplacian matrix of a directed graph.
`shortest_path`(csgraph[, method, directed, ...])	Perform a shortest-path graph search on a positive directed or undirected gra
`dijkstra`(csgraph[, directed, indices, ...])	Dijkstra algorithm using Fibonacci Heaps
`floyd_warshall`(csgraph[, directed, ...])	Compute the shortest path lengths using the Floyd-Warshall algorithm
`bellman_ford`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using the Bellman-Ford algorithm.
`johnson`(csgraph[, directed, indices, ...])	Compute the shortest path lengths using Johnson's algorithm.
`breadth_first_order`(csgraph, i_start[, ...])	Return a breadth-first ordering starting with specified node.
`depth_first_order`(csgraph, i_start[, ...])	Return a depth-first ordering starting with specified node.
`breadth_first_tree`(csgraph, i_start[, directed])	Return the tree generated by a breadth-first search
`depth_first_tree`(csgraph, i_start[, directed])	Return a tree generated by a depth-first search.
`minimum_spanning_tree`(csgraph[, overwrite])	Return a minimum spanning tree of an undirected graph
`reverse_cuthill_mckee`	Returns the permutation array that orders a sparse CSR or CSC matrix in Re
`maximum_bipartite_matching`	Returns an array of row or column permutations that makes the diagonal of a

`scipy.sparse.csgraph.`**`connected_components`**(*csgraph*, *directed=True*, *connection='weak'*, *return_labels=True*)

Analyze the connected components of a sparse graph

New in version 0.11.0.

Parameters

csgraph : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

connection : str, optional

['weak'|'strong']. For directed graphs, the type of connection to use. Nodes i and j are strongly connected if a path exists both from i to j and from j to i. Nodes i and j are weakly connected if only one of these paths exists. If directed == False, this keyword is not referenced.

return_labels : str, optional

If True (default), then return the labels for each of the connected components.

Returns

n_components: int

The number of connected components.

labels: ndarray

The length-N array of labels of the connected components.

References

[R204]

`scipy.sparse.csgraph.`**`laplacian`**(*csgraph*, *normed=False*, *return_diag=False*, *use_out_degree=False*)

Return the Laplacian matrix of a directed graph.

Parameters **csgraph** : array_like or sparse matrix, 2 dimensions

compressed-sparse graph, with shape (N, N).

normed : bool, optional

If True, then compute normalized Laplacian.

return_diag : bool, optional

If True, then also return an array related to vertex degrees.

use_out_degree : bool, optional

If True, then use out-degree instead of in-degree. This distinction matters only if the graph is asymmetric. Default: False.

Returns **lap** : ndarray

The N x N laplacian matrix of graph.

diag : ndarray, optional

The length-N diagonal of the Laplacian matrix. For the normalized Laplacian, this is the array of square roots of vertex degrees or 1 if the degree is zero.

Notes

The Laplacian matrix of a graph is sometimes referred to as the “Kirchoff matrix” or the “admittance matrix”, and is useful in many parts of spectral graph theory. In particular, the eigen-decomposition of the laplacian matrix can give insight into many properties of the graph.

Examples

```
>>> from scipy.sparse import csgraph
>>> G = np.arange(5) * np.arange(5)[:, np.newaxis]
>>> G
array([[ 0,  0,  0,  0,  0],
       [ 0,  1,  2,  3,  4],
       [ 0,  2,  4,  6,  8],
       [ 0,  3,  6,  9, 12],
       [ 0,  4,  8, 12, 16]])
>>> csgraph.laplacian(G, normed=False)
array([[  0,   0,   0,   0,   0],
       [  0,   9,  -2,  -3,  -4],
       [  0,  -2,  16,  -6,  -8],
       [  0,  -3,  -6,  21, -12],
       [  0,  -4,  -8, -12,  24]])
```

`scipy.sparse.csgraph.`**`shortest_path`**(*csgraph*, *method='auto'*, *directed=True*, *return_predecessors=False*, *unweighted=False*, *overwrite=False*)

Perform a shortest-path graph search on a positive directed or undirected graph.

New in version 0.11.0.

Parameters **csgraph** : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

method : string ['auto'|'FW'|'D'], optional

Algorithm to use for shortest paths. Options are:

'auto' – (default) select the best among 'FW', 'D', 'BF', or 'J'

based on the input data.

'FW' – Floyd-Warshall algorithm. Computational cost is

approximately `O[N^3]`. The input csgraph will be converted to a dense representation.

'D' – Dijkstra's algorithm with Fibonacci heaps. Computational

cost is approximately `O[N(N*k + N*log(N))]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'BF' – Bellman-Ford algorithm. This algorithm can be used when

weights are negative. If a negative cycle is encountered, an error will be raised. Computational cost is approximately `O[N(N^2 k)]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'J' – Johnson's algorithm. Like the Bellman-Ford algorithm,

Johnson's algorithm is designed for use when the weights are negative. It combines the Bellman-Ford algorithm with Dijkstra's algorithm for faster computation.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite : bool, optional

If True, overwrite csgraph with the result. This applies only if method == 'FW' and csgraph is a dense, c-ordered array with dtype=float64.

Returns

dist_matrix : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:

if there are negative cycles in the graph

Notes

As currently implemented, Dijkstra's algorithm and Johnson's algorithm do not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are non-equal edges, method='D' may yield an incorrect result.

`scipy.sparse.csgraph.`**`dijkstra`**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Dijkstra algorithm using Fibonacci Heaps

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of non-negative distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

limit : float, optional

The maximum distance to calculate, must be >= 0. Using a smaller limit will decrease computation time by aborting calculations between pairs that are separated by a distance > limit. For such pairs, the distance will be equal to np.inf (i.e., not connected). .. versionadded:: 0.14.0

Returns

dist_matrix : ndarray

The matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Notes

As currently implemented, Dijkstra's algorithm does not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are not equal and both are nonzero, setting directed=False will not yield the correct result.

Also, this routine does not work for graphs with negative distances. Negative distances can lead to infinite cycles that must be handled by specialized algorithms such as Bellman-Ford's algorithm or Johnson's algorithm.

`scipy.sparse.csgraph.`**`floyd_warshall`**(*csgraph*, *directed=True*, *return_predecessors=False*, *unweighted=False*, *overwrite=False*)

Compute the shortest path lengths using the Floyd-Warshall algorithm

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite : bool, optional

If True, overwrite csgraph with the result. This applies only if csgraph is a dense, c-ordered array with dtype=float64.

Returns **dist_matrix** : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

`scipy.sparse.csgraph.`**`bellman_ford`**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Compute the shortest path lengths using the Bellman-Ford algorithm.

The Bellman-ford algorithm can robustly deal with graphs with negative weights. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra's algorithm may be faster.

New in version 0.11.0.

Parameters **csgraph** : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns **dist_matrix** : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

`scipy.sparse.csgraph.`**`johnson`**`(`*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*`)`

Compute the shortest path lengths using Johnson's algorithm.

Johnson's algorithm combines the Bellman-Ford algorithm and Dijkstra's algorithm to quickly find shortest paths in a way that is robust to the presence of negative cycles. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra() may be faster.

New in version 0.11.0.

Parameters

csgraph : array, matrix, or sparse matrix, 2 dimensions

The N x N array of distances representing the input graph.

directed : bool, optional

If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices : array_like or int, optional

if specified, only compute the paths for the points at the given indices.

return_predecessors : bool, optional

If True, return the size (N, N) predecesor matrix

unweighted : bool, optional

If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

dist_matrix : ndarray

The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors : ndarray

Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises **NegativeCycleError:**

if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

`scipy.sparse.csgraph.`**`breadth_first_order`**`(`*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*`)`

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique, but the tree which it generates is unique.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix

The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors : bool, optional

If True (default), then return the predecesor array (see below).

Returns **node_array** : ndarray, one dimension

The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors : ndarray, one dimension

Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

`scipy.sparse.csgraph.`**`depth_first_order`**(*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*)

Return a depth-first ordering starting with specified node.

Note that a depth-first order is not unique. Furthermore, for graphs with cycles, the tree generated by a depth-first search is not unique either.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix

The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors : bool, optional

If True (default), then return the predecesor array (see below).

Returns **node_array** : ndarray, one dimension

The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors : ndarray, one dimension

Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

`scipy.sparse.csgraph.`**`breadth_first_tree`**(*csgraph*, *i_start*, *directed=True*)

Return the tree generated by a breadth-first search

Note that a breadth-first tree from a specified node is unique.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns **cstree** : csr matrix

The N x N directed compressed-sparse representation of the breadth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
 input graph          breadth first tree from (0)

     (0)                         (0)
    /   \                       /   \
   3     8                     3     8
  /       \                   /       \
(3)---5---(1)               (3)       (1)
  \       /                           /
   6     2                           2
    \   /                           /
     (2)                         (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = breadth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 3],
       [0, 0, 2, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. A breadth-first tree from a given node is unique.

`scipy.sparse.csgraph.`**`depth_first_tree`**(*csgraph*, *i_start*, *directed=True*)

Return a tree generated by a depth-first search.

Note that a tree generated by a depth-first search is not unique: it depends on the order that the children of each node are searched.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix

The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start : int

The index of starting node.

directed : bool, optional

If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns **cstree** : csr matrix

The N x N directed compressed-sparse representation of the depth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
 input graph           depth first tree from (0)

     (0)                         (0)
    /   \                           \
   3     8                           8
  /       \                           \
(3)---5---(1)               (3)       (1)
  \       /                   \       /
   6     2                     6     2
    \   /                       \   /
     (2)                         (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = depth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 0],
       [0, 0, 2, 0],
       [0, 0, 0, 6],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. Unlike a breadth-first tree, a depth-first tree of a given graph is not unique if the graph contains cycles. If the above solution had begun with the edge connecting nodes 0 and 3, the result would have been different.

`scipy.sparse.csgraph.`**`minimum_spanning_tree`**(*csgraph*, *overwrite=False*)

Return a minimum spanning tree of an undirected graph

A minimum spanning tree is a graph consisting of the subset of edges which together connect all connected nodes, while minimizing the total sum of weights on the edges. This is computed using the Kruskal algorithm.

New in version 0.11.0.

Parameters **csgraph** : array_like or sparse matrix, 2 dimensions

The N x N matrix representing an undirected graph over N nodes (see notes below).

overwrite : bool, optional

if true, then parts of the input graph will be overwritten for efficiency.

Returns **span_tree** : csr matrix

The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).

Notes

This routine uses undirected graphs as input and output. That is, if graph[i, j] and graph[j, i] are both zero, then nodes i and j do not have an edge connecting them. If either is nonzero, then the two are connected by the minimum nonzero value of the two.

Examples

The following example shows the computation of a minimum spanning tree over a simple four-component graph:

```
 input graph             minimum spanning tree

     (0)                         (0)
    /   \                       /
   3     8                     3
  /       \                   /
(3)---5---(1)               (3)---5---(1)
  \       /                           /
   6     2                           2
    \   /                           /
     (2)                         (2)
```

It is easy to see from inspection that the minimum spanning tree involves removing the edges with weights 8 and 6. In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import minimum_spanning_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = minimum_spanning_tree(X)
>>> Tcsr.toarray().astype(int)
array([[0, 0, 0, 3],
       [0, 0, 2, 5],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

`scipy.sparse.csgraph.`**`reverse_cuthill_mckee`**`()`

Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.

It is assumed by default, `symmetric_mode=False`, that the input matrix is not symmetric and works on the matrix `A+A.T`. If you are guaranteed that the matrix is symmetric in structure (values of matrix elements do not matter) then set `symmetric_mode=True`.

Parameters **graph** : sparse matrix

Input sparse in CSC or CSR sparse matrix format.

symmetric_mode : bool, optional

Is input matrix guaranteed to be symmetric.

Returns **perm** : ndarray

Array of permuted row and column indices.

Notes

New in version 0.15.0.

References

E. Cuthill and J. McKee, "Reducing the Bandwidth of Sparse Symmetric Matrices", ACM '69 Proceedings of the 1969 24th national conference, (1969).

`scipy.sparse.csgraph.`**`maximum_bipartite_matching`**`()`

Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.

Such a permutation is always possible provided that the matrix is nonsingular. This function looks at the structure of the matrix only. The input matrix will be converted to CSC matrix format if necessary.

Parameters **graph** : sparse matrix

Input sparse in CSC format

perm_type : str, {'row', 'column'}

Type of permutation to generate.

Returns **perm** : ndarray

Array of row or column permutations.

Notes

This function relies on a maximum cardinality bipartite matching algorithm based on a breadth-first search (BFS) of the underlying graph.

New in version 0.15.0.

References

I. S. Duff, K. Kaya, and B. Ucar, "Design, Implementation, and Analysis of Maximum Transversal Algorithms", ACM Trans. Math. Softw. 38, no. 2, (2011).

5.30.2 Graph Representations

This module uses graphs which are stored in a matrix format. A graph with N nodes can be represented by an (N x N) adjacency matrix G. If there is a connection from node i to node j, then G[i, j] = w, where w is the weight of the connection. For nodes i and j which are not connected, the value depends on the representation:

- for dense array representations, non-edges are represented by G[i, j] = 0, infinity, or NaN.
- for dense masked representations (of type np.ma.MaskedArray), non-edges are represented by masked values. This can be useful when graphs with zero-weight edges are desired.
- for sparse array representations, non-edges are represented by non-entries in the matrix. This sort of sparse representation also allows for edges with zero weights.

As a concrete example, imagine that you would like to represent the following undirected graph:

```
      G

     (0)
    /   \
   1     2
  /       \
(2)       (1)
```

This graph has three nodes, where node 0 and 1 are connected by an edge of weight 2, and nodes 0 and 2 are connected by an edge of weight 1. We can construct the dense, masked, and sparse representations as follows, keeping in mind that an undirected graph is represented by a symmetric matrix:

```
>>> G_dense = np.array([[0, 2, 1],
...                     [2, 0, 0],
...                     [1, 0, 0]])
>>> G_masked = np.ma.masked_values(G_dense, 0)
>>> from scipy.sparse import csr_matrix
>>> G_sparse = csr_matrix(G_dense)
```

This becomes more difficult when zero edges are significant. For example, consider the situation when we slightly modify the above graph:

```
     G2

     (0)
    /   \
   0     2
  /       \
(2)       (1)
```

This is identical to the previous graph, except nodes 0 and 2 are connected by an edge of zero weight. In this case, the dense representation above leads to ambiguities: how can non-edges be represented if zero is a meaningful value? In this case, either a masked or sparse representation must be used to eliminate the ambiguity:

```
>>> G2_data = np.array([[np.inf, 2,      0     ],
...                     [2,      np.inf, np.inf],
...                     [0,      np.inf, np.inf]])
>>> G2_masked = np.ma.masked_invalid(G2_data)
>>> from scipy.sparse.csgraph import csgraph_from_dense
>>> # G2_sparse = csr_matrix(G2_data) would give the wrong result
>>> G2_sparse = csgraph_from_dense(G2_data, null_value=np.inf)
>>> G2_sparse.data
array([ 2.,  0.,  2.,  0.])
```

Here we have used a utility routine from the csgraph submodule in order to convert the dense representation to a sparse representation which can be understood by the algorithms in submodule. By viewing the data array, we can see that the zero values are explicitly encoded in the graph.

Directed vs. Undirected

Matrices may represent either directed or undirected graphs. This is specified throughout the csgraph module by a boolean keyword. Graphs are assumed to be directed by default. In a directed graph, traversal from node i to node j can be accomplished over the edge G[i, j], but not the edge G[j, i]. In a non-directed graph, traversal from node i to node j can be accomplished over either G[i, j] or G[j, i]. If both edges are not null, and the two have unequal weights, then the smaller of the two is used. Note that a symmetric matrix will represent an undirected graph, regardless of whether the 'directed' keyword is set to True or False. In this case, using `directed=True` generally leads to more efficient computation.

The routines in this module accept as input either scipy.sparse representations (csr, csc, or lil format), masked representations, or dense representations with non-edges indicated by zeros, infinities, and NaN entries.

5.31 Spatial algorithms and data structures (`scipy.spatial`)

5.31.1 Nearest-neighbor Queries

`KDTree`(data[, leafsize])	kd-tree for quick nearest-neighbor lookup
`cKDTree`	kd-tree for quick nearest-neighbor lookup
`distance`	

class `scipy.spatial.`**`KDTree`**(*data*, *leafsize=10*)

kd-tree for quick nearest-neighbor lookup

This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

Parameters **data** : (N,K) array_like

The data points to be indexed. This array is not copied, and so modifying this data will result in bogus results.

leafsize : int, optional

The number of points at which the algorithm switches over to brute-force. Has to be positive.

Raises **RuntimeError**

The maximum recursion limit can be exceeded for large data sets. If this happens, either increase the value for the *leafsize* parameter or increase the recursion limit by:

```
>>> import sys
>>> sys.setrecursionlimit(10000)
```

Notes

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary tree, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the “sliding midpoint” rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

The tree also supports all-neighbors queries, both with arrays of points and with other kd-trees. These do use a reasonably efficient algorithm, but the kd-tree is not necessarily the best data structure for this sort of calculation.

Methods

`count_neighbors`(other, r[, p])	Count how many nearby pairs can be formed.
`innernode`(split_dim, split, less, greater)	
`leafnode`(idx)	
`node`	

Continued on next page

Table 5.192 – continued from previous page

`query`(x[, k, eps, p, distance_upper_bound])	Query the kd-tree for nearest neighbors
`query_ball_point`(x, r[, p, eps])	Find all points within distance r of point(s) x.
`query_ball_tree`(other, r[, p, eps])	Find all pairs of points whose distance is at most r
`query_pairs`(r[, p, eps])	Find all pairs of points within a distance.
`sparse_distance_matrix`(other, max_distance)	Compute a sparse distance matrix

`KDTree.`**`count_neighbors`**(*other*, *r*, *p=2.0*)

Count how many nearby pairs can be formed.

Count the number of pairs (x1,x2) can be formed, with x1 drawn from self and x2 drawn from *other*, and where `distance(x1, x2, p) <= r`. This is the “two-point correlation” described in Gray and Moore 2000, “N-body problems in statistical learning”, and the code here is based on their algorithm.

Parameters

other : KDTree instance

The other tree to draw points from.

r : float or one-dimensional array of floats

The radius to produce a count for. Multiple radii are searched with a single tree traversal.

p : float, 1<=p<=infinity, optional

Which Minkowski p-norm to use

Returns

result : int or 1-D array of ints

The number of pairs. Note that this is internally stored in a numpy int, and so may overflow if very large (2e9).

`KDTree.`**`query`**(*x*, *k=1*, *eps=0*, *p=2*, *distance_upper_bound=inf*)

Query the kd-tree for nearest neighbors

Parameters

x : array_like, last dimension self.m

An array of points to query.

k : int, optional

The number of nearest neighbors to return.

eps : nonnegative float, optional

Return approximate nearest neighbors; the kth returned value is guaranteed to be no further than (1+eps) times the distance to the real kth nearest neighbor.

p : float, 1<=p<=infinity, optional

Which Minkowski p-norm to use. 1 is the sum-of-absolute-values “Manhattan” distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance

distance_upper_bound : nonnegative float, optional

Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

Returns

d : float or array of floats

The distances to the nearest neighbors. If x has shape tuple+(self.m,), then d has shape tuple if k is one, or tuple+(k,) if k is larger than one. Missing neighbors (e.g. when k > n or distance_upper_bound is given) are indicated with infinite distances. If k is None, then d is an object array of shape tuple, containing lists of distances. In either case the hits are sorted by distance (nearest first).

i : integer or array of integers

The locations of the neighbors in self.data. i is the same shape as d.

Examples

```
>>> from scipy import spatial
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = spatial.KDTree(list(zip(x.ravel(), y.ravel())))
>>> tree.data
array([[0, 2],
       [0, 3],
       [0, 4],
       [0, 5],
       [0, 6],
       [0, 7],
       [1, 2],
       [1, 3],
       [1, 4],
       [1, 5],
       [1, 6],
       [1, 7],
       [2, 2],
       [2, 3],
       [2, 4],
       [2, 5],
       [2, 6],
       [2, 7],
       [3, 2],
       [3, 3],
       [3, 4],
       [3, 5],
       [3, 6],
       [3, 7],
       [4, 2],
       [4, 3],
       [4, 4],
       [4, 5],
       [4, 6],
       [4, 7]])
>>> pts = np.array([[0, 0], [2.1, 2.9]])
>>> tree.query(pts)
(array([ 2.        ,  0.14142136]), array([ 0, 13]))
>>> tree.query(pts[0])
(2.0, 0)
```

`KDTree.`**`query_ball_point`**(*x*, *r*, *p=2.0*, *eps=0*)

Find all points within distance r of point(s) x.

Parameters **x** : array_like, shape tuple + (self.m,)

The point or points to search for neighbors of.

r : positive float

The radius of points to return.

p : float, optional

Which Minkowski p-norm to use. Should be in the range [1, inf].

eps : nonnegative float, optional

Approximate search. Branches of the tree are not explored if their nearest points are further than `r / (1 + eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1 + eps)`.

Returns **results** : list or array of lists

If *x* is a single point, returns a list of the indices of the neighbors of *x*. If *x* is an array of points, returns an object array of shape tuple containing lists of neighbors.

Notes

If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a KDTree and using query_ball_tree.

Examples

```
>>> from scipy import spatial
>>> x, y = np.mgrid[0:4, 0:4]
>>> points = zip(x.ravel(), y.ravel())
>>> tree = spatial.KDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```

`KDTree.`**`query_ball_tree`**`(`*other*, *r*, *p=2.0*, *eps=0*`)`

Find all pairs of points whose distance is at most r

Parameters

other : KDTree instance
The tree containing points to search against.

r : float
The maximum distance, has to be positive.

p : float, optional
Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

eps : float, optional
Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns

results : list of lists
For each element `self.data[i]` of this tree, `results[i]` is a list of the indices of its neighbors in `other.data`.

`KDTree.`**`query_pairs`**`(`*r*, *p=2.0*, *eps=0*`)`

Find all pairs of points within a distance.

Parameters

r : positive float
The maximum distance.

p : float, optional
Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

eps : float, optional
Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns

results : set
Set of pairs `(i,j)`, with `i < j`, for which the corresponding positions are close.

`KDTree.`**`sparse_distance_matrix`**`(`*other*, *max_distance*, *p=2.0*`)`

Compute a sparse distance matrix

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than max_distance.

Parameters **other** : KDTree

max_distance : positive float

p : float, optional

Returns **result** : dok_matrix

Sparse matrix representing the results in "dictionary of keys" format.

class `scipy.spatial.`**`cKDTree`**

kd-tree for quick nearest-neighbor lookup

This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary trie, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the "sliding midpoint" rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

Parameters **data** : array_like, shape (n,m)

The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles, and so modifying this data will result in bogus results. The data are also copied if the kd-tree is built with copy_data=True.

leafsize : positive int, optional

The number of points at which the algorithm switches over to brute-force. Default: 16.

compact_nodes : bool, optional

If True, the kd-tree is built to shrink the hyperrectangles to the actual data range. This usually gives a more compact tree and faster queries at the expense of longer build time. Default: True.

copy_data : bool, optional

If True the data is always copied to protect the kd-tree against data corruption. Default: False.

balanced_tree : bool, optional

If True, the median is used to split the hyperrectangles instead of the midpoint. This usually gives a more compact tree and faster queries at the expense of longer build time. Default: True.

Attributes

`data`
`indices`
`leafsize`
`m`
`maxes`
`mins`
`n`
`tree`

cKDTree.**data**

cKDTree.**indices**

cKDTree.**leafsize**

cKDTree.**m**

cKDTree.**maxes**

cKDTree.**mins**

cKDTree.**n**

cKDTree.**tree**

Methods

`count_neighbors`(self, other, r[, p])	Count how many nearby pairs can be formed.
`query`(self, x[, k, eps, p, ...])	Query the kd-tree for nearest neighbors
`query_ball_point`(self, x, r[, p, eps])	Find all points within distance r of point(s) x.
`query_ball_tree`(self, other, r[, p, eps])	Find all pairs of points whose distance is at most r
`query_pairs`(self, r[, p, eps])	Find all pairs of points whose distance is at most r.
`sparse_distance_matrix`(self, other, max_distance)	Compute a sparse distance matrix

cKDTree.**count_neighbors**(*self*, *other*, *r*, *p=2.*)

Count how many nearby pairs can be formed.

Count the number of pairs (x1,x2) can be formed, with x1 drawn from self and x2 drawn from *other*, and where `distance(x1, x2, p) <= r`. This is the "two-point correlation" described in Gray and Moore 2000, "N-body problems in statistical learning", and the code here is based on their algorithm.

Parameters **other** : KDTree instance

The other tree to draw points from.

r : float or one-dimensional array of floats

The radius to produce a count for. Multiple radii are searched with a single tree traversal.

p : float, 1<=p<=infinity

Which Minkowski p-norm to use

Returns **result** : int or 1-D array of ints

The number of pairs. Note that this is internally stored in a numpy int, and so may overflow if very large (2e9).

cKDTree.**query**(*self*, *x*, *k=1*, *eps=0*, *p=2*, *distance_upper_bound=np.inf*, *n_jobs=1*)

Query the kd-tree for nearest neighbors

Parameters **x** : array_like, last dimension self.m

An array of points to query.

k : integer

The number of nearest neighbors to return.

eps : non-negative float

Return approximate nearest neighbors; the k-th returned value is guaranteed to be no further than (1+eps) times the distance to the real k-th nearest neighbor.

p : float, 1<=p<=infinity

Which Minkowski p-norm to use. 1 is the sum-of-absolute-values "Manhattan" distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance

distance_upper_bound : nonnegative float

Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

n_jobs : int, optional

Number of jobs to schedule for parallel processing. If -1 is given all processors are used. Default: 1.

Returns

d : array of floats

The distances to the nearest neighbors. If x has shape tuple+(self.m,), then d has shape tuple+(k,). Missing neighbors are indicated with infinite distances.

i : ndarray of ints

The locations of the neighbors in self.data. If *x* has shape tuple+(self.m,), then *i* has shape tuple+(k,). Missing neighbors are indicated with self.n.

`cKDTree.`**`query_ball_point`**(*self*, *x*, *r*, *p=2.*, *eps=0*)

Find all points within distance r of point(s) x.

Parameters

x : array_like, shape tuple + (self.m,)

The point or points to search for neighbors of.

r : positive float

The radius of points to return.

p : float, optional

Which Minkowski p-norm to use. Should be in the range [1, inf].

eps : nonnegative float, optional

Approximate search. Branches of the tree are not explored if their nearest points are further than `r / (1 + eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1 + eps)`.

Returns

results : list or array of lists

If *x* is a single point, returns a list of the indices of the neighbors of *x*. If *x* is an array of points, returns an object array of shape tuple containing lists of neighbors.

Notes

If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a cKDTree and using query_ball_tree.

Examples

```
>>> from scipy import spatial
>>> x, y = np.mgrid[0:4, 0:4]
>>> points = zip(x.ravel(), y.ravel())
>>> tree = spatial.cKDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```

`cKDTree.`**`query_ball_tree`**(*self*, *other*, *r*, *p=2.*, *eps=0*)

Find all pairs of points whose distance is at most r

Parameters **other** : KDTree instance

The tree containing points to search against.

r : float

The maximum distance, has to be positive.

p : float, optional

Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

eps : float, optional

Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns **results** : list of lists

For each element `self.data[i]` of this tree, `results[i]` is a list of the indices of its neighbors in `other.data`.

`cKDTree.`**`query_pairs`**(*self*, *r*, *p=2.*, *eps=0*)

Find all pairs of points whose distance is at most r.

Parameters **r** : positive float

The maximum distance.

p : float, optional

Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

eps : float, optional

Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns **results** : set

Set of pairs `(i,j)`, with `i < j`, for which the corresponding positions are close.

`cKDTree.`**`sparse_distance_matrix`**(*self*, *other*, *max_distance*, *p=2.*)

Compute a sparse distance matrix

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than max_distance.

Parameters **other** : cKDTree

max_distance : positive float

p : float, 1<=p<=infinity

Which Minkowski p-norm to use.

Returns **result** : dok_matrix

Sparse matrix representing the results in “dictionary of keys” format. FIXME: Internally, built as a COO matrix, it would be more efficient to return this COO matrix.

Distance computations (`scipy.spatial.distance`)

Function Reference Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

`pdist`(X[, metric, p, w, V, VI])	Pairwise distances between observations in n-dimensional space.
`cdist`(XA, XB[, metric, p, V, VI, w])	Computes distance between each pair of the two collections of inputs.

Continued on next page

Table 5.195 – continued from previous page

squareform(X[, force, checks])	Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.

`scipy.spatial.distance.`**`pdist`**(*X*, *metric='euclidean'*, *p=2*, *w=None*, *V=None*, *VI=None*)

Pairwise distances between observations in n-dimensional space.

The following are common calling conventions.

1. `Y = pdist(X, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.

2. `Y = pdist(X, 'minkowski', p)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.

3. `Y = pdist(X, 'cityblock')`

   Computes the city block or Manhattan distance between the points.

4. `Y = pdist(X, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

$$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.

5. `Y = pdist(X, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = pdist(X, 'cosine')`

   Computes the cosine distance between vectors u and v,

$$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of `u` and `v`.

7. `Y = pdist(X, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

$$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.

8. `Y = pdist(X, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.

9. `Y = pdist(X, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree where at least one of them is non-zero.

10. `Y = pdist(X, 'chebyshev')`

   Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

$$d(u, v) = \max_i |u_i - v_i|$$

11. `Y = pdist(X, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u,v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}$$

12. `Y = pdist(X, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u,v) = \frac{\sum_i u_i - v_i}{\sum_i u_i + v_i}$$

13. `Y = pdist(X, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $(u - v)(1/V)(u - v)^T$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

14. `Y = pdist(X, 'yule')`

    Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

15. `Y = pdist(X, 'matching')`

    Computes the matching distance between each pair of boolean vectors. (see matching function documentation)

16. `Y = pdist(X, 'dice')`

    Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

17. `Y = pdist(X, 'kulsinski')`

    Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

18. `Y = pdist(X, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

19. `Y = pdist(X, 'russellrao')`

    Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

20. `Y = pdist(X, 'sokalmichener')`

    Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

21. `Y = pdist(X, 'sokalsneath')`

    Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)

22. `Y = pdist(X, 'wminkowski')`

    Computes the weighted Minkowski distance between each pair of vectors. (see wminkowski function documentation)

23. `Y = pdist(X, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

    ```
    dm = pdist(X, lambda u, v: np.sqrt(((u-v)**2).sum()))
    ```

    Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

    ```
    dm = pdist(X, sokalsneath)
    ```

    would calculate the pair-wise distances between the vectors in X using the Python function sokalsneath. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax.:

    ```
    dm = pdist(X, 'sokalsneath')
    ```

Parameters

X : ndarray

An m by n array of m original observations in an n-dimensional space.

metric : str or function, optional

The distance metric to use. The distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'yule'.

w : ndarray, optional

The weight vector (for weighted Minkowski).

p : double, optional

The p-norm to apply (for Minkowski, weighted and unweighted)

V : ndarray, optional

The variance vector (for standardized Euclidean).

VI : ndarray, optional

The inverse of the covariance matrix (for Mahalanobis).

Returns

Y : ndarray

Returns a condensed distance matrix Y. For each i and j (where $i < j < n$), the metric `dist(u=X[i], v=X[j])` is computed and stored in entry `ij`.

See also:

`squareform`converts between condensed distance matrices and square distance matrices.

Notes

See `squareform` for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

`scipy.spatial.distance.`**`cdist`**(*XA*, *XB*, *metric='euclidean'*, *p=2*, *V=None*, *VI=None*, *w=None*)

Computes distance between each pair of the two collections of inputs.

The following are common calling conventions:

1. `Y = cdist(XA, XB, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.

2. `Y = cdist(XA, XB, 'minkowski', p)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.

3. `Y = cdist(XA, XB, 'cityblock')`

   Computes the city block or Manhattan distance between the points.

4. `Y = cdist(XA, XB, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}.$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.

5. `Y = cdist(XA, XB, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = cdist(XA, XB, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of u and v.

7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.

8. `Y = cdist(XA, XB, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.

9. `Y = cdist(XA, XB, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree where at least one of them is non-zero.

10. `Y = cdist(XA, XB, 'chebyshev')`

    Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

    $$d(u, v) = \max_i |u_i - v_i|.$$

11. `Y = cdist(XA, XB, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

12. `Y = cdist(XA, XB, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u,v) = \frac{\sum_i (u_i - v_i)}{\sum_i (u_i + v_i)}$$

13. `Y = cdist(XA, XB, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $(u-v)(1/V)(u-v)^T$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

14. `Y = cdist(XA, XB, 'yule')`

    Computes the Yule distance between the boolean vectors. (see `yule` function documentation)

15. `Y = cdist(XA, XB, 'matching')`

    Computes the matching distance between the boolean vectors. (see `matching` function documentation)

16. `Y = cdist(XA, XB, 'dice')`

    Computes the Dice distance between the boolean vectors. (see `dice` function documentation)

17. `Y = cdist(XA, XB, 'kulsinski')`

    Computes the Kulsinski distance between the boolean vectors. (see `kulsinski` function documentation)

18. `Y = cdist(XA, XB, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between the boolean vectors. (see `rogerstanimoto` function documentation)

19. `Y = cdist(XA, XB, 'russellrao')`

    Computes the Russell-Rao distance between the boolean vectors. (see `russellrao` function documentation)

20. `Y = cdist(XA, XB, 'sokalmichener')`

    Computes the Sokal-Michener distance between the boolean vectors. (see `sokalmichener` function documentation)

21. `Y = cdist(XA, XB, 'sokalsneath')`

    Computes the Sokal-Sneath distance between the vectors. (see `sokalsneath` function documentation)

22. `Y = cdist(XA, XB, 'wminkowski')`

    Computes the weighted Minkowski distance between the vectors. (see `wminkowski` function documentation)

23. `Y = cdist(XA, XB, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

```
dm = cdist(XA, XB, lambda u, v: np.sqrt(((u-v)**2).sum()))
```

Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

```
dm = cdist(XA, XB, sokalsneath)
```

would calculate the pair-wise distances between the vectors in X using the Python function `sokalsneath`. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax:

```
dm = cdist(XA, XB, 'sokalsneath')
```

Parameters

XA : ndarray

An m_A by n array of m_A original observations in an n-dimensional space. Inputs are converted to float type.

XB : ndarray

An m_B by n array of m_B original observations in an n-dimensional space. Inputs are converted to float type.

metric : str or callable, optional

The distance metric to use. If a string, the distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'wminkowski', 'yule'.

w : ndarray, optional

The weight vector (for weighted Minkowski).

p : scalar, optional

The p-norm to apply (for Minkowski, weighted and unweighted)

V : ndarray, optional

The variance vector (for standardized Euclidean).

VI : ndarray, optional

The inverse of the covariance matrix (for Mahalanobis).

Returns

Y : ndarray

A m_A by m_B distance matrix is returned. For each i and j, the metric `dist(u=XA[i], v=XB[j])` is computed and stored in the ij th entry.

Raises

ValueError

An exception is thrown if *XA* and *XB* do not have the same number of columns.

Examples

Find the Euclidean distances between four 2-D coordinates:

```
>>> from scipy.spatial import distance
>>> coords = [(35.0456, -85.2672),
...           (35.1174, -89.9711),
...           (35.9728, -83.9422),
...           (36.1667, -86.7833)]
>>> distance.cdist(coords, coords, 'euclidean')
array([[ 0.    ,  4.7044,  1.6172,  1.8856],
       [ 4.7044,  0.    ,  6.0893,  3.3561],
       [ 1.6172,  6.0893,  0.    ,  2.8477],
       [ 1.8856,  3.3561,  2.8477,  0.    ]])
```

Find the Manhattan distance from a 3-D point to the corners of the unit cube:

```
>>> a = np.array([[0, 0, 0],
                  [0, 0, 1],
                  [0, 1, 0],
                  [0, 1, 1],
                  [1, 0, 0],
                  [1, 0, 1],
                  [1, 1, 0],
                  [1, 1, 1]])
>>> b = np.array([[ 0.1,  0.2,  0.4]])
>>> distance.cdist(a, b, 'cityblock')
array([[ 0.7],
       [ 0.9],
       [ 1.3],
       [ 1.5],
       [ 1.5],
       [ 1.7],
       [ 2.1],
       [ 2.3]])
```

`scipy.spatial.distance.`**`squareform`**`(`*X*, *force='no'*, *checks=True*`)`

Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.

Parameters

X : ndarray

Either a condensed or redundant distance matrix.

force : str, optional

As with MATLAB(TM), if force is equal to 'tovector' or 'tomatrix', the input will be treated as a distance matrix or distance vector respectively.

checks : bool, optional

If *checks* is set to False, no checks will be made for matrix symmetry nor zero diagonals. This is useful if it is known that `X - X.T1` is small and `diag(X)` is close to zero. These values are ignored any way so they do not disrupt the squareform transformation.

Returns

Y : ndarray

If a condensed distance matrix is passed, a redundant one is returned, or if a redundant one is passed, a condensed distance matrix is returned.

Notes

1.v = squareform(X)

Given a square d-by-d symmetric distance matrix X, `v=squareform(X)` returns a `d * (d-1) / 2` (or *${n choose 2}$*) sized vector v.

v[{n choose 2}-{n-i choose 2} + (j-i-1)] is the distance between points i and j. If X is non-square or asymmetric, an error is returned.

2.X = squareform(v)

Given a d*d(-1)/2 sized v for some integer d>=2 encoding distances as described, X=squareform(v) returns a d by d distance matrix X. The X[i, j] and X[j, i] values are set to v[{n choose 2}-{n-i choose 2} + (j-u-1)] and all diagonal elements are zero.

Predicates for checking the validity of distance matrices, both condensed and redundant. Also contained in this module are functions for computing the number of observations in a distance matrix.

`is_valid_dm`(D[, tol, throw, name, warning])	Returns True if input array is a valid distance matrix.

Continue

Table 5.196 – continued from previous page

`is_valid_y`(y[, warning, throw, name])	Returns True if the input array is a valid condensed distance matrix.
`num_obs_dm`(d)	Returns the number of original observations that correspond to a square, redundant
`num_obs_y`(Y)	Returns the number of original observations that correspond to a condensed distan

`scipy.spatial.distance.`**`is_valid_dm`**(*D*, *tol=0.0*, *throw=False*, *name='D'*, *warning=False*)

Returns True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays containing doubles. They must have a zero-diagonal, and they must be symmetric.

Parameters

D : ndarray
The candidate object to test for validity.

tol : float, optional
The distance matrix should be symmetric. *tol* is the maximum difference between entries `ij` and `ji` for the distance metric to be considered symmetric.

throw : bool, optional
An exception is thrown if the distance matrix passed is not valid.

name : str, optional
The name of the variable to checked. This is useful if throw is set to True so the offending variable can be identified in the exception message when an exception is thrown.

warning : bool, optional
Instead of throwing an exception, a warning message is raised.

Returns

valid : bool
True if the variable *D* passed is a valid distance matrix.

Notes

Small numerical differences in *D* and *D.T* and non-zeroness of the diagonal are ignored if they are within the tolerance specified by *tol*.

`scipy.spatial.distance.`**`is_valid_y`**(*y*, *warning=False*, *throw=False*, *name=None*)

Returns True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays containing doubles. Their length must be a binomial coefficient $\binom{n}{2}$ for some positive integer n.

Parameters

y : ndarray
The condensed distance matrix.

warning : bool, optional
Invokes a warning if the variable passed is not a valid condensed distance matrix. The warning message explains why the distance matrix is not valid. *name* is used when referencing the offending variable.

throw : bool, optional
Throws an exception if the variable passed is not a valid condensed distance matrix.

name : bool, optional
Used when referencing the offending variable in the warning or exception message.

`scipy.spatial.distance.`**`num_obs_dm`**(*d*)

Returns the number of original observations that correspond to a square, redundant distance matrix.

Parameters

d : ndarray
The target distance matrix.

Returns

num_obs_dm : int

The number of observations in the redundant distance matrix.

`scipy.spatial.distance.`**`num_obs_y`**`(`*Y*`)`

Returns the number of original observations that correspond to a condensed distance matrix.

Parameters **Y** : ndarray

Condensed distance matrix.

Returns **n** : int

The number of observations in the condensed distance matrix *Y*.

Distance functions between two vectors `u` and `v`. Computing distances over a large collection of vectors is inefficient for these functions. Use `pdist` for this purpose.

`braycurtis`(u, v)	Computes the Bray-Curtis distance between two 1-D arrays.
`canberra`(u, v)	Computes the Canberra distance between two 1-D arrays.
`chebyshev`(u, v)	Computes the Chebyshev distance.
`cityblock`(u, v)	Computes the City Block (Manhattan) distance.
`correlation`(u, v)	Computes the correlation distance between two 1-D arrays.
`cosine`(u, v)	Computes the Cosine distance between 1-D arrays.
`dice`(u, v)	Computes the Dice dissimilarity between two boolean 1-D arrays.
`euclidean`(u, v)	Computes the Euclidean distance between two 1-D arrays.
`hamming`(u, v)	Computes the Hamming distance between two 1-D arrays.
`jaccard`(u, v)	Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
`kulsinski`(u, v)	Computes the Kulsinski dissimilarity between two boolean 1-D arrays.
`mahalanobis`(u, v, VI)	Computes the Mahalanobis distance between two 1-D arrays.
`matching`(u, v)	Computes the Matching dissimilarity between two boolean 1-D arrays.
`minkowski`(u, v, p)	Computes the Minkowski distance between two 1-D arrays.
`rogerstanimoto`(u, v)	Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
`russellrao`(u, v)	Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.
`seuclidean`(u, v, V)	Returns the standardized Euclidean distance between two 1-D arrays.
`sokalmichener`(u, v)	Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.
`sokalsneath`(u, v)	Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.
`sqeuclidean`(u, v)	Computes the squared Euclidean distance between two 1-D arrays.
`wminkowski`(u, v, p, w)	Computes the weighted Minkowski distance between two 1-D arrays.
`yule`(u, v)	Computes the Yule dissimilarity between two boolean 1-D arrays.

`scipy.spatial.distance.`**`braycurtis`**`(`*u*, *v*`)`

Computes the Bray-Curtis distance between two 1-D arrays.

Bray-Curtis distance is defined as

$$\sum |u_i - v_i| / \sum |u_i + v_i|$$

The Bray-Curtis distance is in the range [0, 1] if all coordinates are positive, and is undefined if the inputs are of length zero.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **braycurtis** : double

The Bray-Curtis distance between 1-D arrays *u* and *v*.

`scipy.spatial.distance.`**`canberra`**`(`*u*, *v*`)`

Computes the Canberra distance between two 1-D arrays.

The Canberra distance is defined as

$$d(u,v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **canberra** : double

The Canberra distance between vectors *u* and *v*.

Notes

When *u[i]* and *v[i]* are 0 for given i, then the fraction 0/0 = 0 is used in the calculation.

`scipy.spatial.distance.`**`chebyshev`**`(`*u*, *v*`)`

Computes the Chebyshev distance.

Computes the Chebyshev distance between two 1-D arrays *u* and *v*, which is defined as

$$\max_i |u_i - v_i|.$$

Parameters **u** : (N,) array_like

Input vector.

v : (N,) array_like

Input vector.

Returns **chebyshev** : double

The Chebyshev distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`cityblock`**`(`*u*, *v*`)`

Computes the City Block (Manhattan) distance.

Computes the Manhattan distance between two 1-D arrays *u* and *v*, which is defined as

$$\sum_i |u_i - v_i|.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **cityblock** : double

The City Block (Manhattan) distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`correlation`**`(`*u*, *v*`)`

Computes the correlation distance between two 1-D arrays.

The correlation distance between *u* and *v*, is defined as

$$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{{||(u - \bar{u})||}_2 {||(v - \bar{v})||}_2}$$

where $\bar{u}$ is the mean of the elements of *u* and $x \cdot y$ is the dot product of x and y.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **correlation** : double

The correlation distance between 1-D array *u* and *v*.

`scipy.spatial.distance.`**`cosine`**(*u*, *v*)

Computes the Cosine distance between 1-D arrays.

The Cosine distance between *u* and *v*, is defined as

$$1 - \frac{u \cdot v}{||u||_2||v||_2}.$$

where $u \cdot v$ is the dot product of u and v.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **cosine** : double

The Cosine distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`dice`**(*u*, *v*)

Computes the Dice dissimilarity between two boolean 1-D arrays.

The Dice dissimilarity between *u* and *v*, is

$$\frac{c_{TF} + c_{FT}}{2c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) ndarray, bool

Input 1-D array.

v : (N,) ndarray, bool

Input 1-D array.

Returns **dice** : double

The Dice dissimilarity between 1-D arrays *u* and *v*.

`scipy.spatial.distance.`**`euclidean`**(*u*, *v*)

Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays *u* and *v*, is defined as

$$||u - v||_2$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **euclidean** : double

The Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`hamming`**(*u*, *v*)

Computes the Hamming distance between two 1-D arrays.

The Hamming distance between 1-D arrays *u* and *v*, is simply the proportion of disagreeing components in *u* and *v*. If *u* and *v* are boolean vectors, the Hamming distance is

$$\frac{c_{01} + c_{10}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **hamming** : double

The Hamming distance between vectors *u* and *v*.

scipy.spatial.distance.**jaccard**(*u*, *v*)

Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.

The Jaccard-Needham dissimilarity between 1-D boolean arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT}}{c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **jaccard** : double

The Jaccard distance between vectors *u* and *v*.

scipy.spatial.distance.**kulsinski**(*u*, *v*)

Computes the Kulsinski dissimilarity between two boolean 1-D arrays.

The Kulsinski dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT} - c_{TT} + n}{c_{FT} + c_{TF} + n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **kulsinski** : double

The Kulsinski distance between vectors *u* and *v*.

scipy.spatial.distance.**mahalanobis**(*u*, *v*, *VI*)

Computes the Mahalanobis distance between two 1-D arrays.

The Mahalanobis distance between 1-D arrays *u* and *v*, is defined as

$$\sqrt{(u-v)V^{-1}(u-v)^T}$$

where `V` is the covariance matrix. Note that the argument *VI* is the inverse of `V`.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

VI : ndarray

The inverse of the covariance matrix.

Returns **mahalanobis** : double

The Mahalanobis distance between vectors *u* and *v*.

scipy.spatial.distance.**matching**(*u*, *v*)

Computes the Matching dissimilarity between two boolean 1-D arrays.

The Matching dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **matching** : double

The Matching dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`minkowski`**(*u*, *v*, *p*)

Computes the Minkowski distance between two 1-D arrays.

The Minkowski distance between 1-D arrays *u* and *v*, is defined as

$$||u-v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

p : int

The order of the norm of the difference $||u-v||_p$.

Returns **d** : double

The Minkowski distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`rogerstanimoto`**(*u*, *v*)

Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.

The Rogers-Tanimoto dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{c_{TT} + c_{FF} + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **rogerstanimoto** : double

The Rogers-Tanimoto dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`russellrao`**(*u*, *v*)

Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.

The Russell-Rao dissimilarity between two boolean 1-D arrays, *u* and *v*, is defined as

$$\frac{n - c_{TT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **russellrao** : double

The Russell-Rao dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`seuclidean`**(*u*, *v*, *V*)

Returns the standardized Euclidean distance between two 1-D arrays.

The standardized Euclidean distance between *u* and *v*.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

V : (N,) array_like

V is an 1-D array of component variances. It is usually computed among a larger collection vectors.

Returns **seuclidean** : double

The standardized Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`sokalmichener`**`(`*u*, *v*`)`

Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.

The Sokal-Michener dissimilarity between boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{S+R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$, $R = 2 * (c_{TF} + c_{FT})$ and $S = c_{FF} + c_{TT}$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **sokalmichener** : double

The Sokal-Michener dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`sokalsneath`**`(`*u*, *v*`)`

Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.

The Sokal-Sneath dissimilarity between *u* and *v*,

$$\frac{R}{c_{TT}+R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **sokalsneath** : double

The Sokal-Sneath dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`sqeuclidean`**`(`*u*, *v*`)`

Computes the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between *u* and *v* is defined as

$$||u - v||_2^2.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **sqeuclidean** : double

The squared Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`wminkowski`**`(`*u*, *v*, *p*, *w*`)`

Computes the weighted Minkowski distance between two 1-D arrays.

The weighted Minkowski distance between *u* and *v*, defined as

$$\left(\sum (w_i |u_i - v_i|^p)\right)^{1/p}.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

p : int

The order of the norm of the difference $||u - v||_p$.

w : (N,) array_like

The weight vector.

Returns **wminkowski** : double

The weighted Minkowski distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`yule`**`(u, v)`

Computes the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

$$\frac{R}{c_{TT} * c_{FF} + \frac{R}{2}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2.0 * c_{TF} * c_{FT}$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **yule** : double

The Yule dissimilarity between vectors *u* and *v*.

Functions

`braycurtis`(u, v)	Computes the Bray-Curtis distance between two 1-D arrays.
`callable`((object) -> bool)	Return whether the object is callable (i.e., some kind of function).
`canberra`(u, v)	Computes the Canberra distance between two 1-D arrays.
`cdist`(XA, XB[, metric, p, V, VI, w])	Computes distance between each pair of the two collections of inputs.
`chebyshev`(u, v)	Computes the Chebyshev distance.
`cityblock`(u, v)	Computes the City Block (Manhattan) distance.
`correlation`(u, v)	Computes the correlation distance between two 1-D arrays.
`cosine`(u, v)	Computes the Cosine distance between 1-D arrays.
`dice`(u, v)	Computes the Dice dissimilarity between two boolean 1-D arrays.
`euclidean`(u, v)	Computes the Euclidean distance between two 1-D arrays.
`hamming`(u, v)	Computes the Hamming distance between two 1-D arrays.
`is_valid_dm`(D[, tol, throw, name, warning])	Returns True if input array is a valid distance matrix.
`is_valid_y`(y[, warning, throw, name])	Returns True if the input array is a valid condensed distance matrix.
`jaccard`(u, v)	Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
`kulsinski`(u, v)	Computes the Kulsinski dissimilarity between two boolean 1-D arrays.
`mahalanobis`(u, v, VI)	Computes the Mahalanobis distance between two 1-D arrays.
`matching`(u, v)	Computes the Matching dissimilarity between two boolean 1-D arrays.
`minkowski`(u, v, p)	Computes the Minkowski distance between two 1-D arrays.
`norm`(a[, ord])	Matrix or vector norm.
`num_obs_dm`(d)	Returns the number of original observations that correspond to a square, redundant
`num_obs_y`(Y)	Returns the number of original observations that correspond to a condensed distanc
`pdist`(X[, metric, p, w, V, VI])	Pairwise distances between observations in n-dimensional space.
`rogerstanimoto`(u, v)	Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
`russellrao`(u, v)	Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.
`seuclidean`(u, v, V)	Returns the standardized Euclidean distance between two 1-D arrays.

Continue

Table 5.198 – continued from previous page

`sokalmichener`(u, v)	Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.
`sokalsneath`(u, v)	Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.
`sqeuclidean`(u, v)	Computes the squared Euclidean distance between two 1-D arrays.
`squareform`(X[, force, checks])	Converts a vector-form distance vector to a square-form distance matrix, and vice-
`wminkowski`(u, v, p, w)	Computes the weighted Minkowski distance between two 1-D arrays.
`yule`(u, v)	Computes the Yule dissimilarity between two boolean 1-D arrays.

Classes

`xrange`	xrange(stop) -> xrange object

5.31.2 Delaunay Triangulation, Convex Hulls and Voronoi Diagrams

`Delaunay`(points[, furthest_site, ...])	Delaunay tesselation in N dimensions.
`ConvexHull`(points[, incremental, qhull_options])	Convex hulls in N dimensions.
`Voronoi`(points[, furthest_site, ...])	Voronoi diagrams in N dimensions.

class `scipy.spatial.`**`Delaunay`**(*points*, *furthest_site=False*, *incremental=False*, *qhull_options=None*)

Delaunay tesselation in N dimensions.

New in version 0.9.

Parameters

points : ndarray of floats, shape (npoints, ndim)

Coordinates of points to triangulate

furthest_site : bool, optional

Whether to compute a furthest-site Delaunay triangulation. Default: False

New in version 0.12.0.

incremental : bool, optional

Allow adding new points incrementally. This takes up some additional resources.

qhull_options : str, optional

Additional options to pass to Qhull. See Qhull manual for details. Option “Qt” is always enabled. Default:”Qbb Qc Qz Qx” for ndim > 4 and “Qbb Qc Qz” otherwise. Incremental mode omits “Qz”.

New in version 0.12.0.

Raises

QhullError

Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError

Raised if an incompatible array is given as input.

Notes

The tesselation is computed using the Qhull library Qhull library.

Note: Unless you pass in the Qhull option “QJ”, Qhull does not guarantee that each input point appears as a vertex in the Delaunay triangulation. Omitted points are listed in the *coplanar* attribute.

Do not call the `add_points` method from a `__del__` destructor.

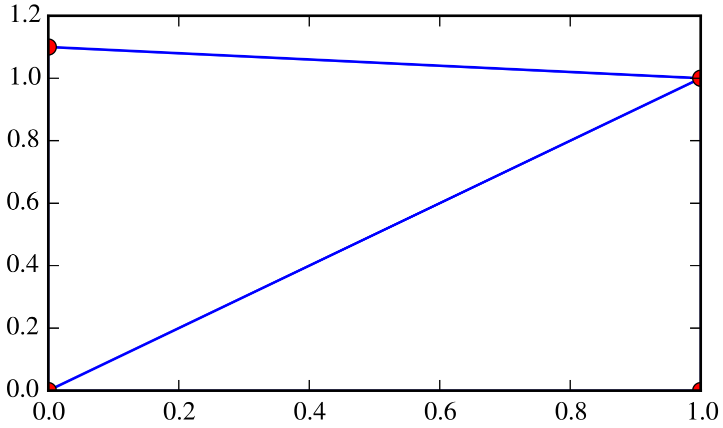
Examples

Triangulation of a set of points:

```
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> from scipy.spatial import Delaunay
>>> tri = Delaunay(points)
```

We can plot it:

```
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices.copy())
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> plt.show()
```



Point indices and coordinates for the two triangles forming the triangulation:

```
>>> tri.simplices
array([[3, 2, 0],
       [3, 1, 0]], dtype=int32)
>>> points[tri.simplices]
array([[[ 1. ,  1. ],
        [ 1. ,  0. ],
        [ 0. ,  0. ]],
       [[ 1. ,  1. ],
        [ 0. ,  1.1],
        [ 0. ,  0. ]]])
```

Triangle 0 is the only neighbor of triangle 1, and it's opposite to vertex 1 of triangle 1:

```
>>> tri.neighbors[1]
array([-1,  0, -1], dtype=int32)
>>> points[tri.simplices[1,1]]
array([ 0. ,  1.1])
```

We can find out which triangle points are in:

```
>>> p = np.array([(0.1, 0.2), (1.5, 0.5)])
>>> tri.find_simplex(p)
array([ 1, -1], dtype=int32)
```

We can also compute barycentric coordinates in triangle 1 for these points:

```
>>> b = tri.transform[1,:2].dot(p - tri.transform[1,2])
>>> np.c_[b, 1 - b.sum(axis=1)]
array([[ 0.1       ,  0.2       ,  0.7       ],
       [ 1.27272727,  0.27272727, -0.54545455]])
```

The coordinates for the first point are all positive, meaning it is indeed inside the triangle.

Attributes

`transform`	Affine transform from `x` to the barycentric coordinates `c`.
`vertex_to_simplex`	Lookup array, from a vertex, to some simplex which it is a part of.
`convex_hull`	Vertices of facets forming the convex hull of the point set.
`vertex_neighbor_vertices`	Neighboring vertices of vertices.

`Delaunay.`**`transform`**

Affine transform from `x` to the barycentric coordinates `c`.

Type ndarray of double, shape (nsimplex, ndim+1, ndim)

This is defined by:

```
T c = x - r
```

At vertex `j`, `c_j = 1` and the other coordinates zero.

For simplex `i`, `transform[i,:ndim,:ndim]` contains inverse of the matrix `T`, and `transform[i,ndim,:]` contains the vector `r`.

`Delaunay.`**`vertex_to_simplex`**

Lookup array, from a vertex, to some simplex which it is a part of.

Type ndarray of int, shape (npoints,)

`Delaunay.`**`convex_hull`**

Vertices of facets forming the convex hull of the point set.

Type ndarray of int, shape (nfaces, ndim)

The array contains the indices of the points belonging to the (N-1)-dimensional facets that form the convex hull of the triangulation.

Note: Computing convex hulls via the Delaunay triangulation is inefficient and subject to increased numerical instability. Use `ConvexHull` instead.

`Delaunay.`**`vertex_neighbor_vertices`**

Neighboring vertices of vertices.

Tuple of two ndarrays of int: (indices, indptr). The indices of neighboring vertices of vertex *k* are `indptr[indices[k]:indices[k+1]]`.

points	(ndarray of double, shape (npoints, ndim)) Coordinates of input points.
simplices	(ndarray of ints, shape (nsimplex, ndim+1)) Indices of the points forming the simplices in the triangulation. For 2-D, the points are oriented counterclockwise.
neighbors	(ndarray of ints, shape (nsimplex, ndim+1)) Indices of neighbor simplices for each simplex. The kth neighbor is opposite to the kth vertex. For simplices at the boundary, -1 denotes no neighbor.
equations	(ndarray of double, shape (nsimplex, ndim+2)) [normal, offset] forming the hyperplane equation of the facet on the paraboloid (see Qhull documentation for more).
paraboloid_scale, paraboloid_shift	(float) Scale and shift for the extra paraboloid dimension (see Qhull documentation for more).
coplanar	(ndarray of int, shape (ncoplanar, 3)) Indices of coplanar points and the corresponding indices of the nearest facet and the nearest vertex. Coplanar points are input points which were *not* included in the triangulation due to numerical precision issues. If option “Qc” is not specified, this list is not computed. .. versionadded:: 0.12.0
vertices	Same as *simplices*, but deprecated.

Methods

`add_points`(points[, restart])	Process a set of additional new points.
`close`()	Finish incremental processing.
`find_simplex`(self, xi[, bruteforce, tol])	Find the simplices containing the given points.
`lift_points`(self, x)	Lift points to the Qhull paraboloid.
`plane_distance`(self, xi)	Compute hyperplane distances to the point *xi* from all simplices.

`Delaunay.`**`add_points`**(*points*, *restart=False*)

Process a set of additional new points.

Parameters **points** : ndarray

New points to add. The dimensionality should match that of the initial points.

restart : bool, optional

Whether to restart processing from scratch, rather than adding points incrementally.

Raises **QhullError**

Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

`close`

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after `close` has been called.

`Delaunay.`**`close`**()

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

`Delaunay.`**`find_simplex`**(*self*, *xi*, *bruteforce=False*, *tol=None*)

Find the simplices containing the given points.

Parameters **tri** : DelaunayInfo

Delaunay triangulation

xi : ndarray of double, shape (..., ndim)

Points to locate

bruteforce : bool, optional

Whether to only perform a brute-force search

tol : float, optional

Tolerance allowed in the inside-triangle check. Default is `100*eps`.

Returns **i** : ndarray of int, same shape as *xi*

Indices of simplices containing each point. Points outside the triangulation get the value -1.

Notes

This uses an algorithm adapted from Qhull's `qh_findbestfacet`, which makes use of the connection between a convex hull and a Delaunay triangulation. After finding the simplex closest to the point in N+1 dimensions, the algorithm falls back to directed search in N dimensions.

`Delaunay.`**`lift_points`**(*self*, *x*)

Lift points to the Qhull paraboloid.

`Delaunay.`**`plane_distance`**(*self*, *xi*)

Compute hyperplane distances to the point *xi* from all simplices.

class `scipy.spatial.`**`ConvexHull`**(*points*, *incremental=False*, *qhull_options=None*)

Convex hulls in N dimensions.

New in version 0.12.0.

Parameters **points** : ndarray of floats, shape (npoints, ndim)

Coordinates of points to construct a convex hull from

incremental : bool, optional

Allow adding new points incrementally. This takes up some additional resources.

qhull_options : str, optional

Additional options to pass to Qhull. See Qhull manual for details. (Default: "Qx" for ndim > 4 and "" otherwise) Option "Qt" is always enabled.

Raises **QhullError**

Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError

Raised if an incompatible array is given as input.

Notes

The convex hull is computed using the Qhull library.

Do not call the `add_points` method from a `__del__` destructor.

References

[Qhull]

Examples

Convex hull of a random set of points:

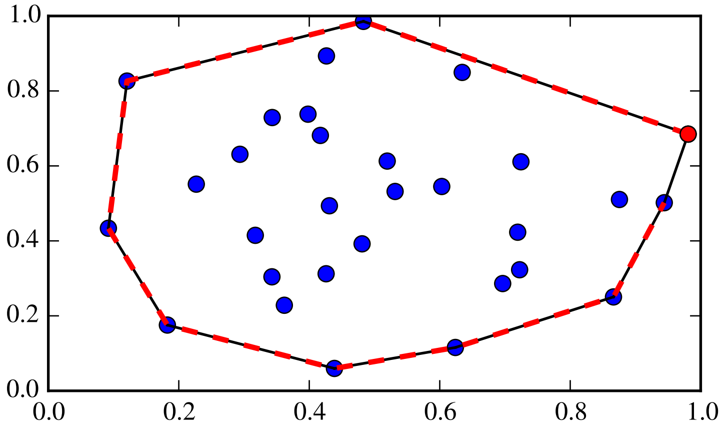
```
>>> from scipy.spatial import ConvexHull
>>> points = np.random.rand(30, 2)   # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

Plot it:

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
...     plt.plot(points[simplex, 0], points[simplex, 1], 'k-')
```

We could also have directly used the vertices of the hull, which for 2-D are guaranteed to be in counterclockwise order:

```
>>> plt.plot(points[hull.vertices,0], points[hull.vertices,1], 'r--', lw=2)
>>> plt.plot(points[hull.vertices[0],0], points[hull.vertices[0],1], 'ro')
>>> plt.show()
```



Attributes

points	(ndarray of double, shape (npoints, ndim)) Coordinates of input points.
vertices	(ndarray of ints, shape (nvertices,)) Indices of points forming the vertices of the convex hull. For 2-D convex hulls, the vertices are in counterclockwise order. For other dimensions, they are in input order.
simplices	(ndarray of ints, shape (nfacet, ndim)) Indices of points forming the simplical facets of the convex hull.
neighbors	(ndarray of ints, shape (nfacet, ndim)) Indices of neighbor facets for each facet. The kth neighbor is opposite to the kth vertex. -1 denotes no neighbor.
equations	(ndarray of double, shape (nfacet, ndim+1)) [normal, offset] forming the hyperplane equation of the facet (see Qhull documentation for more).
coplanar	(ndarray of int, shape (ncoplanar, 3)) Indices of coplanar points and the corresponding indices of the nearest facets and nearest vertex indices. Coplanar points are input points which were *not* included in the triangulation due to numerical precision issues. If option "Qc" is not specified, this list is not computed.

Methods

`add_points`(points[, restart])	Process a set of additional new points.
`close`()	Finish incremental processing.

`ConvexHull.`**`add_points`**(*points*, *restart=False*)

Process a set of additional new points.

Parameters	**points** : ndarray	
		New points to add. The dimensionality should match that of the initial points.
	restart : bool, optional	
		Whether to restart processing from scratch, rather than adding points incrementally.
Raises	**QhullError**	
		Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

`close`

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after `close` has been called.

`ConvexHull.`**`close`**()

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

class `scipy.spatial.`**`Voronoi`**(*points*, *furthest_site=False*, *incremental=False*, *qhull_options=None*)

Voronoi diagrams in N dimensions.

New in version 0.12.0.

Parameters	**points** : ndarray of floats, shape (npoints, ndim)	
		Coordinates of points to construct a convex hull from
	furthest_site : bool, optional	
		Whether to compute a furthest-site Voronoi diagram. Default: False
	incremental : bool, optional	
		Allow adding new points incrementally. This takes up some additional resources.
	qhull_options : str, optional	
		Additional options to pass to Qhull. See Qhull manual for details. (Default: “Qbb Qc Qz Qx” for ndim > 4 and “Qbb Qc Qz” otherwise. Incremental mode omits “Qz”.)
Raises	**QhullError**	
		Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.
	ValueError	
		Raised if an incompatible array is given as input.

Notes

The Voronoi diagram is computed using the Qhull library.

Do not call the `add_points` method from a `__del__` destructor.

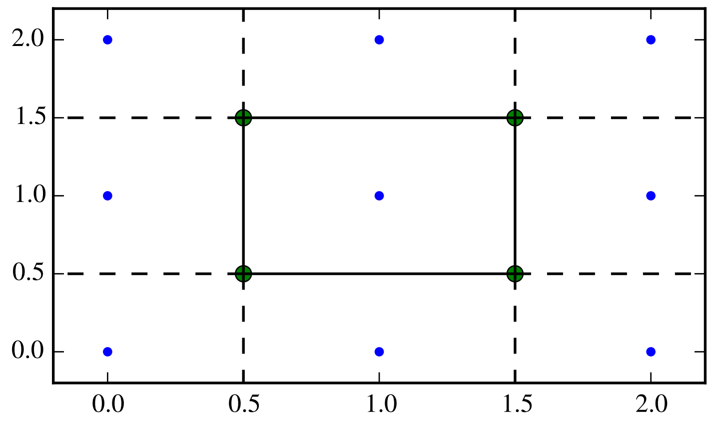
Examples

Voronoi diagram for a set of point:

```
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
...                    [2, 0], [2, 1], [2, 2]])
>>> from scipy.spatial import Voronoi, voronoi_plot_2d
>>> vor = Voronoi(points)
```

Plot it:

```
>>> import matplotlib.pyplot as plt
>>> voronoi_plot_2d(vor)
>>> plt.show()
```



The Voronoi vertices:

```
>>> vor.vertices
array([[ 0.5,  0.5],
       [ 1.5,  0.5],
       [ 0.5,  1.5],
       [ 1.5,  1.5]])
```

There is a single finite Voronoi region, and four finite Voronoi ridges:

```
>>> vor.regions
[[], [-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [3, 2, 0, 1], [2, -1, 0], [3, -
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1, 3], [-1, 2], [0, 2],
```

The ridges are perpendicular between lines drawn between the following input points:

```
>>> vor.ridge_points
array([[0, 1],
       [0, 3],
       [6, 3],
       [6, 7],
       [3, 4],
       [5, 8],
       [5, 2],
```

```
       [5, 4],
       [8, 7],
       [2, 1],
       [4, 1],
       [4, 7]], dtype=int32)
```

Attributes

points	(ndarray of double, shape (npoints, ndim)) Coordinates of input points.
vertices	(ndarray of double, shape (nvertices, ndim)) Coordinates of the Voronoi vertices.
ridge_points	(ndarray of ints, shape `(nridges, 2)`) Indices of the points between which each Voronoi ridge lies.
ridge_vertices	(list of list of ints, shape `(nridges, *)`) Indices of the Voronoi vertices forming each Voronoi ridge.
regions	(list of list of ints, shape `(nregions, *)`) Indices of the Voronoi vertices forming each Voronoi region. -1 indicates vertex outside the Voronoi diagram.
point_region	(list of ints, shape (npoints)) Index of the Voronoi region for each input point. If qhull option "Qc" was not specified, the list will contain -1 for points that are not associated with a Voronoi region.

Methods

`add_points`(points[, restart])	Process a set of additional new points.
`close`()	Finish incremental processing.

`Voronoi.`**`add_points`**`(`*points*, *restart=False*`)`

Process a set of additional new points.

Parameters **points** : ndarray

New points to add. The dimensionality should match that of the initial points.

restart : bool, optional

Whether to restart processing from scratch, rather than adding points incrementally.

Raises **QhullError**

Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

`close`

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after `close` has been called.

`Voronoi.`**`close`**`()`

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

5.31.3 Plotting Helpers

`delaunay_plot_2d`(tri[, ax])	Plot the given Delaunay triangulation in 2-D
`convex_hull_plot_2d`(hull[, ax])	Plot the given convex hull diagram in 2-D
`voronoi_plot_2d`(vor[, ax])	Plot the given Voronoi diagram in 2-D

`scipy.spatial.`**`delaunay_plot_2d`**(*tri*, *ax=None*)

Plot the given Delaunay triangulation in 2-D

Parameters **tri** : scipy.spatial.Delaunay instance

Triangulation to plot

ax : matplotlib.axes.Axes instance, optional

Axes to plot on

Returns **fig** : matplotlib.figure.Figure instance

Figure for the plot

See also:

`Delaunay`, `matplotlib.pyplot.triplot`

Notes

Requires Matplotlib.

`scipy.spatial.`**`convex_hull_plot_2d`**(*hull*, *ax=None*)

Plot the given convex hull diagram in 2-D

Parameters **hull** : scipy.spatial.ConvexHull instance

Convex hull to plot

ax : matplotlib.axes.Axes instance, optional

Axes to plot on

Returns **fig** : matplotlib.figure.Figure instance

Figure for the plot

See also:

`ConvexHull`

Notes

Requires Matplotlib.

`scipy.spatial.`**`voronoi_plot_2d`**(*vor*, *ax=None*)

Plot the given Voronoi diagram in 2-D

Parameters **vor** : scipy.spatial.Voronoi instance

Diagram to plot

ax : matplotlib.axes.Axes instance, optional

Axes to plot on

Returns **fig** : matplotlib.figure.Figure instance

Figure for the plot

See also:

`Voronoi`

Notes

Requires Matplotlib.

See also:

Tutorial

5.31.4 Simplex representation

The simplices (triangles, tetrahedra, ...) appearing in the Delaunay tesselation (N-dim simplices), convex hull facets, and Voronoi ridges (N-1 dim simplices) are represented in the following scheme:

```
tess = Delaunay(points)
hull = ConvexHull(points)
voro = Voronoi(points)

# coordinates of the j-th vertex of the i-th simplex
tess.points[tess.simplices[i, j], :]        # tesselation element
hull.points[hull.simplices[i, j], :]        # convex hull facet
voro.vertices[voro.ridge_vertices[i, j], :] # ridge between Voronoi cells
```

For Delaunay triangulations and convex hulls, the neighborhood structure of the simplices satisfies the condition:

> `tess.neighbors[i,j]` is the neighboring simplex of the i-th simplex, opposite to the j-vertex. It is -1 in case of no neighbor.

Convex hull facets also define a hyperplane equation:

```
(hull.equations[i,:-1] * coord).sum() + hull.equations[i,-1] == 0
```

Similar hyperplane equations for the Delaunay triangulation correspond to the convex hull facets on the corresponding N+1 dimensional paraboloid.

The Delaunay triangulation objects offer a method for locating the simplex containing a given point, and barycentric coordinate computations.

Functions

`tsearch`(tri, xi)	Find simplices containing the given points.
`distance_matrix`(x, y[, p, threshold])	Compute the distance matrix.
`minkowski_distance`(x, y[, p])	Compute the L**p distance between two arrays.
`minkowski_distance_p`(x, y[, p])	Compute the p-th power of the L**p distance between two arrays.
`procrustes`(data1, data2)	Procrustes analysis, a similarity test for two data sets.

`scipy.spatial.`**`tsearch`**(*tri*, *xi*)

Find simplices containing the given points. This function does the same thing as `Delaunay.find_simplex`.

New in version 0.9.

See also:

`Delaunay.find_simplex`

`scipy.spatial.`**`distance_matrix`**(*x*, *y*, *p=2*, *threshold=1000000*)

Compute the distance matrix.

Returns the matrix of all pair-wise distances.

Parameters

x : (M, K) array_like

TODO: description needed

y : (N, K) array_like

TODO: description needed

p : float, 1 <= p <= infinity

Which Minkowski p-norm to use.

threshold : positive int
If `M * N * K` > *threshold*, algorithm uses a Python loop instead of large temporary arrays.

Returns **result** : (M, N) ndarray
Distance matrix.

Examples

```
>>> distance_matrix([[0,0],[0,1]], [[1,0],[1,1]])
array([[ 1.        ,  1.41421356],
       [ 1.41421356,  1.        ]])
```

`scipy.spatial.`**`minkowski_distance`**(*x*, *y*, *p=2*)

Compute the L**p distance between two arrays.

Parameters **x** : (M, K) array_like
Input array.
y : (N, K) array_like
Input array.
p : float, 1 <= p <= infinity
Which Minkowski p-norm to use.

Examples

```
>>> minkowski_distance([[0,0],[0,0]], [[1,1],[0,1]])
array([ 1.41421356,  1.        ])
```

`scipy.spatial.`**`minkowski_distance_p`**(*x*, *y*, *p=2*)

Compute the p-th power of the L**p distance between two arrays.

For efficiency, this function computes the L**p distance but does not extract the pth root. If *p* is 1 or infinity, this is equal to the actual L**p distance.

Parameters **x** : (M, K) array_like
Input array.
y : (N, K) array_like
Input array.
p : float, 1 <= p <= infinity
Which Minkowski p-norm to use.

Examples

```
>>> minkowski_distance_p([[0,0],[0,0]], [[1,1],[0,1]])
array([2, 1])
```

`scipy.spatial.`**`procrustes`**(*data1*, *data2*)

Procrustes analysis, a similarity test for two data sets.

Each input matrix is a set of points or vectors (the rows of the matrix). The dimension of the space is the number of columns of each matrix. Given two identically sized matrices, procrustes standardizes both such that:

- $tr(AA^T) = 1$.
- Both sets of points are centered around the origin.

Procrustes ([R273], [R274]) then applies the optimal transform to the second matrix (including scaling/dilation, rotations, and reflections) to minimize $M^2 = \sum(data1 - data2)^2$, or the sum of the squares of the pointwise differences between the two input datasets.

This function was not designed to handle datasets with different numbers of datapoints (rows). If two data sets have different dimensionality (different number of columns), simply add columns of zeros the smaller of the two.

Parameters **data1** : array_like

Matrix, n rows represent points in k (columns) space *data1* is the reference data, after it is standardised, the data from *data2* will be transformed to fit the pattern in *data1* (must have >1 unique points).

data2 : array_like

n rows of data in k space to be fit to *data1*. Must be the same shape `(numrows, numcols)` as data1 (must have >1 unique points).

Returns **mtx1** : array_like

A standardized version of *data1*.

mtx2 : array_like

The orientation of *data2* that best fits *data1*. Centered, but not necessarily $tr(AA^T) = 1$.

disparity : float

M^2 as defined above.

Raises **ValueError**

If the input arrays are not two-dimensional. If the shape of the input arrays is different. If the input arrays have zero columns or zero rows.

See also:

`scipy.linalg.orthogonal_procrustes`

Notes

- The disparity should not depend on the order of the input matrices, but the output matrices will, as only the first output matrix is guaranteed to be scaled such that $tr(AA^T) = 1$.
- Duplicate data points are generally ok, duplicating a data point will increase its effect on the procrustes fit.
- The disparity scales as the number of points per input matrix.

References

[R273], [R274]

Examples

```
>>> from scipy.spatial import procrustes
```

The matrix `b` is a rotated, shifted, scaled and mirrored version of `a` here:

```
>>> a = np.array([[1, 3], [1, 2], [1, 1], [2, 1]], 'd')
>>> b = np.array([[4, -2], [4, -4], [4, -6], [2, -6]], 'd')
>>> mtx1, mtx2, disparity = procrustes(a, b)
>>> round(disparity)
0.0
```

5.32 Distance computations (`scipy.spatial.distance`)

5.32.1 Function Reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

`pdist`(X[, metric, p, w, V, VI])	Pairwise distances between observations in n-dimensional space.
`cdist`(XA, XB[, metric, p, V, VI, w])	Computes distance between each pair of the two collections of inputs.
`squareform`(X[, force, checks])	Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.

`scipy.spatial.distance.`**`pdist`**(*X*, *metric='euclidean'*, *p=2*, *w=None*, *V=None*, *VI=None*)

Pairwise distances between observations in n-dimensional space.

The following are common calling conventions.

1. `Y = pdist(X, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.
2. `Y = pdist(X, 'minkowski', p)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.
3. `Y = pdist(X, 'cityblock')`

   Computes the city block or Manhattan distance between the points.
4. `Y = pdist(X, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.
5. `Y = pdist(X, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.
6. `Y = pdist(X, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of `u` and `v`.
7. `Y = pdist(X, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.
8. `Y = pdist(X, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.
9. `Y = pdist(X, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree where at least one of them is non-zero.
10. `Y = pdist(X, 'chebyshev')`

    Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

    $$d(u, v) = \max_i |u_i - v_i|$$

11. `Y = pdist(X, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u,v)=\sum_i \frac{|u_i-v_i|}{|u_i|+|v_i|}$$

12. `Y = pdist(X, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u,v)=\frac{\sum_i u_i-v_i}{\sum_i u_i+v_i}$$

13. `Y = pdist(X, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $(u-v)(1/V)(u-v)^T$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

14. `Y = pdist(X, 'yule')`

    Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

15. `Y = pdist(X, 'matching')`

    Computes the matching distance between each pair of boolean vectors. (see matching function documentation)

16. `Y = pdist(X, 'dice')`

    Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

17. `Y = pdist(X, 'kulsinski')`

    Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

18. `Y = pdist(X, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

19. `Y = pdist(X, 'russellrao')`

    Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

20. `Y = pdist(X, 'sokalmichener')`

    Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

21. `Y = pdist(X, 'sokalsneath')`

    Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)

22. `Y = pdist(X, 'wminkowski')`

    Computes the weighted Minkowski distance between each pair of vectors. (see wminkowski function documentation)

23. `Y = pdist(X, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

    ```
    dm = pdist(X, lambda u, v: np.sqrt(((u-v)**2).sum()))
    ```

    Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

    ```
    dm = pdist(X, sokalsneath)
    ```

    would calculate the pair-wise distances between the vectors in X using the Python function sokalsneath. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax.:

    ```
    dm = pdist(X, 'sokalsneath')
    ```

Parameters

X : ndarray
: An m by n array of m original observations in an n-dimensional space.

metric : str or function, optional
: The distance metric to use. The distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'yule'.

w : ndarray, optional
: The weight vector (for weighted Minkowski).

p : double, optional
: The p-norm to apply (for Minkowski, weighted and unweighted)

V : ndarray, optional
: The variance vector (for standardized Euclidean).

VI : ndarray, optional
: The inverse of the covariance matrix (for Mahalanobis).

Returns

Y : ndarray
: Returns a condensed distance matrix Y. For each i and j (where $i < j < n$), the metric `dist(u=X[i], v=X[j])` is computed and stored in entry `ij`.

See also:

`squareform` converts between condensed distance matrices and square distance matrices.

Notes

See `squareform` for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

`scipy.spatial.distance.`**`cdist`**(*XA*, *XB*, *metric='euclidean'*, *p=2*, *V=None*, *VI=None*, *w=None*)

Computes distance between each pair of the two collections of inputs.

The following are common calling conventions:

1. `Y = cdist(XA, XB, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.
2. `Y = cdist(XA, XB, 'minkowski', p)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.
3. `Y = cdist(XA, XB, 'cityblock')`

   Computes the city block or Manhattan distance between the points.
4. `Y = cdist(XA, XB, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}.$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.
5. `Y = cdist(XA, XB, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.
6. `Y = cdist(XA, XB, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of u and v.
7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.
8. `Y = cdist(XA, XB, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.
9. `Y = cdist(XA, XB, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree where at least one of them is non-zero.
10. `Y = cdist(XA, XB, 'chebyshev')`

    Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

    $$d(u, v) = \max_i |u_i - v_i|.$$
11. `Y = cdist(XA, XB, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

12. `Y = cdist(XA, XB, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u,v) = \frac{\sum_i (u_i - v_i)}{\sum_i (u_i + v_i)}$$

13. `Y = cdist(XA, XB, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $(u-v)(1/V)(u-v)^T$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

14. `Y = cdist(XA, XB, 'yule')`

    Computes the Yule distance between the boolean vectors. (see `yule` function documentation)

15. `Y = cdist(XA, XB, 'matching')`

    Computes the matching distance between the boolean vectors. (see `matching` function documentation)

16. `Y = cdist(XA, XB, 'dice')`

    Computes the Dice distance between the boolean vectors. (see `dice` function documentation)

17. `Y = cdist(XA, XB, 'kulsinski')`

    Computes the Kulsinski distance between the boolean vectors. (see `kulsinski` function documentation)

18. `Y = cdist(XA, XB, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between the boolean vectors. (see `rogerstanimoto` function documentation)

19. `Y = cdist(XA, XB, 'russellrao')`

    Computes the Russell-Rao distance between the boolean vectors. (see `russellrao` function documentation)

20. `Y = cdist(XA, XB, 'sokalmichener')`

    Computes the Sokal-Michener distance between the boolean vectors. (see `sokalmichener` function documentation)

21. `Y = cdist(XA, XB, 'sokalsneath')`

    Computes the Sokal-Sneath distance between the vectors. (see `sokalsneath` function documentation)

22. `Y = cdist(XA, XB, 'wminkowski')`

    Computes the weighted Minkowski distance between the vectors. (see `wminkowski` function documentation)

23. `Y = cdist(XA, XB, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

```
dm = cdist(XA, XB, lambda u, v: np.sqrt(((u-v)**2).sum()))
```

Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

```
dm = cdist(XA, XB, sokalsneath)
```

would calculate the pair-wise distances between the vectors in X using the Python function `sokalsneath`. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax:

```
dm = cdist(XA, XB, 'sokalsneath')
```

Parameters

XA : ndarray

An m_A by n array of m_A original observations in an n-dimensional space. Inputs are converted to float type.

XB : ndarray

An m_B by n array of m_B original observations in an n-dimensional space. Inputs are converted to float type.

metric : str or callable, optional

The distance metric to use. If a string, the distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'wminkowski', 'yule'.

w : ndarray, optional

The weight vector (for weighted Minkowski).

p : scalar, optional

The p-norm to apply (for Minkowski, weighted and unweighted)

V : ndarray, optional

The variance vector (for standardized Euclidean).

VI : ndarray, optional

The inverse of the covariance matrix (for Mahalanobis).

Returns

Y : ndarray

A m_A by m_B distance matrix is returned. For each i and j, the metric `dist(u=XA[i], v=XB[j])` is computed and stored in the ij th entry.

Raises

ValueError

An exception is thrown if *XA* and *XB* do not have the same number of columns.

Examples

Find the Euclidean distances between four 2-D coordinates:

```
>>> from scipy.spatial import distance
>>> coords = [(35.0456, -85.2672),
...           (35.1174, -89.9711),
...           (35.9728, -83.9422),
...           (36.1667, -86.7833)]
>>> distance.cdist(coords, coords, 'euclidean')
array([[ 0.    ,  4.7044,  1.6172,  1.8856],
       [ 4.7044,  0.    ,  6.0893,  3.3561],
       [ 1.6172,  6.0893,  0.    ,  2.8477],
       [ 1.8856,  3.3561,  2.8477,  0.    ]])
```

Find the Manhattan distance from a 3-D point to the corners of the unit cube:

```
>>> a = np.array([[0, 0, 0],
                  [0, 0, 1],
                  [0, 1, 0],
                  [0, 1, 1],
                  [1, 0, 0],
                  [1, 0, 1],
                  [1, 1, 0],
                  [1, 1, 1]])
>>> b = np.array([[ 0.1,  0.2,  0.4]])
>>> distance.cdist(a, b, 'cityblock')
array([[ 0.7],
       [ 0.9],
       [ 1.3],
       [ 1.5],
       [ 1.5],
       [ 1.7],
       [ 2.1],
       [ 2.3]])
```

`scipy.spatial.distance.`**`squareform`**`(`*X*, *force='no'*, *checks=True*`)`

Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.

Parameters **X** : ndarray

Either a condensed or redundant distance matrix.

force : str, optional

As with MATLAB(TM), if force is equal to 'tovector' or 'tomatrix', the input will be treated as a distance matrix or distance vector respectively.

checks : bool, optional

If *checks* is set to False, no checks will be made for matrix symmetry nor zero diagonals. This is useful if it is known that `X - X.T1` is small and `diag(X)` is close to zero. These values are ignored any way so they do not disrupt the squareform transformation.

Returns **Y** : ndarray

If a condensed distance matrix is passed, a redundant one is returned, or if a redundant one is passed, a condensed distance matrix is returned.

Notes

1.v = squareform(X)

Given a square d-by-d symmetric distance matrix X, `v=squareform(X)` returns a `d * (d-1) / 2` (or *${n choose 2}$*) sized vector v.

v[{n choose 2}-{n-i choose 2} + (j-i-1)] is the distance between points i and j. If X is non-square or asymmetric, an error is returned.

2.X = squareform(v)

Given a d*d(-1)/2 sized v for some integer d>=2 encoding distances as described, X=squareform(v) returns a d by d distance matrix X. The X[i, j] and X[j, i] values are set to v[{n choose 2}-{n-i choose 2} + (j-u-1)] and all diagonal elements are zero.

Predicates for checking the validity of distance matrices, both condensed and redundant. Also contained in this module are functions for computing the number of observations in a distance matrix.

`is_valid_dm`(D[, tol, throw, name, warning])	Returns True if input array is a valid distance matrix.

Continue

Table 5.208 – continued from previous page

is_valid_y(y[, warning, throw, name])	Returns True if the input array is a valid condensed distance matrix.
num_obs_dm(d)	Returns the number of original observations that correspond to a square, redundant
num_obs_y(Y)	Returns the number of original observations that correspond to a condensed distan

scipy.spatial.distance.**is_valid_dm**(*D*, *tol=0.0*, *throw=False*, *name='D'*, *warning=False*)

Returns True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays containing doubles. They must have a zero-diagonal, and they must be symmetric.

Parameters

D : ndarray

The candidate object to test for validity.

tol : float, optional

The distance matrix should be symmetric. *tol* is the maximum difference between entries `ij` and `ji` for the distance metric to be considered symmetric.

throw : bool, optional

An exception is thrown if the distance matrix passed is not valid.

name : str, optional

The name of the variable to checked. This is useful if throw is set to True so the offending variable can be identified in the exception message when an exception is thrown.

warning : bool, optional

Instead of throwing an exception, a warning message is raised.

Returns

valid : bool

True if the variable *D* passed is a valid distance matrix.

Notes

Small numerical differences in *D* and *D.T* and non-zeroness of the diagonal are ignored if they are within the tolerance specified by *tol*.

scipy.spatial.distance.**is_valid_y**(*y*, *warning=False*, *throw=False*, *name=None*)

Returns True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays containing doubles. Their length must be a binomial coefficient $\binom{n}{2}$ for some positive integer n.

Parameters

y : ndarray

The condensed distance matrix.

warning : bool, optional

Invokes a warning if the variable passed is not a valid condensed distance matrix. The warning message explains why the distance matrix is not valid. *name* is used when referencing the offending variable.

throw : bool, optional

Throws an exception if the variable passed is not a valid condensed distance matrix.

name : bool, optional

Used when referencing the offending variable in the warning or exception message.

scipy.spatial.distance.**num_obs_dm**(*d*)

Returns the number of original observations that correspond to a square, redundant distance matrix.

Parameters

d : ndarray

The target distance matrix.

Returns

num_obs_dm : int

The number of observations in the redundant distance matrix.

`scipy.spatial.distance.`**`num_obs_y`**`(`*Y*`)`

Returns the number of original observations that correspond to a condensed distance matrix.

Parameters **Y** : ndarray

Condensed distance matrix.

Returns **n** : int

The number of observations in the condensed distance matrix *Y*.

Distance functions between two vectors `u` and `v`. Computing distances over a large collection of vectors is inefficient for these functions. Use `pdist` for this purpose.

`braycurtis`(u, v)	Computes the Bray-Curtis distance between two 1-D arrays.
`canberra`(u, v)	Computes the Canberra distance between two 1-D arrays.
`chebyshev`(u, v)	Computes the Chebyshev distance.
`cityblock`(u, v)	Computes the City Block (Manhattan) distance.
`correlation`(u, v)	Computes the correlation distance between two 1-D arrays.
`cosine`(u, v)	Computes the Cosine distance between 1-D arrays.
`dice`(u, v)	Computes the Dice dissimilarity between two boolean 1-D arrays.
`euclidean`(u, v)	Computes the Euclidean distance between two 1-D arrays.
`hamming`(u, v)	Computes the Hamming distance between two 1-D arrays.
`jaccard`(u, v)	Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
`kulsinski`(u, v)	Computes the Kulsinski dissimilarity between two boolean 1-D arrays.
`mahalanobis`(u, v, VI)	Computes the Mahalanobis distance between two 1-D arrays.
`matching`(u, v)	Computes the Matching dissimilarity between two boolean 1-D arrays.
`minkowski`(u, v, p)	Computes the Minkowski distance between two 1-D arrays.
`rogerstanimoto`(u, v)	Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
`russellrao`(u, v)	Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.
`seuclidean`(u, v, V)	Returns the standardized Euclidean distance between two 1-D arrays.
`sokalmichener`(u, v)	Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.
`sokalsneath`(u, v)	Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.
`sqeuclidean`(u, v)	Computes the squared Euclidean distance between two 1-D arrays.
`wminkowski`(u, v, p, w)	Computes the weighted Minkowski distance between two 1-D arrays.
`yule`(u, v)	Computes the Yule dissimilarity between two boolean 1-D arrays.

`scipy.spatial.distance.`**`braycurtis`**`(`*u*, *v*`)`

Computes the Bray-Curtis distance between two 1-D arrays.

Bray-Curtis distance is defined as

$$\sum |u_i - v_i| / \sum |u_i + v_i|$$

The Bray-Curtis distance is in the range [0, 1] if all coordinates are positive, and is undefined if the inputs are of length zero.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **braycurtis** : double

The Bray-Curtis distance between 1-D arrays *u* and *v*.

`scipy.spatial.distance.`**`canberra`**`(`*u*, *v*`)`

Computes the Canberra distance between two 1-D arrays.

The Canberra distance is defined as

$$d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

Parameters **u** : (N,) array_like
Input array.
v : (N,) array_like
Input array.

Returns **canberra** : double
The Canberra distance between vectors *u* and *v*.

Notes

When *u[i]* and *v[i]* are 0 for given i, then the fraction 0/0 = 0 is used in the calculation.

`scipy.spatial.distance.`**`chebyshev`**(*u*, *v*)

Computes the Chebyshev distance.

Computes the Chebyshev distance between two 1-D arrays *u* and *v*, which is defined as

$$\max_i |u_i - v_i|.$$

Parameters **u** : (N,) array_like
Input vector.
v : (N,) array_like
Input vector.

Returns **chebyshev** : double
The Chebyshev distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`cityblock`**(*u*, *v*)

Computes the City Block (Manhattan) distance.

Computes the Manhattan distance between two 1-D arrays *u* and *v*, which is defined as

$$\sum_i |u_i - v_i|.$$

Parameters **u** : (N,) array_like
Input array.
v : (N,) array_like
Input array.

Returns **cityblock** : double
The City Block (Manhattan) distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`correlation`**(*u*, *v*)

Computes the correlation distance between two 1-D arrays.

The correlation distance between *u* and *v*, is defined as

$$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{{||(u - \bar{u})||}_2 {||(v - \bar{v})||}_2}$$

where $\bar{u}$ is the mean of the elements of *u* and $x \cdot y$ is the dot product of x and y.

Parameters **u** : (N,) array_like
Input array.
v : (N,) array_like
Input array.

Returns **correlation** : double
The correlation distance between 1-D array *u* and *v*.

`scipy.spatial.distance.`**`cosine`**(*u*, *v*)

Computes the Cosine distance between 1-D arrays.

The Cosine distance between *u* and *v*, is defined as

$$1 - \frac{u \cdot v}{||u||_2 ||v||_2}.$$

where $u \cdot v$ is the dot product of u and v.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **cosine** : double

The Cosine distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`dice`**(*u*, *v*)

Computes the Dice dissimilarity between two boolean 1-D arrays.

The Dice dissimilarity between *u* and *v*, is

$$\frac{c_{TF} + c_{FT}}{2c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) ndarray, bool

Input 1-D array.

v : (N,) ndarray, bool

Input 1-D array.

Returns **dice** : double

The Dice dissimilarity between 1-D arrays *u* and *v*.

`scipy.spatial.distance.`**`euclidean`**(*u*, *v*)

Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays *u* and *v*, is defined as

$$||u - v||_2$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **euclidean** : double

The Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`hamming`**(*u*, *v*)

Computes the Hamming distance between two 1-D arrays.

The Hamming distance between 1-D arrays *u* and *v*, is simply the proportion of disagreeing components in *u* and *v*. If *u* and *v* are boolean vectors, the Hamming distance is

$$\frac{c_{01} + c_{10}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **hamming** : double

The Hamming distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`jaccard`**(*u*, *v*)

Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.

The Jaccard-Needham dissimilarity between 1-D boolean arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT}}{c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **jaccard** : double

The Jaccard distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`kulsinski`**(*u*, *v*)

Computes the Kulsinski dissimilarity between two boolean 1-D arrays.

The Kulsinski dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT} - c_{TT} + n}{c_{FT} + c_{TF} + n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **kulsinski** : double

The Kulsinski distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`mahalanobis`**(*u*, *v*, *VI*)

Computes the Mahalanobis distance between two 1-D arrays.

The Mahalanobis distance between 1-D arrays *u* and *v*, is defined as

$$\sqrt{(u-v)V^{-1}(u-v)^T}$$

where `V` is the covariance matrix. Note that the argument *VI* is the inverse of `V`.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

VI : ndarray

The inverse of the covariance matrix.

Returns **mahalanobis** : double

The Mahalanobis distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`matching`**(*u*, *v*)

Computes the Matching dissimilarity between two boolean 1-D arrays.

The Matching dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool
Input array.
v : (N,) array_like, bool
Input array.

Returns **matching** : double
The Matching dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`minkowski`**(*u*, *v*, *p*)

Computes the Minkowski distance between two 1-D arrays.

The Minkowski distance between 1-D arrays *u* and *v*, is defined as

$$||u - v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$

Parameters **u** : (N,) array_like
Input array.
v : (N,) array_like
Input array.
p : int
The order of the norm of the difference $||u - v||_p$.

Returns **d** : double
The Minkowski distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`rogerstanimoto`**(*u*, *v*)

Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.

The Rogers-Tanimoto dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{c_{TT} + c_{FF} + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters **u** : (N,) array_like, bool
Input array.
v : (N,) array_like, bool
Input array.

Returns **rogerstanimoto** : double
The Rogers-Tanimoto dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`russellrao`**(*u*, *v*)

Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.

The Russell-Rao dissimilarity between two boolean 1-D arrays, *u* and *v*, is defined as

$$\frac{n - c_{TT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$.

Parameters **u** : (N,) array_like, bool
Input array.
v : (N,) array_like, bool
Input array.

Returns **russellrao** : double
The Russell-Rao dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`seuclidean`**(*u*, *v*, *V*)

Returns the standardized Euclidean distance between two 1-D arrays.

The standardized Euclidean distance between *u* and *v*.

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

V : (N,) array_like

V is an 1-D array of component variances. It is usually computed among a larger collection vectors.

Returns **seuclidean** : double

The standardized Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`sokalmichener`**`(`*u*, *v*`)`

Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.

The Sokal-Michener dissimilarity between boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{S+R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$, $R = 2 * (c_{TF} + c_{FT})$ and $S = c_{FF} + c_{TT}$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **sokalmichener** : double

The Sokal-Michener dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`sokalsneath`**`(`*u*, *v*`)`

Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.

The Sokal-Sneath dissimilarity between *u* and *v*,

$$\frac{R}{c_{TT}+R}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **sokalsneath** : double

The Sokal-Sneath dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`sqeuclidean`**`(`*u*, *v*`)`

Computes the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between *u* and *v* is defined as

$$||u - v||_2^2.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

Returns **sqeuclidean** : double

The squared Euclidean distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`wminkowski`**`(`*u*, *v*, *p*, *w*`)`

Computes the weighted Minkowski distance between two 1-D arrays.

The weighted Minkowski distance between *u* and *v*, defined as

$$\left(\sum(w_i|u_i - v_i|^p)\right)^{1/p}.$$

Parameters **u** : (N,) array_like

Input array.

v : (N,) array_like

Input array.

p : int

The order of the norm of the difference $||u - v||_p$.

w : (N,) array_like

The weight vector.

Returns **wminkowski** : double

The weighted Minkowski distance between vectors *u* and *v*.

`scipy.spatial.distance.`**`yule`**`(`*u*, *v*`)`

Computes the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

$$\frac{R}{c_{TT} * c_{FF} + \frac{R}{2}}$$

where c_{ij} is the number of occurrences of $\mathtt{u[k]} = i$ and $\mathtt{v[k]} = j$ for $k < n$ and $R = 2.0 * c_{TF} * c_{FT}$.

Parameters **u** : (N,) array_like, bool

Input array.

v : (N,) array_like, bool

Input array.

Returns **yule** : double

The Yule dissimilarity between vectors *u* and *v*.

5.33 Special functions (`scipy.special`)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules. Exceptions are noted.

5.33.1 Error handling

Errors are handled by returning nans, or other appropriate values. Some of the special function routines will emit warnings when an error occurs. By default this is disabled. To enable such messages use `errprint(1)`, and to disable such messages use `errprint(0)`.

Example:

```
>>> print scipy.special.bdtr(-1,10,0.3)
>>> scipy.special.errprint(1)
>>> print scipy.special.bdtr(-1,10,0.3)
```

`errprint`([inflag])	Sets or returns the error printing flag for special functions.
`SpecialFunctionWarning`	Warning that can be issued with `errprint(True)`

`scipy.special.`**`errprint`**`(`*inflag=None*`)`

Sets or returns the error printing flag for special functions.

Parameters **inflag** : bool, optional

Whether warnings concerning evaluation of special functions in scipy.special are shown. If omitted, no change is made to the current setting.

Returns old_flag

Previous value of the error flag

exception `scipy.special.`**`SpecialFunctionWarning`**

Warning that can be issued with `errprint(True)`

5.33.2 Available functions

Airy functions

`airy`(z)	Airy functions and their derivatives.
`airye`(z)	Exponentially scaled Airy functions and their derivatives.
`ai_zeros`(nt)	Compute the zeros of Airy Functions Ai(x) and Ai’(x), a and a’ respectively, and the associated values of Ai(a’) and
`bi_zeros`(nt)	Compute the zeros of Airy Functions Bi(x) and Bi’(x), b and b’ respectively, and the associated values of Ai(b’) and
`itairy`(x)	Integrals of Airy functios

`scipy.special.`**`airy`**`(z)` **= <ufunc ‘airy’>**

Airy functions and their derivatives.

Parameters **z** : float or complex

Argument.

Returns Ai, Aip, Bi, Bip

Airy functions Ai and Bi, and their derivatives Aip and Bip

Notes

The Airy functions Ai and Bi are two independent solutions of y’‘(x) = x y.

`scipy.special.`**`airye`**`(z)` **= <ufunc ‘airye’>**

Exponentially scaled Airy functions and their derivatives.

Scaling:

```
eAi  = Ai  * exp(2.0/3.0*z*sqrt(z))
eAip = Aip * exp(2.0/3.0*z*sqrt(z))
eBi  = Bi  * exp(-abs((2.0/3.0*z*sqrt(z)).real))
eBip = Bip * exp(-abs((2.0/3.0*z*sqrt(z)).real))
```

Parameters **z** : float or complex

Argument.

Returns eAi, eAip, eBi, eBip

Airy functions Ai and Bi, and their derivatives Aip and Bip

`scipy.special.`**`ai_zeros`**`(nt)`

Compute the zeros of Airy Functions Ai(x) and Ai’(x), a and a’ respectively, and the associated values of Ai(a’) and Ai’(a).

Returns a[l-1] – the lth zero of Ai(x)
ap[l-1] – the lth zero of Ai’(x)
ai[l-1] – Ai(ap[l-1])
aip[l-1] – Ai’(a[l-1])

`scipy.special.`**`bi_zeros`**`(nt)`

Compute the zeros of Airy Functions Bi(x) and Bi’(x), b and b’ respectively, and the associated values of Ai(b’) and Ai’(b).

Returns	b[l-1] – the lth zero of Bi(x) bp[l-1] – the lth zero of Bi’(x) bi[l-1] – Bi(bp[l-1]) bip[l-1] – Bi’(b[l-1])

`scipy.special.`**`itairy`**`(`*x*`)` **= <ufunc ‘itairy’>**

Integrals of Airy functios

Calculates the integral of Airy functions from 0 to x

Returns Apt, Bpt

Integrals for positive arguments

Ant, Bnt

Integrals for negative arguments

Elliptic Functions and Integrals

`ellipj`(u, m)	Jacobian elliptic functions
`ellipk`(m)	Complete elliptic integral of the first kind
`ellipkm1`(p)	Complete elliptic integral of the first kind around m = 1
`ellipkinc`(phi, m)	Incomplete elliptic integral of the first kind
`ellipe`(m)	Complete elliptic integral of the second kind
`ellipeinc`(phi, m)	Incomplete elliptic integral of the second kind

`scipy.special.`**`ellipj`**`(`*u*, *m*`)` **= <ufunc ‘ellipj’>**

Jacobian elliptic functions

Calculates the Jacobian elliptic functions of parameter m between 0 and 1, and real u.

Parameters **m, u**

Parameters

Returns sn, cn, dn, ph

The returned functions:

`sn(u|m), cn(u|m), dn(u|m)`

The value `ph` is such that if `u = ellik(ph, m)`, then `sn(u|m) = sin(ph)` and `cn(u|m) = cos(ph)`.

`scipy.special.`**`ellipk`**`(`*m*`)`

Complete elliptic integral of the first kind

This function is defined as

$$K(m) = \int_0^{\pi/2} [1 - m\sin(t)^2]^{-1/2} dt$$

Parameters **m** : array_like

The parameter of the elliptic integral.

Returns **K** : array_like

Value of the elliptic integral.

See also:

`ellipkm1`	Complete elliptic integral of the first kind around m = 1
`ellipkinc`	Incomplete elliptic integral of the first kind
`ellipe`	Complete elliptic integral of the second kind
`ellipeinc`	Incomplete elliptic integral of the second kind

Notes

For more precision around point m = 1, use `ellipkm1`.

`scipy.special.`**`ellipkm1`**(*p*) **= <ufunc 'ellipkm1'>**

Complete elliptic integral of the first kind around m = 1

This function is defined as

$$K(p) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{-1/2} dt$$

where *m = 1 - p*.

Parameters	**p** : array_like	Defines the parameter of the elliptic integral as m = 1 - p.
Returns	**K** : ndarray	Value of the elliptic integral.

See also:

`ellipk`	Complete elliptic integral of the first kind
`ellipkinc`	Incomplete elliptic integral of the first kind
`ellipe`	Complete elliptic integral of the second kind
`ellipeinc`	Incomplete elliptic integral of the second kind

`scipy.special.`**`ellipkinc`**(*phi*, *m*) **= <ufunc 'ellipkinc'>**

Incomplete elliptic integral of the first kind

This function is defined as

$$K(\phi, m) = \int_0^{\phi} [1 - m \sin(t)^2]^{-1/2} dt$$

Parameters	**phi** : array_like	amplitude of the elliptic integral
	m : array_like	parameter of the elliptic integral
Returns	**K** : ndarray	Value of the elliptic integral

See also:

`ellipkm1`	Complete elliptic integral of the first kind, near m = 1
`ellipk`	Complete elliptic integral of the first kind
`ellipe`	Complete elliptic integral of the second kind
`ellipeinc`	Incomplete elliptic integral of the second kind

Notes

This function is also called `F(phi, m)`.

`scipy.special.`**`ellipe`**(*m*) **= <ufunc 'ellipe'>**

Complete elliptic integral of the second kind

This function is defined as

$$E(m) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{1/2} dt$$

Parameters	**m** : array_like	Defines the parameter of the elliptic integral.
Returns	**E** : ndarray	Value of the elliptic integral.

See also:

`ellipkm1`	Complete elliptic integral of the first kind, near m = 1
`ellipk`	Complete elliptic integral of the first kind
`ellipkinc`	Incomplete elliptic integral of the first kind
`ellipeinc`	Incomplete elliptic integral of the second kind

`scipy.special.`**`ellipeinc`**(*phi*, *m*) **= <ufunc 'ellipeinc'>**

Incomplete elliptic integral of the second kind

This function is defined as

$$E(\phi, m) = \int_0^{\phi} [1 - m \sin(t)^2]^{1/2} dt$$

Parameters **phi** : array_like

amplitude of the elliptic integral.

m : array_like

parameter of the elliptic integral.

Returns **E** : ndarray

Value of the elliptic integral.

See also:

`ellipkm1`	Complete elliptic integral of the first kind, near m = 1
`ellipk`	Complete elliptic integral of the first kind
`ellipkinc`	Incomplete elliptic integral of the first kind
`ellipe`	Complete elliptic integral of the second kind

Bessel Functions

`jv`(v, z)	Bessel function of the first kind of real order v
`jve`(v, z)	Exponentially scaled Bessel function of order v
`yn`(n,x)	Bessel function of the second kind of integer order
`yv`(v,z)	Bessel function of the second kind of real order
`yve`(v,z)	Exponentially scaled Bessel function of the second kind of real order
`kn`(n, x)	Modified Bessel function of the second kind of integer order n
`kv`(v,z)	Modified Bessel function of the second kind of real order v
`kve`(v,z)	Exponentially scaled modified Bessel function of the second kind.
`iv`(v,z)	Modified Bessel function of the first kind of real order
`ive`(v,z)	Exponentially scaled modified Bessel function of the first kind
`hankel1`(v, z)	Hankel function of the first kind
`hankel1e`(v, z)	Exponentially scaled Hankel function of the first kind
`hankel2`(v, z)	Hankel function of the second kind
`hankel2e`(v, z)	Exponentially scaled Hankel function of the second kind

`scipy.special.`**`jv`**(*v*, *z*) **= <ufunc 'jv'>**

Bessel function of the first kind of real order v

`scipy.special.`**`jve`**(*v*, *z*) **= <ufunc 'jve'>**

Exponentially scaled Bessel function of order v

Defined as:

```
jve(v,z) = jv(v,z) * exp(-abs(z.imag))
```

`scipy.special.`**`yn`**`(`n, x`)` **= <ufunc 'yn'>**

Bessel function of the second kind of integer order

Returns the Bessel function of the second kind of integer order n at x.

`scipy.special.`**`yv`**`(`v, z`)` **= <ufunc 'yv'>**

Bessel function of the second kind of real order

Returns the Bessel function of the second kind of real order v at complex z.

`scipy.special.`**`yve`**`(`v, z`)` **= <ufunc 'yve'>**

Exponentially scaled Bessel function of the second kind of real order

Returns the exponentially scaled Bessel function of the second kind of real order v at complex z:

```
yve(v,z) = yv(v,z) * exp(-abs(z.imag))
```

`scipy.special.`**`kn`**`(`n, x`)` **= <ufunc 'kn'>**

Modified Bessel function of the second kind of integer order n

These are also sometimes called functions of the third kind.

`scipy.special.`**`kv`**`(`v, z`)` **= <ufunc 'kv'>**

Modified Bessel function of the second kind of real order v

Returns the modified Bessel function of the second kind (sometimes called the third kind) for real order v at complex z.

`scipy.special.`**`kve`**`(`v, z`)` **= <ufunc 'kve'>**

Exponentially scaled modified Bessel function of the second kind.

Returns the exponentially scaled, modified Bessel function of the second kind (sometimes called the third kind) for real order v at complex z:

```
kve(v,z) = kv(v,z) * exp(z)
```

`scipy.special.`**`iv`**`(`v, z`)` **= <ufunc 'iv'>**

Modified Bessel function of the first kind of real order

Parameters **v**

Order. If z is of real type and negative, v must be integer valued.

z

Argument.

`scipy.special.`**`ive`**`(`v, z`)` **= <ufunc 'ive'>**

Exponentially scaled modified Bessel function of the first kind

Defined as:

```
ive(v,z) = iv(v,z) * exp(-abs(z.real))
```

`scipy.special.`**`hankel1`**`(`v, z`)` **= <ufunc 'hankel1'>**

Hankel function of the first kind

Parameters **v** : float

Order

z : float or complex

Argument

`scipy.special.`**`hankel1e`**(*v*, *z*) **= <ufunc 'hankel1e'>**

Exponentially scaled Hankel function of the first kind

Defined as:

```
hankel1e(v,z) = hankel1(v,z) * exp(-1j * z)
```

Parameters **v** : float

Order

z : complex

Argument

`scipy.special.`**`hankel2`**(*v*, *z*) **= <ufunc 'hankel2'>**

Hankel function of the second kind

Parameters **v** : float

Order

z : complex

Argument

`scipy.special.`**`hankel2e`**(*v*, *z*) **= <ufunc 'hankel2e'>**

Exponentially scaled Hankel function of the second kind

Defined as:

```
hankel1e(v,z) = hankel1(v,z) * exp(1j * z)
```

Parameters **v** : float

Order

z : complex

Argument

The following is not an universal function:

`lmbda`(v, x)	Compute sequence of lambda functions with arbitrary order v and their derivatives.

`scipy.special.`**`lmbda`**(*v*, *x*)

Compute sequence of lambda functions with arbitrary order v and their derivatives. Lv0(x)..Lv(x) are computed with v0=v-int(v).

Zeros of Bessel Functions

These are not universal functions:

`jnjnp_zeros`(nt)	Compute nt (<=1200) zeros of the Bessel functions Jn and Jn' and arange them in order of their magni
`jnyn_zeros`(n, nt)	Compute nt zeros of the Bessel functions Jn(x), Jn'(x), Yn(x), and Yn'(x), respectively.
`jn_zeros`(n, nt)	Compute nt zeros of the Bessel function Jn(x).
`jnp_zeros`(n, nt)	Compute nt zeros of the Bessel function Jn'(x).
`yn_zeros`(n, nt)	Compute nt zeros of the Bessel function Yn(x).
`ynp_zeros`(n, nt)	Compute nt zeros of the Bessel function Yn'(x).
`y0_zeros`(nt[, complex])	Returns nt (complex or real) zeros of Y0(z), z0, and the value of Y0'(z0) = -Y1(z0) at each zero.
`y1_zeros`(nt[, complex])	Returns nt (complex or real) zeros of Y1(z), z1, and the value of Y1'(z1) = Y0(z1) at each zero.
`y1p_zeros`(nt[, complex])	Returns nt (complex or real) zeros of Y1'(z), z1', and the value of Y1(z1') at each zero.

`scipy.special.`**`jnjnp_zeros`**`(`*nt*`)`

Compute nt (<=1200) zeros of the Bessel functions Jn and Jn' and arange them in order of their magnitudes.

Returns	**zo[l-1]** : ndarray Value of the lth zero of Jn(x) and Jn'(x). Of length *nt*. **n[l-1]** : ndarray Order of the Jn(x) or Jn'(x) associated with lth zero. Of length *nt*. **m[l-1]** : ndarray Serial number of the zeros of Jn(x) or Jn'(x) associated with lth zero. Of length *nt*. **t[l-1]** : ndarray 0 if lth zero in zo is zero of Jn(x), 1 if it is a zero of Jn'(x). Of length *nt*.

See also:

`jn_zeros`, `jnp_zeros`

`scipy.special.`**`jnyn_zeros`**`(`*n*, *nt*`)`

Compute nt zeros of the Bessel functions Jn(x), Jn'(x), Yn(x), and Yn'(x), respectively. Returns 4 arrays of length nt.

See jn_zeros, jnp_zeros, yn_zeros, ynp_zeros to get separate arrays.

`scipy.special.`**`jn_zeros`**`(`*n*, *nt*`)`

Compute nt zeros of the Bessel function Jn(x).

`scipy.special.`**`jnp_zeros`**`(`*n*, *nt*`)`

Compute nt zeros of the Bessel function Jn'(x).

`scipy.special.`**`yn_zeros`**`(`*n*, *nt*`)`

Compute nt zeros of the Bessel function Yn(x).

`scipy.special.`**`ynp_zeros`**`(`*n*, *nt*`)`

Compute nt zeros of the Bessel function Yn'(x).

`scipy.special.`**`y0_zeros`**`(`*nt*, *complex=0*`)`

Returns nt (complex or real) zeros of Y0(z), z0, and the value of Y0'(z0) = -Y1(z0) at each zero.

`scipy.special.`**`y1_zeros`**`(`*nt*, *complex=0*`)`

Returns nt (complex or real) zeros of Y1(z), z1, and the value of Y1'(z1) = Y0(z1) at each zero.

`scipy.special.`**`y1p_zeros`**`(`*nt*, *complex=0*`)`

Returns nt (complex or real) zeros of Y1'(z), z1', and the value of Y1(z1') at each zero.

Faster versions of common Bessel Functions

`j0`(x)	Bessel function the first kind of order 0
`j1`(x)	Bessel function of the first kind of order 1
`y0`(x)	Bessel function of the second kind of order 0
`y1`(x)	Bessel function of the second kind of order 1
`i0`(x)	Modified Bessel function of order 0
`i0e`(x)	Exponentially scaled modified Bessel function of order 0.
`i1`(x)	Modified Bessel function of order 1
`i1e`(x)	Exponentially scaled modified Bessel function of order 0.
`k0`(x)	Modified Bessel function K of order 0
`k0e`(x)	Exponentially scaled modified Bessel function K of order 0
`k1`(x)	Modified Bessel function of the first kind of order 1
`k1e`(x)	Exponentially scaled modified Bessel function K of order 1

`scipy.special.`**`j0`**`(`*x*`)` **= <ufunc 'j0'>**
Bessel function the first kind of order 0

`scipy.special.`**`j1`**`(`*x*`)` **= <ufunc 'j1'>**
Bessel function of the first kind of order 1

`scipy.special.`**`y0`**`(`*x*`)` **= <ufunc 'y0'>**
Bessel function of the second kind of order 0

Returns the Bessel function of the second kind of order 0 at x.

`scipy.special.`**`y1`**`(`*x*`)` **= <ufunc 'y1'>**
Bessel function of the second kind of order 1

Returns the Bessel function of the second kind of order 1 at x.

`scipy.special.`**`i0`**`(`*x*`)` **= <ufunc 'i0'>**
Modified Bessel function of order 0

`scipy.special.`**`i0e`**`(`*x*`)` **= <ufunc 'i0e'>**
Exponentially scaled modified Bessel function of order 0.

Defined as:

```
i0e(x) = exp(-abs(x)) * i0(x).
```

`scipy.special.`**`i1`**`(`*x*`)` **= <ufunc 'i1'>**
Modified Bessel function of order 1

`scipy.special.`**`i1e`**`(`*x*`)` **= <ufunc 'i1e'>**
Exponentially scaled modified Bessel function of order 0.

Defined as:

```
i1e(x) = exp(-abs(x)) * i1(x)
```

`scipy.special.`**`k0`**`(`*x*`)` **= <ufunc 'k0'>**
Modified Bessel function K of order 0

Modified Bessel function of the second kind (sometimes called the third kind) of order 0.

`scipy.special.`**`k0e`**`(`*x*`)` **= <ufunc 'k0e'>**
Exponentially scaled modified Bessel function K of order 0

Defined as:

```
k0e(x) = exp(x) * k0(x).
```

`scipy.special.`**`k1`**`(`*x*`)` **= <ufunc 'k1'>**
Modified Bessel function of the first kind of order 1

`scipy.special.`**`k1e`**`(`*x*`)` **= <ufunc 'k1e'>**
Exponentially scaled modified Bessel function K of order 1

Defined as:

```
k1e(x) = exp(x) * k1(x)
```

Continued on next page

Table 5.217 – continued from previous page

Integrals of Bessel Functions

`itj0y0`(x)	Integrals of Bessel functions of order 0
`it2j0y0`(x)	Integrals related to Bessel functions of order 0
`iti0k0`(x)	Integrals of modified Bessel functions of order 0
`it2i0k0`(x)	Integrals related to modified Bessel functions of order 0
`besselpoly`(a, lmb, nu)	Weighed integral of a Bessel function.

`scipy.special.`**`itj0y0`**(*x*) **= <ufunc 'itj0y0'>**

Integrals of Bessel functions of order 0

Returns simple integrals from 0 to x of the zeroth order Bessel functions j0 and y0.

Returns ij0, iy0

`scipy.special.`**`it2j0y0`**(*x*) **= <ufunc 'it2j0y0'>**

Integrals related to Bessel functions of order 0

Returns ij0

`integral((1-j0(t))/t, t=0..x)`

iy0

`integral(y0(t)/t, t=x..inf)`

`scipy.special.`**`iti0k0`**(*x*) **= <ufunc 'iti0k0'>**

Integrals of modified Bessel functions of order 0

Returns simple integrals from 0 to x of the zeroth order modified Bessel functions i0 and k0.

Returns ii0, ik0

`scipy.special.`**`it2i0k0`**(*x*) **= <ufunc 'it2i0k0'>**

Integrals related to modified Bessel functions of order 0

Returns ii0

`integral((i0(t)-1)/t, t=0..x)`

ik0

`int(k0(t)/t,t=x..inf)`

`scipy.special.`**`besselpoly`**(*a*, *lmb*, *nu*) **= <ufunc 'besselpoly'>**

Weighed integral of a Bessel function.

$$\int_0^1 x^\lambda J_v(\nu, 2ax)\,dx$$

where J_v is a Bessel function and $\lambda = lmb$, $\nu = nu$.

Derivatives of Bessel Functions

`jvp`(v, z[, n])	Return the nth derivative of Jv(z) with respect to z.
`yvp`(v, z[, n])	Return the nth derivative of Yv(z) with respect to z.
`kvp`(v, z[, n])	Return the nth derivative of Kv(z) with respect to z.
`ivp`(v, z[, n])	Return the nth derivative of Iv(z) with respect to z.
`h1vp`(v, z[, n])	Return the nth derivative of H1v(z) with respect to z.
`h2vp`(v, z[, n])	Return the nth derivative of H2v(z) with respect to z.

`scipy.special.`**`jvp`**(*v*, *z*, *n=1*)
Return the nth derivative of Jv(z) with respect to z.

`scipy.special.`**`yvp`**(*v*, *z*, *n=1*)
Return the nth derivative of Yv(z) with respect to z.

`scipy.special.`**`kvp`**(*v*, *z*, *n=1*)
Return the nth derivative of Kv(z) with respect to z.

`scipy.special.`**`ivp`**(*v*, *z*, *n=1*)
Return the nth derivative of Iv(z) with respect to z.

`scipy.special.`**`h1vp`**(*v*, *z*, *n=1*)
Return the nth derivative of H1v(z) with respect to z.

`scipy.special.`**`h2vp`**(*v*, *z*, *n=1*)
Return the nth derivative of H2v(z) with respect to z.

Spherical Bessel Functions

These are not universal functions:

`sph_jn`(n, z)	Compute the spherical Bessel function jn(z) and its derivative for all orders up to and including n.
`sph_yn`(n, z)	Compute the spherical Bessel function yn(z) and its derivative for all orders up to and including n.
`sph_jnyn`(n, z)	Compute the spherical Bessel functions, jn(z) and yn(z) and their derivatives for all orders up to and including n.
`sph_in`(n, z)	Compute the spherical Bessel function in(z) and its derivative for all orders up to and including n.
`sph_kn`(n, z)	Compute the spherical Bessel function kn(z) and its derivative for all orders up to and including n.
`sph_inkn`(n, z)	Compute the spherical Bessel functions, in(z) and kn(z) and their derivatives for all orders up to and including n.

`scipy.special.`**`sph_jn`**(*n*, *z*)
Compute the spherical Bessel function jn(z) and its derivative for all orders up to and including n.

`scipy.special.`**`sph_yn`**(*n*, *z*)
Compute the spherical Bessel function yn(z) and its derivative for all orders up to and including n.

`scipy.special.`**`sph_jnyn`**(*n*, *z*)
Compute the spherical Bessel functions, jn(z) and yn(z) and their derivatives for all orders up to and including n.

`scipy.special.`**`sph_in`**(*n*, *z*)
Compute the spherical Bessel function in(z) and its derivative for all orders up to and including n.

`scipy.special.`**`sph_kn`**(*n*, *z*)
Compute the spherical Bessel function kn(z) and its derivative for all orders up to and including n.

`scipy.special.`**`sph_inkn`**(*n*, *z*)
Compute the spherical Bessel functions, in(z) and kn(z) and their derivatives for all orders up to and including n.

Riccati-Bessel Functions

These are not universal functions:

`riccati_jn`(n, x)	Compute the Ricatti-Bessel function of the first kind and its derivative for all orders up to and including n.
`riccati_yn`(n, x)	Compute the Ricatti-Bessel function of the second kind and its derivative for all orders up to and including n.

`scipy.special.`**`riccati_jn`**(*n*, *x*)
Compute the Ricatti-Bessel function of the first kind and its derivative for all orders up to and including n.

`scipy.special.`**`riccati_yn`**`(`*n*, *x*`)`

Compute the Ricatti-Bessel function of the second kind and its derivative for all orders up to and including n.

Struve Functions

`struve`(v,x)	Struve function
`modstruve`(v, x)	Modified Struve function
`itstruve0`(x)	Integral of the Struve function of order 0
`it2struve0`(x)	Integral related to Struve function of order 0
`itmodstruve0`(x)	Integral of the modified Struve function of order 0

`scipy.special.`**`struve`**`(`*v*, *x*`)` **= <ufunc 'struve'>**

Struve function

Computes the struve function Hv(x) of order v at x, x must be positive unless v is an integer.

`scipy.special.`**`modstruve`**`(`*v*, *x*`)` **= <ufunc 'modstruve'>**

Modified Struve function

Returns the modified Struve function Lv(x) of order v at x, x must be positive unless v is an integer.

`scipy.special.`**`itstruve0`**`(`*x*`)` **= <ufunc 'itstruve0'>**

Integral of the Struve function of order 0

Returns i

`integral(H0(t), t=0..x)`

`scipy.special.`**`it2struve0`**`(`*x*`)` **= <ufunc 'it2struve0'>**

Integral related to Struve function of order 0

Returns i

`integral(H0(t)/t, t=x..inf)`

`scipy.special.`**`itmodstruve0`**`(`*x*`)` **= <ufunc 'itmodstruve0'>**

Integral of the modified Struve function of order 0

Returns i

`integral(L0(t), t=0..x)`

Raw Statistical Functions

See also:

`scipy.stats`: Friendly versions of these functions.

`bdtr`(k, n, p)	Binomial distribution cumulative distribution function.
`bdtrc`(k, n, p)	Binomial distribution survival function.
`bdtri`(k, n, y)	Inverse function to bdtr vs.
`bdtrik`(y, n, p)	Inverse function to bdtr vs k
`bdtrin`(k, y, p)	Inverse function to bdtr vs n
`btdtr`(a,b,x)	Cumulative beta distribution.
`btdtri`(a,b,p)	p-th quantile of the beta distribution.
`btdtria`(p, b, x)	Inverse of btdtr vs a
`btdtrib`(a, p, x)	Inverse of btdtr vs b
`fdtr`(dfn, dfd, x)	F cumulative distribution function

Continued on next page

Table 5.222 – continued from previous page

`fdtrc`(dfn, dfd, x)	F survival function
`fdtri`(dfn, dfd, p)	Inverse to fdtr vs x
`gdtr`(a,b,x)	Gamma distribution cumulative density function.
`gdtrc`(a,b,x)	Gamma distribution survival function.
`gdtria`(p, b, x[, out])	Inverse of gdtr vs a.
`gdtrib`(a, p, x[, out])	Inverse of gdtr vs b.
`gdtrix`(a, b, p[, out])	Inverse of gdtr vs x.
`nbdtr`(k, n, p)	Negative binomial cumulative distribution function
`nbdtrc`(k,n,p)	Negative binomial survival function
`nbdtri`(k, n, y)	Inverse of nbdtr vs p
`nbdtrik`(y,n,p)	Inverse of nbdtr vs k
`nbdtrin`(k,y,p)	Inverse of nbdtr vs n
`ncfdtr`(dfn, dfd, nc, f)	Cumulative distribution function of the non-central F distribution.
`ncfdtridfd`(p, f, dfn, nc)	Calculate degrees of freedom (denominator) for the noncentral F-distribution.
`ncfdtridfn`(p, f, dfd, nc)	Calculate degrees of freedom (numerator) for the noncentral F-distribution.
`ncfdtri`(p, dfn, dfd, nc)	Inverse cumulative distribution function of the non-central F distribution.
`ncfdtrinc`(p, f, dfn, dfd)	Calculate non-centrality parameter for non-central F distribution.
`nctdtr`(df, nc, t)	Cumulative distribution function of the non-central t distribution.
`nctdtridf`(p, nc, t)	Calculate degrees of freedom for non-central t distribution.
`nctdtrit`(df, nc, p)	Inverse cumulative distribution function of the non-central t distribution.
`nctdtrinc`(df, p, t)	Calculate non-centrality parameter for non-central t distribution.
`nrdtrimn`(p, x, std)	Calculate mean of normal distribution given other params.
`nrdtrisd`(p, x, mn)	Calculate standard deviation of normal distribution given other params.
`pdtr`(k, m)	Poisson cumulative distribution function
`pdtrc`(k, m)	Poisson survival function
`pdtri`(k,y)	Inverse to pdtr vs m
`pdtrik`(p,m)	Inverse to pdtr vs k
`stdtr`(df,t)	Student t distribution cumulative density function
`stdtridf`(p,t)	Inverse of stdtr vs df
`stdtrit`(df,p)	Inverse of stdtr vs t
`chdtr`(v, x)	Chi square cumulative distribution function
`chdtrc`(v,x)	Chi square survival function
`chdtri`(v,p)	Inverse to chdtrc
`chdtriv`(p, x)	Inverse to chdtr vs v
`ndtr`(x)	Gaussian cumulative distribution function
`log_ndtr`(x)	Logarithm of Gaussian cumulative distribution function
`ndtri`(y)	Inverse of ndtr vs x
`chndtr`(x, df, nc)	Non-central chi square cumulative distribution function
`chndtridf`(x, p, nc)	Inverse to chndtr vs df
`chndtrinc`(x, df, p)	Inverse to chndtr vs nc
`chndtrix`(p, df, nc)	Inverse to chndtr vs x
`smirnov`(n, e)	Kolmogorov-Smirnov complementary cumulative distribution function
`smirnovi`(n, y)	Inverse to smirnov
`kolmogorov`(y)	Complementary cumulative distribution function of Kolmogorov distribution
`kolmogi`(p)	Inverse function to kolmogorov
`tklmbda`(x, lmbda)	Tukey-Lambda cumulative distribution function
`logit`(x)	Logit ufunc for ndarrays.
`expit`(x)	Expit ufunc for ndarrays.
`boxcox`(x, lmbda)	Compute the Box-Cox transformation.
`boxcox1p`(x, lmbda)	Compute the Box-Cox transformation of $1 + x$.

`scipy.special.`**`bdtr`**`(`*k*, *n*, *p*`)` **= <ufunc 'bdtr'>**

Binomial distribution cumulative distribution function.

Sum of the terms 0 through k of the Binomial probability density.

```
y = sum(nCj p**j (1-p)**(n-j),j=0..k)
```

Parameters	**k, n** : int	Terms to include
	p : float	Probability
Returns	**y** : float	Sum of terms

`scipy.special.`**`bdtrc`**`(`*k*, *n*, *p*`)` **= <ufunc 'bdtrc'>**

Binomial distribution survival function.

Sum of the terms k+1 through n of the Binomial probability density

```
y = sum(nCj p**j (1-p)**(n-j), j=k+1..n)
```

Parameters	**k, n** : int	Terms to include
	p : float	Probability
Returns	**y** : float	Sum of terms

`scipy.special.`**`bdtri`**`(`*k*, *n*, *y*`)` **= <ufunc 'bdtri'>**

Inverse function to bdtr vs. p

Finds probability *p* such that for the cumulative binomial probability `bdtr(k, n, p) == y`.

`scipy.special.`**`bdtrik`**`(`*y*, *n*, *p*`)` **= <ufunc 'bdtrik'>**

Inverse function to bdtr vs k

`scipy.special.`**`bdtrin`**`(`*k*, *y*, *p*`)` **= <ufunc 'bdtrin'>**

Inverse function to bdtr vs n

`scipy.special.`**`btdtr`**`(`*a*, *b*, *x*`)` **= <ufunc 'btdtr'>**

Cumulative beta distribution.

Returns the area from zero to x under the beta density function:

```
gamma(a+b)/(gamma(a)*gamma(b)))*integral(t**(a-1) (1-t)**(b-1), t=0..x)
```

See also:

`betainc`

`scipy.special.`**`btdtri`**`(`*a*, *b*, *p*`)` **= <ufunc 'btdtri'>**

p-th quantile of the beta distribution.

This is effectively the inverse of btdtr returning the value of x for which `btdtr(a,b,x) = p`

See also:

`betaincinv`

`scipy.special.`**`btdtria`**`(`*p*, *b*, *x*`)` **= <ufunc 'btdtria'>**

Inverse of btdtr vs a

`scipy.special.`**`btdtrib`**(*a*, *p*, *x*) = **<ufunc 'btdtrib'>**

Inverse of btdtr vs b

`scipy.special.`**`fdtr`**(*dfn*, *dfd*, *x*) = **<ufunc 'fdtr'>**

F cumulative distribution function

Returns the area from zero to x under the F density function (also known as Snedcor's density or the variance ratio density). This is the density of X = (unum/dfn)/(uden/dfd), where unum and uden are random variables having Chi square distributions with dfn and dfd degrees of freedom, respectively.

`scipy.special.`**`fdtrc`**(*dfn*, *dfd*, *x*) = **<ufunc 'fdtrc'>**

F survival function

Returns the complemented F distribution function.

`scipy.special.`**`fdtri`**(*dfn*, *dfd*, *p*) = **<ufunc 'fdtri'>**

Inverse to fdtr vs x

Finds the F density argument x such that `fdtr(dfn, dfd, x) == p`.

`scipy.special.`**`gdtr`**(*a*, *b*, *x*) = **<ufunc 'gdtr'>**

Gamma distribution cumulative density function.

Returns the integral from zero to x of the gamma probability density function:

```
a**b / gamma(b) * integral(t**(b-1) exp(-at),t=0..x).
```

The arguments a and b are used differently here than in other definitions.

`scipy.special.`**`gdtrc`**(*a*, *b*, *x*) = **<ufunc 'gdtrc'>**

Gamma distribution survival function.

Integral from x to infinity of the gamma probability density function.

See also:

`gdtr`, `gdtri`

`scipy.special.`**`gdtria`**(*p*, *b*, *x*, *out=None*) = **<ufunc 'gdtria'>**

Inverse of gdtr vs a.

Returns the inverse with respect to the parameter *a* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution.

Parameters	**p** : array_like	Probability values.
	b : array_like	*b* parameter values of *gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.
	x : array_like	Nonnegative real values, from the domain of the gamma distribution.
	out : ndarray, optional	If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.
Returns	**a** : ndarray	Values of the *a* parameter such that *p = gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.

See also:

`gdtr`	CDF of the gamma distribution.
`gdtrib`	Inverse with respect to *b* of *gdtr(a, b, x)*.

gdtrix	Inverse with respect to *x* of *gdtr(a, b, x)*.

Examples

First evaluate `gdtr`.

```
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtria(p, 3.4, 5.6)
1.2
```

`scipy.special.`**`gdtrib`**(*a*, *p*, *x*, *out=None*) **= <ufunc 'gdtrib'>**

Inverse of gdtr vs b.

Returns the inverse with respect to the parameter *b* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution.

Parameters **a** : array_like

a parameter values of *gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.

p : array_like

Probability values.

x : array_like

Nonnegative real values, from the domain of the gamma distribution.

out : ndarray, optional

If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.

Returns **b** : ndarray

Values of the *b* parameter such that *p = gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.

See also:

gdtr	CDF of the gamma distribution.
gdtria	Inverse with respect to *a* of *gdtr(a, b, x)*.
gdtrix	Inverse with respect to *x* of *gdtr(a, b, x)*.

Examples

First evaluate `gdtr`.

```
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtrib(1.2, p, 5.6)
3.3999999999723882
```

`scipy.special.`**`gdtrix`**(*a*, *b*, *p*, *out=None*) **= <ufunc 'gdtrix'>**

Inverse of gdtr vs x.

Returns the inverse with respect to the parameter *x* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution. This is also known as the p'th quantile of the distribution.

Parameters **a** : array_like

a parameter values of *gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.

b : array_like

b parameter values of *gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.

p : array_like

Probability values.

out : ndarray, optional

If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.

Returns **x** : ndarray

Values of the *x* parameter such that *p = gdtr(a, b, x)*.

See also:

`gdtr`	CDF of the gamma distribution.
`gdtria`	Inverse with respect to *a* of *gdtr(a, b, x)*.
`gdtrib`	Inverse with respect to *b* of *gdtr(a, b, x)*.

Examples

First evaluate `gdtr`.

```
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtrix(1.2, 3.4, p)
5.5999999999999996
```

`scipy.special.`**`nbdtr`**(*k*, *n*, *p*) **= <ufunc 'nbdtr'>**

Negative binomial cumulative distribution function

Returns the sum of the terms 0 through k of the negative binomial distribution:

```
sum((n+j-1)Cj p**n (1-p)**j,j=0..k).
```

In a sequence of Bernoulli trials this is the probability that k or fewer failures precede the nth success.

`scipy.special.`**`nbdtrc`**(*k*, *n*, *p*) **= <ufunc 'nbdtrc'>**

Negative binomial survival function

Returns the sum of the terms k+1 to infinity of the negative binomial distribution.

`scipy.special.`**`nbdtri`**(*k*, *n*, *y*) **= <ufunc 'nbdtri'>**

Inverse of nbdtr vs p

Finds the argument p such that `nbdtr(k,n,p) = y`.

`scipy.special.`**`nbdtrik`**(*y*, *n*, *p*) **= <ufunc 'nbdtrik'>**

Inverse of nbdtr vs k

Finds the argument k such that `nbdtr(k,n,p) = y`.

`scipy.special.`**`nbdtrin`**(*k*, *y*, *p*) **= <ufunc 'nbdtrin'>**

Inverse of nbdtr vs n

Finds the argument n such that `nbdtr(k,n,p) = y`.

`scipy.special.`**`ncfdtr`**(*dfn*, *dfd*, *nc*, *f*) **= <ufunc 'ncfdtr'>**

Cumulative distribution function of the non-central F distribution.

Parameters

dfn : array_like

Degrees of freedom of the numerator sum of squares. Range (0, inf).

dfd : array_like

Degrees of freedom of the denominator sum of squares. Range (0, inf).

nc : array_like

Noncentrality parameter. Should be in range (0, 1e4).

f : array_like

Quantiles, i.e. the upper limit of integration.

Returns

cdf : float or ndarray

The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise it will be an array.

See also:

`ncdfdtri`	Inverse CDF (iCDF) of the non-central F distribution.
`ncdfdtridfd`	Calculate dfd, given CDF and iCDF values.
`ncdfdtridfn`	Calculate dfn, given CDF and iCDF values.
`ncdfdtrinc`	Calculate noncentrality parameter, given CDF, iCDF, dfn, dfd.

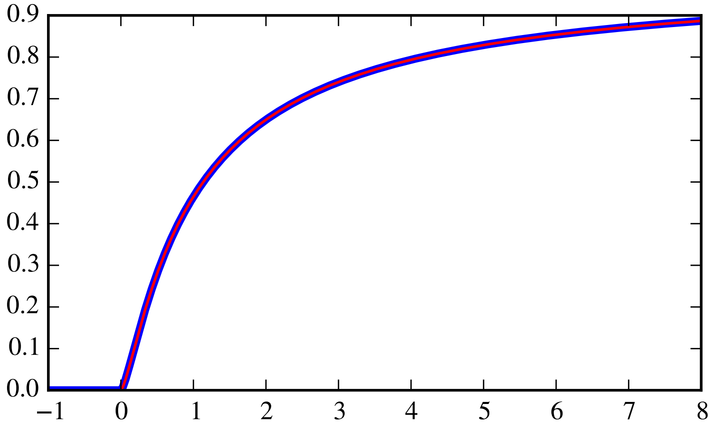
Examples

```
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Plot the CDF of the non-central F distribution, for nc=0. Compare with the F-distribution from scipy.stats:

```
>>> x = np.linspace(-1, 8, num=500)
>>> dfn = 3
>>> dfd = 2
>>> ncf_stats = stats.f.cdf(x, dfn, dfd)
>>> ncf_special = special.ncfdtr(dfn, dfd, 0, x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, ncf_stats, 'b-', lw=3)
>>> ax.plot(x, ncf_special, 'r-')
>>> plt.show()
```



`scipy.special.`**`ncfdtridfd`**(*p*, *f*, *dfn*, *nc*) **= <ufunc 'ncfdtridfd'>**

Calculate degrees of freedom (denominator) for the noncentral F-distribution.

See `ncfdtr` for more details.

`scipy.special.`**`ncfdtridfn`**(*p*, *f*, *dfd*, *nc*) **= <ufunc 'ncfdtridfn'>**

Calculate degrees of freedom (numerator) for the noncentral F-distribution.

See `ncfdtr` for more details.

`scipy.special.`**`ncfdtri`**(*p*, *dfn*, *dfd*, *nc*) **= <ufunc 'ncfdtri'>**

Inverse cumulative distribution function of the non-central F distribution.

See `ncfdtr` for more details.

`scipy.special.`**`ncfdtrinc`**(*p*, *f*, *dfn*, *dfd*) **= <ufunc 'ncfdtrinc'>**

Calculate non-centrality parameter for non-central F distribution.

See `ncfdtr` for more details.

`scipy.special.`**`nctdtr`**(*df*, *nc*, *t*) **= <ufunc 'nctdtr'>**

Cumulative distribution function of the non-central t distribution.

Parameters

df : array_like

Degrees of freedom of the distribution. Should be in range (0, inf).

nc : array_like

Noncentrality parameter. Should be in range (-1e6, 1e6).

t : array_like

Quantiles, i.e. the upper limit of integration.

Returns

cdf : float or ndarray

The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise it will be an array.

See also:

`nctdtrit`	Inverse CDF (iCDF) of the non-central t distribution.
`nctdtridf`	Calculate degrees of freedom, given CDF and iCDF values.
`nctdtrinc`	Calculate non-centrality parameter, given CDF iCDF values.

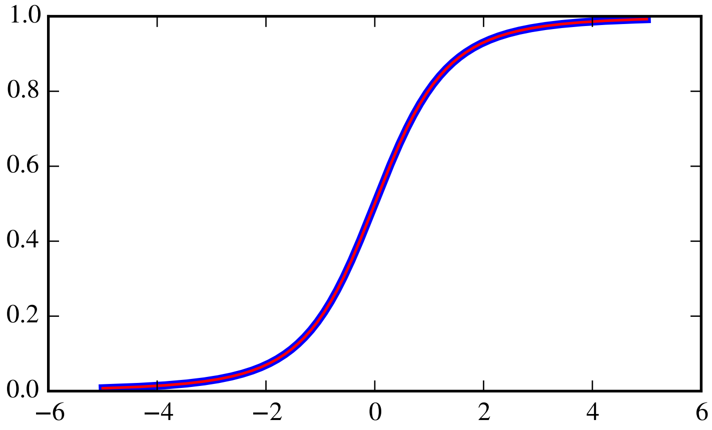
Examples

```
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Plot the CDF of the non-central t distribution, for nc=0. Compare with the t-distribution from scipy.stats:

```
>>> x = np.linspace(-5, 5, num=500)
>>> df = 3
>>> nct_stats = stats.t.cdf(x, df)
>>> nct_special = special.nctdtr(df, 0, x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, nct_stats, 'b-', lw=3)
>>> ax.plot(x, nct_special, 'r-')
>>> plt.show()
```



`scipy.special.`**`nctdtridf`**(*p*, *nc*, *t*) **= <ufunc 'nctdtridf'>**

Calculate degrees of freedom for non-central t distribution.

See `nctdtr` for more details.

Parameters **p** : array_like

CDF values, in range (0, 1].

nc : array_like

Noncentrality parameter. Should be in range (-1e6, 1e6).

t : array_like

Quantiles, i.e. the upper limit of integration.

`scipy.special.`**`nctdtrit`**(*df*, *nc*, *p*) **= <ufunc 'nctdtrit'>**

Inverse cumulative distribution function of the non-central t distribution.

See `nctdtr` for more details.

Parameters **df** : array_like

Degrees of freedom of the distribution. Should be in range (0, inf).

nc : array_like
Noncentrality parameter. Should be in range (-1e6, 1e6).

p : array_like
CDF values, in range (0, 1].

`scipy.special.`**`nctdtrinc`**`(`*df*, *p*, *t*`)` **= <ufunc 'nctdtrinc'>**

Calculate non-centrality parameter for non-central t distribution.

See `nctdtr` for more details.

Parameters **df** : array_like
Degrees of freedom of the distribution. Should be in range (0, inf).

p : array_like
CDF values, in range (0, 1].

t : array_like
Quantiles, i.e. the upper limit of integration.

`scipy.special.`**`nrdtrimn`**`(`*p*, *x*, *std*`)` **= <ufunc 'nrdtrimn'>**

Calculate mean of normal distribution given other params.

Parameters **p** : array_like
CDF values, in range (0, 1].

x : array_like
Quantiles, i.e. the upper limit of integration.

std : array_like
Standard deviation.

Returns **mn** : float or ndarray
The mean of the normal distribution.

See also:

`nrdtrimn`, `ndtr`

`scipy.special.`**`nrdtrisd`**`(`*p*, *x*, *mn*`)` **= <ufunc 'nrdtrisd'>**

Calculate standard deviation of normal distribution given other params.

Parameters **p** : array_like
CDF values, in range (0, 1].

x : array_like
Quantiles, i.e. the upper limit of integration.

mn : float or ndarray
The mean of the normal distribution.

Returns **std** : array_like
Standard deviation.

See also:

`nrdtristd`, `ndtr`

`scipy.special.`**`pdtr`**`(`*k*, *m*`)` **= <ufunc 'pdtr'>**

Poisson cumulative distribution function

Returns the sum of the first k terms of the Poisson distribution: sum(exp(-m) * m**j / j!, j=0..k) = gammaincc(k+1, m). Arguments must both be positive and k an integer.

`scipy.special.`**`pdtrc`**`(`*k*, *m*`)` **= <ufunc 'pdtrc'>**

Poisson survival function

Returns the sum of the terms from k+1 to infinity of the Poisson distribution: sum(exp(-m) * m**j / j!, j=k+1..inf) = gammainc(k+1, m). Arguments must both be positive and k an integer.

`scipy.special.`**`pdtri`**`(`*k*, *y*`)` **= <ufunc 'pdtri'>**

Inverse to pdtr vs m

Returns the Poisson variable m such that the sum from 0 to k of the Poisson density is equal to the given probability y: calculated by gammaincinv(k+1, y). k must be a nonnegative integer and y between 0 and 1.

`scipy.special.`**`pdtrik`**`(`*p*, *m*`)` **= <ufunc 'pdtrik'>**

Inverse to pdtr vs k

Returns the quantile k such that `pdtr(k, m) = p`

`scipy.special.`**`stdtr`**`(`*df*, *t*`)` **= <ufunc 'stdtr'>**

Student t distribution cumulative density function

Returns the integral from minus infinity to t of the Student t distribution with df > 0 degrees of freedom:

```
gamma((df+1)/2)/(sqrt(df*pi)*gamma(df/2)) *
integral((1+x**2/df)**(-df/2-1/2), x=-inf..t)
```

`scipy.special.`**`stdtridf`**`(`*p*, *t*`)` **= <ufunc 'stdtridf'>**

Inverse of stdtr vs df

Returns the argument df such that stdtr(df,t) is equal to p.

`scipy.special.`**`stdtrit`**`(`*df*, *p*`)` **= <ufunc 'stdtrit'>**

Inverse of stdtr vs t

Returns the argument t such that stdtr(df,t) is equal to p.

`scipy.special.`**`chdtr`**`(`*v*, *x*`)` **= <ufunc 'chdtr'>**

Chi square cumulative distribution function

Returns the area under the left hand tail (from 0 to x) of the Chi square probability density function with v degrees of freedom:

```
1/(2**(v/2) * gamma(v/2)) * integral(t**(v/2-1) * exp(-t/2), t=0..x)
```

`scipy.special.`**`chdtrc`**`(`*v*, *x*`)` **= <ufunc 'chdtrc'>**

Chi square survival function

Returns the area under the right hand tail (from x to infinity) of the Chi square probability density function with v degrees of freedom:

```
1/(2**(v/2) * gamma(v/2)) * integral(t**(v/2-1) * exp(-t/2), t=x..inf)
```

`scipy.special.`**`chdtri`**`(`*v*, *p*`)` **= <ufunc 'chdtri'>**

Inverse to chdtrc

Returns the argument x such that `chdtrc(v,x) == p`.

`scipy.special.`**`chdtriv`**`(`*p*, *x*`)` **= <ufunc 'chdtriv'>**

Inverse to chdtr vs v

Returns the argument v such that `chdtr(v, x) == p`.

`scipy.special.`**`ndtr`**`(`*x*`)` **= <ufunc 'ndtr'>**

Gaussian cumulative distribution function

Returns the area under the standard Gaussian probability density function, integrated from minus infinity to x:

```
1/sqrt(2*pi) * integral(exp(-t**2 / 2),t=-inf..x)
```

`scipy.special.`**`log_ndtr`**(*x*) = **<ufunc 'log_ndtr'>**

Logarithm of Gaussian cumulative distribution function

Returns the log of the area under the standard Gaussian probability density function, integrated from minus infinity to x:

```
log(1/sqrt(2*pi) * integral(exp(-t**2 / 2), t=-inf..x))
```

`scipy.special.`**`ndtri`**(*y*) = **<ufunc 'ndtri'>**

Inverse of ndtr vs x

Returns the argument x for which the area under the Gaussian probability density function (integrated from minus infinity to x) is equal to y.

`scipy.special.`**`chndtr`**(*x*, *df*, *nc*) = **<ufunc 'chndtr'>**

Non-central chi square cumulative distribution function

`scipy.special.`**`chndtridf`**(*x*, *p*, *nc*) = **<ufunc 'chndtridf'>**

Inverse to chndtr vs df

`scipy.special.`**`chndtrinc`**(*x*, *df*, *p*) = **<ufunc 'chndtrinc'>**

Inverse to chndtr vs nc

`scipy.special.`**`chndtrix`**(*p*, *df*, *nc*) = **<ufunc 'chndtrix'>**

Inverse to chndtr vs x

`scipy.special.`**`smirnov`**(*n*, *e*) = **<ufunc 'smirnov'>**

Kolmogorov-Smirnov complementary cumulative distribution function

Returns the exact Kolmogorov-Smirnov complementary cumulative distribution function (Dn+ or Dn-) for a one-sided test of equality between an empirical and a theoretical distribution. It is equal to the probability that the maximum difference between a theoretical distribution and an empirical one based on n samples is greater than e.

`scipy.special.`**`smirnovi`**(*n*, *y*) = **<ufunc 'smirnovi'>**

Inverse to smirnov

Returns `e` such that `smirnov(n, e) = y`.

`scipy.special.`**`kolmogorov`**(*y*) = **<ufunc 'kolmogorov'>**

Complementary cumulative distribution function of Kolmogorov distribution

Returns the complementary cumulative distribution function of Kolmogorov's limiting distribution (Kn* for large n) of a two-sided test for equality between an empirical and a theoretical distribution. It is equal to the (limit as n->infinity of the) probability that sqrt(n) * max absolute deviation > y.

`scipy.special.`**`kolmogi`**(*p*) = **<ufunc 'kolmogi'>**

Inverse function to kolmogorov

Returns y such that `kolmogorov(y) == p`.

`scipy.special.`**`tklmbda`**(*x*, *lmbda*) = **<ufunc 'tklmbda'>**

Tukey-Lambda cumulative distribution function

`scipy.special.`**`logit`**(*x*) = **<ufunc 'logit'>**

Logit ufunc for ndarrays.

The logit function is defined as logit(p) = log(p/(1-p)). Note that logit(0) = -inf, logit(1) = inf, and logit(p) for p<0 or p>1 yields nan.

Parameters **x** : ndarray

The ndarray to apply logit to element-wise.

Returns **out** : ndarray

An ndarray of the same shape as x. Its entries are logit of the corresponding entry of x.

Notes

As a ufunc logit takes a number of optional keyword arguments. For more information see ufuncs

New in version 0.10.0.

`scipy.special.`**`expit`**(*x*) **= <ufunc 'expit'>**

Expit ufunc for ndarrays.

The expit function, also known as the logistic function, is defined as expit(x) = 1/(1+exp(-x)). It is the inverse of the logit function.

Parameters	**x** : ndarray	The ndarray to apply expit to element-wise.
Returns	**out** : ndarray	An ndarray of the same shape as x. Its entries are expit of the corresponding entry of x.

Notes

As a ufunc expit takes a number of optional keyword arguments. For more information see ufuncs

New in version 0.10.0.

`scipy.special.`**`boxcox`**(*x*, *lmbda*) **= <ufunc 'boxcox'>**

Compute the Box-Cox transformation.

The Box-Cox transformation is:

```
y = (x**lmbda - 1) / lmbda  if lmbda != 0
    log(x)                  if lmbda == 0
```

Returns *nan* if `x < 0`. Returns *-inf* if `x == 0` and `lmbda < 0`.

Parameters	**x** : array_like	Data to be transformed.
	lmbda : array_like	Power parameter of the Box-Cox transform.
Returns	**y** : array	Transformed data.

Notes

New in version 0.14.0.

Examples

```
>>> boxcox([1, 4, 10], 2.5)
array([   0.        ,   12.4       ,  126.09110641])
>>> boxcox(2, [0, 1, 2])
array([ 0.69314718,  1.        ,  1.5       ])
```

`scipy.special.`**`boxcox1p`**(*x*, *lmbda*) **= <ufunc 'boxcox1p'>**

Compute the Box-Cox transformation of $1 + x$.

The Box-Cox transformation computed by `boxcox1p` is:

```
y = ((1+x)**lmbda - 1) / lmbda  if lmbda != 0
    log(1+x)                    if lmbda == 0
```

Returns *nan* if `x < -1`. Returns *-inf* if `x == -1` and `lmbda < 0`.

Parameters **x** : array_like

Data to be transformed.

lmbda : array_like

Power parameter of the Box-Cox transform.

Returns **y** : array

Transformed data.

Notes

New in version 0.14.0.

Examples

```
>>> boxcox1p(1e-4, [0, 0.5, 1])
array([  9.99950003e-05,   9.99975001e-05,   1.00000000e-04])
>>> boxcox1p([0.01, 0.1], 0.25)
array([ 0.00996272,  0.09645476])
```

Information Theory Functions

`entr`(x)	Elementwise function for computing entropy.
`rel_entr`(x, y)	Elementwise function for computing relative entropy.
`kl_div`(x, y)	Elementwise function for computing Kullback-Leibler divergence.
`huber`(delta, r)	Huber loss function.
`pseudo_huber`(delta, r)	Pseudo-Huber loss function.

`scipy.special.`**`entr`**(*x*) **= <ufunc 'entr'>**

Elementwise function for computing entropy.

$$\text{entr}(x) = \begin{cases} -x\log(x) & x > 0 \\ 0 & x = 0 \\ -\infty & \text{otherwise} \end{cases}$$

Parameters **x** : ndarray

Input array.

Returns **res** : ndarray

The value of the elementwise entropy function at the given points x.

See also:

`kl_div`, `rel_entr`

Notes

This function is concave.

New in version 0.14.0.

`scipy.special.`**`rel_entr`**(*x*, *y*) **= <ufunc 'rel_entr'>**

Elementwise function for computing relative entropy.

$$\text{rel\_entr}(x, y) = \begin{cases} x\log(x/y) & x > 0, y > 0 \\ 0 & x = 0, y \geq 0 \\ \infty & \text{otherwise} \end{cases}$$

Parameters	**x** : ndarray	
		First input array.
	y : ndarray	
		Second input array.
Returns	**res** : ndarray	
		Output array.

See also:

`entr`, `kl_div`

Notes

This function is jointly convex in x and y.

New in version 0.14.0.

`scipy.special.`**`kl_div`**(*x*, *y*) **= <ufunc 'kl_div'>**

Elementwise function for computing Kullback-Leibler divergence.

$$\mathrm{kl\_div}(x, y) = \begin{cases} x \log(x/y) - x + y & x > 0, y > 0 \\ y & x = 0, y \geq 0 \\ \infty & \text{otherwise} \end{cases}$$

Parameters	**x** : ndarray	
		First input array.
	y : ndarray	
		Second input array.
Returns	**res** : ndarray	
		Output array.

See also:

`entr`, `rel_entr`

Notes

This function is non-negative and is jointly convex in x and y.

New in version 0.14.0.

`scipy.special.`**`huber`**(*delta*, *r*) **= <ufunc 'huber'>**

Huber loss function.

$$\mathrm{huber}(\delta, r) = \begin{cases} \infty & \delta < 0 \\ \frac{1}{2}r^2 & 0 \leq \delta, |r| \leq \delta \\ \delta(|r| - \frac{1}{2}\delta) & \text{otherwise} \end{cases}$$

Parameters	**delta** : ndarray	
		Input array, indicating the quadratic vs. linear loss changepoint.
	r : ndarray	
		Input array, possibly representing residuals.
Returns	**res** : ndarray	
		The computed Huber loss function values.

Notes

This function is convex in r.

New in version 0.15.0.

`scipy.special.`**`pseudo_huber`**`(`*delta*, *r*`)` **= <ufunc 'pseudo_huber'>**

Pseudo-Huber loss function.

$$\mathrm{pseudo\_huber}(\delta, r) = \delta^2 \left(\sqrt{ 1 + \left(\frac{r}{\delta} \right)^2 } - 1 \right)$$

Parameters **delta** : ndarray

Input array, indicating the soft quadratic vs. linear loss changepoint.

r : ndarray

Input array, possibly representing residuals.

Returns **res** : ndarray

The computed Pseudo-Huber loss function values.

Notes

This function is convex in r.

New in version 0.15.0.

Gamma and Related Functions

`gamma`(z)	Gamma function
`gammaln`(z)	Logarithm of absolute value of gamma function
`gammasgn`(x)	Sign of the gamma function.
`gammainc`(a, x)	Incomplete gamma function
`gammaincinv`(a, y)	Inverse to gammainc
`gammaincc`(a,x)	Complemented incomplete gamma integral
`gammainccinv`(a,y)	Inverse to gammaincc
`beta`(a, b)	Beta function.
`betaln`(a, b)	Natural logarithm of absolute value of beta function.
`betainc`(a, b, x)	Incomplete beta integral.
`betaincinv`(a, b, y)	Inverse function to beta integral.
`psi`(z)	Digamma function
`rgamma`(z)	Gamma function inverted
`polygamma`(n, x)	Polygamma function which is the nth derivative of the digamma (psi) function.
`multigammaln`(a, d)	Returns the log of multivariate gamma, also sometimes called the generalized gamma.
`digamma`(z)	Digamma function
`poch`(z, m)	Rising factorial (z)_m

`scipy.special.`**`gamma`**`(`*z*`)` **= <ufunc 'gamma'>**

Gamma function

The gamma function is often referred to as the generalized factorial since `z*gamma(z) = gamma(z+1)` and `gamma(n+1) = n!` for natural number *n*.

`scipy.special.`**`gammaln`**`(`*z*`)` **= <ufunc 'gammaln'>**

Logarithm of absolute value of gamma function

Defined as:

```
ln(abs(gamma(z)))
```

See also:

`gammasgn`

`scipy.special.`**`gammasgn`**`(`*x*`)` **= <ufunc 'gammasgn'>**

Sign of the gamma function.

See also:

`gammaln`

`scipy.special.`**`gammainc`**`(`*a*, *x*`)` **= <ufunc 'gammainc'>**

Incomplete gamma function

Defined as:

```
1 / gamma(a) * integral(exp(-t) * t**(a-1), t=0..x)
```

a must be positive and *x* must be >= 0.

`scipy.special.`**`gammaincinv`**`(`*a*, *y*`)` **= <ufunc 'gammaincinv'>**

Inverse to gammainc

Returns *x* such that `gammainc(a, x) = y`.

`scipy.special.`**`gammaincc`**`(`*a*, *x*`)` **= <ufunc 'gammaincc'>**

Complemented incomplete gamma integral

Defined as:

```
1 / gamma(a) * integral(exp(-t) * t**(a-1), t=x..inf) = 1 - gammainc(a,x)
```

a must be positive and *x* must be >= 0.

`scipy.special.`**`gammainccinv`**`(`*a*, *y*`)` **= <ufunc 'gammainccinv'>**

Inverse to gammaincc

Returns *x* such that `gammaincc(a,x) == y`.

`scipy.special.`**`beta`**`(`*a*, *b*`)` **= <ufunc 'beta'>**

Beta function.

```
beta(a,b) =  gamma(a) * gamma(b) / gamma(a+b)
```

`scipy.special.`**`betaln`**`(`*a*, *b*`)` **= <ufunc 'betaln'>**

Natural logarithm of absolute value of beta function.

Computes `ln(abs(beta(x)))`.

`scipy.special.`**`betainc`**`(`*a*, *b*, *x*`)` **= <ufunc 'betainc'>**

Incomplete beta integral.

Compute the incomplete beta integral of the arguments, evaluated from zero to x:

```
gamma(a+b) / (gamma(a)*gamma(b)) * integral(t**(a-1) (1-t)**(b-1), t=0..x).
```

Notes

The incomplete beta is also sometimes defined without the terms in gamma, in which case the above definition is the so-called regularized incomplete beta. Under this definition, you can get the incomplete beta by multiplying the result of the scipy function by beta(a, b).

`scipy.special.`**`betaincinv`**`(`*a*, *b*, *y*`)` **= <ufunc 'betaincinv'>**

Inverse function to beta integral.

Compute x such that betainc(a,b,x) = y.

`scipy.special.`**`psi`**`(z)` **= <ufunc 'psi'>**

Digamma function

The derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

`scipy.special.`**`rgamma`**`(z)` **= <ufunc 'rgamma'>**

Gamma function inverted

Returns `1/gamma(x)`

`scipy.special.`**`polygamma`**`(n, x)`

Polygamma function which is the nth derivative of the digamma (psi) function.

Parameters

n : array_like of int

The order of the derivative of `psi`.

x : array_like

Where to evaluate the polygamma function.

Returns

polygamma : ndarray

The result.

Examples

```
>>> from scipy import special
>>> x = [2, 3, 25.5]
>>> special.polygamma(1, x)
array([ 0.64493407,  0.39493407,  0.03999467])
>>> special.polygamma(0, x) == special.psi(x)
array([ True,  True,  True], dtype=bool)
```

`scipy.special.`**`multigammaln`**`(a, d)`

Returns the log of multivariate gamma, also sometimes called the generalized gamma.

Parameters

a : ndarray

The multivariate gamma is computed for each item of *a*.

d : int

The dimension of the space of integration.

Returns

res : ndarray

The values of the log multivariate gamma at the given points *a*.

Notes

The formal definition of the multivariate gamma of dimension d for a real a is:

```
\Gamma_d(a) = \int_{A>0}{e^{-tr(A)\cdot{|A|}^{a - (m+1)/2}dA}}
```

with the condition `a > (d-1)/2`, and `A > 0` being the set of all the positive definite matrices of dimension s. Note that a is a scalar: the integrand only is multivariate, the argument is not (the function is defined over a subset of the real set).

This can be proven to be equal to the much friendlier equation:

```
\Gamma_d(a) = \pi^{d(d-1)/4}\prod_{i=1}^{d}{\Gamma(a - (i-1)/2)}.
```

References

R. J. Muirhead, Aspects of multivariate statistical theory (Wiley Series in probability and mathematical statistics).

`scipy.special.`**`digamma`**`(`*z*`)` **= <ufunc 'psi'>**

Digamma function

The derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

`scipy.special.`**`poch`**`(`*z*, *m*`)` **= <ufunc 'poch'>**

Rising factorial (z)_m

The Pochhammer symbol (rising factorial), is defined as:

```
(z)_m = gamma(z + m) / gamma(z)
```

For positive integer *m* it reads:

```
(z)_m = z * (z + 1) * ... * (z + m - 1)
```

Error Function and Fresnel Integrals

`erf`(z)	Returns the error function of complex argument.
`erfc`(x)	Complementary error function, 1 - erf(x).
`erfcx`(x)	Scaled complementary error function, exp(x^2) erfc(x).
`erfi`(z)	Imaginary error function, -i erf(i z).
`erfinv`(y)	Inverse function for erf
`erfcinv`(y)	Inverse function for erfc
`wofz`(z)	Faddeeva function
`dawsn`(x)	Dawson's integral.
`fresnel`(z)	Fresnel sin and cos integrals
`fresnel_zeros`(nt)	Compute nt complex zeros of the sine and cosine Fresnel integrals S(z) and C(z).
`modfresnelp`(x)	Modified Fresnel positive integrals
`modfresnelm`(x)	Modified Fresnel negative integrals

`scipy.special.`**`erf`**`(`*z*`)` **= <ufunc 'erf'>**

Returns the error function of complex argument.

It is defined as `2/sqrt(pi)*integral(exp(-t**2), t=0..z)`.

Parameters **x** : ndarray

Input array.

Returns **res** : ndarray

The values of the error function at the given points x.

See also:

`erfc`, `erfinv`, `erfcinv`

Notes

The cumulative of the unit normal distribution is given by `Phi(z) = 1/2[1 + erf(z/sqrt(2))]`.

References

[R282], [R283], [R284]

`scipy.special.`**`erfc`**`(`*x*`)` **= <ufunc 'erfc'>**

Complementary error function, 1 - erf(x).

References

[R285]

`scipy.special.`**`erfcx`**(*x*) **= <ufunc 'erfcx'>**

Scaled complementary error function, exp(x^2) erfc(x).

Notes

New in version 0.12.0.

References

[R286]

`scipy.special.`**`erfi`**(*z*) **= <ufunc 'erfi'>**

Imaginary error function, -i erf(i z).

Notes

New in version 0.12.0.

References

[R287]

`scipy.special.`**`erfinv`**(*y*)

Inverse function for erf

`scipy.special.`**`erfcinv`**(*y*)

Inverse function for erfc

`scipy.special.`**`wofz`**(*z*) **= <ufunc 'wofz'>**

Faddeeva function

Returns the value of the Faddeeva function for complex argument:

```
exp(-z**2)*erfc(-i*z)
```

References

[R292]

`scipy.special.`**`dawsn`**(*x*) **= <ufunc 'dawsn'>**

Dawson's integral.

Computes:

```
exp(-x**2) * integral(exp(t**2),t=0..x).
```

References

[R277]

`scipy.special.`**`fresnel`**(*z*) **= <ufunc 'fresnel'>**

Fresnel sin and cos integrals

Defined as:

```
ssa = integral(sin(pi/2 * t**2),t=0..z)
csa = integral(cos(pi/2 * t**2),t=0..z)
```

Parameters **z** : float or complex array_like

Argument

Returns ssa, csa

Fresnel sin and cos integral values

`scipy.special.`**`fresnel_zeros`**`(`*nt*`)`

Compute nt complex zeros of the sine and cosine Fresnel integrals S(z) and C(z).

`scipy.special.`**`modfresnelp`**`(`*x*`)` **= <ufunc 'modfresnelp'>**

Modified Fresnel positive integrals

Returns fp

Integral `F_+(x): integral(exp(1j*t*t),t=x..inf)`

kp

Integral `K_+(x): 1/sqrt(pi)*exp(-1j*(x*x+pi/4))*fp`

`scipy.special.`**`modfresnelm`**`(`*x*`)` **= <ufunc 'modfresnelm'>**

Modified Fresnel negative integrals

Returns fm

Integral `F_-(x): integral(exp(-1j*t*t),t=x..inf)`

km

Integral `K_-(x): 1/sqrt(pi)*exp(1j*(x*x+pi/4))*fp`

These are not universal functions:

`erf_zeros`(nt)	Compute nt complex zeros of the error function erf(z).
`fresnelc_zeros`(nt)	Compute nt complex zeros of the cosine Fresnel integral C(z).
`fresnels_zeros`(nt)	Compute nt complex zeros of the sine Fresnel integral S(z).

`scipy.special.`**`erf_zeros`**`(`*nt*`)`

Compute nt complex zeros of the error function erf(z).

`scipy.special.`**`fresnelc_zeros`**`(`*nt*`)`

Compute nt complex zeros of the cosine Fresnel integral C(z).

`scipy.special.`**`fresnels_zeros`**`(`*nt*`)`

Compute nt complex zeros of the sine Fresnel integral S(z).

Legendre Functions

`lpmv`(m, v, x)	Associated legendre function of integer order.
`sph_harm`(m, n, theta, phi)	Compute spherical harmonics.

`scipy.special.`**`lpmv`**`(`*m*, *v*, *x*`)` **= <ufunc 'lpmv'>**

Associated legendre function of integer order.

Parameters **m** : int

Order

v : real

Degree. Must be `v>-m-1` or `v<m`

x : complex

Argument. Must be `|x| <= 1`.

`scipy.special.`**`sph_harm`**`(`*m*, *n*, *theta*, *phi*`)` **= <ufunc 'sph_harm'>**

Compute spherical harmonics.

$$Y^m_n(\theta,\phi) = \sqrt{\frac{2n+1}{4\pi}\frac{(n-m)!}{(n+m)!}}e^{im\theta}P^m_n(\cos(\phi))$$

Parameters

m : int

`|m| <= n`; the order of the harmonic.

n : int

where *n* >= 0; the degree of the harmonic. This is often called `l` (lower case L) in descriptions of spherical harmonics.

theta : float

[0, 2*pi]; the azimuthal (longitudinal) coordinate.

phi : float

[0, pi]; the polar (colatitudinal) coordinate.

Returns

y_mn : complex float

The harmonic Y^m_n sampled at *theta* and *phi*

Notes

There are different conventions for the meaning of input arguments *theta* and *phi*. We take *theta* to be the azimuthal angle and *phi* to be the polar angle. It is common to see the opposite convention - that is *theta* as the polar angle and *phi* as the azimuthal angle.

References

[R291]

These are not universal functions:

`clpmn`(m, n, z[, type])	Associated Legendre function of the first kind, Pmn(z)
`lpn`(n, z)	Compute sequence of Legendre functions of the first kind (polynomials), Pn(z) and derivatives for all degree
`lqn`(n, z)	Compute sequence of Legendre functions of the second kind, Qn(z) and derivatives for all degrees from 0 to
`lpmn`(m, n, z)	Associated Legendre function of the first kind, Pmn(z)
`lqmn`(m, n, z)	Associated Legendre functions of the second kind, Qmn(z) and its derivative, `Qmn'(z)` of order m and deg

`scipy.special.`**`clpmn`**(*m*, *n*, *z*, *type=3*)

Associated Legendre function of the first kind, Pmn(z)

Computes the (associated) Legendre function of the first kind of order m and degree n,:

```
Pmn(z) = P_n^m(z)
```

and its derivative, `Pmn'(z)`. Returns two arrays of size `(m+1, n+1)` containing `Pmn(z)` and `Pmn'(z)` for all orders from `0..m` and degrees from `0..n`.

Parameters

m : int

`|m| <= n`; the order of the Legendre function.

n : int

where `n >= 0`; the degree of the Legendre function. Often called `l` (lower case L) in descriptions of the associated Legendre function

z : float or complex

Input value.

type : int, optional

takes values 2 or 3 2: cut on the real axis `|x| > 1` 3: cut on the real axis `-1 < x < 1` (default)

Returns

Pmn_z : (m+1, n+1) array

Values for all orders `0..m` and degrees `0..n`

Pmn_d_z : (m+1, n+1) array

Derivatives for all orders `0..m` and degrees `0..n`

See also:

lpmn	associated Legendre functions of the first kind for real z

Notes

By default, i.e. for `type=3`, phase conventions are chosen according to [R275] such that the function is analytic. The cut lies on the interval (-1, 1). Approaching the cut from above or below in general yields a phase factor with respect to Ferrer's function of the first kind (cf. `lpmn`).

For `type=2` a cut at `|x| > 1` is chosen. Approaching the real values on the interval (-1, 1) in the complex plane yields Ferrer's function of the first kind.

References

[R275]

`scipy.special.`**`lpn`**(*n*, *z*)

Compute sequence of Legendre functions of the first kind (polynomials), Pn(z) and derivatives for all degrees from 0 to n (inclusive).

See also special.legendre for polynomial class.

`scipy.special.`**`lqn`**(*n*, *z*)

Compute sequence of Legendre functions of the second kind, Qn(z) and derivatives for all degrees from 0 to n (inclusive).

`scipy.special.`**`lpmn`**(*m*, *n*, *z*)

Associated Legendre function of the first kind, Pmn(z)

Computes the associated Legendre function of the first kind of order m and degree n,:

```
Pmn(z) = P_n^m(z)
```

and its derivative, `Pmn'(z)`. Returns two arrays of size `(m+1, n+1)` containing `Pmn(z)` and `Pmn'(z)` for all orders from `0..m` and degrees from `0..n`.

This function takes a real argument `z`. For complex arguments `z` use clpmn instead.

Parameters

m : int

`|m| <= n`; the order of the Legendre function.

n : int

where `n >= 0`; the degree of the Legendre function. Often called `l` (lower case L) in descriptions of the associated Legendre function

z : float

Input value.

Returns

Pmn_z : (m+1, n+1) array

Values for all orders 0..m and degrees 0..n

Pmn_d_z : (m+1, n+1) array

Derivatives for all orders 0..m and degrees 0..n

See also:

clpmn	associated Legendre functions of the first kind for complex z

Notes

In the interval (-1, 1), Ferrer's function of the first kind is returned. The phase convention used for the intervals (1, inf) and (-inf, -1) is such that the result is always real.

References

[R290]

`scipy.special.`**`lqmn`**`(`*m*, *n*, *z*`)`

Associated Legendre functions of the second kind, Qmn(z) and its derivative, `Qmn'(z)` of order m and degree n. Returns two arrays of size `(m+1, n+1)` containing `Qmn(z)` and `Qmn'(z)` for all orders from `0..m` and degrees from `0..n`.

z can be complex.

Ellipsoidal Harmonics

`ellip_harm`(h2, k2, n, p, s[, signm, signn])	Ellipsoidal harmonic functions E^p_n(l)
`ellip_harm_2`(h2, k2, n, p, s)	Ellipsoidal harmonic functions F^p_n(l)
`ellip_normal`(h2, k2, n, p)	Ellipsoidal harmonic normalization constants gamma^p_n

`scipy.special.`**`ellip_harm`**`(`*h2*, *k2*, *n*, *p*, *s*, *signm=1*, *signn=1*`)`

Ellipsoidal harmonic functions E^p_n(l)

These are also known as Lame functions of the first kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)E''(s) + s(2s^2 - h^2 - k^2)E'(s) + (a - qs^2)E(s) = 0$$

where $q = (n+1)n$ and a is the eigenvalue (not returned) corresponding to the solutions.

Parameters

h2 : float

`h**2`

k2 : float

`k**2`; should be larger than `h**2`

n : int

Degree

s : float

Coordinate

p : int

Order, can range between [1,2n+1]

signm : {1, -1}, optional

Sign of prefactor of functions. Can be +/-1. See Notes.

signn : {1, -1}, optional

Sign of prefactor of functions. Can be +/-1. See Notes.

Returns

E : float

the harmonic $E^p_n(s)$

See also:

`ellip_harm_2`, `ellip_normal`

Notes

The geometric intepretation of the ellipsoidal functions is explained in [R279], [R280], [R281]. The *signm* and *signn* arguments control the sign of prefactors for functions according to their type:

```
K : +1
L : signm
M : signn
N : signm*signn
```

New in version 0.15.0.

References

[R278], [R279], [R280], [R281]

Examples

```
>>> from scipy.special import ellip_harm
>>> w = ellip_harm(5,8,1,1,2.5)
>>> w
2.5
```

Check that the functions indeed are solutions to the Lame equation:

```
>>> from scipy.interpolate import UnivariateSpline
>>> def eigenvalue(f, df, ddf):
...     r = ((s**2 - h**2)*(s**2 - k**2)*ddf + s*(2*s**2 - h**2 - k**2)*df - n*(n+1)*s**2*f)/f
...     return -r.mean(), r.std()
>>> s = np.linspace(0.1, 10, 200)
>>> k, h, n, p = 8.0, 2.2, 3, 2
>>> E = ellip_harm(h**2, k**2, n, p, s)
>>> E_spl = UnivariateSpline(s, E)
>>> a, a_err = eigenvalue(E_spl(s), E_spl(s,1), E_spl(s,2))
>>> a, a_err
(583.44366156701483, 6.4580890640310646e-11)
```

scipy.special.**ellip_harm_2**(*h2*, *k2*, *n*, *p*, *s*)

Ellipsoidal harmonic functions F^p_n(l)

These are also known as Lame functions of the second kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)F''(s) + s(2s^2 - h^2 - k^2)F'(s) + (a - qs^2)F(s) = 0$$

where $q = (n+1)n$ and a is the eigenvalue (not returned) corresponding to the solutions.

Parameters	**h2** : float	`h**2`
	k2 : float	`k**2`; should be larger than `h**2`
	n : int	Degree.
	p : int	Order, can range between [1,2n+1].
	s : float	Coordinate
Returns	**F** : float	The harmonic $F_n^p(s)$

See also:

`ellip_harm`, `ellip_normal`

Notes

Lame functions of the second kind are related to the functions of the first kind:

$$F_n^p(s) = (2n+1)E_n^p(s)\int_0^{1/s}\frac{du}{(E_n^p(1/u))^2\sqrt{(1-u^2k^2)(1-u^2h^2)}}$$

New in version 0.15.0.

Examples

```
>>> from scipy.special import ellip_harm_2
>>> w = ellip_harm_2(5,8,2,1,10)
>>> w
0.00108056853382
```

`scipy.special.`**`ellip_normal`**`(`*h2*, *k2*, *n*, *p*`)`

Ellipsoidal harmonic normalization constants gamma^p_n

The normalization constant is defined as

$$\gamma^p_n = 8 \int_0^h dx \int_h^k dy \frac{(y^2 - x^2)(E^p_n(y)E^p_n(x))^2}{\sqrt{((k^2 - y^2)(y^2 - h^2)(h^2 - x^2)(k^2 - x^2)}}$$

Parameters

h2 : float

`h**2`

k2 : float

`k**2`; should be larger than `h**2`

n : int

Degree.

p : int

Order, can range between [1,2n+1].

Returns

gamma : float

The normalization constant γ^p_n

See also:

`ellip_harm`, `ellip_harm_2`

Notes

New in version 0.15.0.

Examples

```
>>> from scipy.special import ellip_normal
>>> w = ellip_normal(5,8,3,7)
>>> w
1723.38796997
```

Orthogonal polynomials

The following functions evaluate values of orthogonal polynomials:

`assoc_laguerre`(x, n[, k])	Returns the n-th order generalized (associated) Laguerre polynomial.
`eval_legendre`(n, x[, out])	Evaluate Legendre polynomial at a point.
`eval_chebyt`(n, x[, out])	Evaluate Chebyshev T polynomial at a point.
`eval_chebyu`(n, x[, out])	Evaluate Chebyshev U polynomial at a point.
`eval_chebyc`(n, x[, out])	Evaluate Chebyshev C polynomial at a point.
`eval_chebys`(n, x[, out])	Evaluate Chebyshev S polynomial at a point.
`eval_jacobi`(n, alpha, beta, x[, out])	Evaluate Jacobi polynomial at a point.
`eval_laguerre`(n, x[, out])	Evaluate Laguerre polynomial at a point.
`eval_genlaguerre`(n, alpha, x[, out])	Evaluate generalized Laguerre polynomial at a point.
`eval_hermite`(n, x[, out])	Evaluate Hermite polynomial at a point.

Continued on next page

Table 5.230 – continued from previous page

`eval_hermitenorm`(n, x[, out])	Evaluate normalized Hermite polynomial at a point.
`eval_gegenbauer`(n, alpha, x[, out])	Evaluate Gegenbauer polynomial at a point.
`eval_sh_legendre`(n, x[, out])	Evaluate shifted Legendre polynomial at a point.
`eval_sh_chebyt`(n, x[, out])	Evaluate shifted Chebyshev T polynomial at a point.
`eval_sh_chebyu`(n, x[, out])	Evaluate shifted Chebyshev U polynomial at a point.
`eval_sh_jacobi`(n, p, q, x[, out])	Evaluate shifted Jacobi polynomial at a point.

`scipy.special.`**`assoc_laguerre`**(*x*, *n*, *k=0.0*)

Returns the n-th order generalized (associated) Laguerre polynomial.

The polynomial $L^(alpha)_n(x)$ is orthogonal over `[0, inf)`, with weighting function `exp(-x) * x**alpha` with `alpha > -1`.

Notes

`assoc_laguerre` is a simple wrapper around `eval_genlaguerre`, with reversed argument order `(x, n, k=0.0) --> (n, k, x)`.

`scipy.special.`**`eval_legendre`**(*n*, *x*, *out=None*) **= <ufunc 'eval_legendre'>**

Evaluate Legendre polynomial at a point.

`scipy.special.`**`eval_chebyt`**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyt'>**

Evaluate Chebyshev T polynomial at a point.

This routine is numerically stable for *x* in `[-1, 1]` at least up to order `10000`.

`scipy.special.`**`eval_chebyu`**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyu'>**

Evaluate Chebyshev U polynomial at a point.

`scipy.special.`**`eval_chebyc`**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyc'>**

Evaluate Chebyshev C polynomial at a point.

`scipy.special.`**`eval_chebys`**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebys'>**

Evaluate Chebyshev S polynomial at a point.

`scipy.special.`**`eval_jacobi`**(*n*, *alpha*, *beta*, *x*, *out=None*) **= <ufunc 'eval_jacobi'>**

Evaluate Jacobi polynomial at a point.

`scipy.special.`**`eval_laguerre`**(*n*, *x*, *out=None*) **= <ufunc 'eval_laguerre'>**

Evaluate Laguerre polynomial at a point.

`scipy.special.`**`eval_genlaguerre`**(*n*, *alpha*, *x*, *out=None*) **= <ufunc 'eval_genlaguerre'>**

Evaluate generalized Laguerre polynomial at a point.

`scipy.special.`**`eval_hermite`**(*n*, *x*, *out=None*) **= <ufunc 'eval_hermite'>**

Evaluate Hermite polynomial at a point.

`scipy.special.`**`eval_hermitenorm`**(*n*, *x*, *out=None*) **= <ufunc 'eval_hermitenorm'>**

Evaluate normalized Hermite polynomial at a point.

`scipy.special.`**`eval_gegenbauer`**(*n*, *alpha*, *x*, *out=None*) **= <ufunc 'eval_gegenbauer'>**

Evaluate Gegenbauer polynomial at a point.

`scipy.special.`**`eval_sh_legendre`**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_legendre'>**

Evaluate shifted Legendre polynomial at a point.

`scipy.special.`**`eval_sh_chebyt`**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_chebyt'>**

Evaluate shifted Chebyshev T polynomial at a point.

`scipy.special.`**`eval_sh_chebyu`**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_chebyu'>**

Evaluate shifted Chebyshev U polynomial at a point.

`scipy.special.`**`eval_sh_jacobi`**(*n*, *p*, *q*, *x*, *out=None*) **= <ufunc 'eval_sh_jacobi'>**

Evaluate shifted Jacobi polynomial at a point.

The functions below, in turn, return the polynomial coefficients in `orthopoly1d` objects, which function similarly as *numpy.poly1d*. The `orthopoly1d` class also has an attribute `weights` which returns the roots, weights, and total weights for the appropriate form of Gaussian quadrature. These are returned in an `n x 3` array with roots in the first column, weights in the second column, and total weights in the final column. Note that `orthopoly1d` objects are converted to `poly1d` when doing arithmetic, and lose information of the original orthogonal polynomial.

`legendre`(n[, monic])	Legendre polynomial coefficients
`chebyt`(n[, monic])	Return nth order Chebyshev polynomial of first kind, Tn(x).
`chebyu`(n[, monic])	Return nth order Chebyshev polynomial of second kind, Un(x).
`chebyc`(n[, monic])	Return nth order Chebyshev polynomial of first kind, Cn(x).
`chebys`(n[, monic])	Return nth order Chebyshev polynomial of second kind, Sn(x).
`jacobi`(n, alpha, beta[, monic])	Returns the nth order Jacobi polynomial, P^(alpha,beta)_n(x) orthogonal over [-1,1] with weigh
`laguerre`(n[, monic])	Return the nth order Laguerre polynoimal, L_n(x), orthogonal over
`genlaguerre`(n, alpha[, monic])	Returns the nth order generalized (associated) Laguerre polynomial,
`hermite`(n[, monic])	Return the nth order Hermite polynomial, H_n(x), orthogonal over
`hermitenorm`(n[, monic])	Return the nth order normalized Hermite polynomial, He_n(x), orthogonal
`gegenbauer`(n, alpha[, monic])	Return the nth order Gegenbauer (ultraspherical) polynomial,
`sh_legendre`(n[, monic])	Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weight
`sh_chebyt`(n[, monic])	Return nth order shifted Chebyshev polynomial of first kind, Tn(x).
`sh_chebyu`(n[, monic])	Return nth order shifted Chebyshev polynomial of second kind, Un(x).
`sh_jacobi`(n, p, q[, monic])	Returns the nth order Jacobi polynomial, G_n(p,q,x) orthogonal over [0,1] with weighting funct

`scipy.special.`**`legendre`**(*n*, *monic=False*)

Legendre polynomial coefficients

Returns the nth-order Legendre polynomial, P_n(x), orthogonal over [-1, 1] with weight function 1.

Parameters **n**

Order of the polynomial

monic : bool, optional

If True, output is a monic polynomial (normalized so the leading coefficient is 1). Default is False.

Returns **P** : orthopoly1d

The Legendre polynomial object

Examples

Generate the 3rd-order Legendre polynomial 1/2*(5x^3 + 0x^2 - 3x + 0):

```
>>> legendre(3)
poly1d([ 2.5,  0. , -1.5, -0. ])
```

`scipy.special.`**`chebyt`**(*n*, *monic=False*)

Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal over [-1,1] with weight function (1-x**2)**(-1/2).

`scipy.special.`**`chebyu`**(*n*, *monic=False*)

Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal over [-1,1] with weight function (1-x**2)**(1/2).

`scipy.special.`**`chebyc`**(*n*, *monic=False*)

Return nth order Chebyshev polynomial of first kind, Cn(x). Orthogonal over [-2,2] with weight function (1-(x/2)**2)**(-1/2).

`scipy.special.`**`chebys`**`(`*n*, *monic=False*`)`
Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal over [-2,2] with weight function (1-(x/2)**2)**(1/2).

`scipy.special.`**`jacobi`**`(`*n*, *alpha*, *beta*, *monic=False*`)`
Returns the nth order Jacobi polynomial, P^(alpha,beta)_n(x) orthogonal over [-1,1] with weighting function (1-x)**alpha (1+x)**beta with alpha,beta > -1.

`scipy.special.`**`laguerre`**`(`*n*, *monic=False*`)`
Return the nth order Laguerre polynoimal, L_n(x), orthogonal over [0,inf) with weighting function exp(-x)

`scipy.special.`**`genlaguerre`**`(`*n*, *alpha*, *monic=False*`)`
Returns the nth order generalized (associated) Laguerre polynomial, L^(alpha)_n(x), orthogonal over [0,inf) with weighting function exp(-x) x**alpha with alpha > -1

`scipy.special.`**`hermite`**`(`*n*, *monic=False*`)`
Return the nth order Hermite polynomial, H_n(x), orthogonal over (-inf,inf) with weighting function exp(-x**2)

`scipy.special.`**`hermitenorm`**`(`*n*, *monic=False*`)`
Return the nth order normalized Hermite polynomial, He_n(x), orthogonal over (-inf,inf) with weighting function exp(-(x/2)**2)

`scipy.special.`**`gegenbauer`**`(`*n*, *alpha*, *monic=False*`)`
Return the nth order Gegenbauer (ultraspherical) polynomial, C^(alpha)_n(x), orthogonal over [-1,1] with weighting function (1-x**2)**(alpha-1/2) with alpha > -1/2

`scipy.special.`**`sh_legendre`**`(`*n*, *monic=False*`)`
Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weighting function 1.

`scipy.special.`**`sh_chebyt`**`(`*n*, *monic=False*`)`
Return nth order shifted Chebyshev polynomial of first kind, Tn(x). Orthogonal over [0,1] with weight function (x-x**2)**(-1/2).

`scipy.special.`**`sh_chebyu`**`(`*n*, *monic=False*`)`
Return nth order shifted Chebyshev polynomial of second kind, Un(x). Orthogonal over [0,1] with weight function (x-x**2)**(1/2).

`scipy.special.`**`sh_jacobi`**`(`*n*, *p*, *q*, *monic=False*`)`
Returns the nth order Jacobi polynomial, G_n(p,q,x) orthogonal over [0,1] with weighting function (1-x)**(p-q) (x)**(q-1) with p>q-1 and q > 0.

Warning: Computing values of high-order polynomials (around `order > 20`) using polynomial coefficients is numerically unstable. To evaluate polynomial values, the `eval_*` functions should be used instead.

Hypergeometric Functions

`hyp2f1`(a, b, c, z)	Gauss hypergeometric function 2F1(a, b; c; z).
`hyp1f1`(a, b, x)	Confluent hypergeometric function 1F1(a, b; x)
`hyperu`(a, b, x)	Confluent hypergeometric function U(a, b, x) of the second kind
`hyp0f1`(v, z)	Confluent hypergeometric limit function 0F1.
`hyp2f0`(a, b, x, type)	Hypergeometric function 2F0 in y and an error estimate
`hyp1f2`(a, b, c, x)	Hypergeometric function 1F2 and error estimate
`hyp3f0`(a, b, c, x)	Hypergeometric function 3F0 in y and an error estimate

`scipy.special.`**`hyp2f1`**`(`*a*, *b*, *c*, *z*`)` **= <ufunc 'hyp2f1'>**
Gauss hypergeometric function 2F1(a, b; c; z).

`scipy.special.`**`hyp1f1`**`(`*a*, *b*, *x*`)` **= <ufunc 'hyp1f1'>**
Confluent hypergeometric function 1F1(a, b; x)

`scipy.special.`**`hyperu`**`(`*a*, *b*, *x*`)` **= <ufunc 'hyperu'>**
Confluent hypergeometric function U(a, b, x) of the second kind

`scipy.special.`**`hyp0f1`**`(`*v*, *z*`)`
Confluent hypergeometric limit function 0F1.

Parameters **v, z** : array_like

Input values.

Returns **hyp0f1** : ndarray

The confluent hypergeometric limit function.

Notes

This function is defined as:

$$_0F_1(v,z) = \sum_{k=0}^{\inf} \frac{z^k}{(v)_k k!}.$$

It's also the limit as q -> infinity of `1F1(q;v;z/q)`, and satisfies the differential equation $f''(z) + vf'(z) = f(z)$.

`scipy.special.`**`hyp2f0`**`(`*a*, *b*, *x*, *type*`)` **= <ufunc 'hyp2f0'>**
Hypergeometric function 2F0 in y and an error estimate

The parameter *type* determines a convergence factor and can be either 1 or 2.

Returns y

Value of the function

err

Error estimate

`scipy.special.`**`hyp1f2`**`(`*a*, *b*, *c*, *x*`)` **= <ufunc 'hyp1f2'>**
Hypergeometric function 1F2 and error estimate

Returns y

Value of the function

err

Error estimate

`scipy.special.`**`hyp3f0`**`(`*a*, *b*, *c*, *x*`)` **= <ufunc 'hyp3f0'>**
Hypergeometric function 3F0 in y and an error estimate

Returns y

Value of the function

err

Error estimate

Parabolic Cylinder Functions

`pbdv`(v, x)	Parabolic cylinder function D
`pbvv`(v,x)	Parabolic cylinder function V
`pbwa`(a,x)	Parabolic cylinder function W

`scipy.special.`**`pbdv`**`(`*v*, *x*`)` **= <ufunc 'pbdv'>**
Parabolic cylinder function D

Returns (d,dp) the parabolic cylinder function Dv(x) in d and the derivative, Dv'(x) in dp.

Returns	
d	Value of the function
dp	Value of the derivative vs x

`scipy.special.`**`pbvv`**`(`*v*, *x*`)` **= <ufunc 'pbvv'>**

Parabolic cylinder function V

Returns the parabolic cylinder function Vv(x) in v and the derivative, Vv'(x) in vp.

Returns	
v	Value of the function
vp	Value of the derivative vs x

`scipy.special.`**`pbwa`**`(`*a*, *x*`)` **= <ufunc 'pbwa'>**

Parabolic cylinder function W

Returns the parabolic cylinder function W(a,x) in w and the derivative, W'(a,x) in wp.

> **Warning:** May not be accurate for large (>5) arguments in a and/or x.

Returns	
w	Value of the function
wp	Value of the derivative vs x

These are not universal functions:

`pbdv_seq`(v, x)	Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v)
`pbvv_seq`(v, x)	Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v)
`pbdn_seq`(n, z)	Compute sequence of parabolic cylinder functions Dn(z) and their derivatives for D0(z)..Dn(z).

`scipy.special.`**`pbdv_seq`**`(`*v*, *x*`)`

Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v).

`scipy.special.`**`pbvv_seq`**`(`*v*, *x*`)`

Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v).

`scipy.special.`**`pbdn_seq`**`(`*n*, *z*`)`

Compute sequence of parabolic cylinder functions Dn(z) and their derivatives for D0(z)..Dn(z).

Mathieu and Related Functions

`mathieu_a`(m,q)	Characteristic value of even Mathieu functions
`mathieu_b`(m,q)	Characteristic value of odd Mathieu functions

`scipy.special.`**`mathieu_a`**`(`*m*, *q*`)` **= <ufunc 'mathieu_a'>**

Characteristic value of even Mathieu functions

Returns the characteristic value for the even solution, `ce_m(z,q)`, of Mathieu's equation.

`scipy.special.`**`mathieu_b`**`(`*m*, *q*`)` **= <ufunc 'mathieu_b'>**

Characteristic value of odd Mathieu functions

Returns the characteristic value for the odd solution, `se_m(z,q)`, of Mathieu's equation.

These are not universal functions:

`mathieu_even_coef`(m, q)	Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.
`mathieu_odd_coef`(m, q)	Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.

`scipy.special.`**`mathieu_even_coef`**(*m*, *q*)

Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.

`scipy.special.`**`mathieu_odd_coef`**(*m*, *q*)

Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.

The following return both function and first derivative:

`mathieu_cem`(m,q,x)	Even Mathieu function and its derivative
`mathieu_sem`(m, q, x)	Odd Mathieu function and its derivative
`mathieu_modcem1`(m, q, x)	Even modified Mathieu function of the first kind and its derivative
`mathieu_modcem2`(m, q, x)	Even modified Mathieu function of the second kind and its derivative
`mathieu_modsem1`(m,q,x)	Odd modified Mathieu function of the first kind and its derivative
`mathieu_modsem2`(m, q, x)	Odd modified Mathieu function of the second kind and its derivative

`scipy.special.`**`mathieu_cem`**(*m*, *q*, *x*) **= <ufunc 'mathieu_cem'>**

Even Mathieu function and its derivative

Returns the even Mathieu function, `ce_m(x,q)`, of order m and parameter q evaluated at x (given in degrees). Also returns the derivative with respect to x of ce_m(x,q)

Parameters

m
Order of the function

q
Parameter of the function

x
Argument of the function, *given in degrees, not radians*

Returns

y
Value of the function

yp
Value of the derivative vs x

`scipy.special.`**`mathieu_sem`**(*m*, *q*, *x*) **= <ufunc 'mathieu_sem'>**

Odd Mathieu function and its derivative

Returns the odd Mathieu function, se_m(x,q), of order m and parameter q evaluated at x (given in degrees). Also returns the derivative with respect to x of se_m(x,q).

Parameters

m
Order of the function

q
Parameter of the function

x
Argument of the function, *given in degrees, not radians*.

Returns

y
Value of the function

yp
Value of the derivative vs x

`scipy.special.`**`mathieu_modcem1`**(*m*, *q*, *x*) = **<ufunc ‘mathieu_modcem1’>**

Even modified Mathieu function of the first kind and its derivative

Evaluates the even modified Mathieu function of the first kind, `Mc1m(x,q)`, and its derivative at *x* for order m and parameter *q*.

Returns y

Value of the function

yp

Value of the derivative vs x

`scipy.special.`**`mathieu_modcem2`**(*m*, *q*, *x*) = **<ufunc ‘mathieu_modcem2’>**

Even modified Mathieu function of the second kind and its derivative

Evaluates the even modified Mathieu function of the second kind, Mc2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

Returns y

Value of the function

yp

Value of the derivative vs x

`scipy.special.`**`mathieu_modsem1`**(*m*, *q*, *x*) = **<ufunc ‘mathieu_modsem1’>**

Odd modified Mathieu function of the first kind and its derivative

Evaluates the odd modified Mathieu function of the first kind, Ms1m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

Returns y

Value of the function

yp

Value of the derivative vs x

`scipy.special.`**`mathieu_modsem2`**(*m*, *q*, *x*) = **<ufunc ‘mathieu_modsem2’>**

Odd modified Mathieu function of the second kind and its derivative

Evaluates the odd modified Mathieu function of the second kind, Ms2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

Returns y

Value of the function

yp

Value of the derivative vs x

Spheroidal Wave Functions

`pro_ang1`(m,n,c,x)	Prolate spheroidal angular function of the first kind and its derivative
`pro_rad1`(m,n,c,x)	Prolate spheroidal radial function of the first kind and its derivative
`pro_rad2`(m,n,c,x)	Prolate spheroidal radial function of the secon kind and its derivative
`obl_ang1`(m, n, c, x)	Oblate spheroidal angular function of the first kind and its derivative
`obl_rad1`(m,n,c,x)	Oblate spheroidal radial function of the first kind and its derivative
`obl_rad2`(m,n,c,x)	Oblate spheroidal radial function of the second kind and its derivative.
`pro_cv`(m,n,c)	Characteristic value of prolate spheroidal function
`obl_cv`(m, n, c)	Characteristic value of oblate spheroidal function
`pro_cv_seq`(m, n, c)	Compute a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n’=m
`obl_cv_seq`(m, n, c)	Compute a sequence of characteristic values for the oblate spheroidal wave functions for mode m and n’=m

`scipy.special.`**`pro_ang1`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'pro_ang1'>**

Prolate spheroidal angular function of the first kind and its derivative

Computes the prolate spheroidal angular function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`pro_rad1`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'pro_rad1'>**

Prolate spheroidal radial function of the first kind and its derivative

Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`pro_rad2`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'pro_rad2'>**

Prolate spheroidal radial function of the secon kind and its derivative

Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`obl_ang1`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'obl_ang1'>**

Oblate spheroidal angular function of the first kind and its derivative

Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`obl_rad1`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'obl_rad1'>**

Oblate spheroidal radial function of the first kind and its derivative

Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`obl_rad2`**`(`*m*, *n*, *c*, *x*`)` **= <ufunc 'obl_rad2'>**

Oblate spheroidal radial function of the second kind and its derivative.

Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`pro_cv`**`(`*m*, *n*, *c*`)` **= <ufunc 'pro_cv'>**

Characteristic value of prolate spheroidal function

Computes the characteristic value of prolate spheroidal wave functions of order m,n (n>=m) and spheroidal parameter c.

`scipy.special.`**`obl_cv`**`(`*m*, *n*, *c*`)` **= <ufunc 'obl_cv'>**

Characteristic value of oblate spheroidal function

Computes the characteristic value of oblate spheroidal wave functions of order m,n (n>=m) and spheroidal parameter c.

`scipy.special.`**`pro_cv_seq`**`(`*m*, *n*, *c*`)`

Compute a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

`scipy.special.`**`obl_cv_seq`**`(`*m*, *n*, *c*`)`

Compute a sequence of characteristic values for the oblate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

The following functions require pre-computed characteristic value:

`pro_ang1_cv`(m,n,c,cv,x)	Prolate spheroidal angular function pro_ang1 for precomputed characteristic value
`pro_rad1_cv`(m,n,c,cv,x)	Prolate spheroidal radial function pro_rad1 for precomputed characteristic value
`pro_rad2_cv`(m,n,c,cv,x)	Prolate spheroidal radial function pro_rad2 for precomputed characteristic value
`obl_ang1_cv`(m, n, c, cv, x)	Oblate spheroidal angular function obl_ang1 for precomputed characteristic value
`obl_rad1_cv`(m,n,c,cv,x)	Oblate spheroidal radial function obl_rad1 for precomputed characteristic value
`obl_rad2_cv`(m,n,c,cv,x)	Oblate spheroidal radial function obl_rad2 for precomputed characteristic value

`scipy.special.`**`pro_ang1_cv`**`(`*m*, *n*, *c*, *cv*, *x*`)` **= <ufunc 'pro_ang1_cv'>**

Prolate spheroidal angular function pro_ang1 for precomputed characteristic value

Computes the prolate spheroidal angular function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`pro_rad1_cv`**`(`*m*, *n*, *c*, *cv*, *x*`)` **= <ufunc 'pro_rad1_cv'>**

Prolate spheroidal radial function pro_rad1 for precomputed characteristic value

Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns s

Value of the function

sp

Value of the derivative vs x

`scipy.special.`**`pro_rad2_cv`**`(`*m*, *n*, *c*, *cv*, *x*`)` **= <ufunc 'pro_rad2_cv'>**

Prolate spheroidal radial function pro_rad2 for precomputed characteristic value

Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns	s	
		Value of the function
	sp	
		Value of the derivative vs x

`scipy.special.`**`obl_ang1_cv`**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_ang1_cv'>**

Oblate spheroidal angular function obl_ang1 for precomputed characteristic value

Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns	s	
		Value of the function
	sp	
		Value of the derivative vs x

`scipy.special.`**`obl_rad1_cv`**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_rad1_cv'>**

Oblate spheroidal radial function obl_rad1 for precomputed characteristic value

Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns	s	
		Value of the function
	sp	
		Value of the derivative vs x

`scipy.special.`**`obl_rad2_cv`**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_rad2_cv'>**

Oblate spheroidal radial function obl_rad2 for precomputed characteristic value

Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to x) for mode parameters m>=0 and n>=m, spheroidal parameter c and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns	s	
		Value of the function
	sp	
		Value of the derivative vs x

Kelvin Functions

`kelvin`(x)	Kelvin functions as complex numbers
`kelvin_zeros`(nt)	Compute nt zeros of all the Kelvin functions returned in a length 8 tuple of arrays of length nt.
`ber`(x)	Kelvin function ber.
`bei`(x)	Kelvin function bei
`berp`(x)	Derivative of the Kelvin function ber
`beip`(x)	Derivative of the Kelvin function bei
`ker`(x)	Kelvin function ker
`kei`(x)	Kelvin function ker
`kerp`(x)	Derivative of the Kelvin function ker

Continued on next page

Table 5.240 – continued from previous page

`keip`(x)	Derivative of the Kelvin function kei

`scipy.special.`**`kelvin`**(*x*) = **<ufunc 'kelvin'>**

Kelvin functions as complex numbers

Returns Be, Ke, Bep, Kep

The tuple (Be, Ke, Bep, Kep) contains complex numbers representing the real and imaginary Kelvin functions and their derivatives evaluated at x. For example, kelvin(x)[0].real = ber x and kelvin(x)[0].imag = bei x with similar relationships for ker and kei.

`scipy.special.`**`kelvin_zeros`**(*nt*)

Compute nt zeros of all the Kelvin functions returned in a length 8 tuple of arrays of length nt. The tuple containse the arrays of zeros of (ber, bei, ker, kei, ber', bei', ker', kei')

`scipy.special.`**`ber`**(*x*) = **<ufunc 'ber'>**

Kelvin function ber.

`scipy.special.`**`bei`**(*x*) = **<ufunc 'bei'>**

Kelvin function bei

`scipy.special.`**`berp`**(*x*) = **<ufunc 'berp'>**

Derivative of the Kelvin function ber

`scipy.special.`**`beip`**(*x*) = **<ufunc 'beip'>**

Derivative of the Kelvin function bei

`scipy.special.`**`ker`**(*x*) = **<ufunc 'ker'>**

Kelvin function ker

`scipy.special.`**`kei`**(*x*) = **<ufunc 'kei'>**

Kelvin function ker

`scipy.special.`**`kerp`**(*x*) = **<ufunc 'kerp'>**

Derivative of the Kelvin function ker

`scipy.special.`**`keip`**(*x*) = **<ufunc 'keip'>**

Derivative of the Kelvin function kei

These are not universal functions:

`ber_zeros`(nt)	Compute nt zeros of the Kelvin function ber x
`bei_zeros`(nt)	Compute nt zeros of the Kelvin function bei x
`berp_zeros`(nt)	Compute nt zeros of the Kelvin function ber' x
`beip_zeros`(nt)	Compute nt zeros of the Kelvin function bei' x
`ker_zeros`(nt)	Compute nt zeros of the Kelvin function ker x
`kei_zeros`(nt)	Compute nt zeros of the Kelvin function kei x
`kerp_zeros`(nt)	Compute nt zeros of the Kelvin function ker' x
`keip_zeros`(nt)	Compute nt zeros of the Kelvin function kei' x

`scipy.special.`**`ber_zeros`**(*nt*)

Compute nt zeros of the Kelvin function ber x

`scipy.special.`**`bei_zeros`**(*nt*)

Compute nt zeros of the Kelvin function bei x

`scipy.special.`**`berp_zeros`**(*nt*)

Compute nt zeros of the Kelvin function ber' x

`scipy.special.`**`beip_zeros`**(*nt*)
Compute nt zeros of the Kelvin function bei' x

`scipy.special.`**`ker_zeros`**(*nt*)
Compute nt zeros of the Kelvin function ker x

`scipy.special.`**`kei_zeros`**(*nt*)
Compute nt zeros of the Kelvin function kei x

`scipy.special.`**`kerp_zeros`**(*nt*)
Compute nt zeros of the Kelvin function ker' x

`scipy.special.`**`keip_zeros`**(*nt*)
Compute nt zeros of the Kelvin function kei' x

Combinatorics

`comb`(N, k[, exact, repetition])	The number of combinations of N things taken k at a time.
`perm`(N, k[, exact])	Permutations of N things taken k at a time, i.e., k-permutations of N.

`scipy.special.`**`comb`**(*N*, *k*, *exact=False*, *repetition=False*)
The number of combinations of N things taken k at a time.

This is often expressed as "N choose k".

Parameters **N** : int, ndarray
Number of things.
k : int, ndarray
Number of elements taken.
exact : bool, optional
If *exact* is False, then floating point precision is used, otherwise exact long integer is computed.
repetition : bool, optional
If *repetition* is True, then the number of combinations with repetition is computed.

Returns **val** : int, ndarray
The total number of combinations.

Notes

- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

```
>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([ 120.,  210.])
>>> comb(10, 3, exact=True)
120L
>>> comb(10, 3, exact=True, repetition=True)
220L
```

`scipy.special.`**`perm`**(*N*, *k*, *exact=False*)
Permutations of N things taken k at a time, i.e., k-permutations of N.

It's also known as "partial permutations".

Parameters **N** : int, ndarray

Number of things.

k : int, ndarray

Number of elements taken.

exact : bool, optional

If *exact* is False, then floating point precision is used, otherwise exact long integer is computed.

Returns **val** : int, ndarray

The number of k-permutations of N.

Notes

- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

```
>>> from scipy.special import perm
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> perm(n, k)
array([  720.,  5040.])
>>> perm(10, 3, exact=True)
720
```

Other Special Functions

`agm`(a, b)	Arithmetic, Geometric Mean
`bernoulli`(n)	Return an array of the Bernoulli numbers B0..Bn
`binom`(n, k)	Binomial coefficient
`diric`(x, n)	Return the periodic sinc function, also called the Dirichlet function.
`euler`(n)	Return an array of the Euler numbers E0..En (inclusive)
`expn`(n, x)	Exponential integral E_n
`exp1`(z)	Exponential integral E_1 of complex argument z
`expi`(x)	Exponential integral Ei
`factorial`(n[, exact])	The factorial function, n! = special.gamma(n+1).
`factorial2`(n[, exact])	Double factorial.
`factorialk`(n, k[, exact])	n(!!...!) = multifactorial of order k
`shichi`(x)	Hyperbolic sine and cosine integrals
`sici`(x)	Sine and cosine integrals
`spence`(x)	Dilogarithm integral
`lambertw`(z[, k, tol])	Lambert W function [R599].
`zeta`(x, q)	Hurwitz zeta function
`zetac`(x)	Riemann zeta function minus 1.

`scipy.special.`**`agm`**`(`*a*, *b*`)`

Arithmetic, Geometric Mean

Start with a_0=a and b_0=b and iteratively compute

a_{n+1} = (a_n+b_n)/2 b_{n+1} = sqrt(a_n*b_n)

until a_n=b_n. The result is agm(a,b)

agm(a,b)=agm(b,a) agm(a,a) = a min(a,b) < agm(a,b) < max(a,b)

`scipy.special.`**`bernoulli`**`(`*n*`)`

Return an array of the Bernoulli numbers B0..Bn

`scipy.special.`**`binom`**`(`*n*, *k*`)` **= <ufunc 'binom'>**

Binomial coefficient

`scipy.special.`**`diric`**`(`*x*, *n*`)`

Return the periodic sinc function, also called the Dirichlet function.

The Dirichlet function is defined as:

```
diric(x) = sin(x * n/2) / (n * sin(x / 2)),
```

where n is a positive integer.

Parameters **x** : array_like

Input data

n : int

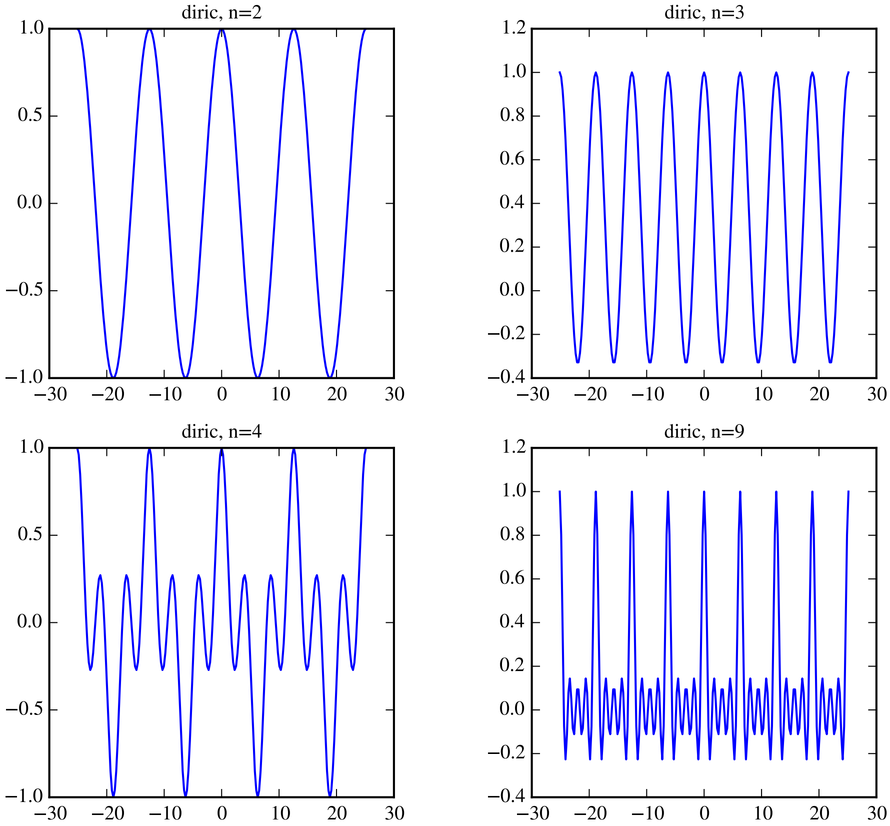
Integer defining the periodicity.

Returns **diric** : ndarray

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-8*np.pi, 8*np.pi, num=201)
>>> plt.figure(figsize=(8,8));
>>> for idx, n in enumerate([2,3,4,9]):
...     plt.subplot(2, 2, idx+1)
...     plt.plot(x, special.diric(x, n))
...     plt.title('diric, n={}'.format(n))
>>> plt.show()
```



`scipy.special.`**`euler`**`(`*n*`)`

Return an array of the Euler numbers E0..En (inclusive)

`scipy.special.`**`expn`**`(`*n, x*`)` **= <ufunc 'expn'>**

Exponential integral E_n

Returns the exponential integral for integer n and non-negative x and n:

```
integral(exp(-x*t) / t**n, t=1..inf).
```

`scipy.special.`**`exp1`**`(`*z*`)` **= <ufunc 'exp1'>**

Exponential integral E_1 of complex argument z

```
integral(exp(-z*t)/t,t=1..inf).
```

`scipy.special.`**`expi`**`(`*x*`)` **= <ufunc 'expi'>**

Exponential integral Ei

Defined as:

```
integral(exp(t)/t,t=-inf..x)
```

See `expn` for a different exponential integral.

`scipy.special.`**`factorial`**`(`*n*, *exact=False*`)`

The factorial function, n! = special.gamma(n+1).

If exact is 0, then floating point precision is used, otherwise exact long integer is computed.

- Array argument accepted only for exact=False case.
- If n<0, the return value is 0.

Parameters **n** : int or array_like of ints

Calculate `n!`. Arrays are only supported with *exact* set to False. If `n < 0`, the return value is 0.

exact : bool, optional

The result can be approximated rapidly using the gamma-formula above. If *exact* is set to True, calculate the answer exactly using integer arithmetic. Default is False.

Returns **nf** : float or int

Factorial of *n*, as an integer or a float depending on *exact*.

Examples

```
>>> from scipy.special import factorial
>>> arr = np.array([3,4,5])
>>> factorial(arr, exact=False)
array([   6.,   24.,  120.])
>>> factorial(5, exact=True)
120L
```

`scipy.special.`**`factorial2`**`(`*n*, *exact=False*`)`

Double factorial.

This is the factorial with every second value skipped, i.e., `7!! = 7 * 5 * 3 * 1`. It can be approximated numerically as:

```
n!! = special.gamma(n/2+1)*2**((m+1)/2)/sqrt(pi)  n odd
    = 2**(n/2) * (n/2)!                           n even
```

Parameters **n** : int or array_like

Calculate `n!!`. Arrays are only supported with *exact* set to False. If `n < 0`, the return value is 0.

exact : bool, optional

The result can be approximated rapidly using the gamma-formula above (default). If *exact* is set to True, calculate the answer exactly using integer arithmetic.

Returns **nff** : float or int

Double factorial of *n*, as an int or a float depending on *exact*.

Examples

```
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
array(105.00000000000001)
```

```
>>> factorial2(7, exact=True)
105L
```

`scipy.special.`**`factorialk`**(*n*, *k*, *exact=True*)

n(!!...!) = multifactorial of order k k times

Parameters **n** : int

Calculate multifactorial. If *n* < 0, the return value is 0.

k : int

Order of multifactorial.

exact : bool, optional

If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns **val** : int

Multi factorial of *n*.

Raises **NotImplementedError**

Raises when exact is False

Examples

```
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120L
>>> factorialk(5, 3, exact=True)
10L
```

`scipy.special.`**`shichi`**(*x*) **= <ufunc 'shichi'>**

Hyperbolic sine and cosine integrals

Returns shi

`integral(sinh(t)/t, t=0..x)`

chi

`eul + ln x + integral((cosh(t)-1)/t, t=0..x)` where `eul` is Euler's constant.

`scipy.special.`**`sici`**(*x*) **= <ufunc 'sici'>**

Sine and cosine integrals

Returns si

`integral(sin(t)/t, t=0..x)`

ci

`eul + ln x + integral((cos(t) - 1)/t, t=0..x)` where `eul` is Euler's constant.

`scipy.special.`**`spence`**(*x*) **= <ufunc 'spence'>**

Dilogarithm integral

Returns the dilogarithm integral:

```
-integral(log t / (t-1),t=1..x)
```

`scipy.special.`**`lambertw`**(*z*, *k=0*, *tol=1e-8*)

Lambert W function [R288].

The Lambert W function *W(z)* is defined as the inverse function of `w * exp(w)`. In other words, the value of `W(z)` is such that `z = W(z) * exp(W(z))` for any complex number `z`.

The Lambert W function is a multivalued function with infinitely many branches. Each branch gives a separate solution of the equation `z = w exp(w)`. Here, the branches are indexed by the integer *k*.

Parameters **z** : array_like

Input argument.

k : int, optional

Branch index.

tol : float, optional

Evaluation tolerance.

Returns **w** : array

w will have the same shape as *z*.

Notes

All branches are supported by `lambertw`:

- `lambertw(z)` gives the principal solution (branch 0)
- `lambertw(z, k)` gives the solution on branch *k*

The Lambert W function has two partially real branches: the principal branch ($k = 0$) is real for real `z > -1/e`, and the `k = -1` branch is real for `-1/e < z < 0`. All branches except `k = 0` have a logarithmic singularity at `z = 0`.

Possible issues

The evaluation can become inaccurate very close to the branch point at `-1/e`. In some corner cases, `lambertw` might currently fail to converge, or can end up on the wrong branch.

Algorithm

Halley's iteration is used to invert `w * exp(w)`, using a first-order asymptotic approximation (O(log(w)) or $O(w)$) as the initial estimate.

The definition, implementation and choice of branches is based on [R289].

References

[R288], [R289]

Examples

The Lambert W function is the inverse of `w exp(w)`:

```
>>> from scipy.special import lambertw
>>> w = lambertw(1)
>>> w
(0.56714329040978384+0j)
>>> w * np.exp(w)
(1.0+0j)
```

Any branch gives a valid inverse:

```
>>> w = lambertw(1, k=3)
>>> w
(-2.8535817554090377+17.113535539412148j)
>>> w*np.exp(w)
(1.0000000000000002+1.609823385706477e-15j)
```

Applications to equation-solving

The Lambert W function may be used to solve various kinds of equations, such as finding the value of the infinite power tower $z^{z^{z^{\cdots}}}$:

```
>>> def tower(z, n):
...     if n == 0:
...         return z
```

```
...         return z ** tower(z, n-1)
...
>>> tower(0.5, 100)
0.641185744504986
>>> -lambertw(-np.log(0.5)) / np.log(0.5)
(0.64118574450498589+0j)
```

`scipy.special.`**`zeta`**`(`*x*, *q*`)` **= <ufunc 'zeta'>**

Hurwitz zeta function

The Riemann zeta function of two arguments (also known as the Hurwitz zeta funtion).

This function is defined as

$$\zeta(x, q) = \sum_{k=0}^{\infty} 1/(k+q)^x,$$

where `x > 1` and `q > 0`.

See also:

`zetac`

`scipy.special.`**`zetac`**`(`*x*`)` **= <ufunc 'zetac'>**

Riemann zeta function minus 1.

This function is defined as

$$\zeta(x) = \sum_{k=2}^{\infty} 1/k^x,$$

where `x > 1`.

See also:

`zeta`

Convenience Functions

`cbrt`(x)	Cube root of x
`exp10`(x)	10**x
`exp2`(x)	2**x
`radian`(d, m, s)	Convert from degrees to radians
`cosdg`(x)	Cosine of the angle x given in degrees.
`sindg`(x)	Sine of angle given in degrees
`tandg`(x)	Tangent of angle x given in degrees.
`cotdg`(x)	Cotangent of the angle x given in degrees.
`log1p`(x)	Calculates log(1+x) for use when x is near zero
`expm1`(x)	exp(x) - 1 for use when x is near zero.
`cosm1`(x)	cos(x) - 1 for use when x is near zero.
`round`(x)	Round to nearest integer
`xlogy`(x, y)	Compute `x*log(y)` so that the result is 0 if *x = 0*.
`xlog1py`(x, y)	Compute `x*log1p(y)` so that the result is 0 if *x = 0*.

`scipy.special.`**`cbrt`**`(`*x*`)` **= <ufunc 'cbrt'>**

Cube root of x

`scipy.special.`**`exp10`**(*x*) **= <ufunc 'exp10'>**

10**x

`scipy.special.`**`exp2`**(*x*) **= <ufunc 'exp2'>**

2**x

`scipy.special.`**`radian`**(*d*, *m*, *s*) **= <ufunc 'radian'>**

Convert from degrees to radians

Returns the angle given in (d)egrees, (m)inutes, and (s)econds in radians.

`scipy.special.`**`cosdg`**(*x*) **= <ufunc 'cosdg'>**

Cosine of the angle x given in degrees.

`scipy.special.`**`sindg`**(*x*) **= <ufunc 'sindg'>**

Sine of angle given in degrees

`scipy.special.`**`tandg`**(*x*) **= <ufunc 'tandg'>**

Tangent of angle x given in degrees.

`scipy.special.`**`cotdg`**(*x*) **= <ufunc 'cotdg'>**

Cotangent of the angle x given in degrees.

`scipy.special.`**`log1p`**(*x*) **= <ufunc 'log1p'>**

Calculates log(1+x) for use when x is near zero

`scipy.special.`**`expm1`**(*x*) **= <ufunc 'expm1'>**

exp(x) - 1 for use when x is near zero.

`scipy.special.`**`cosm1`**(*x*) **= <ufunc 'cosm1'>**

cos(x) - 1 for use when x is near zero.

`scipy.special.`**`round`**(*x*) **= <ufunc 'round'>**

Round to nearest integer

Returns the nearest integer to x as a double precision floating point result. If x ends in 0.5 exactly, the nearest even integer is chosen.

`scipy.special.`**`xlogy`**(*x*, *y*) **= <ufunc 'xlogy'>**

Compute `x*log(y)` so that the result is 0 if *x = 0*.

Parameters	**x** : array_like	Multiplier
	y : array_like	Argument
Returns	**z** : array_like	Computed x*log(y)

Notes

New in version 0.13.0.

`scipy.special.`**`xlog1py`**(*x*, *y*) **= <ufunc 'xlog1py'>**

Compute `x*log1p(y)` so that the result is 0 if *x = 0*.

Parameters	**x** : array_like	Multiplier
	y : array_like	Argument
Returns	**z** : array_like	Computed x*log1p(y)

Notes

New in version 0.13.0.

5.34 Statistical functions (`scipy.stats`)

This module contains a large number of probability distributions as well as a growing library of statistical functions.

Each univariate distribution is an instance of a subclass of `rv_continuous` (`rv_discrete` for discrete distributions):

`rv_continuous`([momtype, a, b, xtol, ...])	A generic continuous random variable class meant for subclassing.
`rv_discrete`([a, b, name, badvalue, ...])	A generic discrete random variable class meant for subclassing.

class `scipy.stats.`**`rv_continuous`**(*momtype=1*, *a=None*, *b=None*, *xtol=1e-14*, *badvalue=None*, *name=None*, *longname=None*, *shapes=None*, *extradoc=None*, *seed=None*)

A generic continuous random variable class meant for subclassing.

`rv_continuous` is a base class to construct specific distribution classes and instances for continuous random variables. It cannot be used directly as a distribution.

Parameters

momtype : int, optional
The type of generic moment calculation to use: 0 for pdf, 1 (default) for ppf.

a : float, optional
Lower bound of the support of the distribution, default is minus infinity.

b : float, optional
Upper bound of the support of the distribution, default is plus infinity.

xtol : float, optional
The tolerance for fixed point calculation for generic ppf.

badvalue : float, optional
The value in a result arrays that indicates a value that for which some argument restriction is violated, default is np.nan.

name : str, optional
The name of the instance. This string is used to construct the default example for distributions.

longname : str, optional
This string is used as part of the first line of the docstring returned when a subclass has no docstring of its own. Note: *longname* exists for backwards compatibility, do not use for new subclasses.

shapes : str, optional
The shape of the distribution. For example `"m, n"` for a distribution that takes two integers as the two shape arguments for all its methods. If not provided, shape parameters will be inferred from the signature of the private methods, `_pdf` and `_cdf` of the instance.

extradoc : str, optional, deprecated
This string is used as the last part of the docstring returned when a subclass has no docstring of its own. Note: *extradoc* exists for backwards compatibility, do not use for new subclasses.

seed : None or int or `numpy.random.RandomState` instance, optional
This parameter defines the RandomState object to use for drawing random variates. If None (or np.random), the global np.random state is used. If integer, it is used to seed the local RandomState instance. Default is None.

Notes

Public methods of an instance of a distribution class (e.g., `pdf`, `cdf`) check their arguments and pass valid arguments to private, computational methods (`_pdf`, `_cdf`). For `pdf(x)`, `x` is valid if it is within the support of a distribution, `self.a <= x <= self.b`. Whether a shape parameter is valid is decided by an `_argcheck` method (which defaults to checking that its arguments are strictly positive.)

Subclassing

New random variables can be defined by subclassing the `rv_continuous` class and re-defining at least the `_pdf` or the `_cdf` method (normalized to location 0 and scale 1).

If positive argument checking is not correct for your RV then you will also need to re-define the `_argcheck` method.

Correct, but potentially slow defaults exist for the remaining methods but for speed and/or accuracy you can over-ride:

```
_logpdf, _cdf, _logcdf, _ppf, _rvs, _isf, _sf, _logsf
```

Rarely would you override `_isf`, `_sf` or `_logsf`, but you could.

Methods that can be overwritten by subclasses

```
_rvs
_pdf
_cdf
_sf
_ppf
_isf
_stats
_munp
_entropy
_argcheck
```

There are additional (internal and private) generic methods that can be useful for cross-checking and for debugging, but might work in all cases when directly called.

A note on `shapes`: subclasses need not specify them explicitly. In this case, *shapes* will be automatically deduced from the signatures of the overridden methods (`pdf`, `cdf` etc). If, for some reason, you prefer to avoid relying on introspection, you can specify `shapes` explicitly as an argument to the instance constructor.

Frozen Distributions

Normally, you must provide shape parameters (and, optionally, location and scale parameters to each call of a method of a distribution.

Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object:

rv = generic(<shape(s)>, loc=0, scale=1)
frozen RV object with the same methods but holding the given shape, location, and scale fixed

Statistics

Statistics are computed using numerical integration by default. For speed you can redefine this using `_stats`:

- take shape parameters and return mu, mu2, g1, g2
- If you can't compute one of these, return it as None
- Can also be defined with a keyword argument `moments`, which is a string composed of "m", "v", "s", and/or "k". Only the components appearing in string should be computed and returned in the order "m", "v", "s", or "k" with missing values returned as None.

Alternatively, you can override `_munp`, which takes `n` and shape parameters and returns the n-th non-central moment of the distribution.

Examples

To create a new Gaussian distribution, we would do the following:

```
>>> from scipy.stats import rv_continuous
>>> class gaussian_gen(rv_continuous):
...     "Gaussian distribution"
...     def _pdf(self, x):
...         return np.exp(-x**2 / 2.) / np.sqrt(2.0 * np.pi)
>>> gaussian = gaussian_gen(name='gaussian')
```

`scipy.stats` distributions are *instances*, so here we subclass `rv_continuous` and create an instance. With this, we now have a fully functional distribution with all relevant methods automagically generated by the framework.

Note that above we defined a standard normal distribution, with zero mean and unit variance. Shifting and scaling of the distribution can be done by using `loc` and `scale` parameters: `gaussian.pdf(x, loc, scale)` essentially computes `y = (x - loc) / scale` and `gaussian._pdf(y) / scale`.

Attributes

`random_state`	Get or set the RandomState object for generating random variates.

`rv_continuous.`**`random_state`**

Get or set the RandomState object for generating random variates.

This can be either None or an existing RandomState object.

If None (or np.random), use the RandomState singleton used by np.random. If already a RandomState instance, use it. If an int, use a new RandomState instance seeded with seed.

Methods

`rvs`(*args, **kwds)	Random variates of given type.
`pdf`(x, *args, **kwds)	Probability density function at x of the given RV.
`logpdf`(x, *args, **kwds)	Log of the probability density function at x of the given RV.
`cdf`(x, *args, **kwds)	Cumulative distribution function of the given RV.
`logcdf`(x, *args, **kwds)	Log of the cumulative distribution function at x of the given RV.
`sf`(x, *args, **kwds)	Survival function (1 - `cdf`) at x of the given RV.
`logsf`(x, *args, **kwds)	Log of the survival function of the given RV.
`ppf`(q, *args, **kwds)	Percent point function (inverse of `cdf`) at q of the given RV.
`isf`(q, *args, **kwds)	Inverse survival function (inverse of `sf`) at q of the given RV.
`moment`(n, *args, **kwds)	n-th order non-central moment of distribution.
`stats`(*args, **kwds)	Some statistics of the given RV.
`entropy`(*args, **kwds)	Differential entropy of the RV.
`expect`([func, args, loc, scale, lb, ub, ...])	Calculate expected value of a function with respect to the distribution.
`median`(*args, **kwds)	Median of the distribution.
`mean`(*args, **kwds)	Mean of the distribution.
`std`(*args, **kwds)	Standard deviation of the distribution.
`var`(*args, **kwds)	Variance of the distribution.
`interval`(alpha, *args, **kwds)	Confidence interval with equal areas around the median.
`__call__`(*args, **kwds)	Freeze the distribution for the given arguments.
`fit`(data, *args, **kwds)	Return MLEs for shape, location, and scale parameters from data.
`fit_loc_scale`(data, *args)	Estimate loc and scale parameters from data using 1st and 2nd moments.

Continued on next page

Table 5.247 – continued from previous page

`nnlf`(theta, x)	Return negative loglikelihood function.

`rv_continuous.`**`rvs`**(**args*, ***kwds*)

Random variates of given type.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

scale : array_like, optional

Scale parameter (default=1).

size : int or tuple of ints, optional

Defining number of random variates (default is 1).

random_state : None or int or `np.random.RandomState` instance, optional

If int or RandomState, use it for drawing the random variates. If None, rely on `self.random_state`. Default is None.

Returns **rvs** : ndarray or scalar

Random variates of given *size*.

`rv_continuous.`**`pdf`**(*x*, **args*, ***kwds*)

Probability density function at x of the given RV.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **pdf** : ndarray

Probability density function evaluated at x

`rv_continuous.`**`logpdf`**(*x*, **args*, ***kwds*)

Log of the probability density function at x of the given RV.

This uses a more numerically accurate calculation if available.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **logpdf** : array_like

Log of the probability density function evaluated at x

`rv_continuous.`**`cdf`**(*x*, **args*, ***kwds*)

Cumulative distribution function of the given RV.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **cdf** : ndarray

Cumulative distribution function evaluated at *x*

`rv_continuous.`**`logcdf`**`(`*x*, **args*, ***kwds*`)`

Log of the cumulative distribution function at x of the given RV.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **logcdf** : array_like

Log of the cumulative distribution function evaluated at x

`rv_continuous.`**`sf`**`(`*x*, **args*, ***kwds*`)`

Survival function (1 - `cdf`) at x of the given RV.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **sf** : array_like

Survival function evaluated at x

`rv_continuous.`**`logsf`**`(`*x*, **args*, ***kwds*`)`

Log of the survival function of the given RV.

Returns the log of the "survival function," defined as (1 - `cdf`), evaluated at *x*.

Parameters **x** : array_like

quantiles

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **logsf** : ndarray

Log of the survival function evaluated at *x*.

`rv_continuous.`**`ppf`**`(`*q*, **args*, ***kwds*`)`

Percent point function (inverse of `cdf`) at q of the given RV.

Parameters **q** : array_like

lower tail probability

arg1, arg2, arg3,... : array_like
The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

Returns **x** : array_like
quantile corresponding to the lower tail probability q.

`rv_continuous.`**`isf`**`(`*q*, **args*, ***kwds*`)`

Inverse survival function (inverse of `sf`) at q of the given RV.

Parameters **q** : array_like
upper tail probability

arg1, arg2, arg3,... : array_like
The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

Returns **x** : ndarray or scalar
Quantile corresponding to the upper tail probability q.

`rv_continuous.`**`moment`**`(`*n*, **args*, ***kwds*`)`

n-th order non-central moment of distribution.

Parameters **n** : int, n >= 1
Order of moment.

arg1, arg2, arg3,... : float
The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

`rv_continuous.`**`stats`**`(`**args*, ***kwds*`)`

Some statistics of the given RV.

Parameters **arg1, arg2, arg3,...** : array_like
The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional
location parameter (default=0)

scale : array_like, optional (continuous RVs only)
scale parameter (default=1)

moments : str, optional
composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

Returns **stats** : sequence
of requested moments.

`rv_continuous.`**`entropy`**`(`**args*, ***kwds*`)`

Differential entropy of the RV.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

scale : array_like, optional (continuous distributions only).

Scale parameter (default=1).

Notes

Entropy is defined base *e*:

```
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

`rv_continuous.`**`expect`**(*func=None*, *args=()*, *loc=0*, *scale=1*, *lb=None*, *ub=None*, *conditional=False*, ***kwds*)

Calculate expected value of a function with respect to the distribution.

The expected value of a function `f(x)` with respect to a distribution `dist` is defined as:

```
        ubound
E[x] = Integral(f(x) * dist.pdf(x))
        lbound
```

Parameters **func** : callable, optional

Function for which integral is calculated. Takes only one argument. The default is the identity mapping f(x) = x.

args : tuple, optional

Shape parameters of the distribution.

loc : float, optional

Location parameter (default=0).

scale : float, optional

Scale parameter (default=1).

lb, ub : scalar, optional

Lower and upper bound for integration. Default is set to the support of the distribution.

conditional : bool, optional

If True, the integral is corrected by the conditional probability of the integration interval. The return value is the expectation of the function, conditional on being in the given interval. Default is False.

Additional keyword arguments are passed to the integration routine.

Returns **expect** : float

The calculated expected value.

Notes

The integration behavior of this function is inherited from *integrate.quad*.

`rv_continuous.`**`median`**(**args*, ***kwds*)

Median of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

Location parameter, Default is 0.

scale : array_like, optional

Scale parameter, Default is 1.

Returns **median** : float

The median of the distribution.

See also:

`stats.distributions.rv_discrete.ppf`
Inverse of the CDF

`rv_continuous.`**`mean`**`(`**args*, ***kwds*`)`

Mean of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **mean** : float

the mean of the distribution

`rv_continuous.`**`std`**`(`**args*, ***kwds*`)`

Standard deviation of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **std** : float

standard deviation of the distribution

`rv_continuous.`**`var`**`(`**args*, ***kwds*`)`

Variance of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **var** : float

the variance of the distribution

`rv_continuous.`**`interval`**`(`*alpha*, **args*, ***kwds*`)`

Confidence interval with equal areas around the median.

Parameters **alpha** : array_like of float

Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].

arg1, arg2, ... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

location parameter, Default is 0.

scale : array_like, optional
scale parameter, Default is 1.

Returns **a, b** : ndarray of float
end-points of range that contain `100 * alpha %` of the rv's possible values.

`rv_continuous.`**`__call__`**`(*args, **kwds)`

Freeze the distribution for the given arguments.

Parameters **arg1, arg2, arg3,...** : array_like
The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns **rv_frozen** : rv_frozen instance
The frozen distribution.

`rv_continuous.`**`fit`**`(data, *args, **kwds)`

Return MLEs for shape, location, and scale parameters from data.

MLE stands for Maximum Likelihood Estimate. Starting estimates for the fit are given by input arguments; for any arguments not provided with starting estimates, `self._fitstart(data)` is called to generate such.

One can hold some parameters fixed to specific values by passing in keyword arguments `f0`, `f1`, ..., `fn` (for shape parameters) and `floc` and `fscale` (for location and scale parameters, respectively).

Parameters **data** : array_like
Data to use in calculating the MLEs.

args : floats, optional
Starting value(s) for any shape-characterizing arguments (those not provided will be determined by a call to `_fitstart(data)`). No default value.

kwds : floats, optional
Starting values for the location and scale parameters; no default. Special keyword arguments are recognized as holding certain parameters fixed:

- f0...fn : hold respective shape parameters fixed. Alternatively, shape parameters to fix can be specified by name. For example, if `self.shapes == "a, b"`, `fa` is equivalent to `f0` and `fb` is equivalent to `f1`.
- floc : hold location parameter fixed to specified value.
- fscale : hold scale parameter fixed to specified value.
- optimizer : The optimizer to use. The optimizer must take `func`, and starting position as the first two arguments, plus `args` (for extra arguments to pass to the function to be optimized) and `disp=0` to suppress output as keyword arguments.

Returns **shape, loc, scale** : tuple of floats
MLEs for any shape statistics, followed by those for location and scale.

Notes

This fit is computed by maximizing a log-likelihood function, with penalty applied for samples outside of range of the distribution. The returned answer is not guaranteed to be the globally optimal MLE, it may only be locally optimal, or the optimization may fail altogether.

Examples

Generate some data to fit: draw random variates from the `beta` distribution

```
>>> from scipy.stats import beta
>>> a, b = 1., 2.
>>> x = beta.rvs(a, b, size=1000)
```

Now we can fit all four parameters (`a`, `b`, `loc` and `scale`):

```
>>> a1, b1, loc1, scale1 = beta.fit(x)
```

We can also use some prior knowledge about the dataset: let's keep `loc` and `scale` fixed:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=1)
>>> loc1, scale1
(0, 1)
```

We can also keep shape parameters fixed by using `f`-keywords. To keep the zero-th shape parameter `a` equal 1, use `f0=1` or, equivalently, `fa=1`:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)
>>> a1
1
```

`rv_continuous.`**`fit_loc_scale`**`(`*data*, **args*`)`

Estimate loc and scale parameters from data using 1st and 2nd moments.

Parameters **data** : array_like

Data to fit.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

Returns **Lhat** : float

Estimated location parameter for the data.

Shat : float

Estimated scale parameter for the data.

`rv_continuous.`**`nnlf`**`(`*theta*, *x*`)`

Return negative loglikelihood function.

Notes

This is `-sum(log pdf(x, theta), axis=0)` where *theta* are the parameters (including loc and scale).

class `scipy.stats.`**`rv_discrete`**`(`*a=0*, *b=inf*, *name=None*, *badvalue=None*, *moment_tol=1e-08*, *values=None*, *inc=1*, *longname=None*, *shapes=None*, *extradoc=None*, *seed=None*`)`

A generic discrete random variable class meant for subclassing.

`rv_discrete` is a base class to construct specific distribution classes and instances for discrete random variables. It can also be used to construct an arbitrary distribution defined by a list of support points and corresponding probabilities.

Parameters **a** : float, optional

Lower bound of the support of the distribution, default: 0

b : float, optional

Upper bound of the support of the distribution, default: plus infinity

moment_tol : float, optional

The tolerance for the generic calculation of moments.

values : tuple of two array_like, optional `(xk, pk)` where `xk` are integers with non-zero probabilities `pk` with `sum(pk) = 1`.

inc : integer, optional

Increment for the support of the distribution. Default is 1. (other values have not been tested)

badvalue : float, optional

The value in a result arrays that indicates a value that for which some argument restriction is violated, default is np.nan.

name : str, optional

The name of the instance. This string is used to construct the default example for distributions.

longname : str, optional

This string is used as part of the first line of the docstring returned when a subclass has no docstring of its own. Note: *longname* exists for backwards compatibility, do not use for new subclasses.

shapes : str, optional

The shape of the distribution. For example "m, n" for a distribution that takes two integers as the two shape arguments for all its methods If not provided, shape parameters will be inferred from the signatures of the private methods, `_pmf` and `_cdf` of the instance.

extradoc : str, optional

This string is used as the last part of the docstring returned when a subclass has no docstring of its own. Note: *extradoc* exists for backwards compatibility, do not use for new subclasses.

seed : None or int or `numpy.random.RandomState` instance, optional

This parameter defines the RandomState object to use for drawing random variates. If None, the global np.random state is used. If integer, it is used to seed the local RandomState instance. Default is None.

Notes

This class is similar to `rv_continuous`, the main differences being:

- the support of the distribution is a set of integers
- instead of the probability density function, `pdf` (and the corresponding private `_pdf`), this class defines the *probability mass function*, `pmf` (and the corresponding private `_pmf`.)
- scale parameter is not defined.

To create a new discrete distribution, we would do the following:

```
>>> from scipy.stats import rv_discrete
>>> class poisson_gen(rv_discrete):
...     "Poisson distribution"
...     def _pmf(self, k, mu):
...         return exp(-mu) * mu**k / factorial(k)
```

and create an instance:

```
>>> poisson = poisson_gen(name="poisson")
```

Note that above we defined the Poisson distribution in the standard form. Shifting the distribution can be done by providing the `loc` parameter to the methods of the instance. For example, `poisson.pmf(x, mu, loc)` delegates the work to `poisson._pmf(x-loc, mu)`.

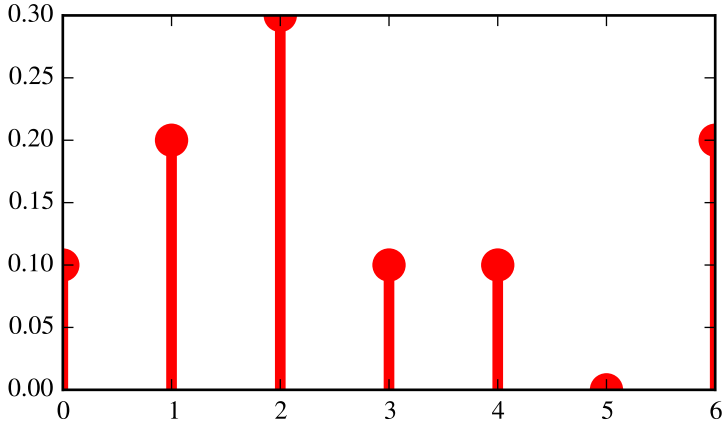
Discrete distributions from a list of probabilities

Alternatively, you can construct an arbitrary discrete rv defined on a finite set of values `xk` with `Prob{X=xk} = pk` by using the `values` keyword argument to the `rv_discrete` constructor.

Examples

Custom made discrete distribution:

```
>>> from scipy import stats
>>> xk = np.arange(7)
>>> pk = (0.1, 0.2, 0.3, 0.1, 0.1, 0.0, 0.2)
>>> custm = stats.rv_discrete(name='custm', values=(xk, pk))
>>>
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
>>> ax.plot(xk, custm.pmf(xk), 'ro', ms=12, mec='r')
>>> ax.vlines(xk, 0, custm.pmf(xk), colors='r', lw=4)
>>> plt.show()
```



Random number generation:

```
>>> R = custm.rvs(size=100)
```

Attributes

`random_state`	Get or set the RandomState object for generating random variates.

`rv_discrete.`**`random_state`**

Get or set the RandomState object for generating random variates.

This can be either None or an existing RandomState object.

If None (or np.random), use the RandomState singleton used by np.random. If already a RandomState instance, use it. If an int, use a new RandomState instance seeded with seed.

Methods

`rvs`(*args, **kwargs)	Random variates of given type.
`pmf`(k, *args, **kwds)	Probability mass function at k of the given RV.

Continued on ne

Table 5.249 – continued from previous page

`logpmf`(k, *args, **kwds)	Log of the probability mass function at k of the given RV.
`cdf`(k, *args, **kwds)	Cumulative distribution function of the given RV.
`logcdf`(k, *args, **kwds)	Log of the cumulative distribution function at k of the given RV.
`sf`(k, *args, **kwds)	Survival function (1 - `cdf`) at k of the given RV.
`logsf`(k, *args, **kwds)	Log of the survival function of the given RV.
`ppf`(q, *args, **kwds)	Percent point function (inverse of `cdf`) at q of the given RV.
`isf`(q, *args, **kwds)	Inverse survival function (inverse of `sf`) at q of the given RV.
`moment`(n, *args, **kwds)	n-th order non-central moment of distribution.
`stats`(*args, **kwds)	Some statistics of the given RV.
`entropy`(*args, **kwds)	Differential entropy of the RV.
`expect`([func, args, loc, lb, ub, conditional])	Calculate expected value of a function with respect to the distribution for discrete dist
`median`(*args, **kwds)	Median of the distribution.
`mean`(*args, **kwds)	Mean of the distribution.
`std`(*args, **kwds)	Standard deviation of the distribution.
`var`(*args, **kwds)	Variance of the distribution.
`interval`(alpha, *args, **kwds)	Confidence interval with equal areas around the median.
`__call__`(*args, **kwds)	Freeze the distribution for the given arguments.

`rv_discrete.`**`rvs`**(**args*, ***kwargs*)

Random variates of given type.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

size : int or tuple of ints, optional

Defining number of random variates (Default is 1). Note that *size* has to be given as keyword, not as positional argument.

random_state : None or int or `np.random.RandomState` instance, optional

If int or RandomState, use it for drawing the random variates. If None, rely on `self.random_state`. Default is None.

Returns **rvs** : ndarray or scalar

Random variates of given *size*.

`rv_discrete.`**`pmf`**(*k*, **args*, ***kwds*)

Probability mass function at k of the given RV.

Parameters **k** : array_like

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

Location parameter (default=0).

Returns **pmf** : array_like

Probability mass function evaluated at k

`rv_discrete.`**`logpmf`**(*k*, **args*, ***kwds*)

Log of the probability mass function at k of the given RV.

Parameters **k** : array_like

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter. Default is 0.

Returns **logpmf** : array_like

Log of the probability mass function evaluated at k.

`rv_discrete.`**`cdf`**(*k*, **args*, ***kwds*)

Cumulative distribution function of the given RV.

Parameters **k** : array_like, int

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **cdf** : ndarray

Cumulative distribution function evaluated at *k*.

`rv_discrete.`**`logcdf`**(*k*, **args*, ***kwds*)

Log of the cumulative distribution function at k of the given RV.

Parameters **k** : array_like, int

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **logcdf** : array_like

Log of the cumulative distribution function evaluated at k.

`rv_discrete.`**`sf`**(*k*, **args*, ***kwds*)

Survival function (1 - `cdf`) at k of the given RV.

Parameters **k** : array_like

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **sf** : array_like

Survival function evaluated at k.

`rv_discrete.`**`logsf`**(*k*, **args*, ***kwds*)

Log of the survival function of the given RV.

Returns the log of the "survival function," defined as 1 - `cdf`, evaluated at *k*.

Parameters **k** : array_like

Quantiles.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **logsf** : ndarray

Log of the survival function evaluated at *k*.

`rv_discrete.`**`ppf`**`(`*q*, **args*, ***kwds*`)`

Percent point function (inverse of `cdf`) at q of the given RV.

Parameters **q** : array_like

Lower tail probability.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **k** : array_like

Quantile corresponding to the lower tail probability, q.

`rv_discrete.`**`isf`**`(`*q*, **args*, ***kwds*`)`

Inverse survival function (inverse of `sf`) at q of the given RV.

Parameters **q** : array_like

Upper tail probability.

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

Returns **k** : ndarray or scalar

Quantile corresponding to the upper tail probability, q.

`rv_discrete.`**`moment`**`(`*n*, **args*, ***kwds*`)`

n-th order non-central moment of distribution.

Parameters **n** : int, n >= 1

Order of moment.

arg1, arg2, arg3,... : float

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

`rv_discrete.`**`stats`**`(`**args*, ***kwds*`)`

Some statistics of the given RV.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional (continuous RVs only)

scale parameter (default=1)

moments : str, optional

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

Returns **stats** : sequence

of requested moments.

`rv_discrete.`**`entropy`**`(`**args*, ***kwds*`)`

Differential entropy of the RV.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

Location parameter (default=0).

scale : array_like, optional (continuous distributions only).

Scale parameter (default=1).

Notes

Entropy is defined base *e*:

```
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

`rv_discrete.`**`expect`**(*func=None*, *args=()*, *loc=0*, *lb=None*, *ub=None*, *conditional=False*)

Calculate expected value of a function with respect to the distribution for discrete distribution.

Parameters

func : callable, optional

Function for which the expectation value is calculated. Takes only one argument. The default is the identity mapping f(k) = k.

args : tuple, optional

Shape parameters of the distribution.

loc : float, optional

Location parameter. Default is 0.

lb, ub : int, optional

Lower and upper bound for integration, default is set to the support of the distribution, inclusive (`ul <= k <= ub`).

conditional : bool, optional

If true then the expectation is corrected by the conditional probability of the summation interval. The return value is the expectation of the function, *func*, conditional on being in the given interval (k such that `ul <= k <= ub`). Default is False.

Returns

expect : float

Expected value.

Notes

- function is not vectorized
- accuracy: uses self.moment_tol as stopping criterium for heavy tailed distribution e.g. zipf(4), accuracy for mean, variance in example is only 1e-5, increasing precision (moment_tol) makes zipf very slow
- suppnmin=100 internal parameter for minimum number of points to evaluate could be added as keyword parameter, to evaluate functions with non-monotonic shapes, points include integers in (-suppnmin, suppnmin)
- uses maxcount=1000 limits the number of points that are evaluated to break loop for infinite sums (a maximum of suppnmin+1000 positive plus suppnmin+1000 negative integers are evaluated)

`rv_discrete.`**`median`**(**args*, ***kwds*)

Median of the distribution.

Parameters

arg1, arg2, arg3,... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

Location parameter, Default is 0.

scale : array_like, optional

Scale parameter, Default is 1.

Returns **median** : float

The median of the distribution.

See also:

`stats.distributions.rv_discrete.ppf`
Inverse of the CDF

`rv_discrete.`**`mean`**`(`**args*, ***kwds*`)`

Mean of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **mean** : float

the mean of the distribution

`rv_discrete.`**`std`**`(`**args*, ***kwds*`)`

Standard deviation of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **std** : float

standard deviation of the distribution

`rv_discrete.`**`var`**`(`**args*, ***kwds*`)`

Variance of the distribution.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array_like, optional

location parameter (default=0)

scale : array_like, optional

scale parameter (default=1)

Returns **var** : float

the variance of the distribution

`rv_discrete.`**`interval`**`(`*alpha*, **args*, ***kwds*`)`

Confidence interval with equal areas around the median.

Parameters **alpha** : array_like of float

Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].

arg1, arg2, ... : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc : array_like, optional

location parameter, Default is 0.

scale : array_like, optional

scale parameter, Default is 1.

Returns **a, b** : ndarray of float end-points of range that contain `100 * alpha %` of the rv's possible values.

`rv_discrete.__call__(*args, **kwds)`

Freeze the distribution for the given arguments.

Parameters **arg1, arg2, arg3,...** : array_like

The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns **rv_frozen** : rv_frozen instance

The frozen distribution.

5.34.1 Continuous distributions

`alpha`	An alpha continuous random variable.
`anglit`	An anglit continuous random variable.
`arcsine`	An arcsine continuous random variable.
`beta`	A beta continuous random variable.
`betaprime`	A beta prime continuous random variable.
`bradford`	A Bradford continuous random variable.
`burr`	A Burr continuous random variable.
`cauchy`	A Cauchy continuous random variable.
`chi`	A chi continuous random variable.
`chi2`	A chi-squared continuous random variable.
`cosine`	A cosine continuous random variable.
`dgamma`	A double gamma continuous random variable.
`dweibull`	A double Weibull continuous random variable.
`erlang`	An Erlang continuous random variable.
`expon`	An exponential continuous random variable.
`exponnorm`	An exponentially modified Normal continuous random variable.
`exponweib`	An exponentiated Weibull continuous random variable.
`exponpow`	An exponential power continuous random variable.
`f`	An F continuous random variable.
`fatiguelife`	A fatigue-life (Birnbaum-Saunders) continuous random variable.
`fisk`	A Fisk continuous random variable.
`foldcauchy`	A folded Cauchy continuous random variable.
`foldnorm`	A folded normal continuous random variable.
`frechet_r`	A Frechet right (or Weibull minimum) continuous random variable.
`frechet_l`	A Frechet left (or Weibull maximum) continuous random variable.
`genlogistic`	A generalized logistic continuous random variable.
`gennorm`	A generalized normal continuous random variable.
`genpareto`	A generalized Pareto continuous random variable.
`genexpon`	A generalized exponential continuous random variable.
`genextreme`	A generalized extreme value continuous random variable.
`gausshyper`	A Gauss hypergeometric continuous random variable.
`gamma`	A gamma continuous random variable.
`gengamma`	A generalized gamma continuous random variable.
`genhalflogistic`	A generalized half-logistic continuous random variable.
`gilbrat`	A Gilbrat continuous random variable.
`gompertz`	A Gompertz (or truncated Gumbel) continuous random variable.
`gumbel_r`	A right-skewed Gumbel continuous random variable.
`gumbel_l`	A left-skewed Gumbel continuous random variable.

Continued on next page

Table 5.250 – continued from previous page

`halfcauchy`	A Half-Cauchy continuous random variable.
`halflogistic`	A half-logistic continuous random variable.
`halfnorm`	A half-normal continuous random variable.
`halfgennorm`	The upper half of a generalized normal continuous random variable.
`hypsecant`	A hyperbolic secant continuous random variable.
`invgamma`	An inverted gamma continuous random variable.
`invgauss`	An inverse Gaussian continuous random variable.
`invweibull`	An inverted Weibull continuous random variable.
`johnsonsb`	A Johnson SB continuous random variable.
`johnsonsu`	A Johnson SU continuous random variable.
`ksone`	General Kolmogorov-Smirnov one-sided test.
`kstwobign`	Kolmogorov-Smirnov two-sided test for large N.
`laplace`	A Laplace continuous random variable.
`logistic`	A logistic (or Sech-squared) continuous random variable.
`loggamma`	A log gamma continuous random variable.
`loglaplace`	A log-Laplace continuous random variable.
`lognorm`	A lognormal continuous random variable.
`lomax`	A Lomax (Pareto of the second kind) continuous random variable.
`maxwell`	A Maxwell continuous random variable.
`mielke`	A Mielke's Beta-Kappa continuous random variable.
`nakagami`	A Nakagami continuous random variable.
`ncx2`	A non-central chi-squared continuous random variable.
`ncf`	A non-central F distribution continuous random variable.
`nct`	A non-central Student's T continuous random variable.
`norm`	A normal continuous random variable.
`pareto`	A Pareto continuous random variable.
`pearson3`	A pearson type III continuous random variable.
`powerlaw`	A power-function continuous random variable.
`powerlognorm`	A power log-normal continuous random variable.
`powernorm`	A power normal continuous random variable.
`rdist`	An R-distributed continuous random variable.
`reciprocal`	A reciprocal continuous random variable.
`rayleigh`	A Rayleigh continuous random variable.
`rice`	A Rice continuous random variable.
`recipinvgauss`	A reciprocal inverse Gaussian continuous random variable.
`semicircular`	A semicircular continuous random variable.
`t`	A Student's T continuous random variable.
`triang`	A triangular continuous random variable.
`truncexpon`	A truncated exponential continuous random variable.
`truncnorm`	A truncated normal continuous random variable.
`tukeylambda`	A Tukey-Lamdba continuous random variable.
`uniform`	A uniform continuous random variable.
`vonmises`	A Von Mises continuous random variable.
`wald`	A Wald continuous random variable.
`weibull_min`	A Frechet right (or Weibull minimum) continuous random variable.
`weibull_max`	A Frechet left (or Weibull maximum) continuous random variable.
`wrapcauchy`	A wrapped Cauchy continuous random variable.

`scipy.stats.`**`alpha`** **= <scipy.stats._continuous_distns.alpha_gen object at 0x7fa40ebcfad0>**

An alpha continuous random variable.

As an instance of the `rv_continuous` class, `alpha` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `alpha` is:

```
alpha.pdf(x, a) = 1/(x**2*Phi(a)*sqrt(2*pi)) * exp(-1/2 * (a-1/x)**2),
```

where `Phi(alpha)` is the normal CDF, `x > 0`, and `a > 0`.

`alpha` takes `a` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `alpha.pdf(x, a, loc, scale)` is identically equivalent to `alpha.pdf(y, a) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import alpha
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 3.57
>>> mean, var, skew, kurt = alpha.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(alpha.ppf(0.01, a),
...                 alpha.ppf(0.99, a), 100)
>>> ax.plot(x, alpha.pdf(x, a),
...        'r-', lw=5, alpha=0.6, label='alpha pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = alpha(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

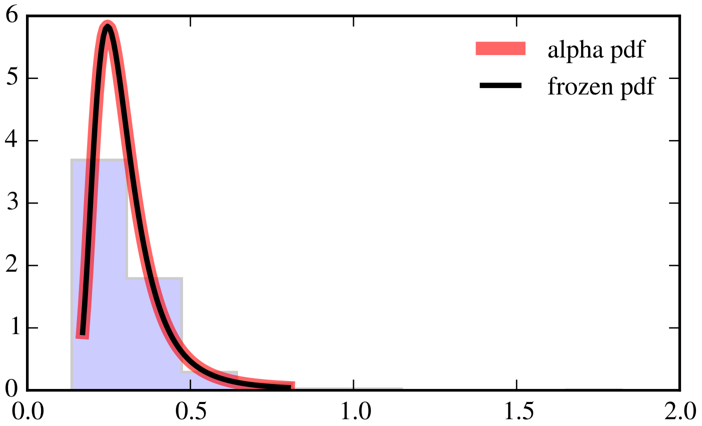
```
>>> vals = alpha.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], alpha.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = alpha.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`anglit`** **= <scipy.stats._continuous_distns.anglit_gen object at 0x7fa40ebcfd90>**

An anglit continuous random variable.

As an instance of the `rv_continuous` class, `anglit` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `anglit` is:

```
anglit.pdf(x) = sin(2*x + pi/2) = cos(2*x),
```

for `-pi/4 <= x <= pi/4`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `anglit.pdf(x, loc, scale)` is identically equivalent to `anglit.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import anglit
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = anglit.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(anglit.ppf(0.01),
...                 anglit.ppf(0.99), 100)
>>> ax.plot(x, anglit.pdf(x),
...        'r-', lw=5, alpha=0.6, label='anglit pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = anglit()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

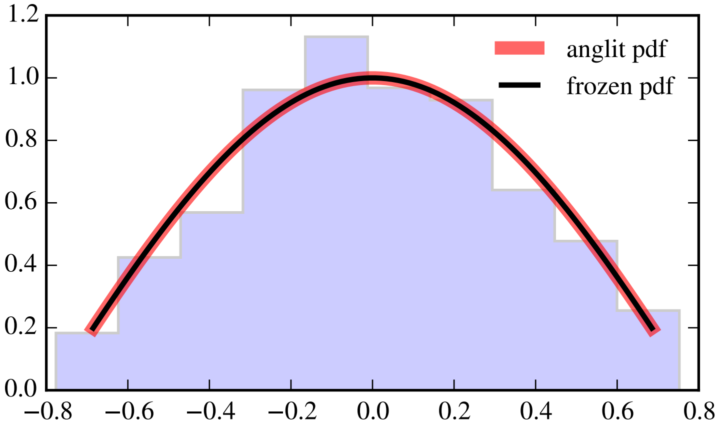
```
>>> vals = anglit.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], anglit.cdf(vals))
True
```

Generate random numbers:

```
>>> r = anglit.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`arcsine`** **= <scipy.stats._continuous_distns.arcsine_gen object at 0x7fa40ebcff90>**

An arcsine continuous random variable.

As an instance of the `rv_continuous` class, `arcsine` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `arcsine` is:

```
arcsine.pdf(x) = 1/(pi*sqrt(x*(1-x)))
```

for `0 < x < 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `arcsine.pdf(x, loc, scale)` is identically equivalent to `arcsine.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import arcsine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = arcsine.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(arcsine.ppf(0.01),
...                 arcsine.ppf(0.99), 100)
>>> ax.plot(x, arcsine.pdf(x),
...        'r-', lw=5, alpha=0.6, label='arcsine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = arcsine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

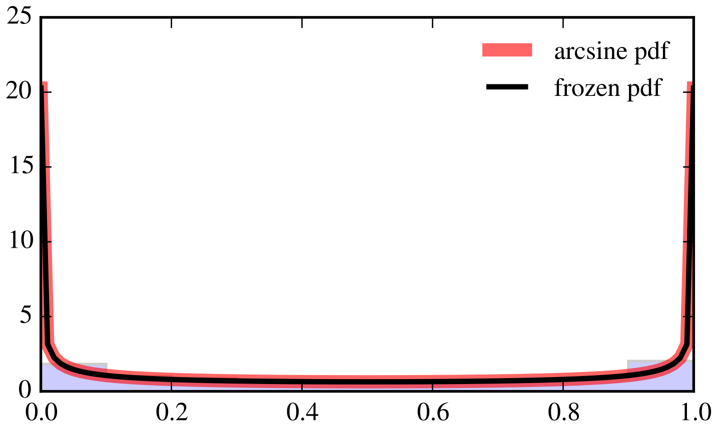
```
>>> vals = arcsine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], arcsine.cdf(vals))
True
```

Generate random numbers:

```
>>> r = arcsine.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`beta`** **= <scipy.stats._continuous_distns.beta_gen object at 0x7fa40ebe51d0>**

A beta continuous random variable.

As an instance of the `rv_continuous` class, `beta` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `beta` is:

```
                     gamma(a+b) * x**(a-1) * (1-x)**(b-1)
beta.pdf(x, a, b) = ------------------------------------
                              gamma(a)*gamma(b)
```

for `0 < x < 1`, `a > 0`, `b > 0`, where `gamma(z)` is the gamma function (`scipy.special.gamma`).

`beta` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `beta.pdf(x, a, b, loc, scale)` is identically equivalent to `beta.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import beta
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 2.31, 0.627
>>> mean, var, skew, kurt = beta.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(beta.ppf(0.01, a, b),
...                 beta.ppf(0.99, a, b), 100)
>>> ax.plot(x, beta.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='beta pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = beta(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

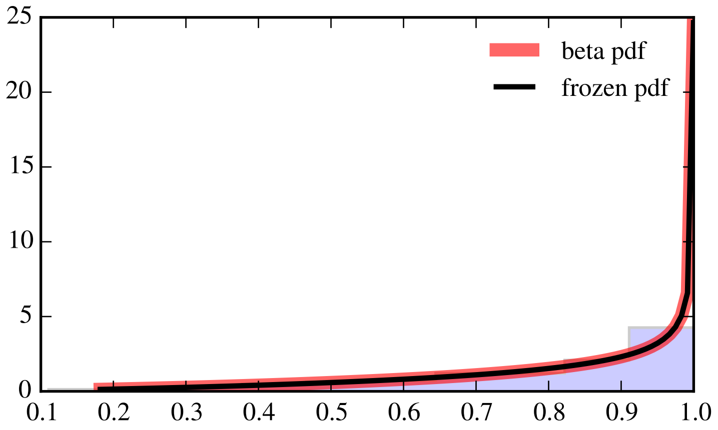
```
>>> vals = beta.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], beta.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = beta.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`betaprime`** **= <scipy.stats._continuous_distns.betaprime_gen object at 0x7fa40ebe5590>**

A beta prime continuous random variable.

As an instance of the `rv_continuous` class, `betaprime` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `betaprime` is:

```
betaprime.pdf(x, a, b) = x**(a-1) * (1+x)**(-a-b) / beta(a, b)
```

for `x > 0`, `a > 0`, `b > 0`, where `beta(a, b)` is the beta function (see `scipy.special.beta`).

`betaprime` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `betaprime.pdf(x, a, b, loc, scale)` is identically equivalent to `betaprime.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import betaprime
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 5, 6
>>> mean, var, skew, kurt = betaprime.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(betaprime.ppf(0.01, a, b),
...                 betaprime.ppf(0.99, a, b), 100)
>>> ax.plot(x, betaprime.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='betaprime pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = betaprime(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

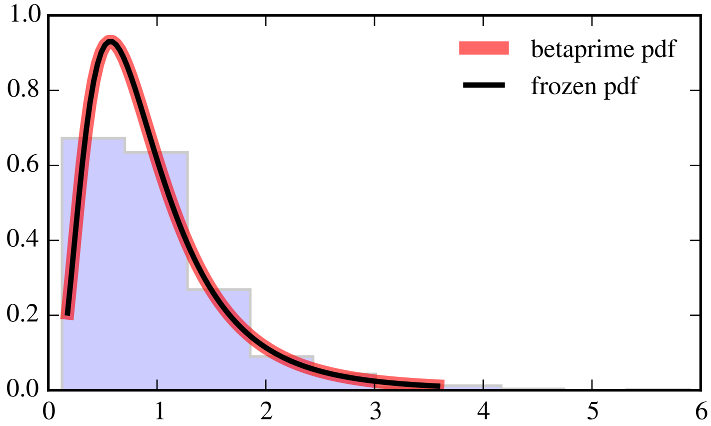
```
>>> vals = betaprime.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], betaprime.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = betaprime.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`bradford`** **= <scipy.stats._continuous_distns.bradford_gen object at 0x7fa40ebe58d0>**

A Bradford continuous random variable.

As an instance of the `rv_continuous` class, `bradford` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `bradford` is:

```
bradford.pdf(x, c) = c / (k * (1+c*x)),
```

for `0 < x < 1`, `c > 0` and `k = log(1+c)`.

`bradford` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `bradford.pdf(x, c, loc, scale)` is identically equivalent to `bradford.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import bradford
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.299
>>> mean, var, skew, kurt = bradford.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(bradford.ppf(0.01, c),
...                 bradford.ppf(0.99, c), 100)
>>> ax.plot(x, bradford.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='bradford pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = bradford(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

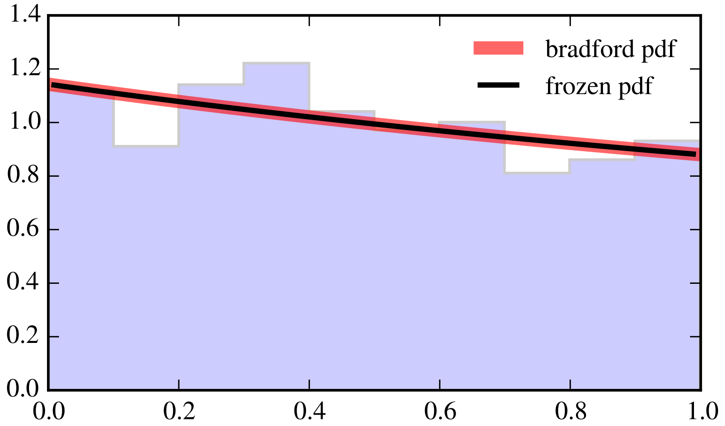
```
>>> vals = bradford.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], bradford.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = bradford.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`burr`** **= <scipy.stats._continuous_distns.burr_gen object at 0x7fa40ebe5bd0>**

A Burr continuous random variable.

As an instance of the `rv_continuous` class, `burr` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`fisk`	a special case of `burr` with `d = 1`

Notes

The probability density function for `burr` is:

```
burr.pdf(x, c, d) = c * d * x**(-c-1) * (1+x**(-c))**(-d-1)
```

for `x > 0`.

`burr` takes `c` and `d` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `burr.pdf(x, c, d, loc, scale)` is identically equivalent to `burr.pdf(y, c, d) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import burr
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c, d = 10.5, 4.3
>>> mean, var, skew, kurt = burr.stats(c, d, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(burr.ppf(0.01, c, d),
...                 burr.ppf(0.99, c, d), 100)
>>> ax.plot(x, burr.pdf(x, c, d),
...        'r-', lw=5, alpha=0.6, label='burr pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = burr(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

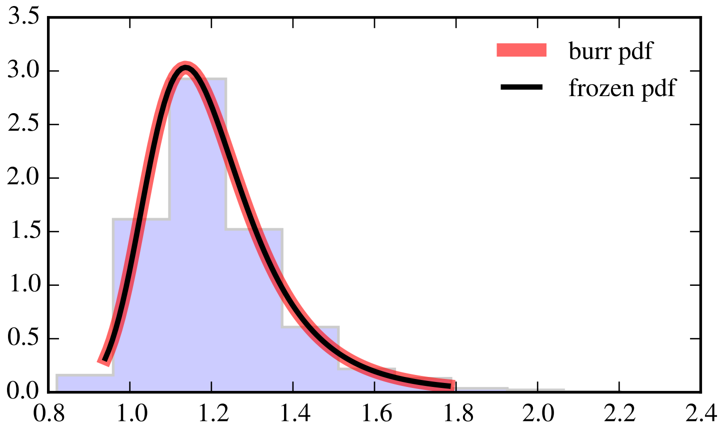
```
>>> vals = burr.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], burr.cdf(vals, c, d))
True
```

Generate random numbers:

```
>>> r = burr.rvs(c, d, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, d, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, d, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, d, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, d, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, d, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, d, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, d, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, d, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, d, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, d, loc=0, scale=1)`	Non-central moment of order n
`stats(c, d, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, d, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, d, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, d, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, d, loc=0, scale=1)`	Median of the distribution.
`mean(c, d, loc=0, scale=1)`	Mean of the distribution.
`var(c, d, loc=0, scale=1)`	Variance of the distribution.
`std(c, d, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, d, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`cauchy`** **= <scipy.stats._continuous_distns.cauchy_gen object at 0x7fa40ebee210>**

A Cauchy continuous random variable.

As an instance of the `rv_continuous` class, `cauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `cauchy` is:

```
cauchy.pdf(x) = 1 / (pi * (1 + x**2))
```

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cauchy.pdf(x, loc, scale)` is identically equivalent to `cauchy.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import cauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = cauchy.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(cauchy.ppf(0.01),
...                 cauchy.ppf(0.99), 100)
>>> ax.plot(x, cauchy.pdf(x),
...        'r-', lw=5, alpha=0.6, label='cauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = cauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

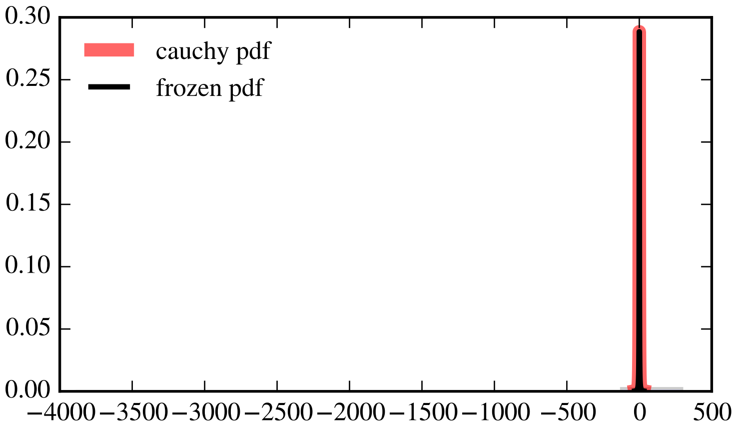
```
>>> vals = cauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cauchy.cdf(vals))
True
```

Generate random numbers:

```
>>> r = cauchy.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`chi`** **= <scipy.stats._continuous_distns.chi_gen object at 0x7fa40ebee450>**

A chi continuous random variable.

As an instance of the `rv_continuous` class, `chi` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `chi` is:

```
chi.pdf(x, df) = x**(df-1) * exp(-x**2/2) / (2**(df/2-1) * gamma(df/2))
```

for `x > 0`.

Special cases of `chi` are:

- `chi(1, loc, scale)` is equivalent to `halfnorm`
- `chi(2, 0, scale)` is equivalent to `rayleigh`
- `chi(3, 0, scale)` is equivalent to `maxwell`

`chi` takes `df` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `chi.pdf(x, df, loc, scale)` is identically equivalent to `chi.pdf(y, df) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import chi
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> df = 78
>>> mean, var, skew, kurt = chi.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(chi.ppf(0.01, df),
...                 chi.ppf(0.99, df), 100)
>>> ax.plot(x, chi.pdf(x, df),
...        'r-', lw=5, alpha=0.6, label='chi pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = chi(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

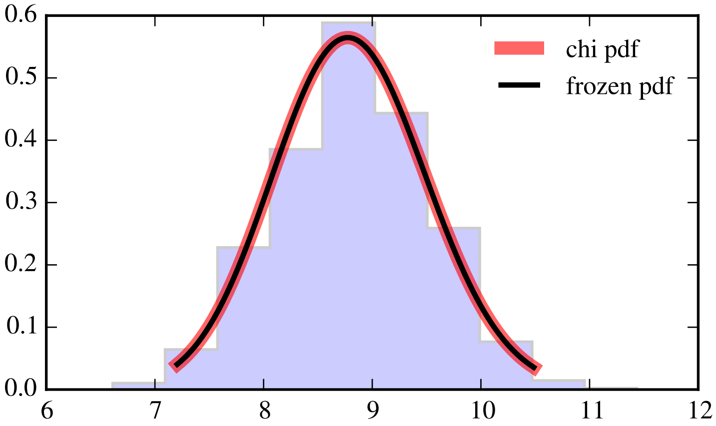
```
>>> vals = chi.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = chi.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(df, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, df, loc=0, scale=1)`	Probability density function.
`logpdf(x, df, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, df, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, df, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, df, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, df, loc=0, scale=1)`	Log of the survival function.
`ppf(q, df, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, df, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, df, loc=0, scale=1)`	Non-central moment of order n
`stats(df, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(df, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, df, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, df, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(df, loc=0, scale=1)`	Median of the distribution.
`mean(df, loc=0, scale=1)`	Mean of the distribution.
`var(df, loc=0, scale=1)`	Variance of the distribution.
`std(df, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, df, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`chi2`** **= <scipy.stats._continuous_distns.chi2_gen object at 0x7fa40ebee710>**

A chi-squared continuous random variable.

As an instance of the `rv_continuous` class, `chi2` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `chi2` is:

```
chi2.pdf(x, df) = 1 / (2*gamma(df/2)) * (x/2)**(df/2-1) * exp(-x/2)
```

`chi2` takes `df` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `chi2.pdf(x, df, loc, scale)` is identically equivalent to `chi2.pdf(y, df) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import chi2
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> df = 55
>>> mean, var, skew, kurt = chi2.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(chi2.ppf(0.01, df),
...                 chi2.ppf(0.99, df), 100)
>>> ax.plot(x, chi2.pdf(x, df),
...        'r-', lw=5, alpha=0.6, label='chi2 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = chi2(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

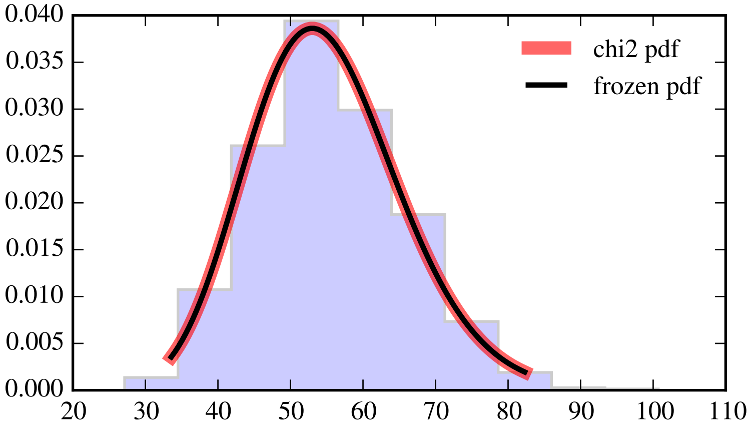
```
>>> vals = chi2.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi2.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = chi2.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(df, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, df, loc=0, scale=1)`	Probability density function.
`logpdf(x, df, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, df, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, df, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, df, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, df, loc=0, scale=1)`	Log of the survival function.
`ppf(q, df, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, df, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, df, loc=0, scale=1)`	Non-central moment of order n
`stats(df, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(df, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, df, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, df, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(df, loc=0, scale=1)`	Median of the distribution.
`mean(df, loc=0, scale=1)`	Mean of the distribution.
`var(df, loc=0, scale=1)`	Variance of the distribution.
`std(df, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, df, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`cosine`** **= <scipy.stats._continuous_distns.cosine_gen object at 0x7fa40ebee9d0>**

A cosine continuous random variable.

As an instance of the `rv_continuous` class, `cosine` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The cosine distribution is an approximation to the normal distribution. The probability density function for `cosine` is:

```
cosine.pdf(x) = 1/(2*pi) * (1+cos(x))
```

for `-pi <= x <= pi`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cosine.pdf(x, loc, scale)` is identically equivalent to `cosine.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import cosine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = cosine.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(cosine.ppf(0.01),
...                 cosine.ppf(0.99), 100)
>>> ax.plot(x, cosine.pdf(x),
...        'r-', lw=5, alpha=0.6, label='cosine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = cosine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

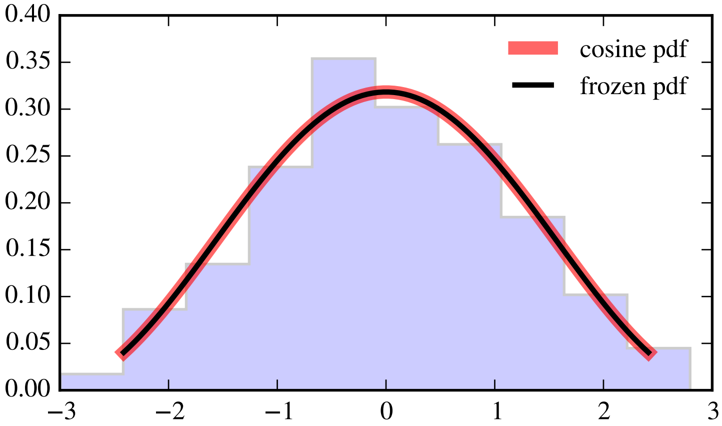
```
>>> vals = cosine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cosine.cdf(vals))
True
```

Generate random numbers:

```
>>> r = cosine.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**dgamma = <scipy.stats._continuous_distns.dgamma_gen object at 0x7fa40ebeebd0>**

A double gamma continuous random variable.

As an instance of the `rv_continuous` class, `dgamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `dgamma` is:

```
dgamma.pdf(x, a) = 1 / (2*gamma(a)) * abs(x)**(a-1) * exp(-abs(x))
```

for `a > 0`.

`dgamma` takes `a` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `dgamma.pdf(x, a, loc, scale)` is identically equivalent to `dgamma.pdf(y, a) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import dgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 1.1
>>> mean, var, skew, kurt = dgamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(dgamma.ppf(0.01, a),
...                 dgamma.ppf(0.99, a), 100)
>>> ax.plot(x, dgamma.pdf(x, a),
...        'r-', lw=5, alpha=0.6, label='dgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = dgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

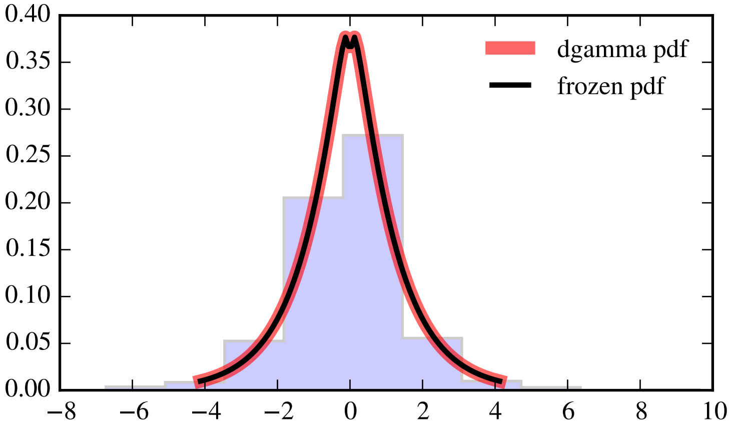
```
>>> vals = dgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], dgamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = dgamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`dweibull`** **= <scipy.stats._continuous_distns.dweibull_gen object at 0x7fa40ebeee90>**

A double Weibull continuous random variable.

As an instance of the `rv_continuous` class, `dweibull` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `dweibull` is:

```
dweibull.pdf(x, c) = c / 2 * abs(x)**(c-1) * exp(-abs(x)**c)
```

`dweibull` takes `d` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `dweibull.pdf(x, c, loc, scale)` is identically equivalent to `dweibull.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import dweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 2.07
>>> mean, var, skew, kurt = dweibull.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(dweibull.ppf(0.01, c),
...                 dweibull.ppf(0.99, c), 100)
>>> ax.plot(x, dweibull.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='dweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = dweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

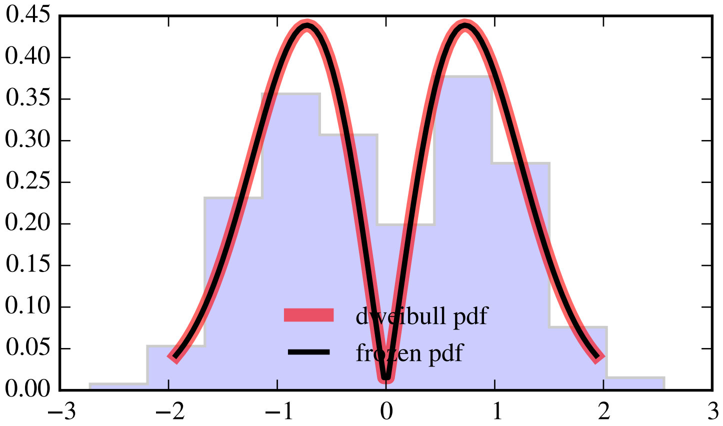
```
>>> vals = dweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], dweibull.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = dweibull.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`erlang`** **= <scipy.stats._continuous_distns.erlang_gen object at 0x7fa40e990190>**

An Erlang continuous random variable.

As an instance of the `rv_continuous` class, `erlang` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gamma`

Notes

The Erlang distribution is a special case of the Gamma distribution, with the shape parameter *a* an integer. Note that this restriction is not enforced by `erlang`. It will, however, generate a warning the first time a non-integer value is used for the shape parameter.

Refer to `gamma` for examples.

Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**expon = <scipy.stats._continuous_distns.expon_gen object at 0x7fa40ebfe190>**

An exponential continuous random variable.

As an instance of the `rv_continuous` class, `expon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `expon` is:

```
expon.pdf(x) = exp(-x)
```

for `x >= 0`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `expon.pdf(x, loc, scale)` is identically equivalent to `expon.pdf(y) / scale` with `y = (x - loc) / scale`.

A common parameterization for `expon` is in terms of the rate parameter `lambda`, such that `pdf = lambda * exp(-lambda * x)`. This parameterization corresponds to using `scale = 1 / lambda`.

Examples

```
>>> from scipy.stats import expon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = expon.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(expon.ppf(0.01),
...                 expon.ppf(0.99), 100)
>>> ax.plot(x, expon.pdf(x),
...        'r-', lw=5, alpha=0.6, label='expon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = expon()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

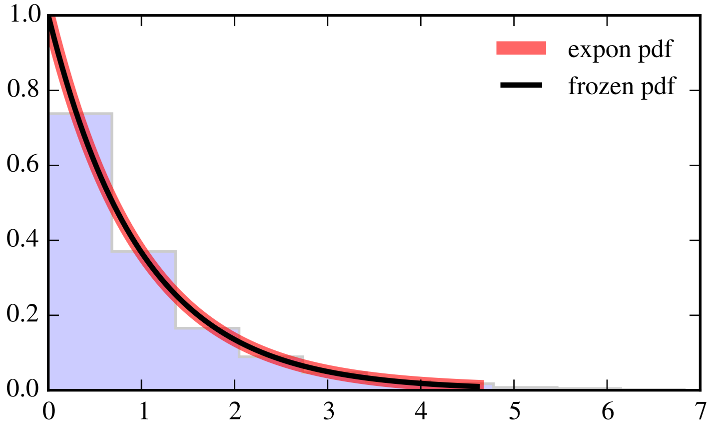
```
>>> vals = expon.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], expon.cdf(vals))
True
```

Generate random numbers:

```
>>> r = expon.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`exponnorm`** **= <scipy.stats._continuous_distns.exponnorm_gen object at 0x7fa40ebfe390>**

An exponentially modified Normal continuous random variable.

As an instance of the `rv_continuous` class, `exponnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `exponnorm` is:

```
exponnorm.pdf(x, K) = 1/(2*K) exp(1/(2 * K**2)) exp(-x / K) * erfc(-(x - 1/K) / sqrt(2))
```

where the shape parameter `K > 0`.

It can be thought of as the sum of a normally distributed random value with mean `loc` and sigma `scale` and an exponentially distributed random number with a pdf proportional to `exp(-lambda * x)` where `lambda = (K * scale)**(-1)`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponnorm.pdf(x, K, loc, scale)` is identically equivalent to `exponnorm.pdf(y, K) / scale` with `y = (x - loc) / scale`.

An alternative parameterization of this distribution (for example, in Wikipedia) involves three parameters, μ, λ and σ. In the present parameterization this corresponds to having `loc` and `scale` equal to μ and σ, respectively, and shape parameter $K = 1/\sigma\lambda$.

New in version 0.16.0.

Examples

```
>>> from scipy.stats import exponnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> K = 1.5
>>> mean, var, skew, kurt = exponnorm.stats(K, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponnorm.ppf(0.01, K),
...                 exponnorm.ppf(0.99, K), 100)
>>> ax.plot(x, exponnorm.pdf(x, K),
...         'r-', lw=5, alpha=0.6, label='exponnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponnorm(K)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

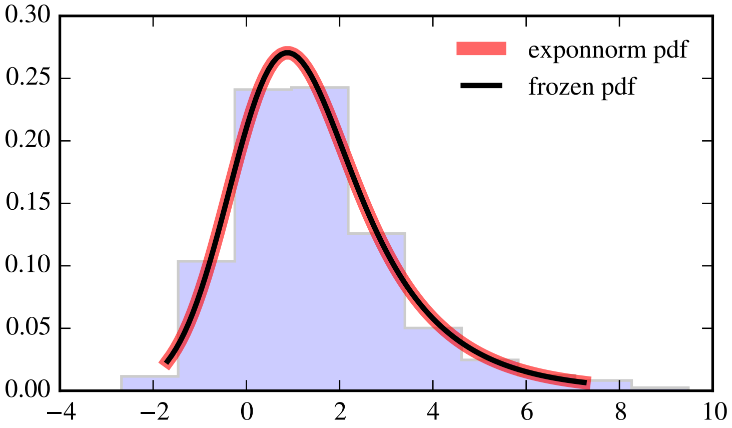
```
>>> vals = exponnorm.ppf([0.001, 0.5, 0.999], K)
>>> np.allclose([0.001, 0.5, 0.999], exponnorm.cdf(vals, K))
True
```

Generate random numbers:

```
>>> r = exponnorm.rvs(K, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(K, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, K, loc=0, scale=1)`	Probability density function.
`logpdf(x, K, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, K, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, K, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, K, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, K, loc=0, scale=1)`	Log of the survival function.
`ppf(q, K, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, K, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, K, loc=0, scale=1)`	Non-central moment of order n
`stats(K, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(K, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, K, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, K, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(K, loc=0, scale=1)`	Median of the distribution.
`mean(K, loc=0, scale=1)`	Mean of the distribution.
`var(K, loc=0, scale=1)`	Variance of the distribution.
`std(K, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, K, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`exponweib`** **= <scipy.stats._continuous_distns.exponweib_gen object at 0x7fa40ebfe650>**

An exponentiated Weibull continuous random variable.

As an instance of the `rv_continuous` class, `exponweib` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `exponweib` is:

```
exponweib.pdf(x, a, c) =
    a * c * (1-exp(-x**c))**(a-1) * exp(-x**c)*x**(c-1)
```

for `x > 0`, `a > 0`, `c > 0`.

`exponweib` takes `a` and `c` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponweib.pdf(x, a, c, loc, scale)` is identically equivalent to `exponweib.pdf(y, a, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import exponweib
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, c = 2.89, 1.95
>>> mean, var, skew, kurt = exponweib.stats(a, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponweib.ppf(0.01, a, c),
...                 exponweib.ppf(0.99, a, c), 100)
>>> ax.plot(x, exponweib.pdf(x, a, c),
...        'r-', lw=5, alpha=0.6, label='exponweib pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponweib(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

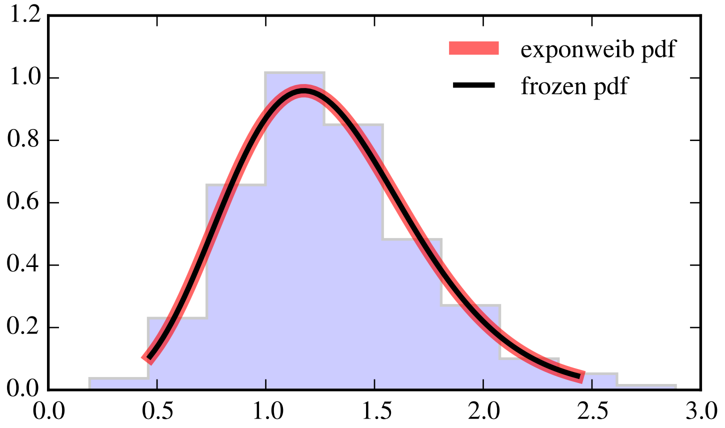
```
>>> vals = exponweib.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], exponweib.cdf(vals, a, c))
True
```

Generate random numbers:

```
>>> r = exponweib.rvs(a, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, c, loc=0, scale=1)`	Non-central moment of order n
`stats(a, c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, c, loc=0, scale=1)`	Median of the distribution.
`mean(a, c, loc=0, scale=1)`	Mean of the distribution.
`var(a, c, loc=0, scale=1)`	Variance of the distribution.
`std(a, c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**exponpow = <scipy.stats._continuous_distns.exponpow_gen object at 0x7fa40ebfe990>**

An exponential power continuous random variable.

As an instance of the `rv_continuous` class, `exponpow` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `exponpow` is:

```
exponpow.pdf(x, b) = b * x**(b-1) * exp(1 + x**b - exp(x**b))
```

for `x >= 0`, `b > 0`. Note that this is a different distribution from the exponential power distribution that is also known under the names "generalized normal" or "generalized Gaussian".

`exponpow` takes `b` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponpow.pdf(x, b, loc, scale)` is identically equivalent to `exponpow.pdf(y, b) / scale` with `y = (x - loc) / scale`.

References

http://www.math.wm.edu/~leemis/chart/UDR/PDFs/Exponentialpower.pdf

Examples

```
>>> from scipy.stats import exponpow
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> b = 2.7
>>> mean, var, skew, kurt = exponpow.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponpow.ppf(0.01, b),
...                 exponpow.ppf(0.99, b), 100)
>>> ax.plot(x, exponpow.pdf(x, b),
...          'r-', lw=5, alpha=0.6, label='exponpow pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponpow(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

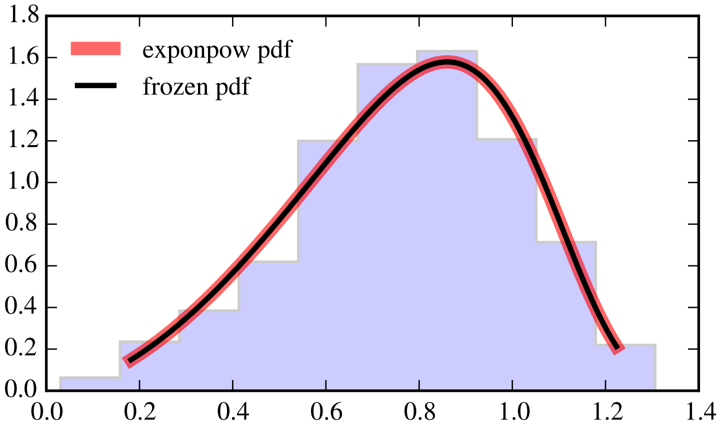
```
>>> vals = exponpow.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], exponpow.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = exponpow.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, b, loc=0, scale=1)`	Non-central moment of order n
`stats(b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(b, loc=0, scale=1)`	Median of the distribution.
`mean(b, loc=0, scale=1)`	Mean of the distribution.
`var(b, loc=0, scale=1)`	Variance of the distribution.
`std(b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**f = <scipy.stats._continuous_distns.f_gen object at 0x7fa40e97e210>**

An F continuous random variable.

As an instance of the `rv_continuous` class, `f` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `f` is:

```
                       df2**(df2/2) * df1**(df1/2) * x**(df1/2-1)
F.pdf(x, df1, df2) = --------------------------------------------
                       (df2+df1*x)**((df1+df2)/2) * B(df1/2, df2/2)
```

for `x > 0`.

`f` takes `dfn` and `dfd` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `f.pdf(x, dfn, dfd, loc, scale)` is identically equivalent to `f.pdf(y, dfn, dfd) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import f
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> dfn, dfd = 29, 18
>>> mean, var, skew, kurt = f.stats(dfn, dfd, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(f.ppf(0.01, dfn, dfd),
...                 f.ppf(0.99, dfn, dfd), 100)
>>> ax.plot(x, f.pdf(x, dfn, dfd),
...        'r-', lw=5, alpha=0.6, label='f pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = f(dfn, dfd)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

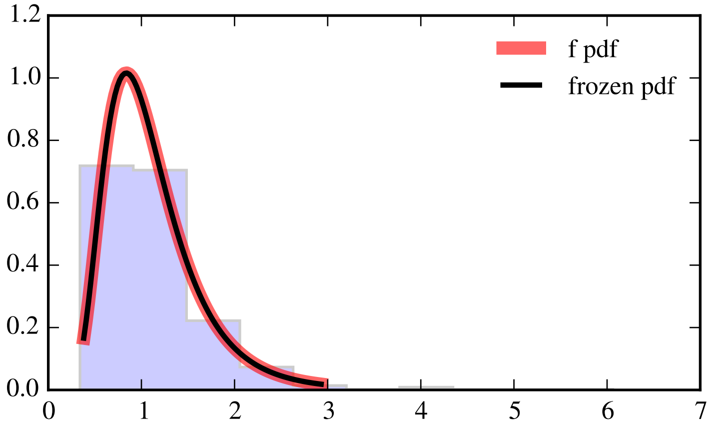
```
>>> vals = f.ppf([0.001, 0.5, 0.999], dfn, dfd)
>>> np.allclose([0.001, 0.5, 0.999], f.cdf(vals, dfn, dfd))
True
```

Generate random numbers:

```
>>> r = f.rvs(dfn, dfd, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(dfn, dfd, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, dfn, dfd, loc=0, scale=1)`	Probability density function.
`logpdf(x, dfn, dfd, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, dfn, dfd, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, dfn, dfd, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, dfn, dfd, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, dfn, dfd, loc=0, scale=1)`	Log of the survival function.
`ppf(q, dfn, dfd, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, dfn, dfd, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, dfn, dfd, loc=0, scale=1)`	Non-central moment of order n
`stats(dfn, dfd, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(dfn, dfd, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, dfn, dfd, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, dfn, dfd, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(dfn, dfd, loc=0, scale=1)`	Median of the distribution.
`mean(dfn, dfd, loc=0, scale=1)`	Mean of the distribution.
`var(dfn, dfd, loc=0, scale=1)`	Variance of the distribution.
`std(dfn, dfd, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, dfn, dfd, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`fatiguelife`** **= <scipy.stats._continuous_distns.fatiguelife_gen object at 0x7fa40ebfec50>**

A fatigue-life (Birnbaum-Saunders) continuous random variable.

As an instance of the `rv_continuous` class, `fatiguelife` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `fatiguelife` is:

```
fatiguelife.pdf(x, c) =
    (x+1) / (2*c*sqrt(2*pi*x**3)) * exp(-(x-1)**2/(2*x*c**2))
```

for `x > 0`.

`fatiguelife` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `fatiguelife.pdf(x, c, loc, scale)` is identically equivalent to `fatiguelife.pdf(y, c) / scale` with `y = (x - loc) / scale`.

References

[R316]

Examples

```
>>> from scipy.stats import fatiguelife
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 29
>>> mean, var, skew, kurt = fatiguelife.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(fatiguelife.ppf(0.01, c),
...                 fatiguelife.ppf(0.99, c), 100)
>>> ax.plot(x, fatiguelife.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='fatiguelife pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = fatiguelife(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

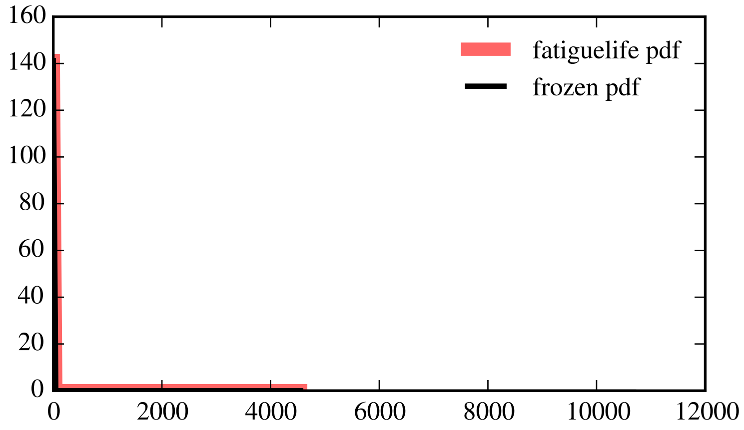
```
>>> vals = fatiguelife.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fatiguelife.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = fatiguelife.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`fisk`** **= <scipy.stats._continuous_distns.fisk_gen object at 0x7fa40ebe5f10>**

A Fisk continuous random variable.

The Fisk distribution is also known as the log-logistic distribution, and equals the Burr distribution with `d == 1`.

`fisk` takes `c` as a shape parameter.

As an instance of the `rv_continuous` class, `fisk` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`burr`

Notes

The probability density function for `fisk` is:

```
fisk.pdf(x, c) = c * x**(-c-1) * (1 + x**(-c))**(-2)
```

for `x > 0`.

`fisk` takes `c` as a shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `fisk.pdf(x, c, loc, scale)` is identically equivalent to `fisk.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import fisk
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 3.09
>>> mean, var, skew, kurt = fisk.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(fisk.ppf(0.01, c),
...                 fisk.ppf(0.99, c), 100)
>>> ax.plot(x, fisk.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='fisk pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = fisk(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

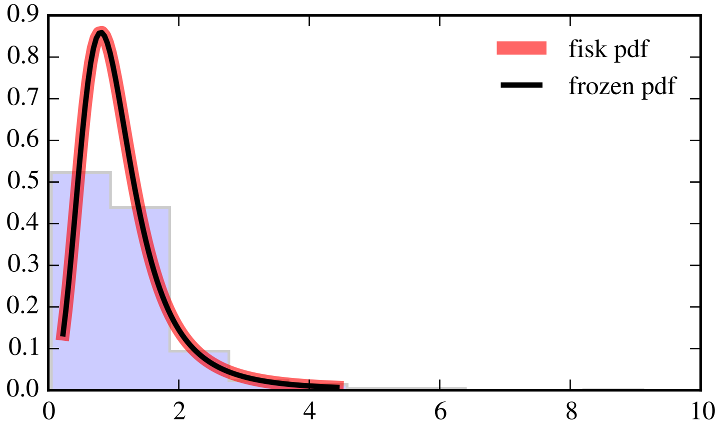
```
>>> vals = fisk.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fisk.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = fisk.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`foldcauchy`** **= <scipy.stats._continuous_distns.foldcauchy_gen object at 0x7fa40ebfef10>**

A folded Cauchy continuous random variable.

As an instance of the `rv_continuous` class, `foldcauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `foldcauchy` is:

```
foldcauchy.pdf(x, c) = 1/(pi*(1+(x-c)**2)) + 1/(pi*(1+(x+c)**2))
```

for `x >= 0`.

`foldcauchy` takes `c` as a shape parameter.

Examples

```
>>> from scipy.stats import foldcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 4.72
>>> mean, var, skew, kurt = foldcauchy.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(foldcauchy.ppf(0.01, c),
...                 foldcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, foldcauchy.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='foldcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = foldcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

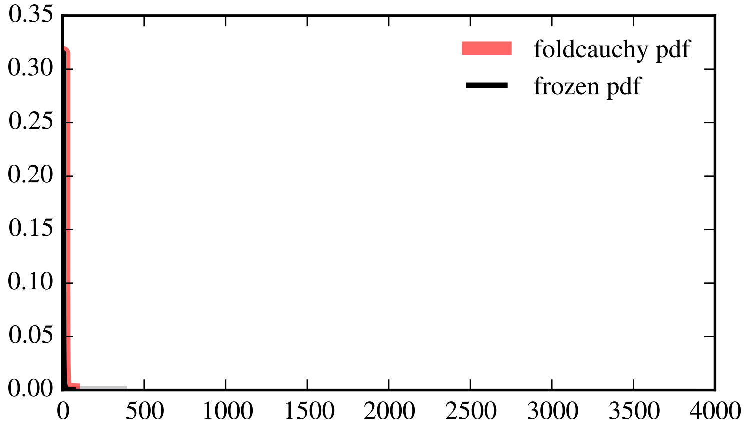
```
>>> vals = foldcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldcauchy.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = foldcauchy.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`foldnorm`** **= <scipy.stats._continuous_distns.foldnorm_gen object at 0x7fa40e97e550>**

A folded normal continuous random variable.

As an instance of the `rv_continuous` class, `foldnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `foldnorm` is:

```
foldnormal.pdf(x, c) = sqrt(2/pi) * cosh(c*x) * exp(-(x**2+c**2)/2)
```

for `c >= 0`.

`foldnorm` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `foldnorm.pdf(x, c, loc, scale)` is identically equivalent to `foldnorm.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import foldnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 1.95
>>> mean, var, skew, kurt = foldnorm.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(foldnorm.ppf(0.01, c),
...                 foldnorm.ppf(0.99, c), 100)
>>> ax.plot(x, foldnorm.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='foldnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = foldnorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

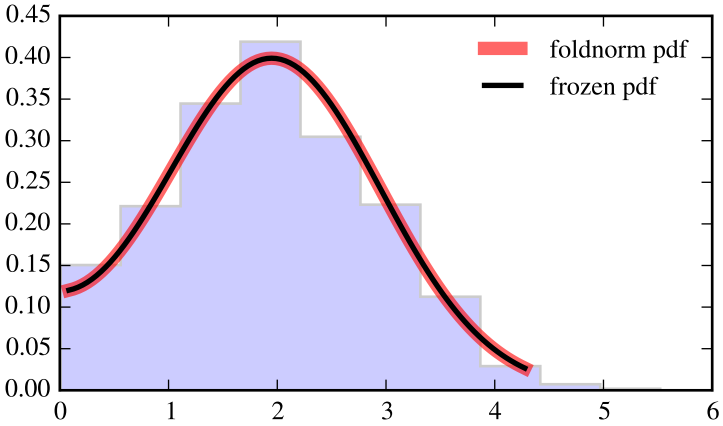
```
>>> vals = foldnorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldnorm.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = foldnorm.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`frechet_r`** **= <scipy.stats._continuous_distns.frechet_r_gen object at 0x7fa40e97e810>**

A Frechet right (or Weibull minimum) continuous random variable.

As an instance of the `rv_continuous` class, `frechet_r` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`weibull_min`

The same distribution as `frechet_r`.

`frechet_l`, `weibull_max`

Notes

The probability density function for `frechet_r` is:

```
frechet_r.pdf(x, c) = c * x**(c-1) * exp(-x**c)
```

for `x > 0`, `c > 0`.

`frechet_r` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `frechet_r.pdf(x, c, loc, scale)` is identically equivalent to `frechet_r.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import frechet_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 1.89
>>> mean, var, skew, kurt = frechet_r.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(frechet_r.ppf(0.01, c),
...                 frechet_r.ppf(0.99, c), 100)
>>> ax.plot(x, frechet_r.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='frechet_r pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = frechet_r(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

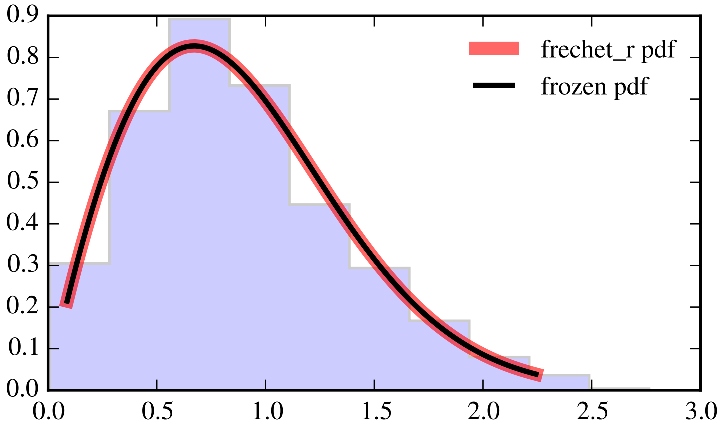
```
>>> vals = frechet_r.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], frechet_r.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = frechet_r.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`frechet_l`** **= <scipy.stats._continuous_distns.frechet_l_gen object at 0x7fa40e97ed50>**

A Frechet left (or Weibull maximum) continuous random variable.

As an instance of the `rv_continuous` class, `frechet_l` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`weibull_max`
The same distribution as `frechet_l`.

`frechet_r`, `weibull_min`

Notes

The probability density function for `frechet_l` is:

```
frechet_l.pdf(x, c) = c * (-x)**(c-1) * exp(-(-x)**c)
```

for `x < 0`, `c > 0`.

`frechet_l` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `frechet_l.pdf(x, c, loc, scale)` is identically equivalent to `frechet_l.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import frechet_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 3.63
>>> mean, var, skew, kurt = frechet_l.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(frechet_l.ppf(0.01, c),
...                 frechet_l.ppf(0.99, c), 100)
>>> ax.plot(x, frechet_l.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='frechet_l pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = frechet_l(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

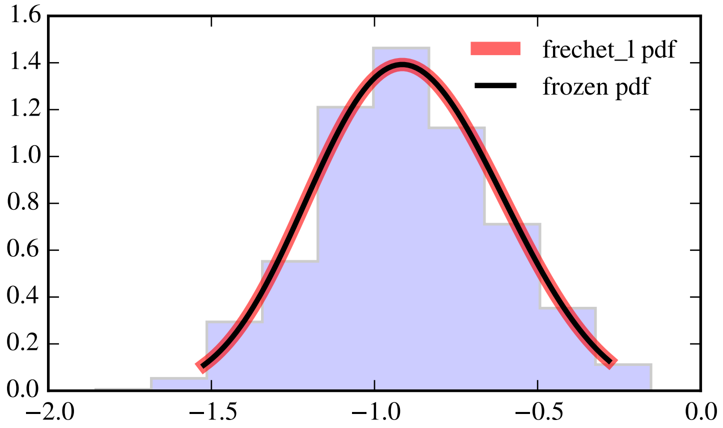
```
>>> vals = frechet_l.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], frechet_l.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = frechet_l.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`genlogistic`** **= <scipy.stats._continuous_distns.genlogistic_gen object at 0x7fa40e9872d0>**

A generalized logistic continuous random variable.

As an instance of the `rv_continuous` class, `genlogistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `genlogistic` is:

```
genlogistic.pdf(x, c) = c * exp(-x) / (1 + exp(-x))**(c+1)
```

for `x > 0`, `c > 0`.

`genlogistic` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genlogistic.pdf(x, c, loc, scale)` is identically equivalent to `genlogistic.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import genlogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.412
>>> mean, var, skew, kurt = genlogistic.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genlogistic.ppf(0.01, c),
...                 genlogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genlogistic.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='genlogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genlogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

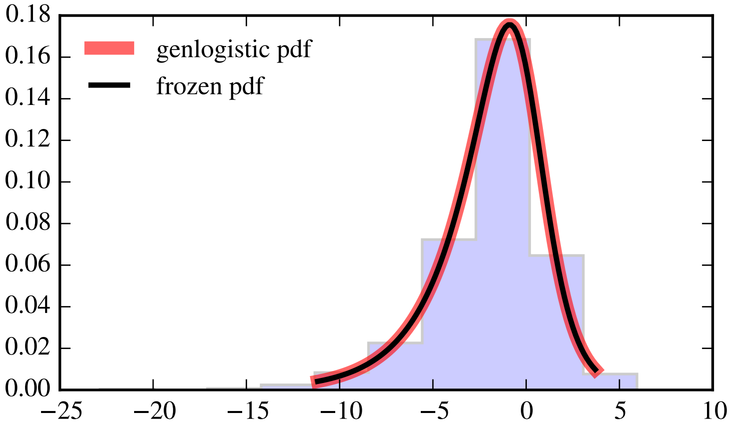
```
>>> vals = genlogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genlogistic.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genlogistic.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gennorm`** **= <scipy.stats._continuous_distns.gennorm_gen object at 0x7fa40e8fdfd0>**
A generalized normal continuous random variable.

As an instance of the `rv_continuous` class, `gennorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`laplace`	Laplace distribution
`norm`	normal distribution

Notes

The probability density function for `gennorm` is [R324]:

```
                             beta
gennorm.pdf(x, beta) =  ---------------  exp(-|x|**beta)
                        2 gamma(1/beta)
```

`gennorm` takes `beta` as a shape parameter. For `beta = 1`, it is identical to a Laplace distribution. For `beta = 2`, it is identical to a normal distribution (with `scale=1/sqrt(2)`).

References

[R324]

Examples

```
>>> from scipy.stats import gennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> beta = 1.3
>>> mean, var, skew, kurt = gennorm.stats(beta, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gennorm.ppf(0.01, beta),
...                 gennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, gennorm.pdf(x, beta),
...        'r-', lw=5, alpha=0.6, label='gennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

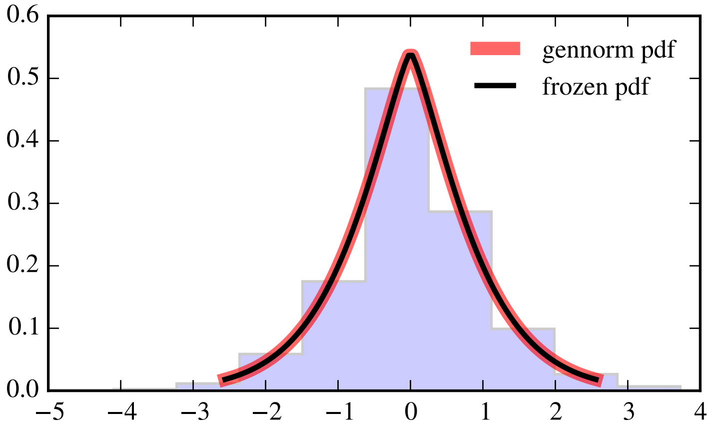
```
>>> vals = gennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], gennorm.cdf(vals, beta))
True
```

Generate random numbers:

```
>>> r = gennorm.rvs(beta, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(beta, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, beta, loc=0, scale=1)`	Probability density function.
`logpdf(x, beta, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, beta, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, beta, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, beta, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, beta, loc=0, scale=1)`	Log of the survival function.
`ppf(q, beta, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, beta, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, beta, loc=0, scale=1)`	Non-central moment of order n
`stats(beta, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(beta, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, beta, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, beta, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(beta, loc=0, scale=1)`	Median of the distribution.
`mean(beta, loc=0, scale=1)`	Mean of the distribution.
`var(beta, loc=0, scale=1)`	Variance of the distribution.
`std(beta, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, beta, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`genpareto`** **= <scipy.stats._continuous_distns.genpareto_gen object at 0x7fa40e987590>**

A generalized Pareto continuous random variable.

As an instance of the `rv_continuous` class, `genpareto` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `genpareto` is:

```
genpareto.pdf(x, c) = (1 + c * x)**(-1 - 1/c)
```

defined for `x >= 0` if `c >=0`, and for `0 <= x <= -1/c` if `c < 0`.

`genpareto` takes `c` as a shape parameter.

For `c == 0`, `genpareto` reduces to the exponential distribution, `expon`:

```
genpareto.pdf(x, c=0) = exp(-x)
```

For `c == -1`, `genpareto` is uniform on `[0, 1]`:

```
genpareto.cdf(x, c=-1) = x
```

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genpareto.pdf(x, c, loc, scale)` is identically equivalent to `genpareto.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import genpareto
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.1
>>> mean, var, skew, kurt = genpareto.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genpareto.ppf(0.01, c),
...                 genpareto.ppf(0.99, c), 100)
>>> ax.plot(x, genpareto.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='genpareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genpareto(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

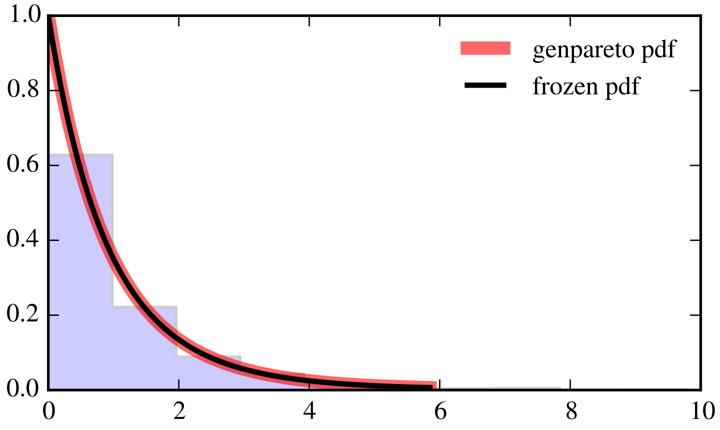
```
>>> vals = genpareto.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genpareto.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genpareto.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**genexpon = <scipy.stats._continuous_distns.genexpon_gen object at 0x7fa40e987850>**

A generalized exponential continuous random variable.

As an instance of the `rv_continuous` class, `genexpon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `genexpon` is:

```
genexpon.pdf(x, a, b, c) = (a + b * (1 - exp(-c*x))) *                                   exp(-a
```

for `x >= 0`, `a, b, c > 0`.

`genexpon` takes `a`, `b` and `c` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genexpon.pdf(x, a, b, c, loc, scale)` is identically equivalent to `genexpon.pdf(y, a, b, c) / scale` with `y = (x - loc) / scale`.

References

H.K. Ryu, "An Extension of Marshall and Olkin's Bivariate Exponential Distribution", Journal of the American Statistical Association, 1993.

N. Balakrishnan, "The Exponential Distribution: Theory, Methods and Applications", Asit P. Basu.

Examples

```
>>> from scipy.stats import genexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b, c = 9.13, 16.2, 3.28
>>> mean, var, skew, kurt = genexpon.stats(a, b, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genexpon.ppf(0.01, a, b, c),
...                 genexpon.ppf(0.99, a, b, c), 100)
>>> ax.plot(x, genexpon.pdf(x, a, b, c),
...        'r-', lw=5, alpha=0.6, label='genexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genexpon(a, b, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

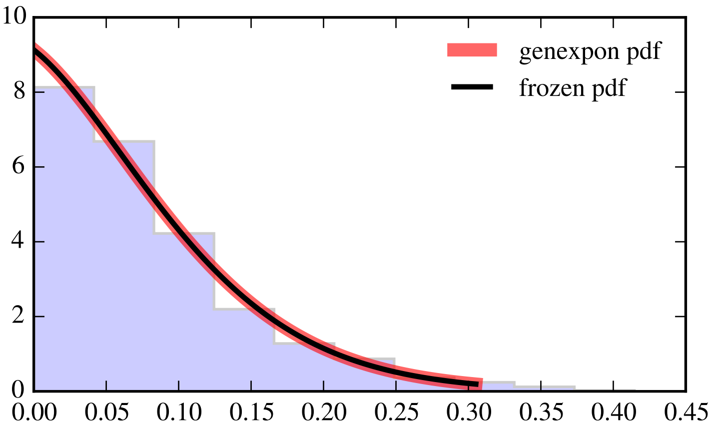
```
>>> vals = genexpon.ppf([0.001, 0.5, 0.999], a, b, c)
>>> np.allclose([0.001, 0.5, 0.999], genexpon.cdf(vals, a, b, c))
True
```

Generate random numbers:

```
>>> r = genexpon.rvs(a, b, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, c, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, c, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, c, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, c, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`genextreme`** **= <scipy.stats._continuous_distns.genextreme_gen object at 0x7fa40e987bd0>**

A generalized extreme value continuous random variable.

As an instance of the `rv_continuous` class, `genextreme` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gumbel_r

Notes

For c=0, genextreme is equal to gumbel_r. The probability density function for genextreme is:

```
genextreme.pdf(x, c) =
    exp(-exp(-x))*exp(-x),                    for c==0
    exp(-(1-c*x)**(1/c))*(1-c*x)**(1/c-1),    for x <= 1/c, c > 0
```

Note that several sources and software packages use the opposite convention for the sign of the shape parameter `c`.

genextreme takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genextreme.pdf(x, c, loc, scale)` is identically equivalent to `genextreme.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import genextreme
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = -0.1
>>> mean, var, skew, kurt = genextreme.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genextreme.ppf(0.01, c),
...                 genextreme.ppf(0.99, c), 100)
>>> ax.plot(x, genextreme.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='genextreme pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genextreme(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

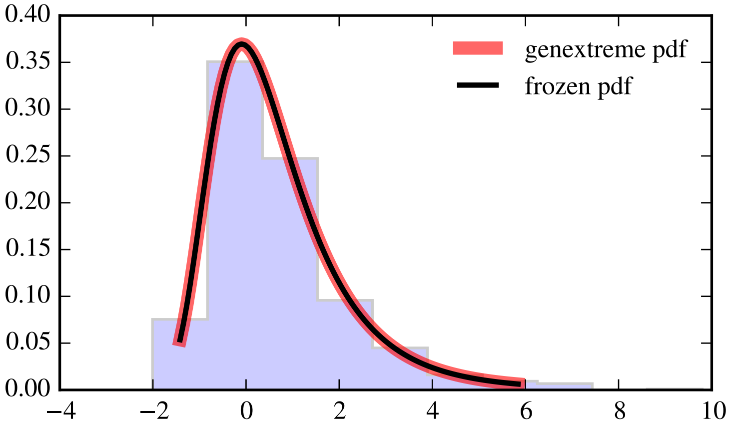
```
>>> vals = genextreme.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genextreme.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genextreme.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gausshyper`** **= <scipy.stats._continuous_distns.gausshyper_gen object at 0x7fa40e9a2950>**

A Gauss hypergeometric continuous random variable.

As an instance of the `rv_continuous` class, `gausshyper` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `gausshyper` is:

```
gausshyper.pdf(x, a, b, c, z) =
    C * x**(a-1) * (1-x)**(b-1) * (1+z*x)**(-c)
```

for `0 <= x <= 1`, `a > 0`, `b > 0`, and `C = 1 / (B(a, b) F[2, 1](c, a; a+b; -z))`

`gausshyper` takes `a`, `b`, `c` and `z` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gausshyper.pdf(x, a, b, c, z, loc, scale)` is identically equivalent to `gausshyper.pdf(y, a, b, c, z) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gausshyper
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b, c, z = 13.8, 3.12, 2.51, 5.18
>>> mean, var, skew, kurt = gausshyper.stats(a, b, c, z, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gausshyper.ppf(0.01, a, b, c, z),
...                 gausshyper.ppf(0.99, a, b, c, z), 100)
>>> ax.plot(x, gausshyper.pdf(x, a, b, c, z),
...          'r-', lw=5, alpha=0.6, label='gausshyper pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gausshyper(a, b, c, z)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

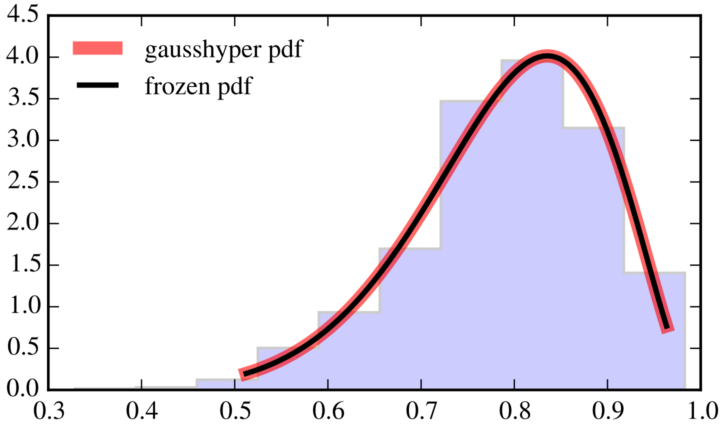
```
>>> vals = gausshyper.ppf([0.001, 0.5, 0.999], a, b, c, z)
>>> np.allclose([0.001, 0.5, 0.999], gausshyper.cdf(vals, a, b, c, z))
True
```

Generate random numbers:

```
>>> r = gausshyper.rvs(a, b, c, z, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, c, z, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, c, z, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, c, z, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, c, z, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, c, z, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, c, z, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, c, z, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, c, z, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, c, z, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, c, z, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, c, z, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, c, z, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, c, z, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, c, z, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, c, z, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, c, z, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, c, z, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, c, z, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, c, z, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**gamma = <scipy.stats._continuous_distns.gamma_gen object at 0x7fa40e987e90>**

A gamma continuous random variable.

As an instance of the `rv_continuous` class, `gamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`erlang`, `expon`

Notes

The probability density function for `gamma` is:

```
gamma.pdf(x, a) = x**(a-1) * exp(-x) / gamma(a)
```

for `x >= 0`, `a > 0`. Here `gamma(a)` refers to the gamma function.

`gamma` has a shape parameter *a* which needs to be set explicitly.

When `a` is an integer, `gamma` reduces to the Erlang distribution, and when `a=1` to the exponential distribution.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gamma.pdf(x, a, loc, scale)` is identically equivalent to `gamma.pdf(y, a) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 1.99
>>> mean, var, skew, kurt = gamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gamma.ppf(0.01, a),
...                 gamma.ppf(0.99, a), 100)
>>> ax.plot(x, gamma.pdf(x, a),
...          'r-', lw=5, alpha=0.6, label='gamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

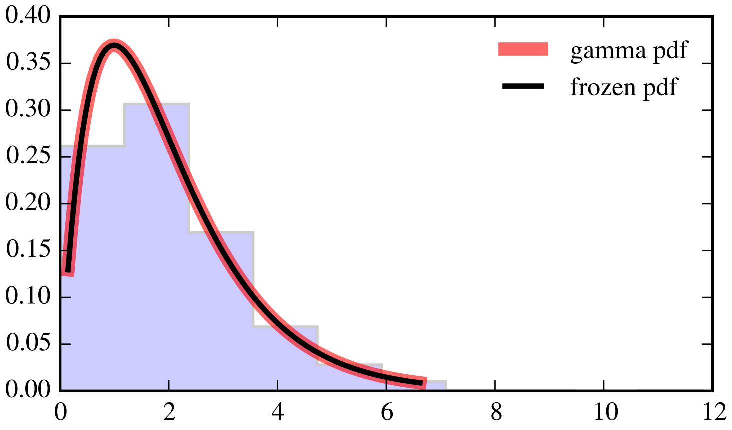
```
>>> vals = gamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], gamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = gamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**gengamma = <scipy.stats._continuous_distns.gengamma_gen object at 0x7fa40e990450>**

A generalized gamma continuous random variable.

As an instance of the `rv_continuous` class, `gengamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `gengamma` is:

```
gengamma.pdf(x, a, c) = abs(c) * x**(c*a-1) * exp(-x**c) / gamma(a)
```

for `x > 0`, `a > 0`, and `c != 0`.

`gengamma` takes `a` and `c` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gengamma.pdf(x, a, c, loc, scale)` is identically equivalent to `gengamma.pdf(y, a, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gengamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, c = 4.42, 3.12
>>> mean, var, skew, kurt = gengamma.stats(a, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gengamma.ppf(0.01, a, c),
...                 gengamma.ppf(0.99, a, c), 100)
>>> ax.plot(x, gengamma.pdf(x, a, c),
...        'r-', lw=5, alpha=0.6, label='gengamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gengamma(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

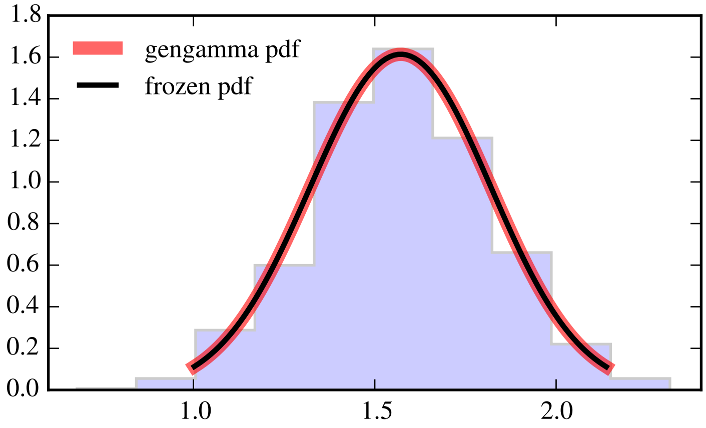
```
>>> vals = gengamma.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], gengamma.cdf(vals, a, c))
True
```

Generate random numbers:

```
>>> r = gengamma.rvs(a, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, c, loc=0, scale=1)`	Non-central moment of order n
`stats(a, c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, c, loc=0, scale=1)`	Median of the distribution.
`mean(a, c, loc=0, scale=1)`	Mean of the distribution.
`var(a, c, loc=0, scale=1)`	Variance of the distribution.
`std(a, c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`genhalflogistic`** **= <scipy.stats._continuous_distns.genhalflogistic_gen object at 0x7fa40e990790>**

A generalized half-logistic continuous random variable.

As an instance of the `rv_continuous` class, `genhalflogistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `genhalflogistic` is:

```
genhalflogistic.pdf(x, c) = 2 * (1-c*x)**(1/c-1) / (1+(1-c*x)**(1/c))**2
```

for `0 <= x <= 1/c`, and `c > 0`.

`genhalflogistic` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genhalflogistic.pdf(x, c, loc, scale)` is identically equivalent to `genhalflogistic.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import genhalflogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.773
>>> mean, var, skew, kurt = genhalflogistic.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genhalflogistic.ppf(0.01, c),
...                 genhalflogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genhalflogistic.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='genhalflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genhalflogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

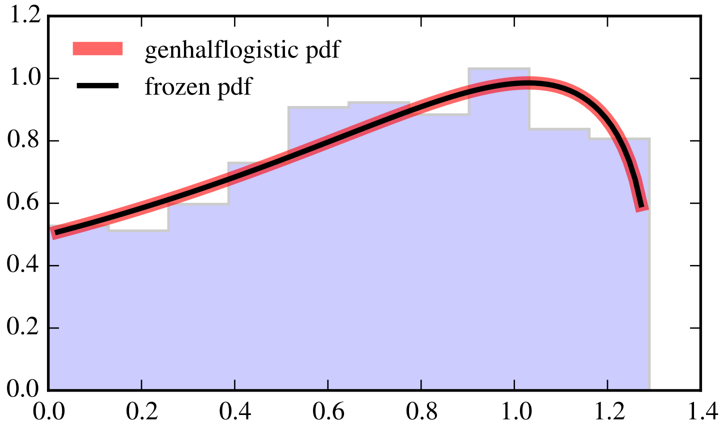
```
>>> vals = genhalflogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genhalflogistic.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genhalflogistic.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gilbrat`** **= <scipy.stats._continuous_distns.gilbrat_gen object at 0x7fa40e93cf50>**

A Gilbrat continuous random variable.

As an instance of the `rv_continuous` class, `gilbrat` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `gilbrat` is:

```
gilbrat.pdf(x) = 1/(x*sqrt(2*pi)) * exp(-1/2*(log(x))**2)
```

`gilbrat` is a special case of `lognorm` with `s = 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gilbrat.pdf(x, loc, scale)` is identically equivalent to `gilbrat.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gilbrat
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = gilbrat.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gilbrat.ppf(0.01),
...                 gilbrat.ppf(0.99), 100)
>>> ax.plot(x, gilbrat.pdf(x),
...        'r-', lw=5, alpha=0.6, label='gilbrat pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gilbrat()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

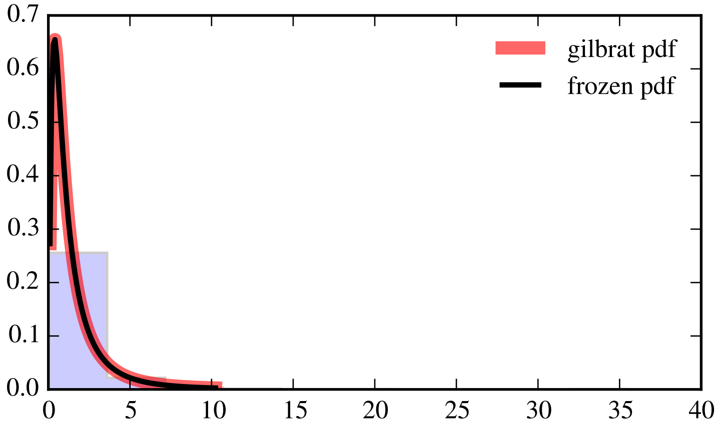
```
>>> vals = gilbrat.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gilbrat.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gilbrat.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gompertz`** **= <scipy.stats._continuous_distns.gompertz_gen object at 0x7fa40e990a50>**

A Gompertz (or truncated Gumbel) continuous random variable.

As an instance of the `rv_continuous` class, `gompertz` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `gompertz` is:

```
gompertz.pdf(x, c) = c * exp(x) * exp(-c*(exp(x)-1))
```

for `x >= 0`, `c > 0`.

`gompertz` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gompertz.pdf(x, c, loc, scale)` is identically equivalent to `gompertz.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gompertz
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.947
>>> mean, var, skew, kurt = gompertz.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gompertz.ppf(0.01, c),
...                 gompertz.ppf(0.99, c), 100)
>>> ax.plot(x, gompertz.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='gompertz pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gompertz(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

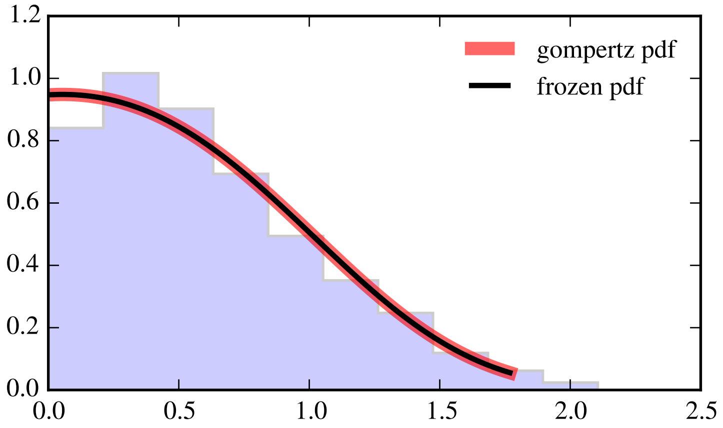
```
>>> vals = gompertz.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], gompertz.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = gompertz.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gumbel_r`** **= <scipy.stats._continuous_distns.gumbel_r_gen object at 0x7fa40e990d10>**

A right-skewed Gumbel continuous random variable.

As an instance of the `rv_continuous` class, `gumbel_r` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gumbel_l`, `gompertz`, `genextreme`

Notes

The probability density function for `gumbel_r` is:

```
gumbel_r.pdf(x) = exp(-(x + exp(-x)))
```

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_r.pdf(x, loc, scale)` is identically equivalent to `gumbel_r.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gumbel_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = gumbel_r.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gumbel_r.ppf(0.01),
...                 gumbel_r.ppf(0.99), 100)
>>> ax.plot(x, gumbel_r.pdf(x),
...        'r-', lw=5, alpha=0.6, label='gumbel_r pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gumbel_r()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

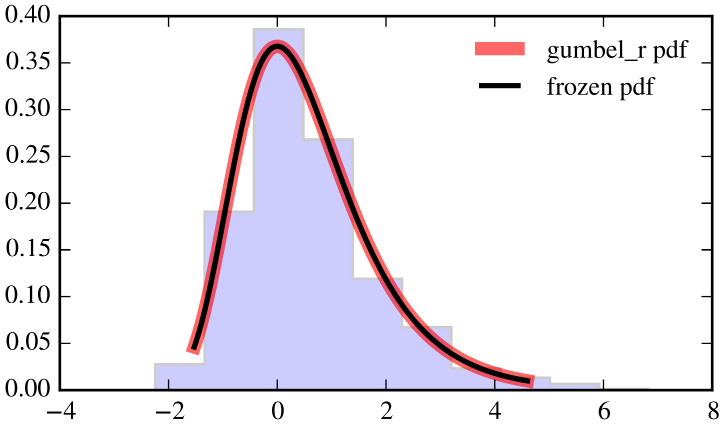
```
>>> vals = gumbel_r.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_r.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gumbel_r.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`gumbel_l`** **= <scipy.stats._continuous_distns.gumbel_l_gen object at 0x7fa40e990f10>**

A left-skewed Gumbel continuous random variable.

As an instance of the `rv_continuous` class, `gumbel_l` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gumbel_r`, `gompertz`, `genextreme`

Notes

The probability density function for `gumbel_l` is:

```
gumbel_l.pdf(x) = exp(x - exp(x))
```

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_l.pdf(x, loc, scale)` is identically equivalent to `gumbel_l.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import gumbel_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = gumbel_l.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gumbel_l.ppf(0.01),
...                 gumbel_l.ppf(0.99), 100)
>>> ax.plot(x, gumbel_l.pdf(x),
...        'r-', lw=5, alpha=0.6, label='gumbel_l pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gumbel_l()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

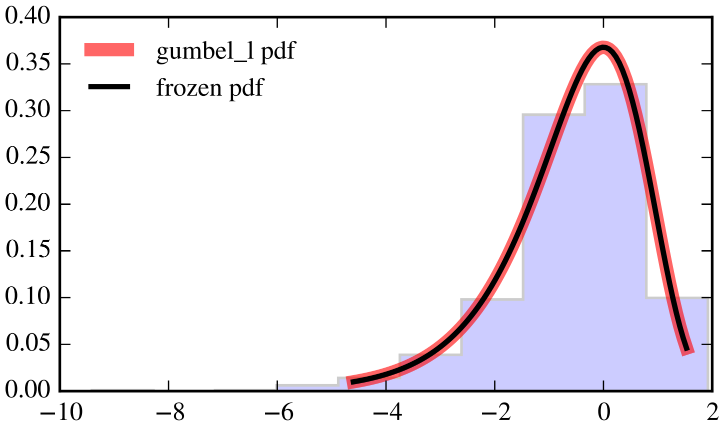
```
>>> vals = gumbel_l.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_l.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gumbel_l.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`halfcauchy`** **= <scipy.stats._continuous_distns.halfcauchy_gen object at 0x7fa40e9a2150>**

A Half-Cauchy continuous random variable.

As an instance of the `rv_continuous` class, `halfcauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `halfcauchy` is:

```
halfcauchy.pdf(x) = 2 / (pi * (1 + x**2))
```

for `x >= 0`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halfcauchy.pdf(x, loc, scale)` is identically equivalent to `halfcauchy.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import halfcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = halfcauchy.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfcauchy.ppf(0.01),
...                 halfcauchy.ppf(0.99), 100)
>>> ax.plot(x, halfcauchy.pdf(x),
...        'r-', lw=5, alpha=0.6, label='halfcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfcauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

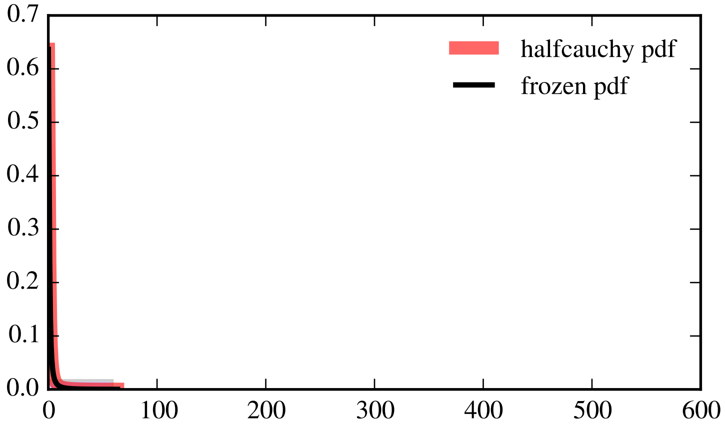
```
>>> vals = halfcauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfcauchy.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halfcauchy.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`halflogistic`** **= <scipy.stats._continuous_distns.halflogistic_gen object at 0x7fa40e9a2350>**

A half-logistic continuous random variable.

As an instance of the `rv_continuous` class, `halflogistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `halflogistic` is:

```
halflogistic.pdf(x) = 2 * exp(-x) / (1+exp(-x))**2 = 1/2 * sech(x/2)**2
```

for `x >= 0`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halflogistic.pdf(x, loc, scale)` is identically equivalent to `halflogistic.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import halflogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = halflogistic.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halflogistic.ppf(0.01),
...                 halflogistic.ppf(0.99), 100)
>>> ax.plot(x, halflogistic.pdf(x),
...        'r-', lw=5, alpha=0.6, label='halflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halflogistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

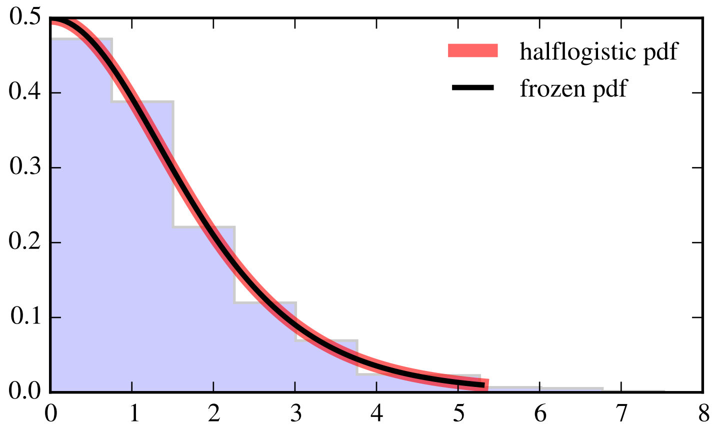
```
>>> vals = halflogistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halflogistic.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halflogistic.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`halfnorm`** **= <scipy.stats._continuous_distns.halfnorm_gen object at 0x7fa40e9a2550>**

A half-normal continuous random variable.

As an instance of the `rv_continuous` class, `halfnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `halfnorm` is:

```
halfnorm.pdf(x) = sqrt(2/pi) * exp(-x**2/2)
```

for `x > 0`.

`halfnorm` is a special case of `chi` with `df == 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halfnorm.pdf(x, loc, scale)` is identically equivalent to `halfnorm.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import halfnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = halfnorm.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfnorm.ppf(0.01),
...                 halfnorm.ppf(0.99), 100)
>>> ax.plot(x, halfnorm.pdf(x),
...        'r-', lw=5, alpha=0.6, label='halfnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfnorm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

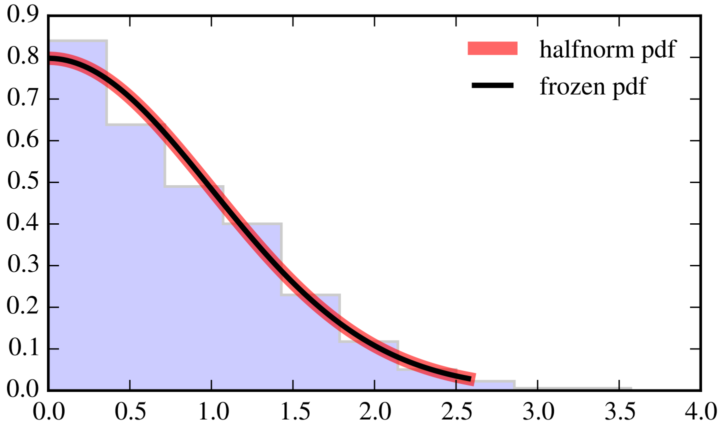
```
>>> vals = halfnorm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfnorm.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halfnorm.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`halfgennorm`** **= <scipy.stats._continuous_distns.halfgennorm_gen object at 0x7fa40e90e2d0>**

The upper half of a generalized normal continuous random variable.

As an instance of the `rv_continuous` class, `halfgennorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gennorm`	generalized normal distribution
`expon`	exponential distribution
`halfnorm`	half normal distribution

Notes

The probability density function for `halfgennorm` is:

```
                              beta
halfgennorm.pdf(x, beta) =  -------------  exp(-|x|**beta)
                            gamma(1/beta)
```

`gennorm` takes `beta` as a shape parameter. For `beta = 1`, it is identical to an exponential distribution. For `beta = 2`, it is identical to a half normal distribution (with `scale=1/sqrt(2)`).

References

[R325]

Examples

```
>>> from scipy.stats import halfgennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> beta = 0.675
>>> mean, var, skew, kurt = halfgennorm.stats(beta, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfgennorm.ppf(0.01, beta),
...                 halfgennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, halfgennorm.pdf(x, beta),
...          'r-', lw=5, alpha=0.6, label='halfgennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfgennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

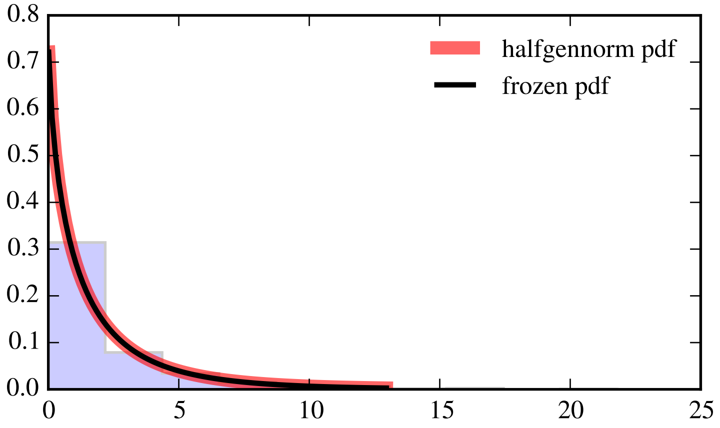
```
>>> vals = halfgennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], halfgennorm.cdf(vals, beta))
True
```

Generate random numbers:

```
>>> r = halfgennorm.rvs(beta, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(beta, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, beta, loc=0, scale=1)`	Probability density function.
`logpdf(x, beta, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, beta, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, beta, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, beta, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, beta, loc=0, scale=1)`	Log of the survival function.
`ppf(q, beta, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, beta, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, beta, loc=0, scale=1)`	Non-central moment of order n
`stats(beta, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(beta, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, beta, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, beta, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(beta, loc=0, scale=1)`	Median of the distribution.
`mean(beta, loc=0, scale=1)`	Mean of the distribution.
`var(beta, loc=0, scale=1)`	Variance of the distribution.
`std(beta, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, beta, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`hypsecant`** **= <scipy.stats._continuous_distns.hypsecant_gen object at 0x7fa40e9a2750>**

A hyperbolic secant continuous random variable.

As an instance of the `rv_continuous` class, `hypsecant` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `hypsecant` is:

```
hypsecant.pdf(x) = 1/pi * sech(x)
```

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `hypsecant.pdf(x, loc, scale)` is identically equivalent to `hypsecant.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import hypsecant
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = hypsecant.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(hypsecant.ppf(0.01),
...                 hypsecant.ppf(0.99), 100)
>>> ax.plot(x, hypsecant.pdf(x),
...        'r-', lw=5, alpha=0.6, label='hypsecant pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = hypsecant()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

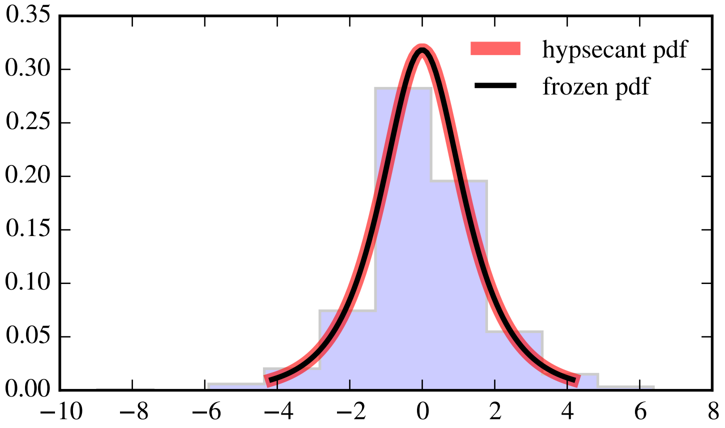
```
>>> vals = hypsecant.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], hypsecant.cdf(vals))
True
```

Generate random numbers:

```
>>> r = hypsecant.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`invgamma`** **= <scipy.stats._continuous_distns.invgamma_gen object at 0x7fa40e9a2c50>**

An inverted gamma continuous random variable.

As an instance of the `rv_continuous` class, `invgamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `invgamma` is:

```
invgamma.pdf(x, a) = x**(-a-1) / gamma(a) * exp(-1/x)
```

for x > 0, a > 0.

`invgamma` takes `a` as a shape parameter.

`invgamma` is a special case of `gengamma` with `c == -1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invgamma.pdf(x, a, loc, scale)` is identically equivalent to `invgamma.pdf(y, a) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import invgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 4.07
>>> mean, var, skew, kurt = invgamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invgamma.ppf(0.01, a),
...                 invgamma.ppf(0.99, a), 100)
>>> ax.plot(x, invgamma.pdf(x, a),
...          'r-', lw=5, alpha=0.6, label='invgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

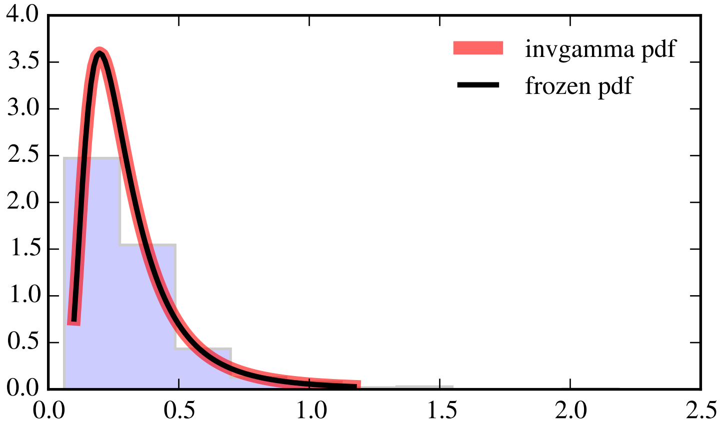
```
>>> vals = invgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], invgamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = invgamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`invgauss`** **= <scipy.stats._continuous_distns.invgauss_gen object at 0x7fa40e9a2f50>**

An inverse Gaussian continuous random variable.

As an instance of the `rv_continuous` class, `invgauss` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `invgauss` is:

```
invgauss.pdf(x, mu) = 1 / sqrt(2*pi*x**3) * exp(-(x-mu)**2/(2*x*mu**2))
```

for `x > 0`.

`invgauss` takes `mu` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invgauss.pdf(x, mu, loc, scale)` is identically equivalent to `invgauss.pdf(y, mu) / scale` with `y = (x - loc) / scale`.

When *mu* is too small, evaluating the cumulative density function will be inaccurate due to `cdf(mu -> 0) = inf * 0`. NaNs are returned for `mu <= 0.0028`.

Examples

```
>>> from scipy.stats import invgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mu = 0.145
>>> mean, var, skew, kurt = invgauss.stats(mu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invgauss.ppf(0.01, mu),
...                 invgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, invgauss.pdf(x, mu),
...        'r-', lw=5, alpha=0.6, label='invgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

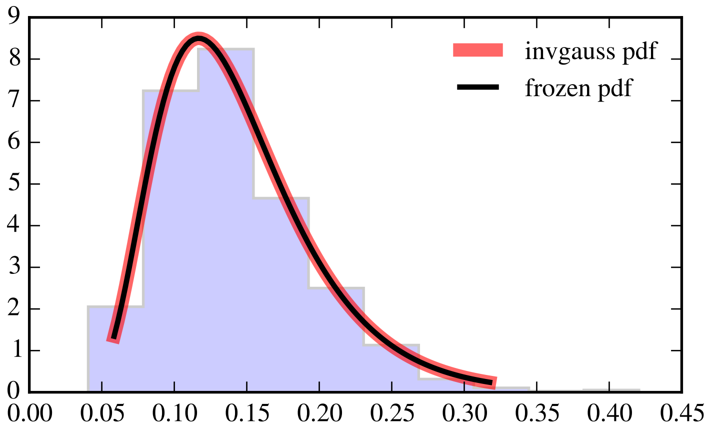
```
>>> vals = invgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], invgauss.cdf(vals, mu))
True
```

Generate random numbers:

```
>>> r = invgauss.rvs(mu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(mu, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, mu, loc=0, scale=1)`	Probability density function.
`logpdf(x, mu, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, mu, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, mu, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, mu, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, mu, loc=0, scale=1)`	Log of the survival function.
`ppf(q, mu, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, mu, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, mu, loc=0, scale=1)`	Non-central moment of order n
`stats(mu, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(mu, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, mu, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, mu, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(mu, loc=0, scale=1)`	Median of the distribution.
`mean(mu, loc=0, scale=1)`	Mean of the distribution.
`var(mu, loc=0, scale=1)`	Variance of the distribution.
`std(mu, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, mu, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`invweibull`** **= <scipy.stats._continuous_distns.invweibull_gen object at 0x7fa40e9b2250>**

An inverted Weibull continuous random variable.

As an instance of the `rv_continuous` class, `invweibull` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `invweibull` is:

```
invweibull.pdf(x, c) = c * x**(-c-1) * exp(-x**(-c))
```

for `x > 0`, `c > 0`.

`invweibull` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invweibull.pdf(x, c, loc, scale)` is identically equivalent to `invweibull.pdf(y, c) / scale` with `y = (x - loc) / scale`.

References

F.R.S. de Gusmao, E.M.M Ortega and G.M. Cordeiro, "The generalized inverse Weibull distribution", Stat. Papers, vol. 52, pp. 591-619, 2011.

Examples

```
>>> from scipy.stats import invweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 10.6
>>> mean, var, skew, kurt = invweibull.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invweibull.ppf(0.01, c),
...                 invweibull.ppf(0.99, c), 100)
>>> ax.plot(x, invweibull.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='invweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

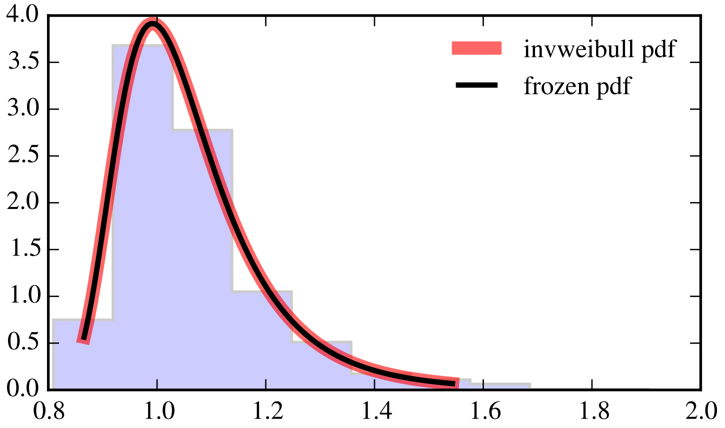
```
>>> vals = invweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], invweibull.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = invweibull.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`johnsonsb`** **= <scipy.stats._continuous_distns.johnsonsb_gen object at 0x7fa40e9b2510>**

A Johnson SB continuous random variable.

As an instance of the `rv_continuous` class, `johnsonsb` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`johnsonsu`

Notes

The probability density function for `johnsonsb` is:

```
johnsonsb.pdf(x, a, b) = b / (x*(1-x)) * phi(a + b * log(x/(1-x)))
```

for `0 < x < 1` and `a, b > 0`, and `phi` is the normal pdf.

`johnsonsb` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `johnsonsb.pdf(x, a, b, loc, scale)` is identically equivalent to `johnsonsb.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import johnsonsb
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 4.32, 3.18
>>> mean, var, skew, kurt = johnsonsb.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(johnsonsb.ppf(0.01, a, b),
...                 johnsonsb.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsb.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='johnsonsb pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = johnsonsb(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

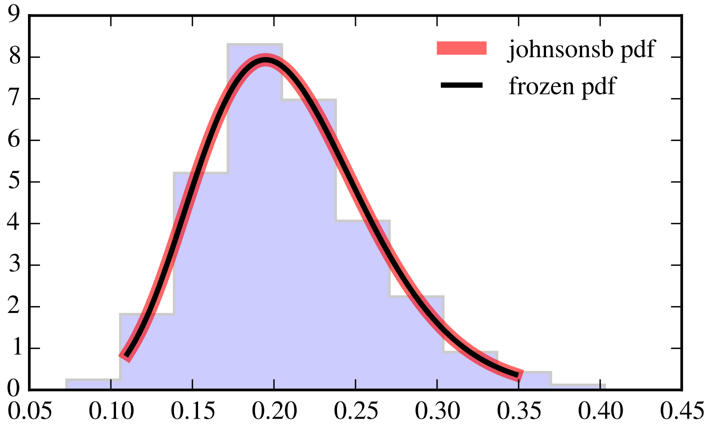
```
>>> vals = johnsonsb.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsb.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = johnsonsb.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`johnsonsu`** **= <scipy.stats._continuous_distns.johnsonsu_gen object at 0x7fa40e9b2850>**

A Johnson SU continuous random variable.

As an instance of the `rv_continuous` class, `johnsonsu` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`johnsonsb`

Notes

The probability density function for `johnsonsu` is:

```
johnsonsu.pdf(x, a, b) = b / sqrt(x**2 + 1) *
                         phi(a + b * log(x + sqrt(x**2 + 1)))
```

for all `x, a, b > 0`, and *phi* is the normal pdf.

`johnsonsu` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `johnsonsu.pdf(x, a, b, loc, scale)` is identically equivalent to `johnsonsu.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import johnsonsu
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 2.55, 2.25
>>> mean, var, skew, kurt = johnsonsu.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(johnsonsu.ppf(0.01, a, b),
...                 johnsonsu.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsu.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='johnsonsu pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = johnsonsu(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

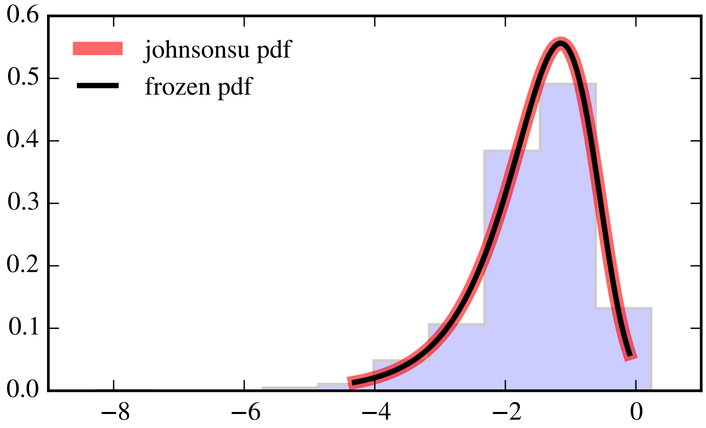
```
>>> vals = johnsonsu.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsu.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = johnsonsu.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`ksone`** **= <scipy.stats._continuous_distns.ksone_gen object at 0x7fa40ebcf450>**

General Kolmogorov-Smirnov one-sided test.

As an instance of the `rv_continuous` class, `ksone` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Methods

`rvs(n, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, n, loc=0, scale=1)`	Probability density function.
`logpdf(x, n, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, n, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, n, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, n, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, n, loc=0, scale=1)`	Log of the survival function.
`ppf(q, n, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, n, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, n, loc=0, scale=1)`	Non-central moment of order n
`stats(n, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(n, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, n, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, n, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(n, loc=0, scale=1)`	Median of the distribution.
`mean(n, loc=0, scale=1)`	Mean of the distribution.
`var(n, loc=0, scale=1)`	Variance of the distribution.
`std(n, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, n, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution
Examples	
`>>> from scipy.stats import ksone`	
`>>> import matplotlib.pyplot as plt`	
`>>> fig, ax = plt.subplots(1, 1)`	
Calculate a few first moments:	
`>>> n = 1e+03`	
`>>> mean, var, skew, kurt = ksone.stats(n, moments='mvsk')`	
Display the probability density function (`pdf`):	

Continued on next page

Table 5.251 – continued from previous page

`>>> x = np.linspace(ksone.ppf(0.01, n),`	
... ksone.ppf(0.99, n), 100)	
`>>> ax.plot(x, ksone.pdf(x, n),`	
... 'r-', lw=5, alpha=0.6, label='ksone pdf')	
Alternatively, the distribution object can be called (as a function)	
to fix the shape, location and scale parameters. This returns a "frozen"	
RV object holding the given parameters fixed.	
Freeze the distribution and display the frozen `pdf`:	
`>>> rv = ksone(n)`	
`>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')`	
Check accuracy of `cdf` and `ppf`:	
`>>> vals = ksone.ppf([0.001, 0.5, 0.999], n)`	
`>>> np.allclose([0.001, 0.5, 0.999], ksone.cdf(vals, n))`	
True	
Generate random numbers:	
`>>> r = ksone.rvs(n, size=1000)`	
And compare the histogram:	
`>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)`	
`>>> ax.legend(loc='best', frameon=False)`	
`>>> plt.show()`	

`scipy.stats.`**`kstwobign`** **= <scipy.stats._continuous_distns.kstwobign_gen object at 0x7fa40ebcf6d0>**

Kolmogorov-Smirnov two-sided test for large N.

As an instance of the `rv_continuous` class, `kstwobign` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.

Continued on next page

Table 5.252 – continued from previous page

`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution
Examples	
`>>> from scipy.stats import kstwobign`	
`>>> import matplotlib.pyplot as plt`	
`>>> fig, ax = plt.subplots(1, 1)`	
Calculate a few first moments:	
`>>> mean, var, skew, kurt = kstwobign.stats(moments='mvsk')`	
Display the probability density function (`pdf`):	
`>>> x = np.linspace(kstwobign.ppf(0.01),`	
... kstwobign.ppf(0.99), 100)	
`>>> ax.plot(x, kstwobign.pdf(x),`	
... 'r-', lw=5, alpha=0.6, label='kstwobign pdf')	
Alternatively, the distribution object can be called (as a function)	
to fix the shape, location and scale parameters. This returns a "frozen"	
RV object holding the given parameters fixed.	
Freeze the distribution and display the frozen `pdf`:	
`>>> rv = kstwobign()`	

Continued on next page

Table 5.252 – continued from previous page

`>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')`	
Check accuracy of `cdf` and `ppf`:	
`>>> vals = kstwobign.ppf([0.001, 0.5, 0.999])`	
`>>> np.allclose([0.001, 0.5, 0.999], kstwobign.cdf(vals))`	
True	
Generate random numbers:	
`>>> r = kstwobign.rvs(size=1000)`	
And compare the histogram:	
`>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)`	
`>>> ax.legend(loc='best', frameon=False)`	
`>>> plt.show()`	

`scipy.stats.`**`laplace`** **= <scipy.stats._continuous_distns.laplace_gen object at 0x7fa40e9b2b90>**

A Laplace continuous random variable.

As an instance of the `rv_continuous` class, `laplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `laplace` is:

```
laplace.pdf(x) = 1/2 * exp(-abs(x))
```

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `laplace.pdf(x, loc, scale)` is identically equivalent to `laplace.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import laplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = laplace.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(laplace.ppf(0.01),
...                 laplace.ppf(0.99), 100)
```

```
>>> ax.plot(x, laplace.pdf(x),
...         'r-', lw=5, alpha=0.6, label='laplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = laplace()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

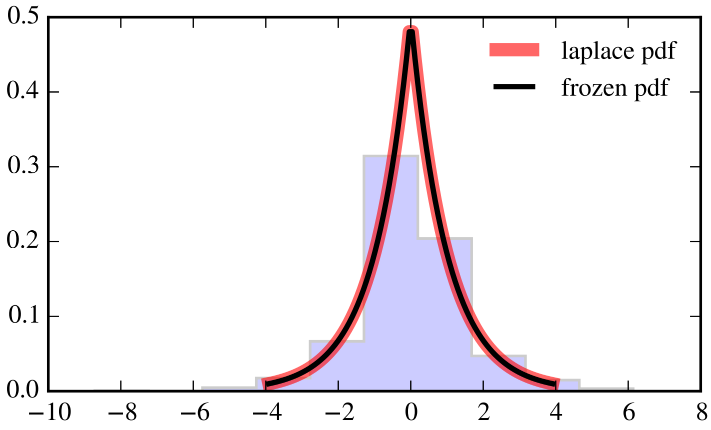
```
>>> vals = laplace.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], laplace.cdf(vals))
True
```

Generate random numbers:

```
>>> r = laplace.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`logistic`** **= <scipy.stats._continuous_distns.logistic_gen object at 0x7fa40e93c510>**

A logistic (or Sech-squared) continuous random variable.

As an instance of the `rv_continuous` class, `logistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `logistic` is:

```
logistic.pdf(x) = exp(-x) / (1+exp(-x))**2
```

`logistic` is a special case of `genlogistic` with `c == 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `logistic.pdf(x, loc, scale)` is identically equivalent to `logistic.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import logistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = logistic.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(logistic.ppf(0.01),
...                 logistic.ppf(0.99), 100)
>>> ax.plot(x, logistic.pdf(x),
...        'r-', lw=5, alpha=0.6, label='logistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = logistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

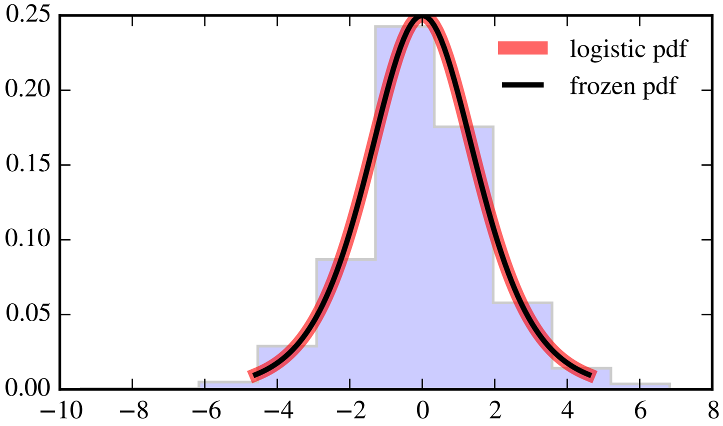
```
>>> vals = logistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], logistic.cdf(vals))
True
```

Generate random numbers:

```
>>> r = logistic.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`loggamma`** **= <scipy.stats._continuous_distns.loggamma_gen object at 0x7fa40e93c710>**

A log gamma continuous random variable.

As an instance of the `rv_continuous` class, `loggamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `loggamma` is:

```
loggamma.pdf(x, c) = exp(c*x-exp(x)) / gamma(c)
```

for all `x, c > 0`.

`loggamma` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loggamma.pdf(x, c, loc, scale)` is identically equivalent to `loggamma.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import loggamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.414
>>> mean, var, skew, kurt = loggamma.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(loggamma.ppf(0.01, c),
...                 loggamma.ppf(0.99, c), 100)
>>> ax.plot(x, loggamma.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='loggamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = loggamma(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

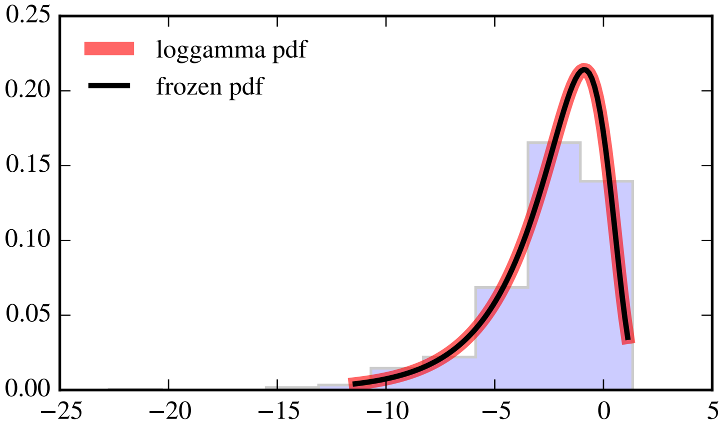
```
>>> vals = loggamma.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loggamma.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = loggamma.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`loglaplace`** **= <scipy.stats._continuous_distns.loglaplace_gen object at 0x7fa40e93c9d0>**

A log-Laplace continuous random variable.

As an instance of the `rv_continuous` class, `loglaplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `loglaplace` is:

```
loglaplace.pdf(x, c) = c / 2 * x**(c-1),   for 0 < x < 1
                     = c / 2 * x**(-c-1),  for x >= 1
```

for `c > 0`.

`loglaplace` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loglaplace.pdf(x, c, loc, scale)` is identically equivalent to `loglaplace.pdf(y, c) / scale` with `y = (x - loc) / scale`.

References

T.J. Kozubowski and K. Podgorski, "A log-Laplace growth rate model", The Mathematical Scientist, vol. 28, pp. 49-60, 2003.

Examples

```
>>> from scipy.stats import loglaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 3.25
>>> mean, var, skew, kurt = loglaplace.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(loglaplace.ppf(0.01, c),
...                 loglaplace.ppf(0.99, c), 100)
>>> ax.plot(x, loglaplace.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='loglaplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = loglaplace(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

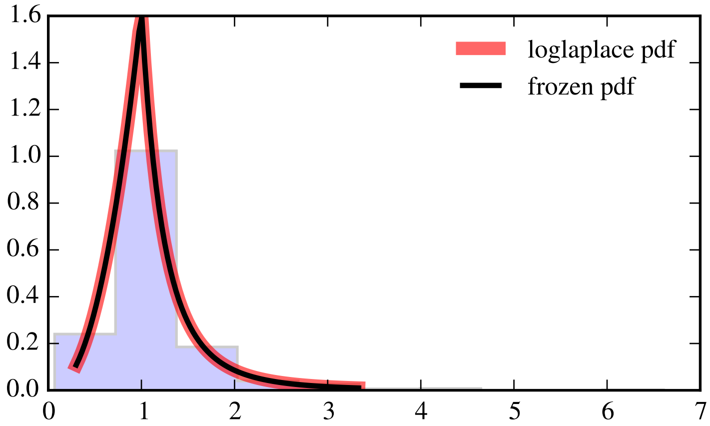
```
>>> vals = loglaplace.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loglaplace.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = loglaplace.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`lognorm`** **= <scipy.stats._continuous_distns.lognorm_gen object at 0x7fa40e93cc90>**

A lognormal continuous random variable.

As an instance of the `rv_continuous` class, `lognorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `lognorm` is:

```
lognorm.pdf(x, s) = 1 / (s*x*sqrt(2*pi)) * exp(-1/2*(log(x)/s)**2)
```

for `x > 0`, `s > 0`.

`lognorm` takes `s` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `lognorm.pdf(x, s, loc, scale)` is identically equivalent to `lognorm.pdf(y, s) / scale` with `y = (x - loc) / scale`.

If `log(x)` is normally distributed with mean `mu` and variance `sigma**2`, then `x` is log-normally distributed with shape parameter sigma and scale parameter `exp(mu)`.

Examples

```
>>> from scipy.stats import lognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> s = 0.954
>>> mean, var, skew, kurt = lognorm.stats(s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(lognorm.ppf(0.01, s),
...                 lognorm.ppf(0.99, s), 100)
>>> ax.plot(x, lognorm.pdf(x, s),
...        'r-', lw=5, alpha=0.6, label='lognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = lognorm(s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

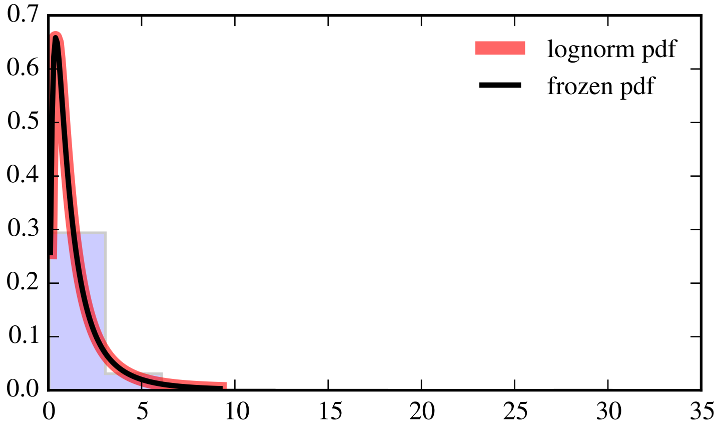
```
>>> vals = lognorm.ppf([0.001, 0.5, 0.999], s)
>>> np.allclose([0.001, 0.5, 0.999], lognorm.cdf(vals, s))
True
```

Generate random numbers:

```
>>> r = lognorm.rvs(s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(s, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, s, loc=0, scale=1)`	Probability density function.
`logpdf(x, s, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, s, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, s, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, s, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, s, loc=0, scale=1)`	Log of the survival function.
`ppf(q, s, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, s, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, s, loc=0, scale=1)`	Non-central moment of order n
`stats(s, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(s, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, s, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, s, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(s, loc=0, scale=1)`	Median of the distribution.
`mean(s, loc=0, scale=1)`	Mean of the distribution.
`var(s, loc=0, scale=1)`	Variance of the distribution.
`std(s, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, s, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`lomax`** **= <scipy.stats._continuous_distns.lomax_gen object at 0x7fa40e95d9d0>**

A Lomax (Pareto of the second kind) continuous random variable.

As an instance of the `rv_continuous` class, `lomax` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The Lomax distribution is a special case of the Pareto distribution, with (loc=-1.0).

The probability density function for `lomax` is:

```
lomax.pdf(x, c) = c / (1+x)**(c+1)
```

for `x >= 0`, `c > 0`.

`lomax` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `lomax.pdf(x, c, loc, scale)` is identically equivalent to `lomax.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import lomax
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 1.88
>>> mean, var, skew, kurt = lomax.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(lomax.ppf(0.01, c),
...                 lomax.ppf(0.99, c), 100)
>>> ax.plot(x, lomax.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='lomax pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = lomax(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

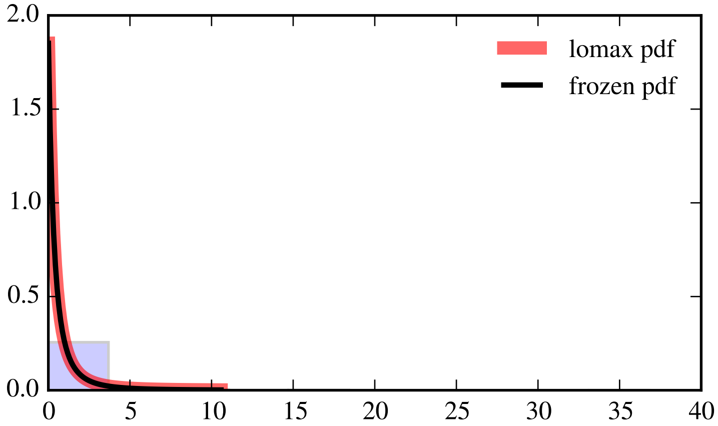
```
>>> vals = lomax.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], lomax.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = lomax.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`maxwell`** **= <scipy.stats._continuous_distns.maxwell_gen object at 0x7fa40e94f190>**

A Maxwell continuous random variable.

As an instance of the `rv_continuous` class, `maxwell` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

A special case of a `chi` distribution, with `df = 3`, `loc = 0.0`, and given `scale = a`, where `a` is the parameter used in the Mathworld description [R333].

The probability density function for `maxwell` is:

```
maxwell.pdf(x) = sqrt(2/pi)x**2 * exp(-x**2/2)
```

for `x > 0`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `maxwell.pdf(x, loc, scale)` is identically equivalent to `maxwell.pdf(y) / scale` with `y = (x - loc) / scale`.

References

[R333]

Examples

```
>>> from scipy.stats import maxwell
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = maxwell.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(maxwell.ppf(0.01),
...                 maxwell.ppf(0.99), 100)
>>> ax.plot(x, maxwell.pdf(x),
...        'r-', lw=5, alpha=0.6, label='maxwell pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = maxwell()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

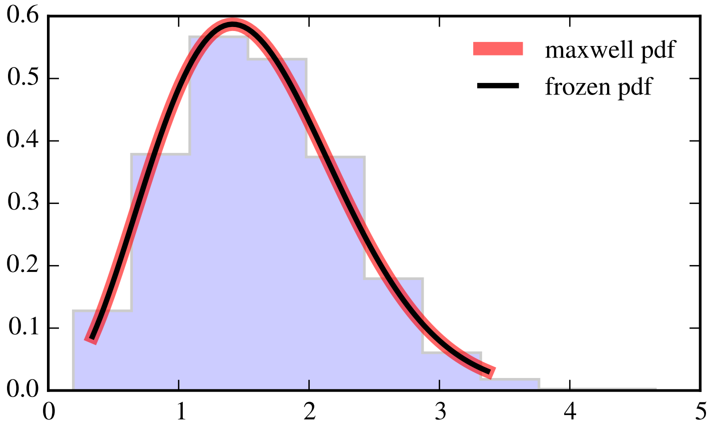
```
>>> vals = maxwell.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], maxwell.cdf(vals))
True
```

Generate random numbers:

```
>>> r = maxwell.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`mielke`** **= <scipy.stats._continuous_distns.mielke_gen object at 0x7fa40e94f390>**

A Mielke's Beta-Kappa continuous random variable.

As an instance of the `rv_continuous` class, `mielke` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `mielke` is:

```
mielke.pdf(x, k, s) = k * x**(k-1) / (1+x**s)**(1+k/s)
```

for `x > 0`.

`mielke` takes `k` and `s` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `mielke.pdf(x, k, s, loc, scale)` is identically equivalent to `mielke.pdf(y, k, s) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import mielke
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> k, s = 10.4, 3.6
>>> mean, var, skew, kurt = mielke.stats(k, s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(mielke.ppf(0.01, k, s),
...                 mielke.ppf(0.99, k, s), 100)
>>> ax.plot(x, mielke.pdf(x, k, s),
...        'r-', lw=5, alpha=0.6, label='mielke pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = mielke(k, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

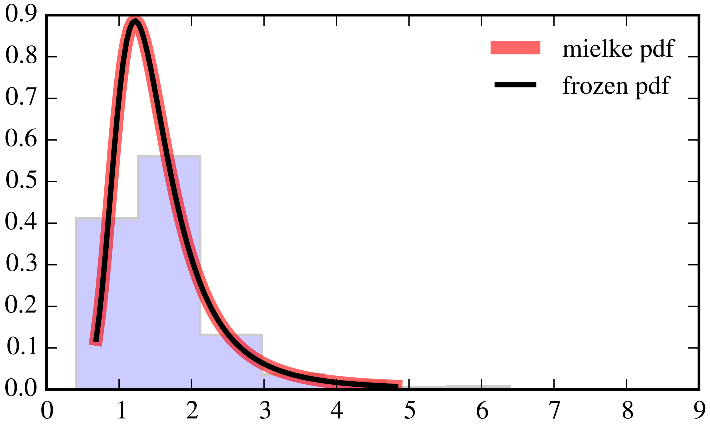
```
>>> vals = mielke.ppf([0.001, 0.5, 0.999], k, s)
>>> np.allclose([0.001, 0.5, 0.999], mielke.cdf(vals, k, s))
True
```

Generate random numbers:

```
>>> r = mielke.rvs(k, s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(k, s, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, k, s, loc=0, scale=1)`	Probability density function.
`logpdf(x, k, s, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, k, s, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, k, s, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, k, s, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, k, s, loc=0, scale=1)`	Log of the survival function.
`ppf(q, k, s, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, k, s, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, k, s, loc=0, scale=1)`	Non-central moment of order n
`stats(k, s, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(k, s, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, k, s, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, k, s, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(k, s, loc=0, scale=1)`	Median of the distribution.
`mean(k, s, loc=0, scale=1)`	Mean of the distribution.
`var(k, s, loc=0, scale=1)`	Variance of the distribution.
`std(k, s, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, k, s, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`nakagami`** **= <scipy.stats._continuous_distns.nakagami_gen object at 0x7fa40e94f6d0>**

A Nakagami continuous random variable.

As an instance of the `rv_continuous` class, `nakagami` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `nakagami` is:

```
nakagami.pdf(x, nu) = 2 * nu**nu / gamma(nu) *
                      x**(2*nu-1) * exp(-nu*x**2)
```

for `x > 0`, `nu > 0`.

`nakagami` takes `nu` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `nakagami.pdf(x, nu, loc, scale)` is identically equivalent to `nakagami.pdf(y, nu) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import nakagami
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> nu = 4.97
>>> mean, var, skew, kurt = nakagami.stats(nu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(nakagami.ppf(0.01, nu),
...                 nakagami.ppf(0.99, nu), 100)
>>> ax.plot(x, nakagami.pdf(x, nu),
...        'r-', lw=5, alpha=0.6, label='nakagami pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = nakagami(nu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

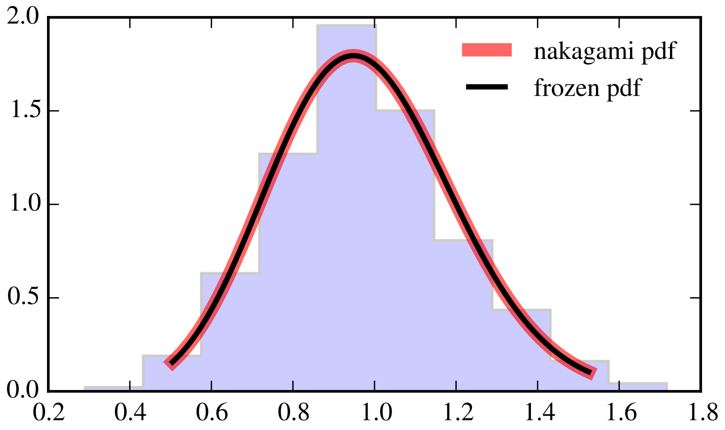
```
>>> vals = nakagami.ppf([0.001, 0.5, 0.999], nu)
>>> np.allclose([0.001, 0.5, 0.999], nakagami.cdf(vals, nu))
True
```

Generate random numbers:

```
>>> r = nakagami.rvs(nu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(nu, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, nu, loc=0, scale=1)`	Probability density function.
`logpdf(x, nu, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, nu, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, nu, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, nu, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, nu, loc=0, scale=1)`	Log of the survival function.
`ppf(q, nu, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, nu, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, nu, loc=0, scale=1)`	Non-central moment of order n
`stats(nu, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(nu, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, nu, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, nu, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(nu, loc=0, scale=1)`	Median of the distribution.
`mean(nu, loc=0, scale=1)`	Mean of the distribution.
`var(nu, loc=0, scale=1)`	Variance of the distribution.
`std(nu, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, nu, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`ncx2`** **= <scipy.stats._continuous_distns.ncx2_gen object at 0x7fa40e94f990>**

A non-central chi-squared continuous random variable.

As an instance of the `rv_continuous` class, `ncx2` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `ncx2` is:

```
ncx2.pdf(x, df, nc) = exp(-(nc+x)/2) * 1/2 * (x/nc)**((df-2)/4)
                      * I[(df-2)/2](sqrt(nc*x))
```

for `x > 0`.

`ncx2` takes `df` and `nc` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncx2.pdf(x, df, nc, loc, scale)` is identically equivalent to `ncx2.pdf(y, df, nc) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import ncx2
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> df, nc = 21, 1.06
>>> mean, var, skew, kurt = ncx2.stats(df, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(ncx2.ppf(0.01, df, nc),
...                 ncx2.ppf(0.99, df, nc), 100)
>>> ax.plot(x, ncx2.pdf(x, df, nc),
...         'r-', lw=5, alpha=0.6, label='ncx2 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = ncx2(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

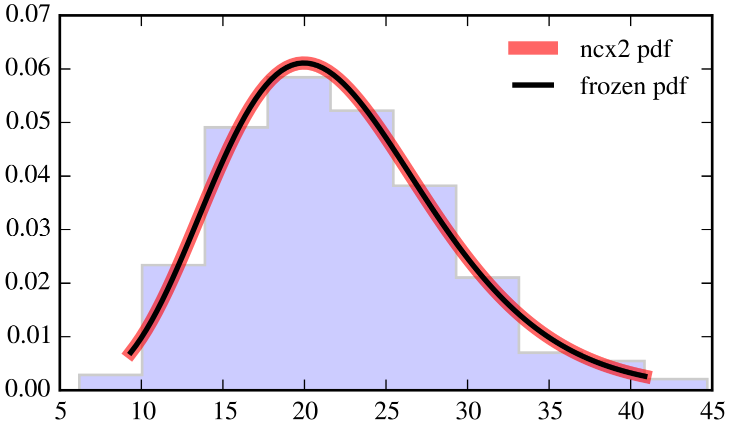
```
>>> vals = ncx2.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncx2.cdf(vals, df, nc))
True
```

Generate random numbers:

```
>>> r = ncx2.rvs(df, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(df, nc, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, df, nc, loc=0, scale=1)`	Probability density function.
`logpdf(x, df, nc, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, df, nc, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, df, nc, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, df, nc, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, df, nc, loc=0, scale=1)`	Log of the survival function.
`ppf(q, df, nc, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, df, nc, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, df, nc, loc=0, scale=1)`	Non-central moment of order n
`stats(df, nc, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(df, nc, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, df, nc, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, df, nc, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(df, nc, loc=0, scale=1)`	Median of the distribution.
`mean(df, nc, loc=0, scale=1)`	Mean of the distribution.
`var(df, nc, loc=0, scale=1)`	Variance of the distribution.
`std(df, nc, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, df, nc, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`ncf`** **= <scipy.stats._continuous_distns.ncf_gen object at 0x7fa40e94fcd0>**

A non-central F distribution continuous random variable.

As an instance of the `rv_continuous` class, `ncf` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `ncf` is:

```
ncf.pdf(x, df1, df2, nc) = exp(nc/2 + nc*df1*x/(2*(df1*x+df2))) *
            df1**(df1/2) * df2**(df2/2) * x**(df1/2-1) *
            (df2+df1*x)**(-(df1+df2)/2) *
            gamma(df1/2)*gamma(1+df2/2) *
            L^{v1/2-1}^{v2/2}(-nc*v1*x/(2*(v1*x+v2))) /
            (B(v1/2, v2/2) * gamma((v1+v2)/2))
```

for `df1, df2, nc > 0`.

`ncf` takes `df1`, `df2` and `nc` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncf.pdf(x, dfn, dfd, nc, loc, scale)` is identically equivalent to `ncf.pdf(y, dfn, dfd, nc) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import ncf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> dfn, dfd, nc = 27, 27, 0.416
>>> mean, var, skew, kurt = ncf.stats(dfn, dfd, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(ncf.ppf(0.01, dfn, dfd, nc),
...                 ncf.ppf(0.99, dfn, dfd, nc), 100)
>>> ax.plot(x, ncf.pdf(x, dfn, dfd, nc),
...          'r-', lw=5, alpha=0.6, label='ncf pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = ncf(dfn, dfd, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

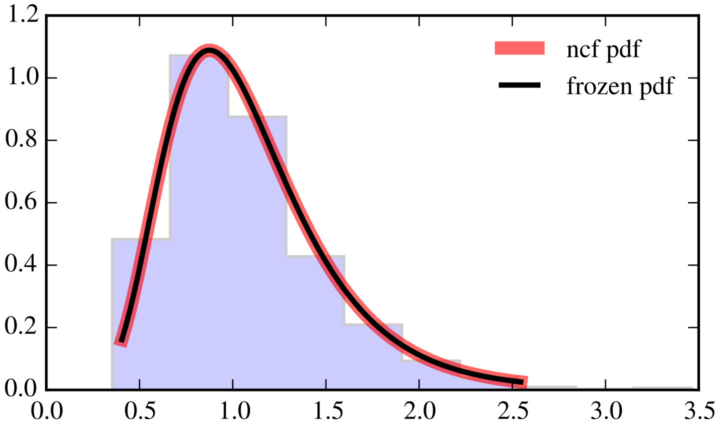
```
>>> vals = ncf.ppf([0.001, 0.5, 0.999], dfn, dfd, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncf.cdf(vals, dfn, dfd, nc))
True
```

Generate random numbers:

```
>>> r = ncf.rvs(dfn, dfd, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(dfn, dfd, nc, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, dfn, dfd, nc, loc=0, scale=1)`	Probability density function.
`logpdf(x, dfn, dfd, nc, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, dfn, dfd, nc, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, dfn, dfd, nc, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, dfn, dfd, nc, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, dfn, dfd, nc, loc=0, scale=1)`	Log of the survival function.
`ppf(q, dfn, dfd, nc, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, dfn, dfd, nc, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, dfn, dfd, nc, loc=0, scale=1)`	Non-central moment of order n
`stats(dfn, dfd, nc, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(dfn, dfd, nc, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, dfn, dfd, nc, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, dfn, dfd, nc, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(dfn, dfd, nc, loc=0, scale=1)`	Median of the distribution.
`mean(dfn, dfd, nc, loc=0, scale=1)`	Mean of the distribution.
`var(dfn, dfd, nc, loc=0, scale=1)`	Variance of the distribution.
`std(dfn, dfd, nc, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, dfn, dfd, nc, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`nct`** **= <scipy.stats._continuous_distns.nct_gen object at 0x7fa40e95d350>**

A non-central Student's T continuous random variable.

As an instance of the `rv_continuous` class, `nct` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `nct` is:

```
                                          df**(df/2) * gamma(df+1)
nct.pdf(x, df, nc) = ----------------------------------------------------
                     2**df*exp(nc**2/2) * (df+x**2)**(df/2) * gamma(df/2)
```

for `df > 0`.

`nct` takes `df` and `nc` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `nct.pdf(x, df, nc, loc, scale)` is identically equivalent to `nct.pdf(y, df, nc) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import nct
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> df, nc = 14, 0.24
>>> mean, var, skew, kurt = nct.stats(df, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(nct.ppf(0.01, df, nc),
...                 nct.ppf(0.99, df, nc), 100)
>>> ax.plot(x, nct.pdf(x, df, nc),
...          'r-', lw=5, alpha=0.6, label='nct pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = nct(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

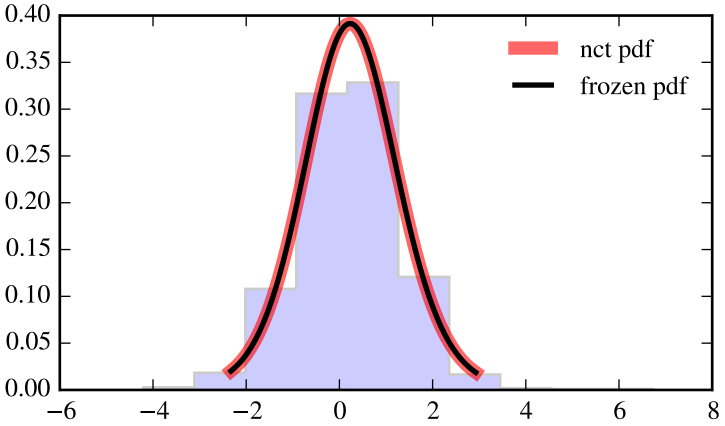
```
>>> vals = nct.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], nct.cdf(vals, df, nc))
True
```

Generate random numbers:

```
>>> r = nct.rvs(df, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(df, nc, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, df, nc, loc=0, scale=1)`	Probability density function.
`logpdf(x, df, nc, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, df, nc, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, df, nc, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, df, nc, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, df, nc, loc=0, scale=1)`	Log of the survival function.
`ppf(q, df, nc, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, df, nc, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, df, nc, loc=0, scale=1)`	Non-central moment of order n
`stats(df, nc, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(df, nc, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, df, nc, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, df, nc, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(df, nc, loc=0, scale=1)`	Median of the distribution.
`mean(df, nc, loc=0, scale=1)`	Mean of the distribution.
`var(df, nc, loc=0, scale=1)`	Variance of the distribution.
`std(df, nc, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, df, nc, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`norm`** **= <scipy.stats._continuous_distns.norm_gen object at 0x7fa40ebcf8d0>**
A normal continuous random variable.

The location (loc) keyword specifies the mean. The scale (scale) keyword specifies the standard deviation.

As an instance of the `rv_continuous` class, `norm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `norm` is:

```
norm.pdf(x) = exp(-x**2/2)/sqrt(2*pi)
```

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `norm.pdf(x, loc, scale)` is identically equivalent to `norm.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import norm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = norm.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(norm.ppf(0.01),
...                 norm.ppf(0.99), 100)
>>> ax.plot(x, norm.pdf(x),
...        'r-', lw=5, alpha=0.6, label='norm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = norm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

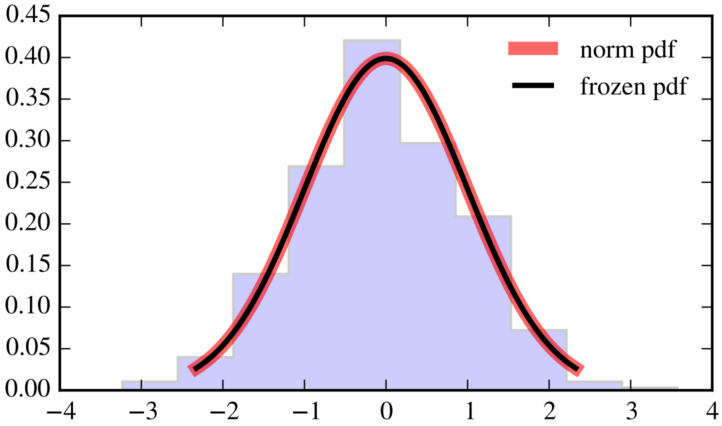
```
>>> vals = norm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], norm.cdf(vals))
True
```

Generate random numbers:

```
>>> r = norm.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`pareto`** **= <scipy.stats._continuous_distns.pareto_gen object at 0x7fa40e95d6d0>**

A Pareto continuous random variable.

As an instance of the `rv_continuous` class, `pareto` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `pareto` is:

```
pareto.pdf(x, b) = b / x**(b+1)
```

for `x >= 1`, `b > 0`.

`pareto` takes `b` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pareto.pdf(x, b, loc, scale)` is identically equivalent to `pareto.pdf(y, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import pareto
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> b = 2.62
>>> mean, var, skew, kurt = pareto.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(pareto.ppf(0.01, b),
...                 pareto.ppf(0.99, b), 100)
>>> ax.plot(x, pareto.pdf(x, b),
...        'r-', lw=5, alpha=0.6, label='pareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = pareto(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

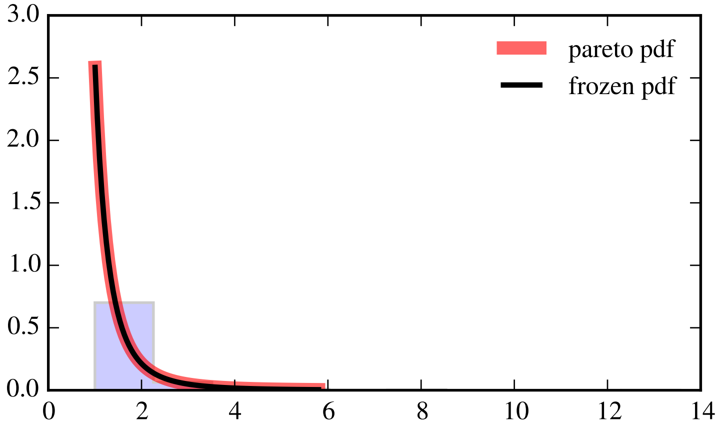
```
>>> vals = pareto.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], pareto.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = pareto.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, b, loc=0, scale=1)`	Non-central moment of order n
`stats(b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(b, loc=0, scale=1)`	Median of the distribution.
`mean(b, loc=0, scale=1)`	Mean of the distribution.
`var(b, loc=0, scale=1)`	Variance of the distribution.
`std(b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`pearson3`** **= <scipy.stats._continuous_distns.pearson3_gen object at 0x7fa40e95dc90>**

A pearson type III continuous random variable.

As an instance of the `rv_continuous` class, `pearson3` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `pearson3` is:

```
pearson3.pdf(x, skew) = abs(beta) / gamma(alpha) *
    (beta * (x - zeta))**(alpha - 1) * exp(-beta*(x - zeta))
```

where:

```
beta = 2 / (skew * stddev)
alpha = (stddev * beta)**2
zeta = loc - alpha / beta
```

`pearson3` takes `skew` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pearson3.pdf(x, skew, loc, scale)` is identically equivalent to `pearson3.pdf(y, skew) / scale` with `y = (x - loc) / scale`.

References

R.W. Vogel and D.E. McMartin, "Probability Plot Goodness-of-Fit and Skewness Estimation Procedures for the Pearson Type 3 Distribution", Water Resources Research, Vol.27, 3149-3158 (1991).

L.R. Salvosa, "Tables of Pearson's Type III Function", Ann. Math. Statist., Vol.1, 191-198 (1930).

"Using Modern Computing Tools to Fit the Pearson Type III Distribution to Aviation Loads Data", Office of Aviation Research (2003).

Examples

```
>>> from scipy.stats import pearson3
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> skew = 0.1
>>> mean, var, skew, kurt = pearson3.stats(skew, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(pearson3.ppf(0.01, skew),
...                 pearson3.ppf(0.99, skew), 100)
>>> ax.plot(x, pearson3.pdf(x, skew),
...        'r-', lw=5, alpha=0.6, label='pearson3 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = pearson3(skew)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

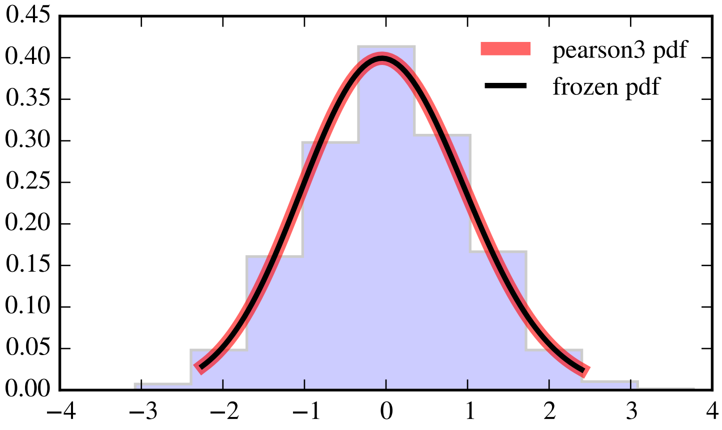
```
>>> vals = pearson3.ppf([0.001, 0.5, 0.999], skew)
>>> np.allclose([0.001, 0.5, 0.999], pearson3.cdf(vals, skew))
True
```

Generate random numbers:

```
>>> r = pearson3.rvs(skew, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(skew, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, skew, loc=0, scale=1)`	Probability density function.
`logpdf(x, skew, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, skew, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, skew, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, skew, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, skew, loc=0, scale=1)`	Log of the survival function.
`ppf(q, skew, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, skew, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, skew, loc=0, scale=1)`	Non-central moment of order n
`stats(skew, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(skew, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, skew, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, skew, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(skew, loc=0, scale=1)`	Median of the distribution.
`mean(skew, loc=0, scale=1)`	Mean of the distribution.
`var(skew, loc=0, scale=1)`	Variance of the distribution.
`std(skew, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, skew, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`powerlaw`** **= <scipy.stats._continuous_distns.powerlaw_gen object at 0x7fa40e95df50>**

A power-function continuous random variable.

As an instance of the `rv_continuous` class, `powerlaw` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `powerlaw` is:

```
powerlaw.pdf(x, a) = a * x**(a-1)
```

for `0 <= x <= 1`, `a > 0`.

`powerlaw` takes `a` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powerlaw.pdf(x, a, loc, scale)` is identically equivalent to `powerlaw.pdf(y, a) / scale` with `y = (x - loc) / scale`.

`powerlaw` is a special case of `beta` with `b == 1`.

Examples

```
>>> from scipy.stats import powerlaw
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 1.66
>>> mean, var, skew, kurt = powerlaw.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(powerlaw.ppf(0.01, a),
...                 powerlaw.ppf(0.99, a), 100)
>>> ax.plot(x, powerlaw.pdf(x, a),
...        'r-', lw=5, alpha=0.6, label='powerlaw pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = powerlaw(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

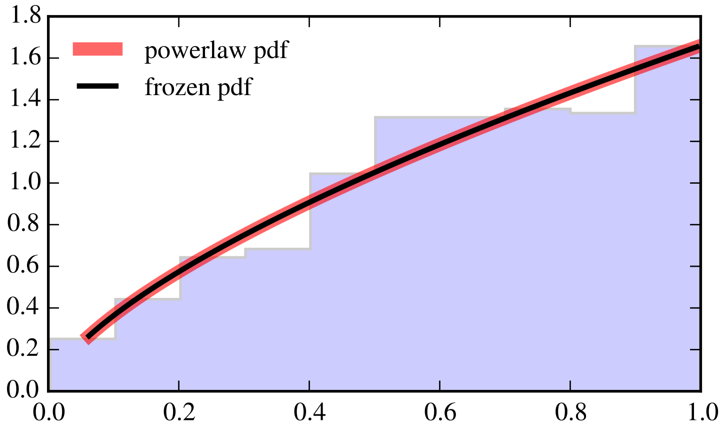
```
>>> vals = powerlaw.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], powerlaw.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = powerlaw.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, loc=0, scale=1)`	Non-central moment of order n
`stats(a, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0, scale=1)`	Median of the distribution.
`mean(a, loc=0, scale=1)`	Mean of the distribution.
`var(a, loc=0, scale=1)`	Variance of the distribution.
`std(a, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`powerlognorm`** **= <scipy.stats._continuous_distns.powerlognorm_gen object at 0x7fa40e965250>**

A power log-normal continuous random variable.

As an instance of the `rv_continuous` class, `powerlognorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `powerlognorm` is:

```
powerlognorm.pdf(x, c, s) = c / (x*s) * phi(log(x)/s) *
                                        (Phi(-log(x)/s))**(c-1),
```

where `phi` is the normal pdf, and `Phi` is the normal cdf, and `x > 0`, `s, c > 0`.

`powerlognorm` takes `c` and `s` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powerlognorm.pdf(x, c, s, loc, scale)` is identically equivalent to `powerlognorm.pdf(y, c, s) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import powerlognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c, s = 2.14, 0.446
>>> mean, var, skew, kurt = powerlognorm.stats(c, s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(powerlognorm.ppf(0.01, c, s),
...                 powerlognorm.ppf(0.99, c, s), 100)
>>> ax.plot(x, powerlognorm.pdf(x, c, s),
...        'r-', lw=5, alpha=0.6, label='powerlognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = powerlognorm(c, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

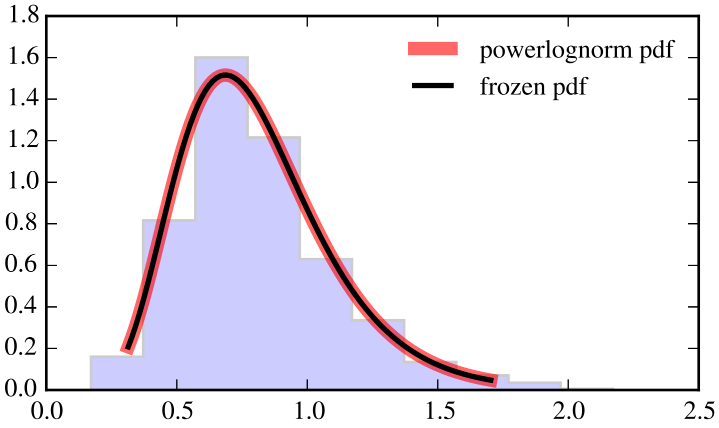
```
>>> vals = powerlognorm.ppf([0.001, 0.5, 0.999], c, s)
>>> np.allclose([0.001, 0.5, 0.999], powerlognorm.cdf(vals, c, s))
True
```

Generate random numbers:

```
>>> r = powerlognorm.rvs(c, s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, s, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, s, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, s, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, s, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, s, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, s, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, s, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, s, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, s, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, s, loc=0, scale=1)`	Non-central moment of order n
`stats(c, s, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, s, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, s, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, s, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, s, loc=0, scale=1)`	Median of the distribution.
`mean(c, s, loc=0, scale=1)`	Mean of the distribution.
`var(c, s, loc=0, scale=1)`	Variance of the distribution.
`std(c, s, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, s, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`powernorm`** **= <scipy.stats._continuous_distns.powernorm_gen object at 0x7fa40e965590>**

A power normal continuous random variable.

As an instance of the `rv_continuous` class, `powernorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `powernorm` is:

```
powernorm.pdf(x, c) = c * phi(x) * (Phi(-x))**(c-1)
```

where `phi` is the normal pdf, and `Phi` is the normal cdf, and `x > 0`, `c > 0`.

`powernorm` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powernorm.pdf(x, c, loc, scale)` is identically equivalent to `powernorm.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import powernorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 4.45
>>> mean, var, skew, kurt = powernorm.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(powernorm.ppf(0.01, c),
...                 powernorm.ppf(0.99, c), 100)
>>> ax.plot(x, powernorm.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='powernorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = powernorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

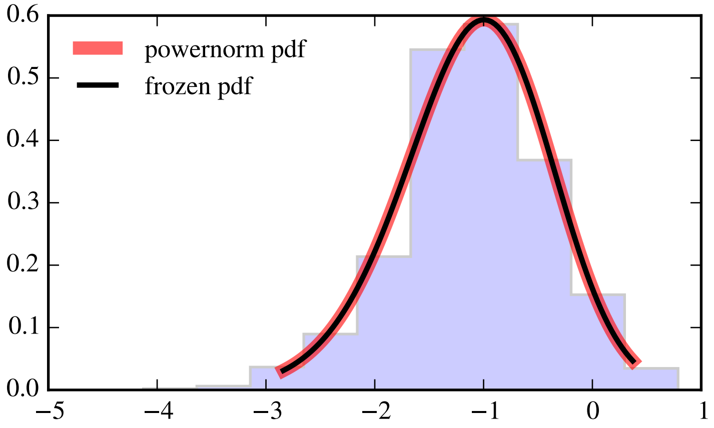
```
>>> vals = powernorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], powernorm.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = powernorm.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`rdist`** **= <scipy.stats._continuous_distns.rdist_gen object at 0x7fa40e965850>**

An R-distributed continuous random variable.

As an instance of the `rv_continuous` class, `rdist` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `rdist` is:

```
rdist.pdf(x, c) = (1-x**2)**(c/2-1) / B(1/2, c/2)
```

for `-1 <= x <= 1`, `c > 0`.

`rdist` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rdist.pdf(x, c, loc, scale)` is identically equivalent to `rdist.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import rdist
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.9
>>> mean, var, skew, kurt = rdist.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rdist.ppf(0.01, c),
...                 rdist.ppf(0.99, c), 100)
>>> ax.plot(x, rdist.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='rdist pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rdist(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

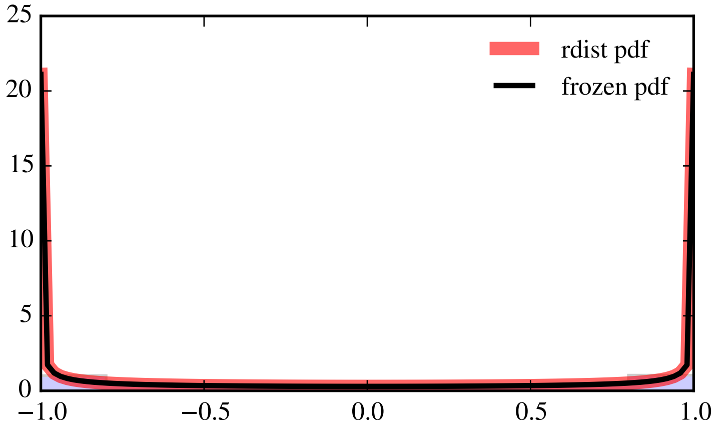
```
>>> vals = rdist.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], rdist.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = rdist.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`reciprocal`** **= <scipy.stats._continuous_distns.reciprocal_gen object at 0x7fa40e965d10>**

A reciprocal continuous random variable.

As an instance of the `rv_continuous` class, `reciprocal` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `reciprocal` is:

```
reciprocal.pdf(x, a, b) = 1 / (x*log(b/a))
```

for `a <= x <= b`, `a, b > 0`.

`reciprocal` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `reciprocal.pdf(x, a, b, loc, scale)` is identically equivalent to `reciprocal.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import reciprocal
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 0.00623, 1.01
>>> mean, var, skew, kurt = reciprocal.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(reciprocal.ppf(0.01, a, b),
...                 reciprocal.ppf(0.99, a, b), 100)
>>> ax.plot(x, reciprocal.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='reciprocal pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = reciprocal(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

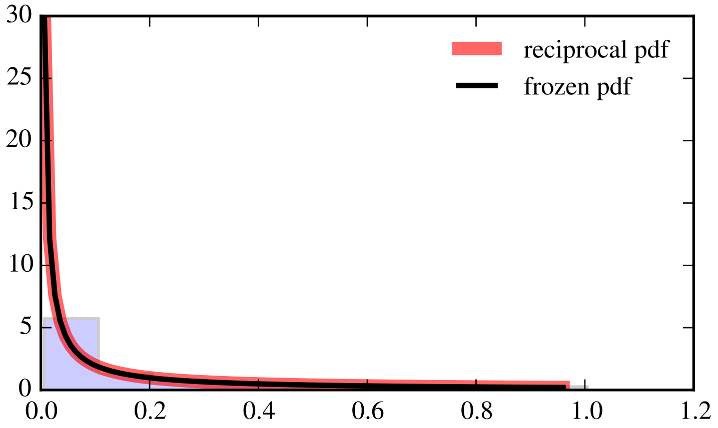
```
>>> vals = reciprocal.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], reciprocal.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = reciprocal.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`rayleigh`** **= <scipy.stats._continuous_distns.rayleigh_gen object at 0x7fa40e965b10>**

A Rayleigh continuous random variable.

As an instance of the `rv_continuous` class, `rayleigh` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `rayleigh` is:

```
rayleigh.pdf(r) = r * exp(-r**2/2)
```

for `x >= 0`.

`rayleigh` is a special case of `chi` with `df == 2`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rayleigh.pdf(x, loc, scale)` is identically equivalent to `rayleigh.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import rayleigh
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = rayleigh.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rayleigh.ppf(0.01),
...                 rayleigh.ppf(0.99), 100)
>>> ax.plot(x, rayleigh.pdf(x),
...        'r-', lw=5, alpha=0.6, label='rayleigh pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rayleigh()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

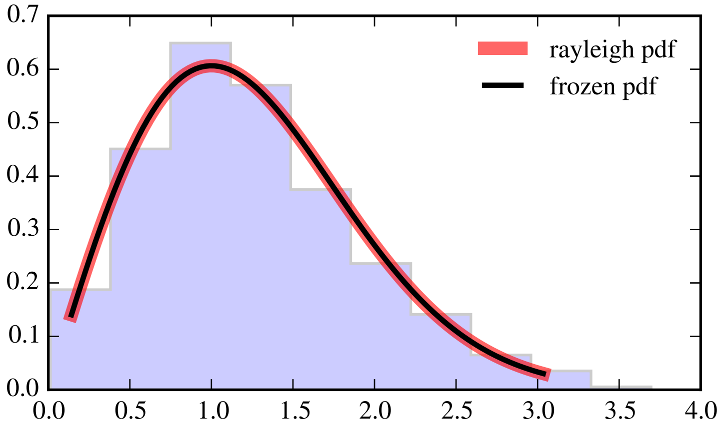
```
>>> vals = rayleigh.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], rayleigh.cdf(vals))
True
```

Generate random numbers:

```
>>> r = rayleigh.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`rice`** **= <scipy.stats._continuous_distns.rice_gen object at 0x7fa40e975090>**

A Rice continuous random variable.

As an instance of the `rv_continuous` class, `rice` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `rice` is:

```
rice.pdf(x, b) = x * exp(-(x**2+b**2)/2) * I[0](x*b)
```

for `x > 0`, `b > 0`.

`rice` takes `b` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rice.pdf(x, b, loc, scale)` is identically equivalent to `rice.pdf(y, b) / scale` with `y = (x - loc) / scale`.

The Rice distribution describes the length, `r`, of a 2-D vector with components `(U+u, V+v)`, where `U, V` are constant, `u, v` are independent Gaussian random variables with standard deviation `s`. Let `R = (U**2 + V**2)**0.5`. Then the pdf of `r` is `rice.pdf(x, R/s, scale=s)`.

Examples

```
>>> from scipy.stats import rice
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> b = 0.775
>>> mean, var, skew, kurt = rice.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rice.ppf(0.01, b),
...                 rice.ppf(0.99, b), 100)
>>> ax.plot(x, rice.pdf(x, b),
...        'r-', lw=5, alpha=0.6, label='rice pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rice(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

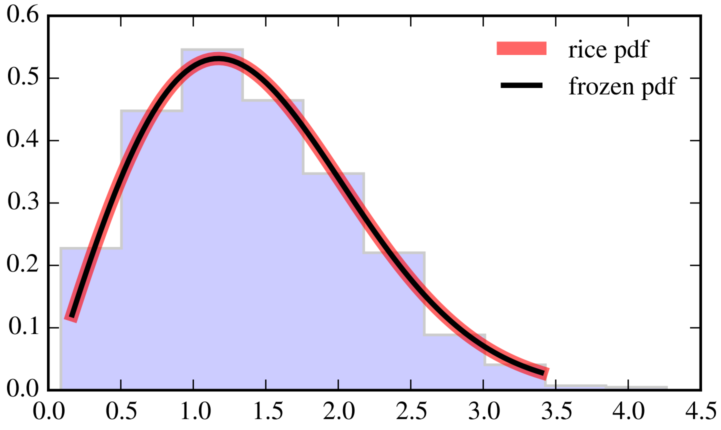
```
>>> vals = rice.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], rice.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = rice.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, b, loc=0, scale=1)`	Non-central moment of order n
`stats(b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(b, loc=0, scale=1)`	Median of the distribution.
`mean(b, loc=0, scale=1)`	Mean of the distribution.
`var(b, loc=0, scale=1)`	Variance of the distribution.
`std(b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`recipinvgauss`** **= <scipy.stats._continuous_distns.recipinvgauss_gen object at 0x7fa40e975350>**

A reciprocal inverse Gaussian continuous random variable.

As an instance of the `rv_continuous` class, `recipinvgauss` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `recipinvgauss` is:

```
recipinvgauss.pdf(x, mu) = 1/sqrt(2*pi*x) * exp(-(1-mu*x)**2/(2*x*mu**2))
```

for `x >= 0`.

`recipinvgauss` takes `mu` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `recipinvgauss.pdf(x, mu, loc, scale)` is identically equivalent to `recipinvgauss.pdf(y, mu) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import recipinvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mu = 0.63
>>> mean, var, skew, kurt = recipinvgauss.stats(mu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(recipinvgauss.ppf(0.01, mu),
...                 recipinvgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, recipinvgauss.pdf(x, mu),
...        'r-', lw=5, alpha=0.6, label='recipinvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = recipinvgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

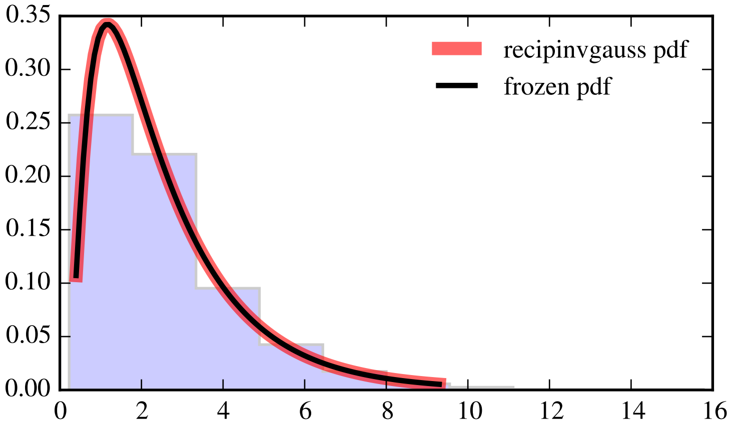
```
>>> vals = recipinvgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], recipinvgauss.cdf(vals, mu))
True
```

Generate random numbers:

```
>>> r = recipinvgauss.rvs(mu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(mu, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, mu, loc=0, scale=1)`	Probability density function.
`logpdf(x, mu, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, mu, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, mu, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, mu, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, mu, loc=0, scale=1)`	Log of the survival function.
`ppf(q, mu, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, mu, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, mu, loc=0, scale=1)`	Non-central moment of order n
`stats(mu, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(mu, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, mu, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, mu, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(mu, loc=0, scale=1)`	Median of the distribution.
`mean(mu, loc=0, scale=1)`	Mean of the distribution.
`var(mu, loc=0, scale=1)`	Variance of the distribution.
`std(mu, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, mu, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`semicircular`** **= <scipy.stats._continuous_distns.semicircular_gen object at 0x7fa40e975610>**

A semicircular continuous random variable.

As an instance of the `rv_continuous` class, `semicircular` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `semicircular` is:

```
semicircular.pdf(x) = 2/pi * sqrt(1-x**2)
```

for `-1 <= x <= 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `semicircular.pdf(x, loc, scale)` is identically equivalent to `semicircular.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import semicircular
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = semicircular.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(semicircular.ppf(0.01),
...                 semicircular.ppf(0.99), 100)
>>> ax.plot(x, semicircular.pdf(x),
...        'r-', lw=5, alpha=0.6, label='semicircular pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = semicircular()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

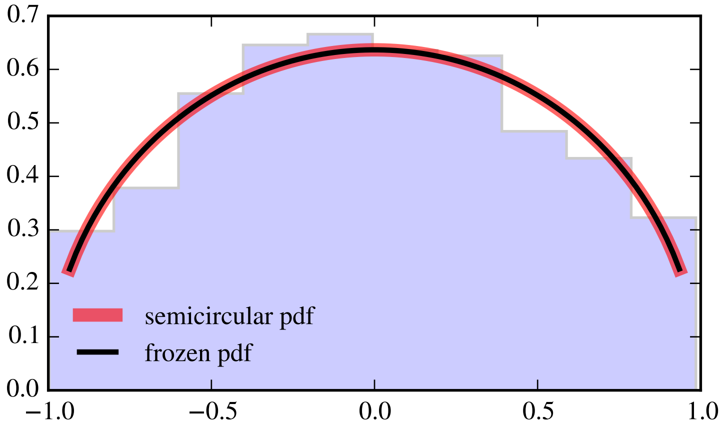
```
>>> vals = semicircular.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], semicircular.cdf(vals))
True
```

Generate random numbers:

```
>>> r = semicircular.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**t = <scipy.stats._continuous_distns.t_gen object at 0x7fa40e95d090>**

A Student's T continuous random variable.

As an instance of the `rv_continuous` class, `t` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `t` is:

```
                                gamma((df+1)/2)
t.pdf(x, df) = ---------------------------------------------------
               sqrt(pi*df) * gamma(df/2) * (1+x**2/df)**((df+1)/2)
```

for `df > 0`.

`t` takes `df` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `t.pdf(x, df, loc, scale)` is identically equivalent to `t.pdf(y, df) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import t
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> df = 2.74
>>> mean, var, skew, kurt = t.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(t.ppf(0.01, df),
...                 t.ppf(0.99, df), 100)
>>> ax.plot(x, t.pdf(x, df),
...        'r-', lw=5, alpha=0.6, label='t pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = t(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

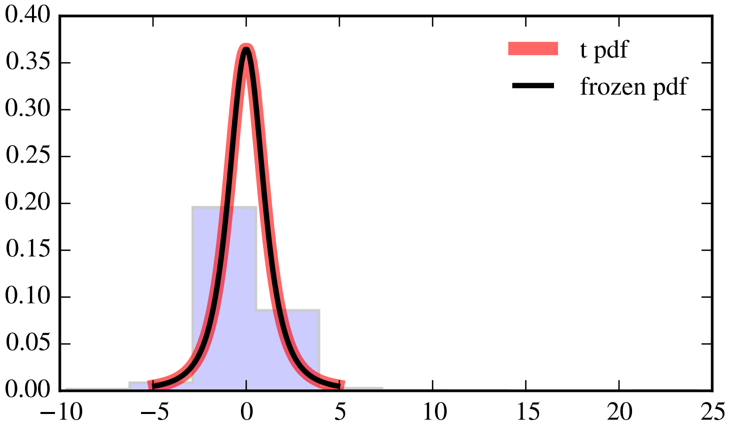
```
>>> vals = t.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], t.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = t.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(df, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, df, loc=0, scale=1)`	Probability density function.
`logpdf(x, df, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, df, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, df, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, df, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, df, loc=0, scale=1)`	Log of the survival function.
`ppf(q, df, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, df, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, df, loc=0, scale=1)`	Non-central moment of order n
`stats(df, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(df, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, df, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, df, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(df, loc=0, scale=1)`	Median of the distribution.
`mean(df, loc=0, scale=1)`	Mean of the distribution.
`var(df, loc=0, scale=1)`	Variance of the distribution.
`std(df, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, df, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`triang`** **= <scipy.stats._continuous_distns.triang_gen object at 0x7fa40e975810>**

A triangular continuous random variable.

As an instance of the `rv_continuous` class, `triang` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The triangular distribution can be represented with an up-sloping line from `loc` to `(loc + c*scale)` and then downsloping for `(loc + c*scale)` to `(loc+scale)`.

`triang` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `triang.pdf(x, c, loc, scale)` is identically equivalent to `triang.pdf(y, c) / scale` with `y = (x - loc) / scale`.

The standard form is in the range [0, 1] with c the mode. The location parameter shifts the start to *loc*. The scale parameter changes the width from 1 to *scale*.

Examples

```
>>> from scipy.stats import triang
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.158
>>> mean, var, skew, kurt = triang.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(triang.ppf(0.01, c),
...                 triang.ppf(0.99, c), 100)
>>> ax.plot(x, triang.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='triang pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = triang(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

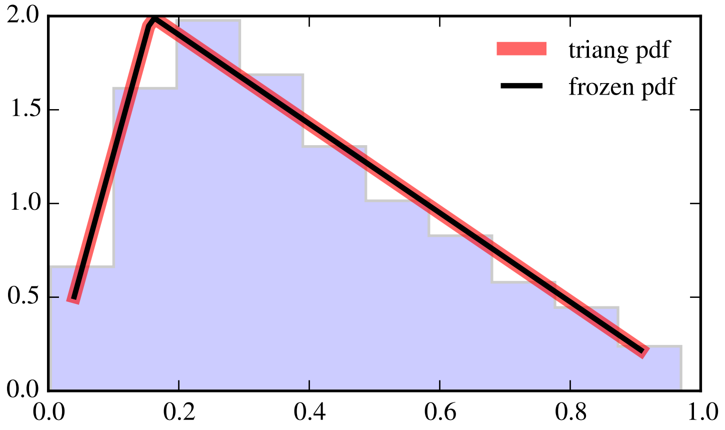
```
>>> vals = triang.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], triang.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = triang.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`truncexpon`** **= <scipy.stats._continuous_distns.truncexpon_gen object at 0x7fa40e975ad0>**

A truncated exponential continuous random variable.

As an instance of the `rv_continuous` class, `truncexpon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `truncexpon` is:

```
truncexpon.pdf(x, b) = exp(-x) / (1-exp(-b))
```

for `0 < x < b`.

`truncexpon` takes `b` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `truncexpon.pdf(x, b, loc, scale)` is identically equivalent to `truncexpon.pdf(y, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import truncexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> b = 4.69
>>> mean, var, skew, kurt = truncexpon.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(truncexpon.ppf(0.01, b),
...                 truncexpon.ppf(0.99, b), 100)
>>> ax.plot(x, truncexpon.pdf(x, b),
...        'r-', lw=5, alpha=0.6, label='truncexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = truncexpon(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

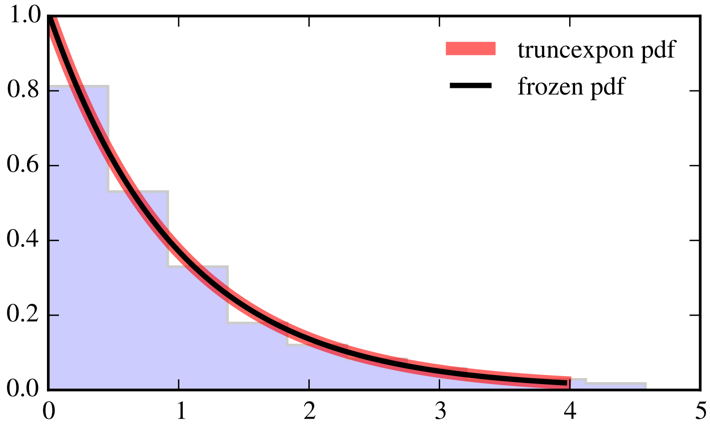
```
>>> vals = truncexpon.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], truncexpon.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = truncexpon.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, b, loc=0, scale=1)`	Non-central moment of order n
`stats(b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(b, loc=0, scale=1)`	Median of the distribution.
`mean(b, loc=0, scale=1)`	Mean of the distribution.
`var(b, loc=0, scale=1)`	Variance of the distribution.
`std(b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`truncnorm`** **= <scipy.stats._continuous_distns.truncnorm_gen object at 0x7fa40e975d90>**

A truncated normal continuous random variable.

As an instance of the `rv_continuous` class, `truncnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The standard form of this distribution is a standard normal truncated to the range [a, b] — notice that a and b are defined over the domain of the standard normal. To convert clip values for a specific mean and standard deviation, use:

```
a, b = (myclip_a - my_mean) / my_std, (myclip_b - my_mean) / my_std
```

`truncnorm` takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `truncnorm.pdf(x, a, b, loc, scale)` is identically equivalent to `truncnorm.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import truncnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a, b = 0.1, 2
>>> mean, var, skew, kurt = truncnorm.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(truncnorm.ppf(0.01, a, b),
...                 truncnorm.ppf(0.99, a, b), 100)
>>> ax.plot(x, truncnorm.pdf(x, a, b),
...        'r-', lw=5, alpha=0.6, label='truncnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = truncnorm(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

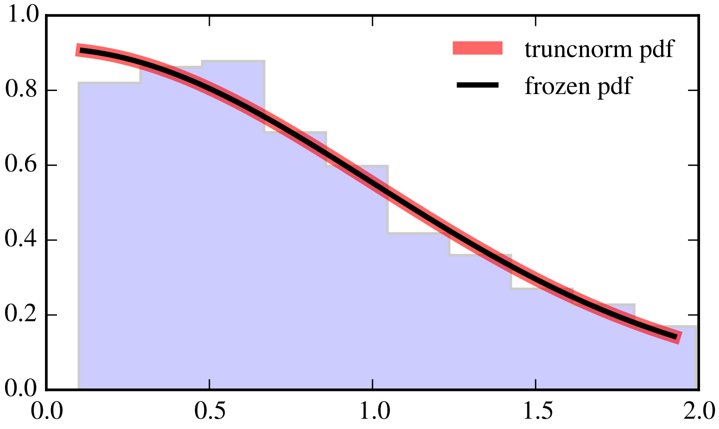
```
>>> vals = truncnorm.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], truncnorm.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = truncnorm.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(a, b, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, a, b, loc=0, scale=1)`	Probability density function.
`logpdf(x, a, b, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, a, b, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, a, b, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, a, b, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, b, loc=0, scale=1)`	Log of the survival function.
`ppf(q, a, b, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, b, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, a, b, loc=0, scale=1)`	Non-central moment of order n
`stats(a, b, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, b, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, a, b, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, b, loc=0, scale=1)`	Median of the distribution.
`mean(a, b, loc=0, scale=1)`	Mean of the distribution.
`var(a, b, loc=0, scale=1)`	Variance of the distribution.
`std(a, b, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, a, b, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`tukeylambda`** **= <scipy.stats._continuous_distns.tukeylambda_gen object at 0x7fa40e8fd110>**

A Tukey-Lamdba continuous random variable.

As an instance of the `rv_continuous` class, `tukeylambda` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

A flexible distribution, able to represent and interpolate between the following distributions:

- Cauchy (lam=-1)
- logistic (lam=0.0)
- approx Normal (lam=0.14)
- u-shape (lam = 0.5)
- uniform from -1 to 1 (lam = 1)

`tukeylambda` takes `lam` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `tukeylambda.pdf(x, lam, loc, scale)` is identically equivalent to `tukeylambda.pdf(y, lam) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import tukeylambda
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> lam = 3.13
>>> mean, var, skew, kurt = tukeylambda.stats(lam, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(tukeylambda.ppf(0.01, lam),
...                 tukeylambda.ppf(0.99, lam), 100)
>>> ax.plot(x, tukeylambda.pdf(x, lam),
...          'r-', lw=5, alpha=0.6, label='tukeylambda pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = tukeylambda(lam)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

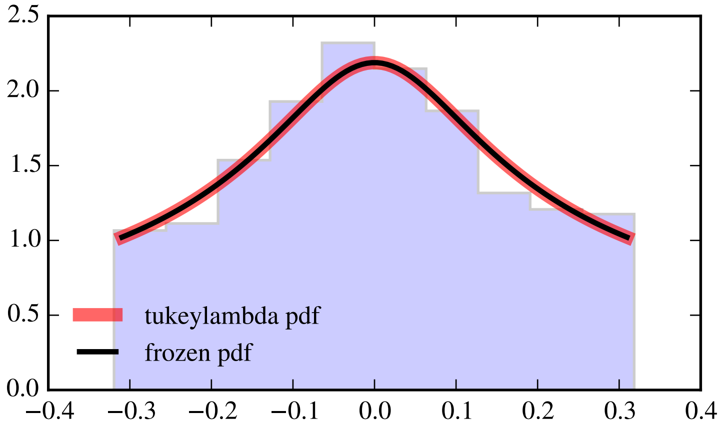
```
>>> vals = tukeylambda.ppf([0.001, 0.5, 0.999], lam)
>>> np.allclose([0.001, 0.5, 0.999], tukeylambda.cdf(vals, lam))
True
```

Generate random numbers:

```
>>> r = tukeylambda.rvs(lam, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(lam, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, lam, loc=0, scale=1)`	Probability density function.
`logpdf(x, lam, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, lam, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, lam, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, lam, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, lam, loc=0, scale=1)`	Log of the survival function.
`ppf(q, lam, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, lam, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, lam, loc=0, scale=1)`	Non-central moment of order n
`stats(lam, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(lam, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, lam, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, lam, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(lam, loc=0, scale=1)`	Median of the distribution.
`mean(lam, loc=0, scale=1)`	Mean of the distribution.
`var(lam, loc=0, scale=1)`	Variance of the distribution.
`std(lam, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, lam, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`uniform`** **= <scipy.stats._continuous_distns.uniform_gen object at 0x7fa40e8fd3d0>**

A uniform continuous random variable.

This distribution is constant between *loc* and `loc + scale`.

As an instance of the `rv_continuous` class, `uniform` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Examples

```
>>> from scipy.stats import uniform
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = uniform.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(uniform.ppf(0.01),
...                 uniform.ppf(0.99), 100)
>>> ax.plot(x, uniform.pdf(x),
...        'r-', lw=5, alpha=0.6, label='uniform pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = uniform()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

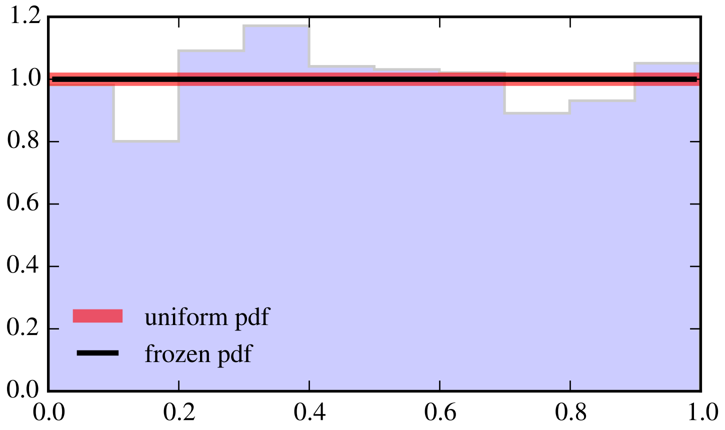
```
>>> vals = uniform.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], uniform.cdf(vals))
True
```

Generate random numbers:

```
>>> r = uniform.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`vonmises`** **= <scipy.stats._continuous_distns.vonmises_gen object at 0x7fa40e8fd5d0>**

A Von Mises continuous random variable.

As an instance of the `rv_continuous` class, `vonmises` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`vonmises_line`
The same distribution, defined on a [-pi, pi] segment of the real line.

Notes

If *x* is not in range or *loc* is not in range it assumes they are angles and converts them to [-pi, pi] equivalents.

The probability density function for `vonmises` is:

```
vonmises.pdf(x, kappa) = exp(kappa * cos(x)) / (2*pi*I[0](kappa))
```

for `-pi <= x <= pi`, `kappa > 0`.

`vonmises` takes `kappa` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `vonmises.pdf(x, kappa, loc, scale)` is identically equivalent to `vonmises.pdf(y, kappa) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import vonmises
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> kappa = 3.99
>>> mean, var, skew, kurt = vonmises.stats(kappa, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(vonmises.ppf(0.01, kappa),
...                 vonmises.ppf(0.99, kappa), 100)
>>> ax.plot(x, vonmises.pdf(x, kappa),
...        'r-', lw=5, alpha=0.6, label='vonmises pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = vonmises(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

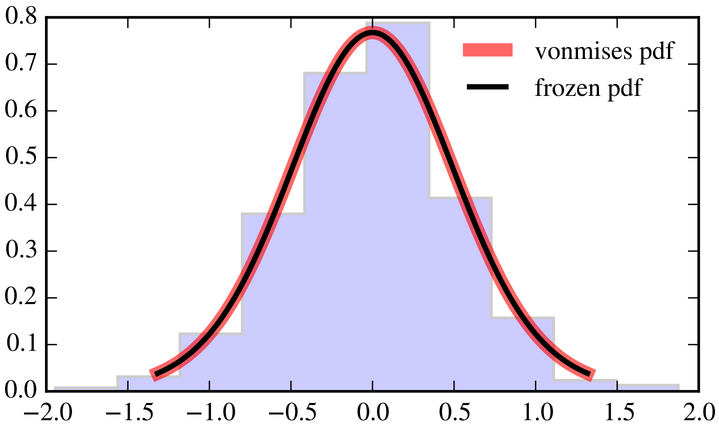
```
>>> vals = vonmises.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], vonmises.cdf(vals, kappa))
True
```

Generate random numbers:

```
>>> r = vonmises.rvs(kappa, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(kappa, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, kappa, loc=0, scale=1)`	Probability density function.
`logpdf(x, kappa, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, kappa, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, kappa, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, kappa, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, kappa, loc=0, scale=1)`	Log of the survival function.
`ppf(q, kappa, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, kappa, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, kappa, loc=0, scale=1)`	Non-central moment of order n
`stats(kappa, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(kappa, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, kappa, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, kappa, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(kappa, loc=0, scale=1)`	Median of the distribution.
`mean(kappa, loc=0, scale=1)`	Mean of the distribution.
`var(kappa, loc=0, scale=1)`	Variance of the distribution.
`std(kappa, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, kappa, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`wald`** **= <scipy.stats._continuous_distns.wald_gen object at 0x7fa40e8fdb10>**

A Wald continuous random variable.

As an instance of the `rv_continuous` class, `wald` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `wald` is:

```
wald.pdf(x) = 1/sqrt(2*pi*x**3) * exp(-(x-1)**2/(2*x))
```

for `x > 0`.

`wald` is a special case of `invgauss` with `mu == 1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `wald.pdf(x, loc, scale)` is identically equivalent to `wald.pdf(y) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import wald
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mean, var, skew, kurt = wald.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(wald.ppf(0.01),
...                 wald.ppf(0.99), 100)
>>> ax.plot(x, wald.pdf(x),
...          'r-', lw=5, alpha=0.6, label='wald pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = wald()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

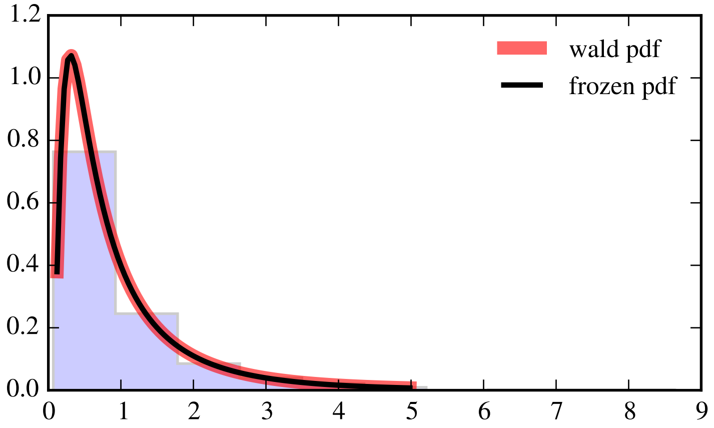
```
>>> vals = wald.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], wald.cdf(vals))
True
```

Generate random numbers:

```
>>> r = wald.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, loc=0, scale=1)`	Probability density function.
`logpdf(x, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, loc=0, scale=1)`	Log of the survival function.
`ppf(q, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, loc=0, scale=1)`	Non-central moment of order n
`stats(loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(loc=0, scale=1)`	Median of the distribution.
`mean(loc=0, scale=1)`	Mean of the distribution.
`var(loc=0, scale=1)`	Variance of the distribution.
`std(loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`weibull_min`** **= <scipy.stats._continuous_distns.frechet_r_gen object at 0x7fa40e97ead0>**

A Frechet right (or Weibull minimum) continuous random variable.

As an instance of the `rv_continuous` class, `weibull_min` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`weibull_min`

The same distribution as `frechet_r`.

`frechet_l`, `weibull_max`

Notes

The probability density function for `frechet_r` is:

```
frechet_r.pdf(x, c) = c * x**(c-1) * exp(-x**c)
```

for `x > 0`, `c > 0`.

`frechet_r` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_min.pdf(x, c, loc, scale)` is identically equivalent to `weibull_min.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import weibull_min
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 1.79
>>> mean, var, skew, kurt = weibull_min.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(weibull_min.ppf(0.01, c),
...                 weibull_min.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_min.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='weibull_min pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = weibull_min(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

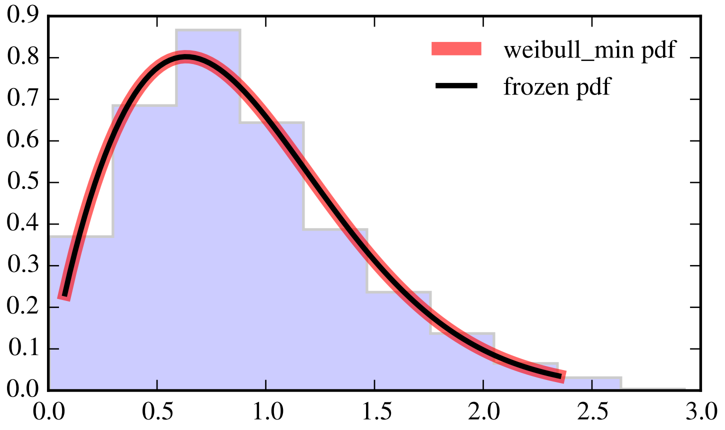
```
>>> vals = weibull_min.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_min.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = weibull_min.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`weibull_max`** **= <scipy.stats._continuous_distns.frechet_l_gen object at 0x7fa40e987050>**

A Frechet left (or Weibull maximum) continuous random variable.

As an instance of the `rv_continuous` class, `weibull_max` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

weibull_max The same distribution as `frechet_l`.

`frechet_r`, `weibull_min`

Notes

The probability density function for `frechet_l` is:

```
frechet_l.pdf(x, c) = c * (-x)**(c-1) * exp(-(-x)**c)
```

for `x < 0`, `c > 0`.

`frechet_l` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_max.pdf(x, c, loc, scale)` is identically equivalent to `weibull_max.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import weibull_max
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 2.87
>>> mean, var, skew, kurt = weibull_max.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(weibull_max.ppf(0.01, c),
...                 weibull_max.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_max.pdf(x, c),
...        'r-', lw=5, alpha=0.6, label='weibull_max pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = weibull_max(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

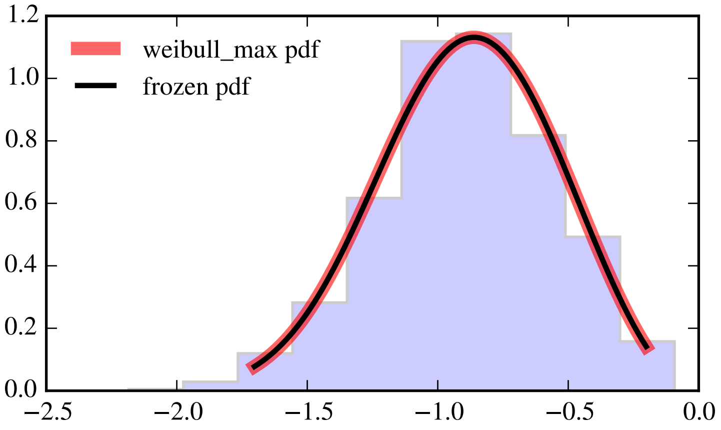
```
>>> vals = weibull_max.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_max.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = weibull_max.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**wrapcauchy = <scipy.stats._continuous_distns.wrapcauchy_gen object at 0x7fa40e8fdd10>**

A wrapped Cauchy continuous random variable.

As an instance of the `rv_continuous` class, `wrapcauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `wrapcauchy` is:

```
wrapcauchy.pdf(x, c) = (1-c**2) / (2*pi*(1+c**2-2*c*cos(x)))
```

for `0 <= x <= 2*pi`, `0 < c < 1`.

`wrapcauchy` takes `c` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `wrapcauchy.pdf(x, c, loc, scale)` is identically equivalent to `wrapcauchy.pdf(y, c) / scale` with `y = (x - loc) / scale`.

Examples

```
>>> from scipy.stats import wrapcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> c = 0.0311
>>> mean, var, skew, kurt = wrapcauchy.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(wrapcauchy.ppf(0.01, c),
...                 wrapcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, wrapcauchy.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='wrapcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = wrapcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

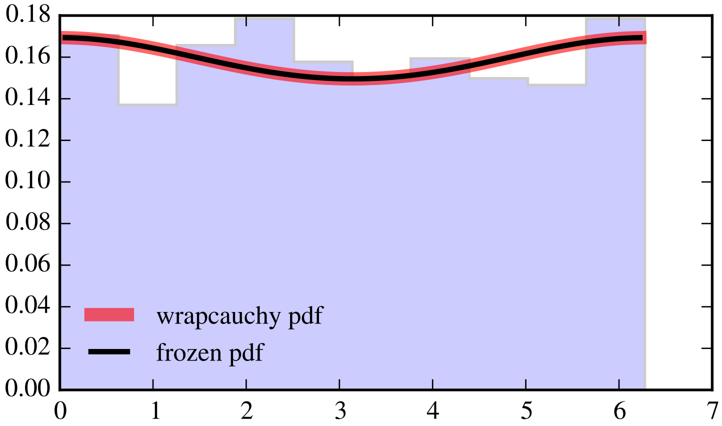
```
>>> vals = wrapcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], wrapcauchy.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = wrapcauchy.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

`rvs(c, loc=0, scale=1, size=1, random_state=None)`	Random variates.
`pdf(x, c, loc=0, scale=1)`	Probability density function.
`logpdf(x, c, loc=0, scale=1)`	Log of the probability density function.
`cdf(x, c, loc=0, scale=1)`	Cumulative density function.
`logcdf(x, c, loc=0, scale=1)`	Log of the cumulative density function.
`sf(x, c, loc=0, scale=1)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, c, loc=0, scale=1)`	Log of the survival function.
`ppf(q, c, loc=0, scale=1)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, c, loc=0, scale=1)`	Inverse survival function (inverse of `sf`).
`moment(n, c, loc=0, scale=1)`	Non-central moment of order n
`stats(c, loc=0, scale=1, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(c, loc=0, scale=1)`	(Differential) entropy of the RV.
`fit(data, c, loc=0, scale=1)`	Parameter estimates for generic data.
`expect(func, c, loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`	Expected value of a function (of one argument) with respect to the distribution.
`median(c, loc=0, scale=1)`	Median of the distribution.
`mean(c, loc=0, scale=1)`	Mean of the distribution.
`var(c, loc=0, scale=1)`	Variance of the distribution.
`std(c, loc=0, scale=1)`	Standard deviation of the distribution.
`interval(alpha, c, loc=0, scale=1)`	Endpoints of the range that contains alpha percent of the distribution

5.34.2 Multivariate distributions

`multivariate_normal`	A multivariate normal random variable.
`dirichlet`	A Dirichlet random variable.
`wishart`	A Wishart random variable.
`invwishart`	An inverse Wishart random variable.

`scipy.stats.`**`multivariate_normal`** **= <scipy.stats._multivariate.multivariate_normal_gen object at 0x7fa40e148e90>**

A multivariate normal random variable.

The *mean* keyword specifies the mean. The *cov* keyword specifies the covariance matrix.

Parameters

x : array_like

Quantiles, with the last axis of *x* denoting the components.

mean : array_like, optional

Mean of the distribution (default zero)

cov : array_like, optional

Covariance matrix of the distribution (default one)

allow_singular : bool, optional

Whether to allow a singular covariance matrix. (Default: False)

random_state : None or int or np.random.RandomState instance, optional

If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the mean and covariance parameters, returning a "frozen" multivariate normal random variable:

rv = multivariate_normal(mean=None, cov=1, allow_singular=False)

- Frozen object with the same methods but holding the given mean and covariance fixed.

Notes

***Setting the parameter* mean *to* None *is equivalent to having* mean**

be the zero-vector. The parameter *cov* can be a scalar, in which case the covariance matrix is the identity times that value, a vector of diagonal entries for the covariance matrix, or a two-dimensional array_like.

The covariance matrix *cov* must be a (symmetric) positive semi-definite matrix. The determinant and inverse of *cov* are computed as the pseudo-determinant and pseudo-inverse, respectively, so that *cov* does not need to have full rank.

The probability density function for `multivariate_normal` is

$$f(x) = \frac{1}{\sqrt{(2\pi)^k \det \Sigma}} \exp\left(-\frac{1}{2}(x-\mu)^T \Sigma^{-1}(x-\mu)\right),$$

where μ is the mean, Σ the covariance matrix, and k is the dimension of the space where x takes values.

New in version 0.14.0.

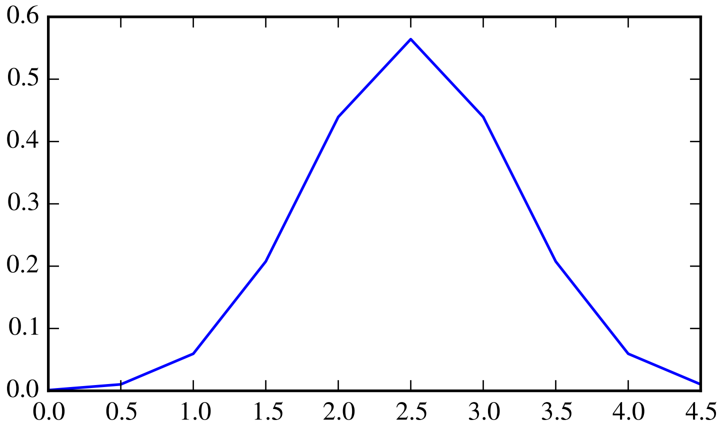
Examples

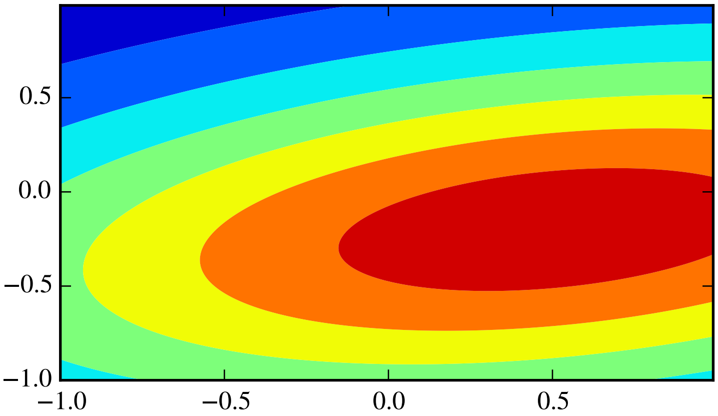
```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import multivariate_normal
```

```
>>> x = np.linspace(0, 5, 10, endpoint=False)
>>> y = multivariate_normal.pdf(x, mean=2.5, cov=0.5); y
array([ 0.00108914,  0.01033349,  0.05946514,  0.20755375,  0.43939129,
        0.56418958,  0.43939129,  0.20755375,  0.05946514,  0.01033349])
>>> fig1 = plt.figure()
>>> ax = fig1.add_subplot(111)
>>> ax.plot(x, y)
```

The input quantiles can be any shape of array, as long as the last axis labels the components. This allows us for instance to display the frozen pdf for a non-isotropic random variable in 2D as follows:

```
>>> x, y = np.mgrid[-1:1:.01, -1:1:.01]
>>> pos = np.empty(x.shape + (2,))
>>> pos[:, :, 0] = x; pos[:, :, 1] = y
>>> rv = multivariate_normal([0.5, -0.2], [[2.0, 0.3], [0.3, 0.5]])
>>> fig2 = plt.figure()
>>> ax2 = fig2.add_subplot(111)
>>> ax2.contourf(x, y, rv.pdf(pos))
```





Methods

`pdf(x, mean=None, cov=1, allow_singular=False)`	Probability density function.
`logpdf(x, mean=None, cov=1, allow_singular=False)`	Log of the probability density function.
`rvs(mean=None, cov=1, size=1, random_state=None)`	Draw random samples from a multivariate normal distribution.
`entropy()`	Compute the differential entropy of the multivariate normal.

`scipy.stats.`**`dirichlet`** **= <scipy.stats._multivariate.dirichlet_gen object at 0x7fa40e148fd0>**

A Dirichlet random variable.

The `alpha` keyword specifies the concentration parameters of the distribution.

New in version 0.15.0.

Parameters

x : array_like

Quantiles, with the last axis of *x* denoting the components.

alpha : array_like

The concentration parameters. The number of entries determines the dimensionality of the distribution.

random_state : None or int or np.random.RandomState instance, optional

If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix concentration parameters, returning a "frozen" Dirichlet random variable:

rv = dirichlet(alpha)

- Frozen object with the same methods but holding the given concentration parameters fixed.

Notes

Each α entry must be positive. The distribution has only support on the simplex defined by

$$\sum_{i=1}^{K} x_i \le 1$$

The probability density function for `dirichlet` is

$$f(x) = \frac{1}{\mathrm{B}(\boldsymbol\alpha)} \prod_{i=1}^{K} x_i^{\alpha_i - 1}$$

where

$$\mathrm{B}(\boldsymbol\alpha) = \frac{\prod_{i=1}^{K} \Gamma(\alpha_i)}{\Gamma\bigl(\sum_{i=1}^{K} \alpha_i\bigr)}$$

and $\boldsymbol\alpha = (\alpha_1, \ldots, \alpha_K)$, the concentration parameters and K is the dimension of the space where x takes values.

Methods

`pdf(x, alpha)`	Probability density function.
`logpdf(x, alpha)`	Log of the probability density function.
`rvs(alpha, size=1, random_state=None)`	Draw random samples from a Dirichlet distribution.
`mean(alpha)`	The mean of the Dirichlet distribution
`var(alpha)`	The variance of the Dirichlet distribution
`entropy(alpha)`	Compute the differential entropy of the multivariate normal.

`scipy.stats.`**`wishart`** **= <scipy.stats._multivariate.wishart_gen object at 0x7fa40e156110>**

A Wishart random variable.

The *df* keyword specifies the degrees of freedom. The *scale* keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal precision matrix (the inverse of the covariance matrix).

Parameters

x : array_like

Quantiles, with the last axis of *x* denoting the components.

df : int

Degrees of freedom, must be greater than or equal to dimension of the scale matrix

scale : array_like

Symmetric positive definite scale matrix of the distribution

random_state : None or int or np.random.RandomState instance, optional

If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a "frozen" Wishart random variable:

rv = wishart(df=1, scale=1)

- Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

`invwishart`, `chi2`

Notes

The scale matrix *scale* must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The Wishart distribution is often denoted

$$W_p(\nu, \Sigma)$$

where ν is the degrees of freedom and Σ is the $p \times p$ scale matrix.

The probability density function for `wishart` has support over positive definite matrices S; if $S \sim W_p(\nu, \Sigma)$, then its PDF is given by:

$$f(S) = \frac{|S|^{\frac{\nu - p - 1}{2}}}{2^{\frac{\nu p}{2}} |\Sigma|^{\frac{\nu}{2}} \Gamma_p\left(\frac{\nu}{2}\right)} \exp\left(-tr(\Sigma^{-1} S) / 2 \right)$$

If $S \sim W_p(\nu, \Sigma)$ (Wishart) then $S^{-1} \sim W_p^{-1}(\nu, \Sigma^{-1})$ (inverse Wishart).

If the scale matrix is 1-dimensional and equal to one, then the Wishart distribution $W_1(\nu, 1)$ collapses to the $\chi^2(\nu)$ distribution.

New in version 0.16.0.

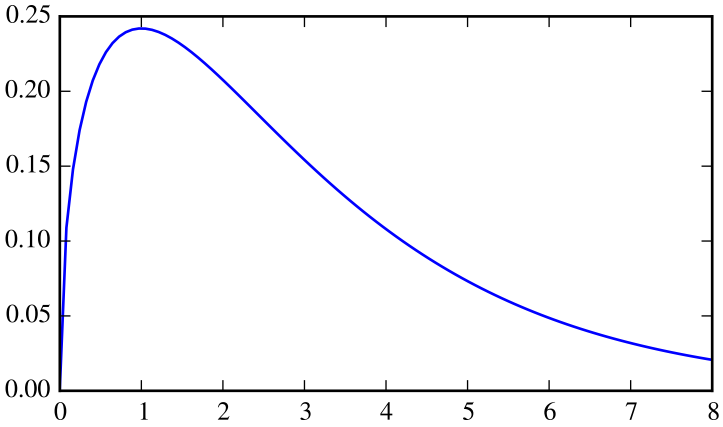
References

[R374], [R375]

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import wishart, chi2
>>> x = np.linspace(1e-5, 8, 100)
>>> w = wishart.pdf(x, df=3, scale=1); w[:5]
array([ 0.00126156,  0.10892176,  0.14793434,  0.17400548,  0.1929669 ])
>>> c = chi2.pdf(x, 3); c[:5]
array([ 0.00126156,  0.10892176,  0.14793434,  0.17400548,  0.1929669 ])
>>> plt.plot(x, w)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.



Methods

`pdf(x, df, scale)`	Probability density function.
`logpdf(x, df, scale)`	Log of the probability density function.
`rvs(df, scale, size=1, random_state=None)`	Draw random samples from a Wishart distribution.
`entropy()`	Compute the differential entropy of the Wishart distribution.

`scipy.stats.`**`invwishart`** **= <scipy.stats._multivariate.invwishart_gen object at 0x7fa40e156390>**

An inverse Wishart random variable.

The *df* keyword specifies the degrees of freedom. The *scale* keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal covariance matrix.

Parameters

x : array_like

Quantiles, with the last axis of *x* denoting the components.

df : int

Degrees of freedom, must be greater than or equal to dimension of the scale matrix

scale : array_like

Symmetric positive definite scale matrix of the distribution

random_state : None or int or np.random.RandomState instance, optional

If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a "frozen" inverse Wishart random variable:

rv = invwishart(df=1, scale=1)

- Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

`wishart`

Notes

The scale matrix *scale* must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The inverse Wishart distribution is often denoted

$$W_p^{-1}(\nu, \Psi)$$

where ν is the degrees of freedom and Ψ is the $p \times p$ scale matrix.

The probability density function for `invwishart` has support over positive definite matrices S; if $S \sim W_p^{-1}(\nu, \Sigma)$, then its PDF is given by:

$$f(S) = \frac{|\Sigma|^{\frac{\nu}{2}}}{2^{\frac{\nu p}{2}} |S|^{\frac{\nu+p+1}{2}} \Gamma_p\left(\frac{\nu}{2}\right)} \exp\left(-tr(\Sigma S^{-1})/2\right)$$

If $S \sim W_p^{-1}(\nu, \Psi)$ (inverse Wishart) then $S^{-1} \sim W_p(\nu, \Psi^{-1})$ (Wishart).

If the scale matrix is 1-dimensional and equal to one, then the inverse Wishart distribution $W_1(\nu, 1)$ collapses to the inverse Gamma distribution with parameters shape = $\frac{\nu}{2}$ and scale = $\frac{1}{2}$.

New in version 0.16.0.

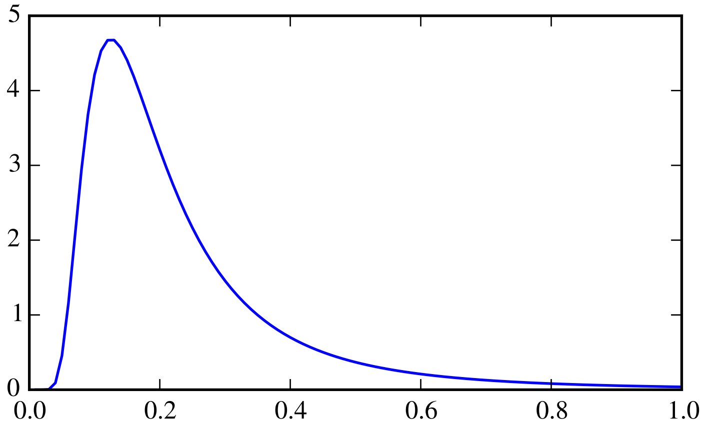
References

[R326], [R327]

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import invwishart, invgamma
>>> x = np.linspace(0.01, 1, 100)
>>> iw = invwishart.pdf(x, df=6, scale=1)
>>> iw[:3]
array([  1.20546865e-15,   5.42497807e-06,   4.45813929e-03])
>>> ig = invgamma.pdf(x, 6/2., scale=1./2)
>>> ig[:3]
array([  1.20546865e-15,   5.42497807e-06,   4.45813929e-03])
>>> plt.plot(x, iw)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.



Methods

`pdf(x, df, scale)`	Probability density function.
`logpdf(x, df, scale)`	Log of the probability density function.
`rvs(df, scale, size=1, random_state=None)`	Draw random samples from an inverse Wishart distribution.

5.34.3 Discrete distributions

`bernoulli`	A Bernoulli discrete random variable.
`binom`	A binomial discrete random variable.
`boltzmann`	A Boltzmann (Truncated Discrete Exponential) random variable.
`dlaplace`	A Laplacian discrete random variable.
`geom`	A geometric discrete random variable.
`hypergeom`	A hypergeometric discrete random variable.

Continued on next page

Table 5.254 – continued from previous page

`logser`	A Logarithmic (Log-Series, Series) discrete random variable.
`nbinom`	A negative binomial discrete random variable.
`planck`	A Planck discrete exponential random variable.
`poisson`	A Poisson discrete random variable.
`randint`	A uniform discrete random variable.
`skellam`	A Skellam discrete random variable.
`zipf`	A Zipf discrete random variable.

`scipy.stats.`**`bernoulli`** **= <scipy.stats._discrete_distns.bernoulli_gen object at 0x7fa40e995310>**

A Bernoulli discrete random variable.

As an instance of the `rv_discrete` class, `bernoulli` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `bernoulli` is:

```
bernoulli.pmf(k) = 1-p  if k = 0
                 = p    if k = 1
```

for `k` in `{0, 1}`.

`bernoulli` takes `p` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `bernoulli.pmf(k, p, loc)` is identically equivalent to `bernoulli.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import bernoulli
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> p = 0.3
>>> mean, var, skew, kurt = bernoulli.stats(p, moments='mvsk')
```

Display the probability mass function (`pmf`):

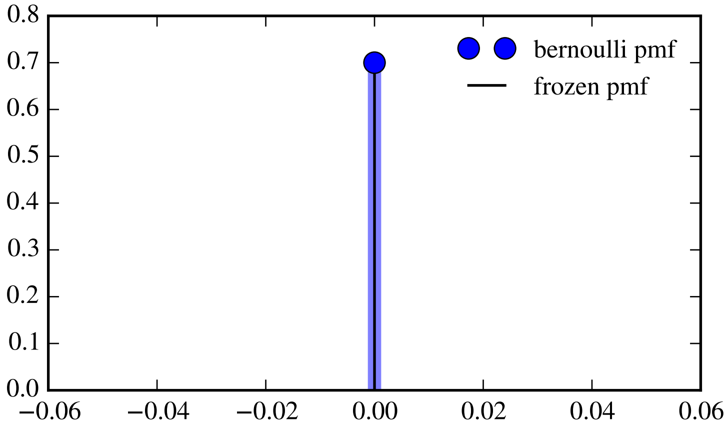
```
>>> x = np.arange(bernoulli.ppf(0.01, p),
...               bernoulli.ppf(0.99, p))
>>> ax.plot(x, bernoulli.pmf(x, p), 'bo', ms=8, label='bernoulli pmf')
>>> ax.vlines(x, 0, bernoulli.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = bernoulli(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
```

```
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = bernoulli.cdf(x, p)
>>> np.allclose(x, bernoulli.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = bernoulli.rvs(p, size=1000)
```

Methods

`rvs(p, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, p, loc=0)`	Probability mass function.
`logpmf(x, p, loc=0)`	Log of the probability mass function.
`cdf(x, p, loc=0)`	Cumulative density function.
`logcdf(x, p, loc=0)`	Log of the cumulative density function.
`sf(x, p, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, p, loc=0)`	Log of the survival function.
`ppf(q, p, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, p, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(p, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(p, loc=0)`	(Differential) entropy of the RV.
`expect(func, p, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(p, loc=0)`	Median of the distribution.
`mean(p, loc=0)`	Mean of the distribution.
`var(p, loc=0)`	Variance of the distribution.
`std(p, loc=0)`	Standard deviation of the distribution.
`interval(alpha, p, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`binom`** **= <scipy.stats._discrete_distns.binom_gen object at 0x7fa40e995090>**

A binomial discrete random variable.

As an instance of the `rv_discrete` class, `binom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `binom` is:

```
binom.pmf(k) = choose(n, k) * p**k * (1-p)**(n-k)
```

for `k` in `{0, 1,..., n}`.

`binom` takes `n` and `p` as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `binom.pmf(k, n, p, loc)` is identically equivalent to `binom.pmf(k - loc, n, p)`.

Examples

```
>>> from scipy.stats import binom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> n, p = 5, 0.4
>>> mean, var, skew, kurt = binom.stats(n, p, moments='mvsk')
```

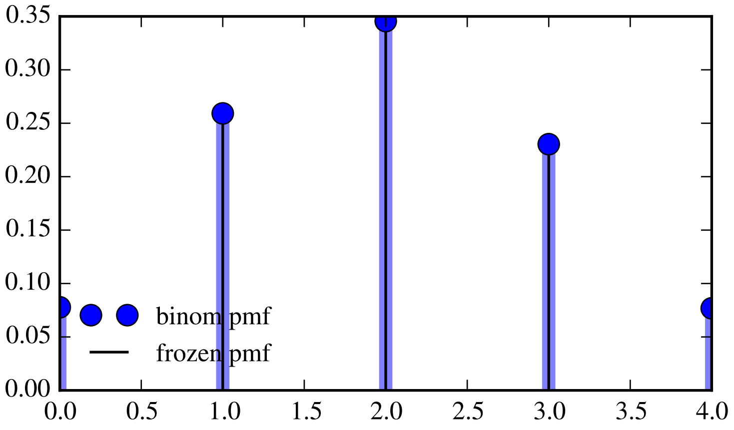
Display the probability mass function (`pmf`):

```
>>> x = np.arange(binom.ppf(0.01, n, p),
...               binom.ppf(0.99, n, p))
>>> ax.plot(x, binom.pmf(x, n, p), 'bo', ms=8, label='binom pmf')
>>> ax.vlines(x, 0, binom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = binom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = binom.cdf(x, n, p)
>>> np.allclose(x, binom.ppf(prob, n, p))
True
```

Generate random numbers:

```
>>> r = binom.rvs(n, p, size=1000)
```

Methods

`rvs(n, p, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, n, p, loc=0)`	Probability mass function.
`logpmf(x, n, p, loc=0)`	Log of the probability mass function.
`cdf(x, n, p, loc=0)`	Cumulative density function.
`logcdf(x, n, p, loc=0)`	Log of the cumulative density function.
`sf(x, n, p, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, n, p, loc=0)`	Log of the survival function.
`ppf(q, n, p, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, n, p, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(n, p, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(n, p, loc=0)`	(Differential) entropy of the RV.
`expect(func, n, p, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(n, p, loc=0)`	Median of the distribution.
`mean(n, p, loc=0)`	Mean of the distribution.
`var(n, p, loc=0)`	Variance of the distribution.
`std(n, p, loc=0)`	Standard deviation of the distribution.
`interval(alpha, n, p, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`boltzmann`** **= <scipy.stats._discrete_distns.boltzmann_gen object at 0x7fa40e9230d0>**

A Boltzmann (Truncated Discrete Exponential) random variable.

As an instance of the `rv_discrete` class, `boltzmann` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `boltzmann` is:

```
boltzmann.pmf(k) = (1-exp(-lambda_)*exp(-lambda_*k)/(1-exp(-lambda_*N))
```

for `k = 0,..., N-1`.

`boltzmann` takes `lambda_` and `N` as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `boltzmann.pmf(k, lambda_, N, loc)` is identically equivalent to `boltzmann.pmf(k - loc, lambda_, N)`.

Examples

```
>>> from scipy.stats import boltzmann
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> lambda_, N = 1.4, 19
>>> mean, var, skew, kurt = boltzmann.stats(lambda_, N, moments='mvsk')
```

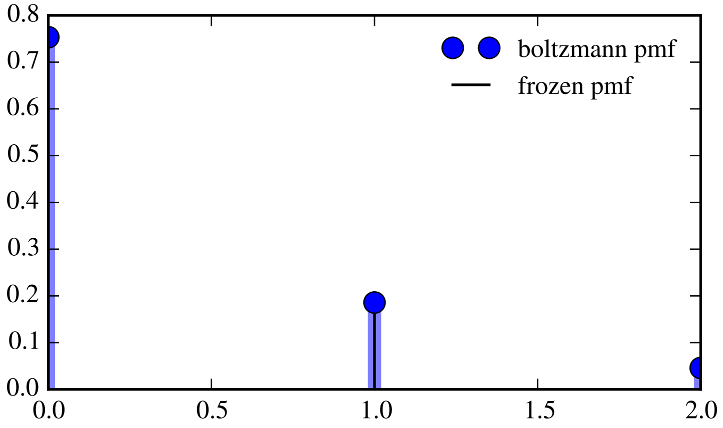
Display the probability mass function (`pmf`):

```
>>> x = np.arange(boltzmann.ppf(0.01, lambda_, N),
...               boltzmann.ppf(0.99, lambda_, N))
>>> ax.plot(x, boltzmann.pmf(x, lambda_, N), 'bo', ms=8, label='boltzmann pmf')
>>> ax.vlines(x, 0, boltzmann.pmf(x, lambda_, N), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = boltzmann(lambda_, N)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = boltzmann.cdf(x, lambda_, N)
>>> np.allclose(x, boltzmann.ppf(prob, lambda_, N))
True
```

Generate random numbers:

```
>>> r = boltzmann.rvs(lambda_, N, size=1000)
```

Methods

`rvs(lambda_, N, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, lambda_, N, loc=0)`	Probability mass function.
`logpmf(x, lambda_, N, loc=0)`	Log of the probability mass function.
`cdf(x, lambda_, N, loc=0)`	Cumulative density function.
`logcdf(x, lambda_, N, loc=0)`	Log of the cumulative density function.
`sf(x, lambda_, N, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, lambda_, N, loc=0)`	Log of the survival function.
`ppf(q, lambda_, N, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, lambda_, N, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(lambda_, N, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(lambda_, N, loc=0)`	(Differential) entropy of the RV.
`expect(func, lambda_, N, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(lambda_, N, loc=0)`	Median of the distribution.
`mean(lambda_, N, loc=0)`	Mean of the distribution.
`var(lambda_, N, loc=0)`	Variance of the distribution.
`std(lambda_, N, loc=0)`	Standard deviation of the distribution.
`interval(alpha, lambda_, N, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`dlaplace`** **= <scipy.stats._discrete_distns.dlaplace_gen object at 0x7fa40e923810>**

A Laplacian discrete random variable.

As an instance of the `rv_discrete` class, `dlaplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `dlaplace` is:

```
dlaplace.pmf(k) = tanh(a/2) * exp(-a*abs(k))
```

for `a > 0`.

`dlaplace` takes `a` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `dlaplace.pmf(k, a, loc)` is identically equivalent to `dlaplace.pmf(k - loc, a)`.

Examples

```
>>> from scipy.stats import dlaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 0.8
>>> mean, var, skew, kurt = dlaplace.stats(a, moments='mvsk')
```

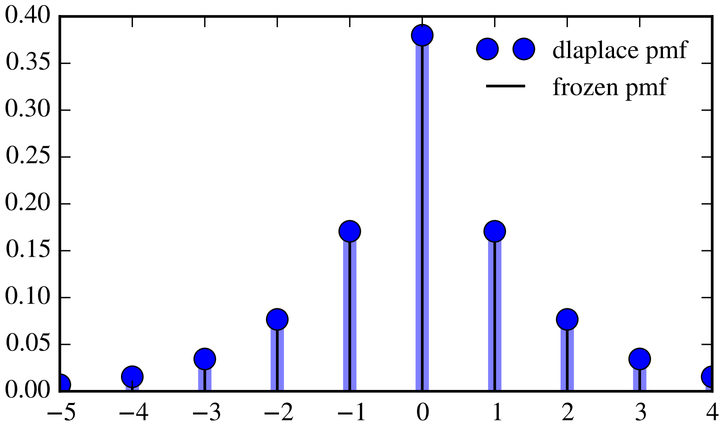
Display the probability mass function (`pmf`):

```
>>> x = np.arange(dlaplace.ppf(0.01, a),
...               dlaplace.ppf(0.99, a))
>>> ax.plot(x, dlaplace.pmf(x, a), 'bo', ms=8, label='dlaplace pmf')
>>> ax.vlines(x, 0, dlaplace.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = dlaplace(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = dlaplace.cdf(x, a)
>>> np.allclose(x, dlaplace.ppf(prob, a))
True
```

Generate random numbers:

```
>>> r = dlaplace.rvs(a, size=1000)
```

Methods

`rvs(a, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, a, loc=0)`	Probability mass function.
`logpmf(x, a, loc=0)`	Log of the probability mass function.
`cdf(x, a, loc=0)`	Cumulative density function.
`logcdf(x, a, loc=0)`	Log of the cumulative density function.
`sf(x, a, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0)`	Log of the survival function.
`ppf(q, a, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(a, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0)`	(Differential) entropy of the RV.
`expect(func, a, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0)`	Median of the distribution.
`mean(a, loc=0)`	Mean of the distribution.
`var(a, loc=0)`	Variance of the distribution.
`std(a, loc=0)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**geom = <scipy.stats._discrete_distns.geom_gen object at 0x7fa40e995790>**

A geometric discrete random variable.

As an instance of the `rv_discrete` class, `geom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `geom` is:

```
geom.pmf(k) = (1-p)**(k-1)*p
```

for `k >= 1`.

`geom` takes `p` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `geom.pmf(k, p, loc)` is identically equivalent to `geom.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import geom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> p = 0.5
>>> mean, var, skew, kurt = geom.stats(p, moments='mvsk')
```

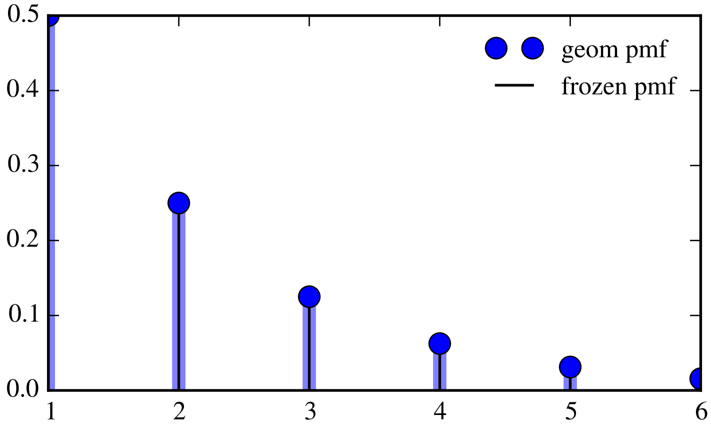
Display the probability mass function (`pmf`):

```
>>> x = np.arange(geom.ppf(0.01, p),
...               geom.ppf(0.99, p))
>>> ax.plot(x, geom.pmf(x, p), 'bo', ms=8, label='geom pmf')
>>> ax.vlines(x, 0, geom.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = geom(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = geom.cdf(x, p)
>>> np.allclose(x, geom.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = geom.rvs(p, size=1000)
```

Methods

`rvs(p, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, p, loc=0)`	Probability mass function.
`logpmf(x, p, loc=0)`	Log of the probability mass function.
`cdf(x, p, loc=0)`	Cumulative density function.
`logcdf(x, p, loc=0)`	Log of the cumulative density function.
`sf(x, p, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, p, loc=0)`	Log of the survival function.
`ppf(q, p, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, p, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(p, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(p, loc=0)`	(Differential) entropy of the RV.
`expect(func, p, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(p, loc=0)`	Median of the distribution.
`mean(p, loc=0)`	Mean of the distribution.
`var(p, loc=0)`	Variance of the distribution.
`std(p, loc=0)`	Standard deviation of the distribution.
`interval(alpha, p, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`hypergeom`** **= <scipy.stats._discrete_distns.hypergeom_gen object at 0x7fa40e995650>**

A hypergeometric discrete random variable.

The hypergeometric distribution models drawing objects from a bin. M is the total number of objects, n is total number of Type I objects. The random variate represents the number of Type I objects in N drawn without replacement from the total population.

As an instance of the `rv_discrete` class, `hypergeom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function is defined as:

```
pmf(k, M, n, N) = choose(n, k) * choose(M - n, N - k) / choose(M, N),
                               for max(0, N - (M-n)) <= k <= min(n, N)
```

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `hypergeom.pmf(k, M, n, N, loc)` is identically equivalent to `hypergeom.pmf(k - loc, M, n, N)`.

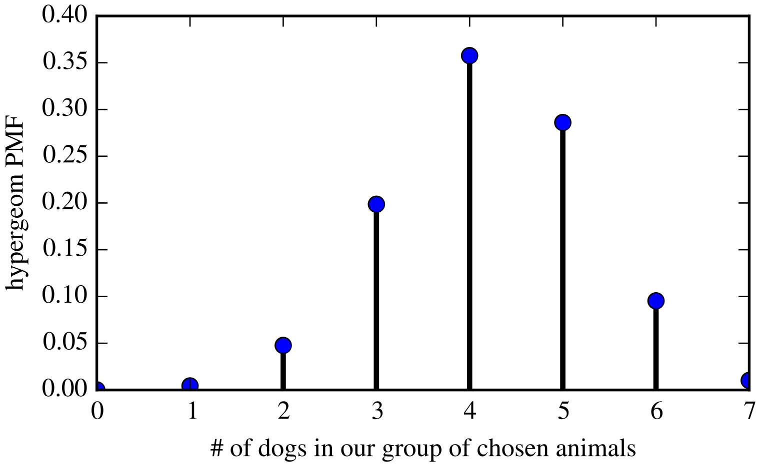
Examples

```
>>> from scipy.stats import hypergeom
>>> import matplotlib.pyplot as plt
```

Suppose we have a collection of 20 animals, of which 7 are dogs. Then if we want to know the probability of finding a given number of dogs if we choose at random 12 of the 20 animals, we can initialize a frozen distribution and plot the probability mass function:

```
>>> [M, n, N] = [20, 7, 12]
>>> rv = hypergeom(M, n, N)
>>> x = np.arange(0, n+1)
>>> pmf_dogs = rv.pmf(x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, pmf_dogs, 'bo')
>>> ax.vlines(x, 0, pmf_dogs, lw=2)
>>> ax.set_xlabel('# of dogs in our group of chosen animals')
>>> ax.set_ylabel('hypergeom PMF')
>>> plt.show()
```



Instead of using a frozen distribution we can also use `hypergeom` methods directly. To for example obtain the cumulative distribution function, use:

```
>>> prb = hypergeom.cdf(x, M, n, N)
```

And to generate random numbers:

```
>>> R = hypergeom.rvs(M, n, N, size=10)
```

Methods

`rvs(M, n, N, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, M, n, N, loc=0)`	Probability mass function.
`logpmf(x, M, n, N, loc=0)`	Log of the probability mass function.
`cdf(x, M, n, N, loc=0)`	Cumulative density function.
`logcdf(x, M, n, N, loc=0)`	Log of the cumulative density function.
`sf(x, M, n, N, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, M, n, N, loc=0)`	Log of the survival function.
`ppf(q, M, n, N, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, M, n, N, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(M, n, N, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(M, n, N, loc=0)`	(Differential) entropy of the RV.
`expect(func, M, n, N, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(M, n, N, loc=0)`	Median of the distribution.
`mean(M, n, N, loc=0)`	Mean of the distribution.
`var(M, n, N, loc=0)`	Variance of the distribution.
`std(M, n, N, loc=0)`	Standard deviation of the distribution.
`interval(alpha, M, n, N, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`logser`** **= <scipy.stats._discrete_distns.logser_gen object at 0x7fa40e995990>**

A Logarithmic (Log-Series, Series) discrete random variable.

As an instance of the `rv_discrete` class, `logser` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `logser` is:

```
logser.pmf(k) = - p**k / (k*log(1-p))
```

for `k >= 1`.

`logser` takes `p` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `logser.pmf(k, p, loc)` is identically equivalent to `logser.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import logser
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> p = 0.6
>>> mean, var, skew, kurt = logser.stats(p, moments='mvsk')
```

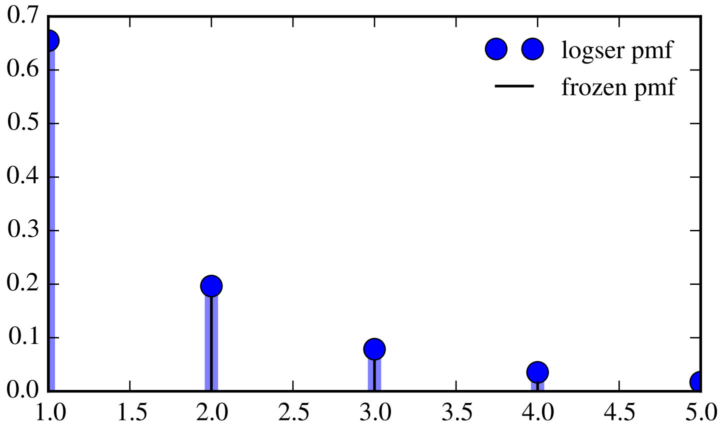
Display the probability mass function (`pmf`):

```
>>> x = np.arange(logser.ppf(0.01, p),
...               logser.ppf(0.99, p))
>>> ax.plot(x, logser.pmf(x, p), 'bo', ms=8, label='logser pmf')
>>> ax.vlines(x, 0, logser.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = logser(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = logser.cdf(x, p)
>>> np.allclose(x, logser.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = logser.rvs(p, size=1000)
```

Methods

`rvs(p, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, p, loc=0)`	Probability mass function.
`logpmf(x, p, loc=0)`	Log of the probability mass function.
`cdf(x, p, loc=0)`	Cumulative density function.
`logcdf(x, p, loc=0)`	Log of the cumulative density function.
`sf(x, p, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, p, loc=0)`	Log of the survival function.
`ppf(q, p, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, p, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(p, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(p, loc=0)`	(Differential) entropy of the RV.
`expect(func, p, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(p, loc=0)`	Median of the distribution.
`mean(p, loc=0)`	Mean of the distribution.
`var(p, loc=0)`	Variance of the distribution.
`std(p, loc=0)`	Standard deviation of the distribution.
`interval(alpha, p, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`nbinom`** **= <scipy.stats._discrete_distns.nbinom_gen object at 0x7fa40e9953d0>**

A negative binomial discrete random variable.

As an instance of the `rv_discrete` class, `nbinom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `nbinom` is:

```
nbinom.pmf(k) = choose(k+n-1, n-1) * p**n * (1-p)**k
```

for `k >= 0`.

`nbinom` takes `n` and `p` as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `nbinom.pmf(k, n, p, loc)` is identically equivalent to `nbinom.pmf(k - loc, n, p)`.

Examples

```
>>> from scipy.stats import nbinom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> n, p = 0.4, 0.4
>>> mean, var, skew, kurt = nbinom.stats(n, p, moments='mvsk')
```

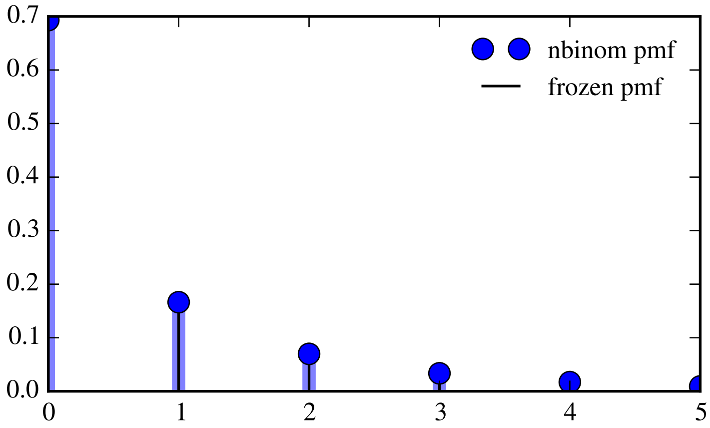
Display the probability mass function (`pmf`):

```
>>> x = np.arange(nbinom.ppf(0.01, n, p),
...               nbinom.ppf(0.99, n, p))
>>> ax.plot(x, nbinom.pmf(x, n, p), 'bo', ms=8, label='nbinom pmf')
>>> ax.vlines(x, 0, nbinom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = nbinom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = nbinom.cdf(x, n, p)
>>> np.allclose(x, nbinom.ppf(prob, n, p))
True
```

Generate random numbers:

```
>>> r = nbinom.rvs(n, p, size=1000)
```

Methods

`rvs(n, p, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, n, p, loc=0)`	Probability mass function.
`logpmf(x, n, p, loc=0)`	Log of the probability mass function.
`cdf(x, n, p, loc=0)`	Cumulative density function.
`logcdf(x, n, p, loc=0)`	Log of the cumulative density function.
`sf(x, n, p, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, n, p, loc=0)`	Log of the survival function.
`ppf(q, n, p, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, n, p, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(n, p, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(n, p, loc=0)`	(Differential) entropy of the RV.
`expect(func, n, p, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(n, p, loc=0)`	Median of the distribution.
`mean(n, p, loc=0)`	Mean of the distribution.
`var(n, p, loc=0)`	Variance of the distribution.
`std(n, p, loc=0)`	Standard deviation of the distribution.
`interval(alpha, n, p, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`planck`** **= <scipy.stats._discrete_distns.planck_gen object at 0x7fa40e995e50>**

A Planck discrete exponential random variable.

As an instance of the `rv_discrete` class, `planck` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `planck` is:

```
planck.pmf(k) = (1-exp(-lambda_))*exp(-lambda_*k)
```

for `k*lambda_ >= 0`.

`planck` takes `lambda_` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `planck.pmf(k, lambda_, loc)` is identically equivalent to `planck.pmf(k - loc, lambda_)`.

Examples

```
>>> from scipy.stats import planck
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> lambda_ = 0.51
>>> mean, var, skew, kurt = planck.stats(lambda_, moments='mvsk')
```

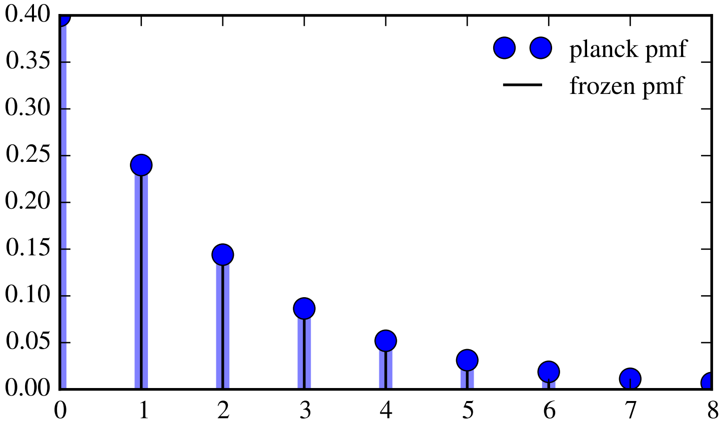
Display the probability mass function (`pmf`):

```
>>> x = np.arange(planck.ppf(0.01, lambda_),
...               planck.ppf(0.99, lambda_))
>>> ax.plot(x, planck.pmf(x, lambda_), 'bo', ms=8, label='planck pmf')
>>> ax.vlines(x, 0, planck.pmf(x, lambda_), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = planck(lambda_)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = planck.cdf(x, lambda_)
>>> np.allclose(x, planck.ppf(prob, lambda_))
True
```

Generate random numbers:

```
>>> r = planck.rvs(lambda_, size=1000)
```

Methods

`rvs(lambda_, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, lambda_, loc=0)`	Probability mass function.
`logpmf(x, lambda_, loc=0)`	Log of the probability mass function.
`cdf(x, lambda_, loc=0)`	Cumulative density function.
`logcdf(x, lambda_, loc=0)`	Log of the cumulative density function.
`sf(x, lambda_, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, lambda_, loc=0)`	Log of the survival function.
`ppf(q, lambda_, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, lambda_, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(lambda_, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(lambda_, loc=0)`	(Differential) entropy of the RV.
`expect(func, lambda_, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(lambda_, loc=0)`	Median of the distribution.
`mean(lambda_, loc=0)`	Mean of the distribution.
`var(lambda_, loc=0)`	Variance of the distribution.
`std(lambda_, loc=0)`	Standard deviation of the distribution.
`interval(alpha, lambda_, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`poisson`** **= <scipy.stats._discrete_distns.poisson_gen object at 0x7fa40e995dd0>**

A Poisson discrete random variable.

As an instance of the `rv_discrete` class, `poisson` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `poisson` is:

```
poisson.pmf(k) = exp(-mu) * mu**k / k!
```

for `k >= 0`.

`poisson` takes `mu` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `poisson.pmf(k, mu, loc)` is identically equivalent to `poisson.pmf(k - loc, mu)`.

Examples

```
>>> from scipy.stats import poisson
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mu = 0.6
>>> mean, var, skew, kurt = poisson.stats(mu, moments='mvsk')
```

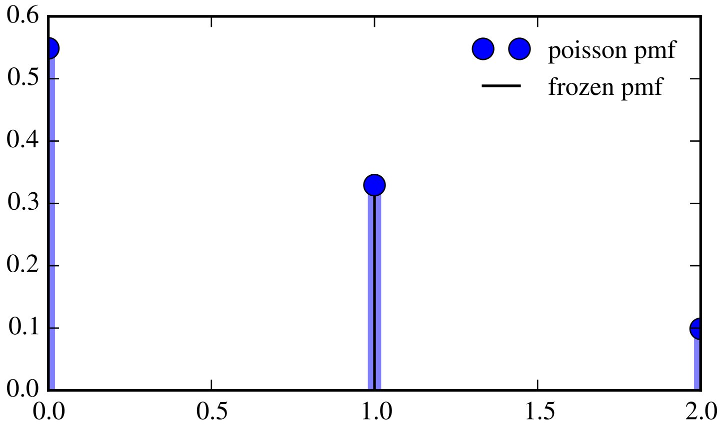
Display the probability mass function (`pmf`):

```
>>> x = np.arange(poisson.ppf(0.01, mu),
...               poisson.ppf(0.99, mu))
>>> ax.plot(x, poisson.pmf(x, mu), 'bo', ms=8, label='poisson pmf')
>>> ax.vlines(x, 0, poisson.pmf(x, mu), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = poisson(mu)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = poisson.cdf(x, mu)
>>> np.allclose(x, poisson.ppf(prob, mu))
True
```

Generate random numbers:

```
>>> r = poisson.rvs(mu, size=1000)
```

Methods

`rvs(mu, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, mu, loc=0)`	Probability mass function.
`logpmf(x, mu, loc=0)`	Log of the probability mass function.
`cdf(x, mu, loc=0)`	Cumulative density function.
`logcdf(x, mu, loc=0)`	Log of the cumulative density function.
`sf(x, mu, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, mu, loc=0)`	Log of the survival function.
`ppf(q, mu, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, mu, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(mu, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(mu, loc=0)`	(Differential) entropy of the RV.
`expect(func, mu, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(mu, loc=0)`	Median of the distribution.
`mean(mu, loc=0)`	Mean of the distribution.
`var(mu, loc=0)`	Variance of the distribution.
`std(mu, loc=0)`	Standard deviation of the distribution.
`interval(alpha, mu, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`randint`** **= <scipy.stats._discrete_distns.randint_gen object at 0x7fa40e923190>**

A uniform discrete random variable.

As an instance of the `rv_discrete` class, `randint` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `randint` is:

```
randint.pmf(k) = 1./(high - low)
```

for `k = low, ..., high - 1`.

`randint` takes `low` and `high` as shape parameters.

Note the difference to the numpy `random_integers` which returns integers on a *closed* interval `[low, high]`.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `randint.pmf(k, low, high, loc)` is identically equivalent to `randint.pmf(k - loc, low, high)`.

Examples

```
>>> from scipy.stats import randint
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> low, high = 7, 31
>>> mean, var, skew, kurt = randint.stats(low, high, moments='mvsk')
```

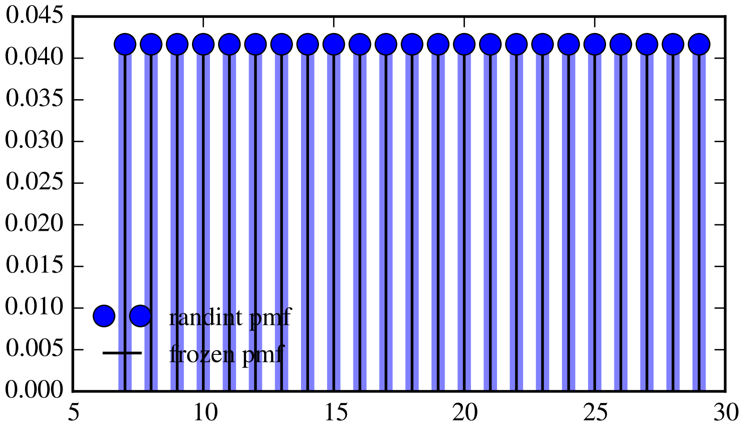
Display the probability mass function (`pmf`):

```
>>> x = np.arange(randint.ppf(0.01, low, high),
...               randint.ppf(0.99, low, high))
>>> ax.plot(x, randint.pmf(x, low, high), 'bo', ms=8, label='randint pmf')
>>> ax.vlines(x, 0, randint.pmf(x, low, high), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = randint(low, high)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = randint.cdf(x, low, high)
>>> np.allclose(x, randint.ppf(prob, low, high))
True
```

Generate random numbers:

```
>>> r = randint.rvs(low, high, size=1000)
```

Methods

`rvs(low, high, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, low, high, loc=0)`	Probability mass function.
`logpmf(x, low, high, loc=0)`	Log of the probability mass function.
`cdf(x, low, high, loc=0)`	Cumulative density function.
`logcdf(x, low, high, loc=0)`	Log of the cumulative density function.
`sf(x, low, high, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, low, high, loc=0)`	Log of the survival function.
`ppf(q, low, high, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, low, high, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(low, high, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(low, high, loc=0)`	(Differential) entropy of the RV.
`expect(func, low, high, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(low, high, loc=0)`	Median of the distribution.
`mean(low, high, loc=0)`	Mean of the distribution.
`var(low, high, loc=0)`	Variance of the distribution.
`std(low, high, loc=0)`	Standard deviation of the distribution.
`interval(alpha, low, high, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`skellam`** **= <scipy.stats._discrete_distns.skellam_gen object at 0x7fa40e9237d0>**

A Skellam discrete random variable.

As an instance of the `rv_discrete` class, `skellam` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

Probability distribution of the difference of two correlated or uncorrelated Poisson random variables.

Let k1 and k2 be two Poisson-distributed r.v. with expected values lam1 and lam2. Then, `k1 - k2` follows a Skellam distribution with parameters `mu1 = lam1 - rho*sqrt(lam1*lam2)` and `mu2 = lam2 - rho*sqrt(lam1*lam2)`, where rho is the correlation coefficient between k1 and k2. If the two Poisson-distributed r.v. are independent then `rho = 0`.

Parameters mu1 and mu2 must be strictly positive.

For details see: http://en.wikipedia.org/wiki/Skellam_distribution

`skellam` takes `mu1` and `mu2` as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `skellam.pmf(k, mu1, mu2, loc)` is identically equivalent to `skellam.pmf(k - loc, mu1, mu2)`.

Examples

```
>>> from scipy.stats import skellam
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> mu1, mu2 = 15, 8
>>> mean, var, skew, kurt = skellam.stats(mu1, mu2, moments='mvsk')
```

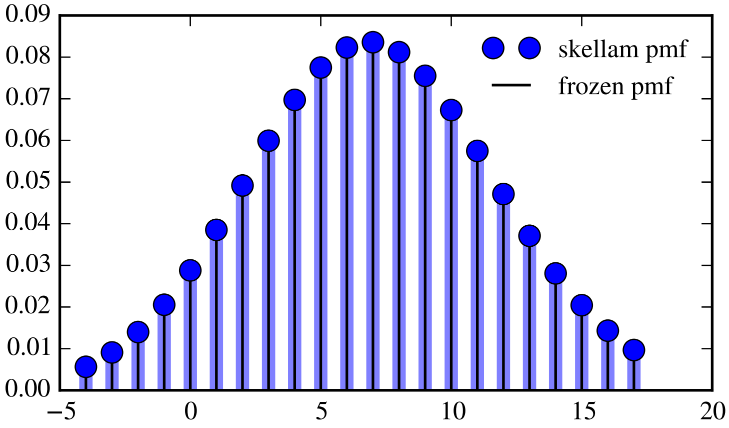
Display the probability mass function (`pmf`):

```
>>> x = np.arange(skellam.ppf(0.01, mu1, mu2),
...               skellam.ppf(0.99, mu1, mu2))
>>> ax.plot(x, skellam.pmf(x, mu1, mu2), 'bo', ms=8, label='skellam pmf')
>>> ax.vlines(x, 0, skellam.pmf(x, mu1, mu2), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = skellam(mu1, mu2)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = skellam.cdf(x, mu1, mu2)
>>> np.allclose(x, skellam.ppf(prob, mu1, mu2))
True
```

Generate random numbers:

```
>>> r = skellam.rvs(mu1, mu2, size=1000)
```

Methods

`rvs(mu1, mu2, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, mu1, mu2, loc=0)`	Probability mass function.
`logpmf(x, mu1, mu2, loc=0)`	Log of the probability mass function.
`cdf(x, mu1, mu2, loc=0)`	Cumulative density function.
`logcdf(x, mu1, mu2, loc=0)`	Log of the cumulative density function.
`sf(x, mu1, mu2, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, mu1, mu2, loc=0)`	Log of the survival function.
`ppf(q, mu1, mu2, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, mu1, mu2, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(mu1, mu2, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(mu1, mu2, loc=0)`	(Differential) entropy of the RV.
`expect(func, mu1, mu2, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(mu1, mu2, loc=0)`	Median of the distribution.
`mean(mu1, mu2, loc=0)`	Mean of the distribution.
`var(mu1, mu2, loc=0)`	Variance of the distribution.
`std(mu1, mu2, loc=0)`	Standard deviation of the distribution.
`interval(alpha, mu1, mu2, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

`scipy.stats.`**`zipf`** **= <scipy.stats._discrete_distns.zipf_gen object at 0x7fa40e923550>**

A Zipf discrete random variable.

As an instance of the `rv_discrete` class, `zipf` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for `zipf` is:

```
zipf.pmf(k, a) = 1/(zeta(a) * k**a)
```

for `k >= 1`.

`zipf` takes `a` as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `zipf.pmf(k, a, loc)` is identically equivalent to `zipf.pmf(k - loc, a)`.

Examples

```
>>> from scipy.stats import zipf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```
>>> a = 6.5
>>> mean, var, skew, kurt = zipf.stats(a, moments='mvsk')
```

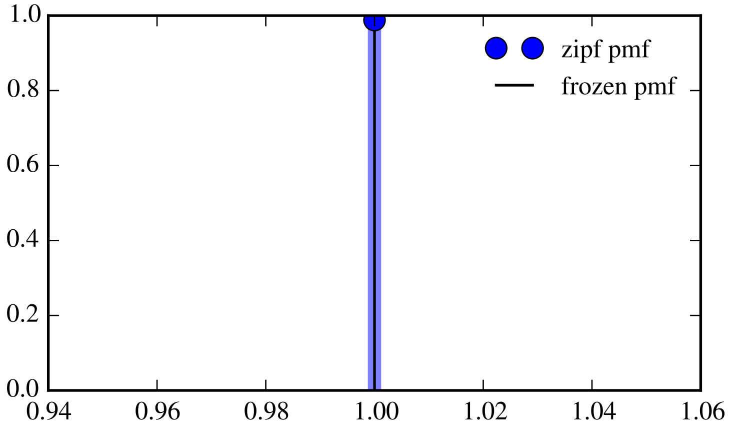
Display the probability mass function (`pmf`):

```
>>> x = np.arange(zipf.ppf(0.01, a),
...               zipf.ppf(0.99, a))
>>> ax.plot(x, zipf.pmf(x, a), 'bo', ms=8, label='zipf pmf')
>>> ax.vlines(x, 0, zipf.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = zipf(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = zipf.cdf(x, a)
>>> np.allclose(x, zipf.ppf(prob, a))
True
```

Generate random numbers:

```
>>> r = zipf.rvs(a, size=1000)
```

Methods

`rvs(a, loc=0, size=1, random_state=None)`	Random variates.
`pmf(x, a, loc=0)`	Probability mass function.
`logpmf(x, a, loc=0)`	Log of the probability mass function.
`cdf(x, a, loc=0)`	Cumulative density function.
`logcdf(x, a, loc=0)`	Log of the cumulative density function.
`sf(x, a, loc=0)`	Survival function (`1 - cdf` — sometimes more accurate).
`logsf(x, a, loc=0)`	Log of the survival function.
`ppf(q, a, loc=0)`	Percent point function (inverse of `cdf` — percentiles).
`isf(q, a, loc=0)`	Inverse survival function (inverse of `sf`).
`stats(a, loc=0, moments='mv')`	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
`entropy(a, loc=0)`	(Differential) entropy of the RV.
`expect(func, a, loc=0, lb=None, ub=None, conditional=False)`	Expected value of a function (of one argument) with respect to the distribution.
`median(a, loc=0)`	Median of the distribution.
`mean(a, loc=0)`	Mean of the distribution.
`var(a, loc=0)`	Variance of the distribution.
`std(a, loc=0)`	Standard deviation of the distribution.
`interval(alpha, a, loc=0)`	Endpoints of the range that contains alpha percent of the distribution

5.34.4 Statistical functions

Several of these functions have a similar version in scipy.stats.mstats which work for masked arrays.

`describe`(a[, axis, ddof])	Computes several descriptive statistics of the passed array.
`gmean`(a[, axis, dtype])	Compute the geometric mean along the specified axis.
`hmean`(a[, axis, dtype])	Calculates the harmonic mean along the specified axis.
`kurtosis`(a[, axis, fisher, bias])	Computes the kurtosis (Fisher or Pearson) of a dataset.
`kurtosistest`(a[, axis])	Tests whether a dataset has normal kurtosis
`mode`(a[, axis])	Returns an array of the modal (most common) value in the passed array.
`moment`(a[, moment, axis])	Calculates the nth moment about the mean for a sample.
`normaltest`(a[, axis])	Tests whether a sample differs from a normal distribution.
`skew`(a[, axis, bias])	Computes the skewness of a data set.
`skewtest`(a[, axis])	Tests whether the skew is different from the normal distribution.
`kstat`(data[, n])	Return the nth k-statistic (1<=n<=4 so far).
`kstatvar`(data[, n])	Returns an unbiased estimator of the variance of the k-statistic.
`tmean`(a[, limits, inclusive])	Compute the trimmed mean.
`tvar`(a[, limits, inclusive])	Compute the trimmed variance
`tmin`(a[, lowerlimit, axis, inclusive])	Compute the trimmed minimum
`tmax`(a[, upperlimit, axis, inclusive])	Compute the trimmed maximum
`tstd`(a[, limits, inclusive])	Compute the trimmed sample standard deviation
`tsem`(a[, limits, inclusive])	Compute the trimmed standard error of the mean.
`nanmean`(*args, **kwds)	`nanmean` is deprecated!
`nanstd`(*args, **kwds)	`nanstd` is deprecated!
`nanmedian`(*args, **kwds)	`nanmedian` is deprecated!

Continued on next page

Table 5.255 – continued from previous page

`variation`(a[, axis])	Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

`scipy.stats.`**`describe`**(*a*, *axis=0*, *ddof=1*)

Computes several descriptive statistics of the passed array.

Parameters

a : array_like

Input data.

axis : int or None, optional

Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

ddof : int, optional

Delta degrees of freedom. Default is 1.

Returns

nobs : int

Number of observations (length of data along *axis*).

minmax: tuple of ndarrays or floats

Minimum and maximum value of data array.

mean : ndarray or float

Arithmetic mean of data along axis.

variance : ndarray or float

Unbiased variance of the data along axis, denominator is number of observations minus one.

skewness : ndarray or float

Biased skewness, based on moment calculations with denominator equal to the number of observations, i.e. no degrees of freedom correction.

kurtosis : ndarray or float

Biased kurtosis (Fisher). The kurtosis is normalized so that it is zero for the normal distribution. No degrees of freedom or bias correction is used.

See also:

`skew`, `kurtosis`

`scipy.stats.`**`gmean`**(*a*, *axis=0*, *dtype=None*)

Compute the geometric mean along the specified axis.

Returns the geometric average of the array elements. That is: n-th root of (x1 * x2 * ... * xn)

Parameters

a : array_like

Input array or object that can be converted to an array.

axis : int or None, optional

Axis along which the geometric mean is computed. Default is 0. If None, compute over the whole array *a*.

dtype : dtype, optional

Type of the returned array and of the accumulator in which the elements are summed. If dtype is not specified, it defaults to the dtype of a, unless a has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

gmean : ndarray

see dtype parameter above

See also:

`numpy.mean`	Arithmetic average
`numpy.average`	Weighted average
`hmean`	Harmonic mean

Notes

The geometric average is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity because masked arrays automatically mask any non-finite values.

`scipy.stats.`**`hmean`**(*a*, *axis=0*, *dtype=None*)

Calculates the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + ... + 1/xn)

Parameters **a** : array_like

Input array, masked array or object that can be converted to an array.

axis : int or None, optional

Axis along which the harmonic mean is computed. Default is 0. If None, compute over the whole array *a*.

dtype : dtype, optional

Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer *dtype* with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns **hmean** : ndarray

see *dtype* parameter above

See also:

`numpy.mean`	Arithmetic average
`numpy.average`	Weighted average
`gmean`	Geometric mean

Notes

The harmonic mean is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity.

`scipy.stats.`**`kurtosis`**(*a*, *axis=0*, *fisher=True*, *bias=True*)

Computes the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use `kurtosistest` to see if result is close enough to normal.

Parameters **a** : array

data for which the kurtosis is calculated

axis : int or None, optional

Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.

fisher : bool, optional

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias : bool, optional

If False, then the calculations are corrected for statistical bias.

Returns **kurtosis** : array

The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[R329]

`scipy.stats.`**`kurtosistest`**(*a*, *axis=0*)

Tests whether a dataset has normal kurtosis

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: `kurtosis = 3(n-1)/(n+1)`.

Parameters **a** : array

array of the sample data

axis : int or None, optional

Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns **statistic** : float

The computed z-score for this test.

pvalue : float

The 2-sided p-value for the hypothesis test

Notes

Valid only for n>20. The Z-score is set to 0 for bad entries.

`scipy.stats.`**`mode`**(*a*, *axis=0*)

Returns an array of the modal (most common) value in the passed array.

If there is more than one such value, only the first is returned. The bin-count for the modal bins is also returned.

Parameters **a** : array_like

n-dimensional array of which to find mode(s).

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

Returns **mode** : ndarray

Array of modal values.

count : ndarray

Array of counts for each mode.

Examples

```
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 7],
...               [8, 1, 8, 4],
...               [5, 3, 0, 5],
...               [4, 7, 5, 9]])
>>> from scipy import stats
>>> stats.mode(a)
(array([[3, 1, 0, 0]]), array([[1, 1, 1, 1]]))
```

To get mode of whole array, specify `axis=None`:

```
>>> stats.mode(a, axis=None)
(array([3]), array([3]))
```

`scipy.stats.`**`moment`**(*a*, *moment=1*, *axis=0*)

Calculates the nth moment about the mean for a sample.

Generally used to calculate coefficients of skewness and kurtosis.

Parameters

a : array_like

data

moment : int, optional

order of central moment that is returned

axis : int or None, optional

Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

Returns

n-th central moment : ndarray or float

The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

`scipy.stats.`**`normaltest`**(*a*, *axis=0*)

Tests whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's [R351], [R352] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters

a : array_like

The array containing the data to be tested.

axis : int or None, optional

Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns

statistic : float or array

s^2 + *k*^2, where `s` is the z-score returned by `skewtest` and *k* is the z-score returned by `kurtosistest`.

pvalue : float or array

A 2-sided chi squared probability for the hypothesis test.

References

[R351], [R352]

`scipy.stats.`**`skew`**(*a*, *axis=0*, *bias=True*)

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left tail of the distribution. The function `skewtest` can be used to determine if the skewness value is close enough to 0, statistically speaking.

Parameters

a : ndarray

data

axis : int or None, optional

Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.

bias : bool, optional

If False, then the calculations are corrected for statistical bias.

Returns

skewness : ndarray

The skewness of values along an axis, returning 0 where all values are equal.

References

[R362]

`scipy.stats.`**`skewtest`**(*a*, *axis=0*)

Tests whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters	**a** : array The data to be tested **axis** : int or None, optional Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.
Returns	**statistic** : float The computed z-score for this test. **pvalue** : float a 2-sided p-value for the hypothesis test

Notes

The sample size must be at least 8.

`scipy.stats.`**`kstat`**`(`*data*, *n=2*`)`

Return the nth k-statistic (1<=n<=4 so far).

The nth k-statistic is the unique symmetric unbiased estimator of the nth cumulant kappa_n.

Parameters	**data** : array_like Input array. **n** : int, {1, 2, 3, 4}, optional Default is equal to 2.
Returns	**kstat** : float The nth k-statistic.

See also:

`kstatvar` Returns an unbiased estimator of the variance of the k-statistic.

Notes

The cumulants are related to central moments but are specifically defined using a power series expansion of the logarithm of the characteristic function (which is the Fourier transform of the PDF). In particular let phi(t) be the characteristic function, then:

```
ln phi(t) = > kappa_n (it)^n / n!    (sum from n=0 to inf)
```

The first few cumulants (kappa_n) in terms of central moments (mu_n) are:

```
kappa_1 = mu_1
kappa_2 = mu_2
kappa_3 = mu_3
kappa_4 = mu_4 - 3*mu_2**2
kappa_5 = mu_5 - 10*mu_2 * mu_3
```

References

http://mathworld.wolfram.com/k-Statistic.html

http://mathworld.wolfram.com/Cumulant.html

`scipy.stats.`**`kstatvar`**`(`*data*, *n=2*`)`

Returns an unbiased estimator of the variance of the k-statistic.

See `kstat` for more details of the k-statistic.

Parameters	**data** : array_like Input array.

n : int, {1, 2}, optional

Default is equal to 2.

Returns **kstatvar** : float

The nth k-statistic variance.

See also:

`kstat`

`scipy.stats.`**`tmean`**`(`*a*, *limits=None*, *inclusive=(True*, *True)*`)`

Compute the trimmed mean.

This function finds the arithmetic mean of given values, ignoring values outside the given *limits*.

Parameters **a** : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tmean** : float

`scipy.stats.`**`tvar`**`(`*a*, *limits=None*, *inclusive=(True*, *True)*`)`

Compute the trimmed variance

This function computes the sample variance of an array of values, while ignoring values which are outside of given *limits*.

Parameters **a** : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tvar** : float

Trimmed variance.

Notes

`tvar` computes the unbiased sample variance, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.`**`tmin`**`(`*a*, *lowerlimit=None*, *axis=0*, *inclusive=True*`)`

Compute the trimmed minimum

This function finds the miminum value of an array *a* along the specified axis, but only considering values greater than a specified lower limit.

Parameters **a** : array_like

array of values

lowerlimit : None or float, optional

Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the lower limit are included. The default value is True.

Returns **tmin** : float

`scipy.stats.`**`tmax`**`(`*a*, *upperlimit=None*, *axis=0*, *inclusive=True*`)`

Compute the trimmed maximum

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters **a** : array_like

array of values

upperlimit : None or float, optional

Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the upper limit are included. The default value is True.

Returns **tmax** : float

`scipy.stats.`**`tstd`**`(`*a*, *limits=None*, *inclusive=(True, True)*`)`

Compute the trimmed sample standard deviation

This function finds the sample standard deviation of given values, ignoring values outside the given *limits*.

Parameters **a** : array_like

array of values

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tstd** : float

Notes

`tstd` computes the unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.`**`tsem`**`(`*a*, *limits=None*, *inclusive=(True, True)*`)`

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given *limits*.

Parameters **a** : array_like

array of values

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tsem** : float

Notes

`tsem` uses unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.`**`nanmean`**`(`**args*, ***kwds*`)`

`nanmean` is deprecated! scipy.stats.nanmean is deprecated in scipy 0.15.0 in favour of numpy.nanmean.

Compute the mean over the given axis ignoring nans.

Parameters **x** : ndarray

Input array.

axis [int or None, optional] Axis along which the mean is computed. Default is 0. If None, compute over the whole array *x*.

Returns **m** : float

The mean of *x*, ignoring nans.

Examples

```
>>> from scipy import stats
>>> a = np.linspace(0, 4, 3)
>>> a
array([ 0.,  2.,  4.])
>>> a[-1] = np.nan
>>> stats.nanmean(a)
1.0
```

`scipy.stats.`**`nanstd`**`(`**args*, ***kwds*`)`

`nanstd` is deprecated! scipy.stats.nanstd is deprecated in scipy 0.15 in favour of numpy.nanstd. Note that numpy.nanstd has a different signature.

Compute the standard deviation over the given axis, ignoring nans.

Parameters **x** : array_like

Input array.

axis [int or None, optional] Axis along which the standard deviation is computed. Default is 0. If None, compute over the whole array *x*.

bias [bool, optional] If True, the biased (normalized by N) definition is used. If False (default), the unbiased definition is used.

Returns **s** : float

The standard deviation.

Examples

```
>>> from scipy import stats
>>> a = np.arange(10, dtype=float)
>>> a[1:3] = np.nan
>>> np.std(a)
nan
>>> stats.nanstd(a)
2.9154759474226504
>>> stats.nanstd(a.reshape(2, 5), axis=1)
array([ 2.0817,  1.5811])
>>> stats.nanstd(a.reshape(2, 5), axis=None)
2.9154759474226504
```

`scipy.stats.`**`nanmedian`**`(`**args*, ***kwds*`)`

`nanmedian` is deprecated! scipy.stats.nanmedian is deprecated in scipy 0.15 in favour of numpy.nanmedian.

Compute the median along the given axis ignoring nan values.

Parameters **x** : array_like

Input array.

axis [int or None, optional] Axis along which the median is computed. Default is 0. If None, compute over the whole array *x*.

Returns **m** : float

The median of *x* along *axis*.

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 3, 1, 5, 5, np.nan])
>>> stats.nanmedian(a)
array(3.0)
```

```
>>> b = np.array([0, 3, 1, 5, 5, np.nan, 5])
>>> stats.nanmedian(b)
array(4.0)
```

Example with axis:

```
>>> c = np.arange(30.).reshape(5,6)
>>> idx = np.array([False, False, False, True, False] * 6).reshape(5,6)
>>> c[idx] = np.nan
>>> c
array([[  0.,   1.,   2.,  nan,   4.,   5.],
       [  6.,   7.,  nan,   9.,  10.,  11.],
       [ 12.,  nan,  14.,  15.,  16.,  17.],
       [ nan,  19.,  20.,  21.,  22.,  nan],
       [ 24.,  25.,  26.,  27.,  nan,  29.]])
>>> stats.nanmedian(c, axis=1)
array([  2. ,   9. ,  15. ,  20.5,  26. ])
```

`scipy.stats.`**`variation`**`(`*a*, *axis=0*`)`

Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters **a** : array_like

Input array.

axis : int or None, optional

Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array *a*.

References

[R372]

`cumfreq`(a[, numbins, defaultreallimits, weights])	Returns a cumulative frequency histogram, using the histogram function.
`histogram2`(*args, **kwds)	`histogram2` is deprecated!
`histogram`(a[, numbins, defaultlimits, ...])	Separates the range into several bins and returns the number of instances in eacl
`itemfreq`(a)	Returns a 2-D array of item frequencies.
`percentileofscore`(a, score[, kind])	The percentile rank of a score relative to a list of scores.
`scoreatpercentile`(a, per[, limit, ...])	Calculate the score at a given percentile of the input sequence.
`relfreq`(a[, numbins, defaultreallimits, weights])	Returns a relative frequency histogram, using the histogram function.

`scipy.stats.`**`cumfreq`**`(`*a*, *numbins=10*, *defaultreallimits=None*, *weights=None*`)`

Returns a cumulative frequency histogram, using the histogram function.

Parameters

a : array_like

Input array.

numbins : int, optional

The number of bins to use for the histogram. Default is 10.

defaultreallimits : tuple (lower, upper), optional

The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in *a* is used. Specifically `(a.min() - s, a.max() + s)`, where `s = (1/2)(a.max() - a.min()) / (numbins - 1)`.

weights : array_like, optional

The weights for each value in *a*. Default is None, which gives each value a weight of 1.0

Returns

cumcount : ndarray

Binned values of cumulative frequency.

lowerlimit : float

Lower real limit

binsize : float

Width of each bin.

extrapoints : int

Extra points.

Examples

```
>>> from scipy import stats
>>> x = [1, 4, 2, 1, 3, 1]
>>> cumfreqs, lowlim, binsize, extrapoints = stats.cumfreq(x, numbins=4)
>>> cumfreqs
array([ 3.,  4.,  5.,  6.])
>>> cumfreqs, lowlim, binsize, extrapoints =     ...     stats.cumfreq(x, numbins=4, defaultreal
>>> cumfreqs
array([ 1.,  2.,  3.,  3.])
>>> extrapoints
3
```

`scipy.stats.`**`histogram2`**`(`**args*, ***kwds*`)`

`histogram2` is deprecated! scipy.stats.histogram2 is deprecated in scipy 0.16.0; use np.histogram2d instead

Compute histogram using divisions in bins.

Count the number of times values from array *a* fall into numerical ranges defined by *bins*. Range x is given by bins[x] <= range_x < bins[x+1] where x =0,N and N is the length of the *bins* array. The last range is given by bins[N] <= range_N < infinity. Values less than bins[0] are not included in the histogram.

Parameters **a** : array_like of rank 1

The array of values to be assigned into bins

bins [array_like of rank 1] Defines the ranges of values to use during histogramming.

Returns **histogram2** : ndarray of rank 1

Each value represents the occurrences for a given bin (range) of values.

`scipy.stats.`**`histogram`**`(`*a*, *numbins=10*, *defaultlimits=None*, *weights=None*, *printextras=False*`)`

Separates the range into several bins and returns the number of instances in each bin.

Parameters **a** : array_like

Array of scores which will be put into bins.

numbins : int, optional

The number of bins to use for the histogram. Default is 10.

defaultlimits : tuple (lower, upper), optional

The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in a is used. Specifically `(a.min() - s, a.max() + s)`, where `s = (1/2)(a.max() - a.min()) / (numbins - 1)`.

weights : array_like, optional

The weights for each value in *a*. Default is None, which gives each value a weight of 1.0

printextras : bool, optional

If True, if there are extra points (i.e. the points that fall outside the bin limits) a warning is raised saying how many of those points there are. Default is False.

Returns **count** : ndarray

Number of points (or sum of weights) in each bin.

lowerlimit : float

Lowest value of histogram, the lower limit of the first bin.

binsize : float

The size of the bins (all bins have the same size).

extrapoints : int

The number of points outside the range of the histogram.

See also:

`numpy.histogram`

Notes

This histogram is based on numpy's histogram but has a larger range by default if default limits is not set.

`scipy.stats.`**`itemfreq`**`(`*a*`)`

Returns a 2-D array of item frequencies.

Parameters **a** : (N,) array_like

Input array.

Returns **itemfreq** : (K, 2) ndarray

A 2-D frequency table. Column 1 contains sorted, unique values from *a*, column 2 contains their respective counts.

Examples

```
>>> from scipy import stats
>>> a = np.array([1, 1, 5, 0, 1, 2, 2, 0, 1, 4])
>>> stats.itemfreq(a)
array([[ 0.,  2.],
       [ 1.,  4.],
       [ 2.,  2.],
       [ 4.,  1.],
       [ 5.,  1.]])
>>> np.bincount(a)
array([2, 4, 2, 0, 1, 1])
```

```
>>> stats.itemfreq(a/10.)
array([[ 0. ,  2. ],
       [ 0.1,  4. ],
       [ 0.2,  2. ],
       [ 0.4,  1. ],
       [ 0.5,  1. ]])
```

`scipy.stats.`**`percentileofscore`**(*a*, *score*, *kind='rank'*)

The percentile rank of a score relative to a list of scores.

A `percentileofscore` of, for example, 80% means that 80% of the scores in *a* are below the given score. In the case of gaps or ties, the exact definition depends on the optional keyword, *kind*.

Parameters **a** : array_like

Array of scores to which *score* is compared.

score : int or float

Score that is compared to the elements in *a*.

kind : {'rank', 'weak', 'strict', 'mean'}, optional

This optional parameter specifies the interpretation of the resulting score:

- ***"rank": Average percentage ranking of score. In case of*** multiple matches, average the percentage rankings of all matching scores.
- ***"weak": This kind corresponds to the definition of a cumulative*** distribution function. A percentileofscore of 80% means that 80% of values are less than or equal to the provided score.
- ***"strict": Similar to "weak", except that only values that are*** strictly less than the given score are counted.
- ***"mean": The average of the "weak" and "strict" scores, often used in*** testing. See http://en.wikipedia.org/wiki/Percentile_rank

Returns **pcos** : float

Percentile-position of score (0-100) relative to *a*.

See also:

`numpy.percentile`

Examples

Three-quarters of the given values lie below a given score:

```
>>> from scipy import stats
>>> stats.percentileofscore([1, 2, 3, 4], 3)
75.0
```

With multiple matches, note how the scores of the two matches, 0.6 and 0.8 respectively, are averaged:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3)
70.0
```

Only 2/5 values are strictly less than 3:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0
```

But 4/5 values are less than or equal to 3:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0
```

The average between the weak and the strict scores is

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0
```

`scipy.stats.`**`scoreatpercentile`**(*a*, *per*, *limit=()*, *interpolation_method='fraction'*, *axis=None*)

Calculate the score at a given percentile of the input sequence.

For example, the score at *per=50* is the median. If the desired quantile lies between two data points, we interpolate between them, according to the value of *interpolation*. If the parameter *limit* is provided, it should be a tuple (lower, upper) of two values.

Parameters

a : array_like

A 1-D array of values from which to extract score.

per : array_like

Percentile(s) at which to extract score. Values should be in range [0,100].

limit : tuple, optional

Tuple of two scalars, the lower and upper limits within which to compute the percentile. Values of *a* outside this (closed) interval will be ignored.

interpolation_method : {'fraction', 'lower', 'higher'}, optional

This optional parameter specifies the interpolation method to use, when the desired quantile lies between two data points *i* and *j*

- fraction: `i + (j - i) * fraction` where `fraction` is the fractional part of the index surrounded by `i` and `j`.
- lower: `i`.
- higher: `j`.

axis : int, optional

Axis along which the percentiles are computed. Default is None. If None, compute over the whole array *a*.

Returns

score : float or ndarray

Score at percentile(s).

See also:

`percentileofscore`, `numpy.percentile`

Notes

This function will become obsolete in the future. For Numpy 1.9 and higher, `numpy.percentile` provides all the functionality that `scoreatpercentile` provides. And it's significantly faster. Therefore it's recommended to use `numpy.percentile` for users that have numpy >= 1.9.

Examples

```
>>> from scipy import stats
>>> a = np.arange(100)
>>> stats.scoreatpercentile(a, 50)
49.5
```

`scipy.stats.`**`relfreq`**(*a*, *numbins=10*, *defaultreallimits=None*, *weights=None*)

Returns a relative frequency histogram, using the histogram function.

Parameters

a : array_like

Input array.

numbins : int, optional

The number of bins to use for the histogram. Default is 10.

defaultreallimits : tuple (lower, upper), optional

The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in a is used. Specifically `(a.min() - s, a.max() + s)`, where `s = (1/2)(a.max() - a.min()) / (numbins - 1)`.

weights : array_like, optional

The weights for each value in *a*. Default is None, which gives each value a weight of 1.0

Returns

frequency : ndarray

Binned values of relative frequency.

lowerlimit : float

Lower real limit

binsize : float

Width of each bin.

extrapoints : int

Extra points.

Examples

```
>>> from scipy import stats
>>> a = np.array([1, 4, 2, 1, 3, 1])
>>> relfreqs, lowlim, binsize, extrapoints = stats.relfreq(a, numbins=4)
>>> relfreqs
array([ 0.5       ,  0.16666667,  0.16666667,  0.16666667])
>>> np.sum(relfreqs)  # relative frequencies should add up to 1
0.99999999999999989
```

`binned_statistic`(x, values[, statistic, ...])	Compute a binned statistic for a set of data.
`binned_statistic_2d`(x, y, values[, ...])	Compute a bidimensional binned statistic for a set of data.
`binned_statistic_dd`(sample, values[, ...])	Compute a multidimensional binned statistic for a set of data.

`scipy.stats.`**`binned_statistic`**(*x*, *values*, *statistic='mean'*, *bins=10*, *range=None*)

Compute a binned statistic for a set of data.

This is a generalization of a histogram function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values within each bin.

Parameters

x : array_like

A sequence of values to be binned.

values : array_like

The values on which the statistic will be computed. This must be the same shape as *x*.

statistic : string or callable, optional

The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins : int or sequence of scalars, optional

If *bins* is an int, it defines the number of equal-width bins in the given range (10 by default). If *bins* is a sequence, it defines the bin edges, including the rightmost edge, allowing for non-uniform bin widths. Values in *x* that are smaller than lowest bin edge are assigned to bin number 0, values beyond the highest bin are assigned to `bins[-1]`.

range : (float, float) or [(float, float)], optional

The lower and upper range of the bins. If not provided, range is simply `(x.min(), x.max())`. Values outside the range are ignored.

Returns

statistic : array

The values of the selected statistic in each bin.

bin_edges : array of dtype float

Return the bin edges `(length(statistic)+1)`.

binnumber : 1-D ndarray of ints

This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as values.

See also:

`numpy.histogram`, `binned_statistic_2d`, `binned_statistic_dd`

Notes

All but the last (righthand-most) bin is half-open. In other words, if *bins* is `[1, 2, 3, 4]`, then the first bin is `[1, 2)` (including 1, but excluding 2) and the second `[2, 3)`. The last bin, however, is `[3, 4]`, which *includes* 4.

New in version 0.11.0.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

First a basic example:

```
>>> stats.binned_statistic([1, 2, 1, 2, 4], np.arange(5), statistic='mean',
...                        bins=3)
(array([ 1.,  2.,  4.]), array([ 1.,  2.,  3.,  4.]), array([1, 2, 1, 2, 3]))
```

As a second example, we now generate some random data of sailing boat speed as a function of wind speed, and then determine how fast our boat is for certain wind speeds:

```
>>> windspeed = 8 * np.random.rand(500)
>>> boatspeed = .3 * windspeed**.5 + .2 * np.random.rand(500)
>>> bin_means, bin_edges, binnumber = stats.binned_statistic(windspeed,
...                 boatspeed, statistic='median', bins=[1,2,3,4,5,6,7])
>>> plt.figure()
>>> plt.plot(windspeed, boatspeed, 'b.', label='raw data')
>>> plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=5,
...            label='binned statistic of data')
>>> plt.legend()
```

Now we can use `binnumber` to select all datapoints with a windspeed below 1:

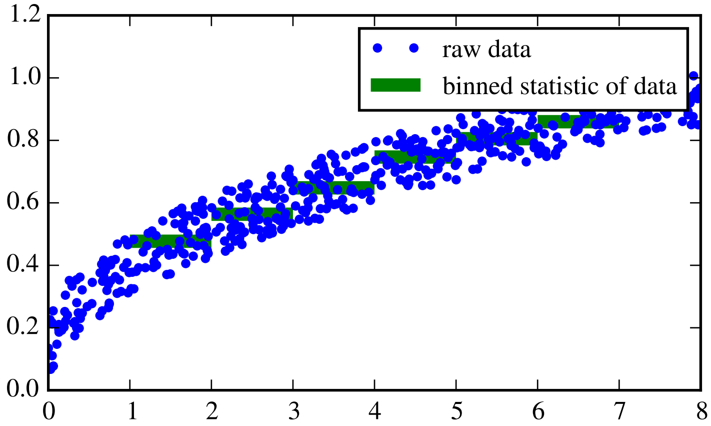
```
>>> low_boatspeed = boatspeed[binnumber == 0]
```

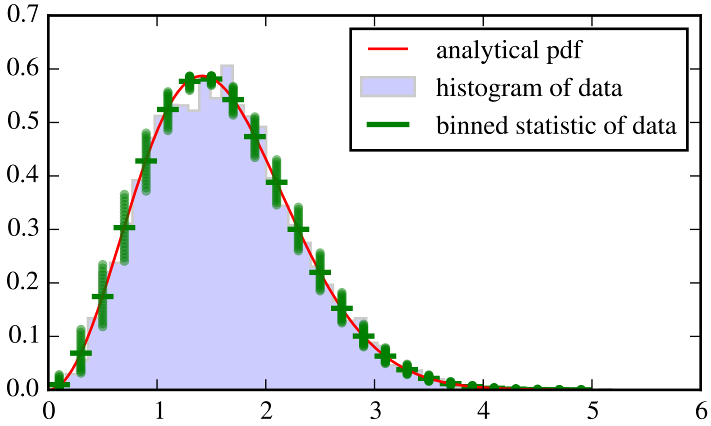
As a final example, we will use `bin_edges` and `binnumber` to make a plot of a distribution that shows the mean and distribution around that mean per bin, on top of a regular histogram and the probability distribution function:

```
>>> x = np.linspace(0, 5, num=500)
>>> x_pdf = stats.maxwell.pdf(x)
>>> samples = stats.maxwell.rvs(size=10000)
```

```
>>> bin_means, bin_edges, binnumber = stats.binned_statistic(x, x_pdf,
...         statistic='mean', bins=25)
>>> bin_width = (bin_edges[1] - bin_edges[0])
>>> bin_centers = bin_edges[1:] - bin_width/2
```

```
>>> plt.figure()
>>> plt.hist(samples, bins=50, normed=True, histtype='stepfilled', alpha=0.2,
...          label='histogram of data')
>>> plt.plot(x, x_pdf, 'r-', label='analytical pdf')
>>> plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=2,
...            label='binned statistic of data')
>>> plt.plot((binnumber - 0.5) * bin_width, x_pdf, 'g.', alpha=0.5)
>>> plt.legend(fontsize=10)
>>> plt.show()
```





`scipy.stats.`**`binned_statistic_2d`**(*x*, *y*, *values*, *statistic='mean'*, *bins=10*, *range=None*)

Compute a bidimensional binned statistic for a set of data.

This is a generalization of a histogram2d function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values within each bin.

Parameters

x : (N,) array_like

A sequence of values to be binned along the first dimension.

y : (M,) array_like

A sequence of values to be binned along the second dimension.

values : (N,) array_like

The values on which the statistic will be computed. This must be the same shape as *x*.

statistic : string or callable, optional

The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins : int or [int, int] or array_like or [array, array], optional

The bin specification:

- the number of bins for the two dimensions (nx=ny=bins),
- the number of bins in each dimension (nx, ny = bins),
- the bin edges for the two dimensions (x_edges = y_edges = bins),
- the bin edges in each dimension (x_edges, y_edges = bins).

range : (2,2) array_like, optional

The leftmost and rightmost edges of the bins along each dimension (if not specified explicitly in the *bins* parameters): [[xmin, xmax], [ymin, ymax]]. All values outside of this range will be considered outliers and not tallied in the histogram.

Returns

statistic : (nx, ny) ndarray

The values of the selected statistic in each two-dimensional bin

x_edges : (nx + 1) ndarray

The bin edges along the first dimension.

y_edges : (ny + 1) ndarray

The bin edges along the second dimension.

binnumber : 1-D ndarray of ints

This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as *values*.

See also:

`numpy.histogram2d`, `binned_statistic`, `binned_statistic_dd`

Notes

New in version 0.11.0.

`scipy.stats.`**`binned_statistic_dd`**(*sample*, *values*, *statistic='mean'*, *bins=10*, *range=None*)

Compute a multidimensional binned statistic for a set of data.

This is a generalization of a histogramdd function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values within each bin.

Parameters

sample : array_like

Data to histogram passed as a sequence of D arrays of length N, or as an (N,D) array.

values : array_like

The values on which the statistic will be computed. This must be the same shape as x.

statistic : string or callable, optional

The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins : sequence or int, optional

The bin specification:

- A sequence of arrays describing the bin edges along each dimension.
- The number of bins for each dimension (nx, ny, ... =bins)
- The number of bins for all dimensions (nx=ny=...=bins).

range : sequence, optional

A sequence of lower and upper bin edges to be used if the edges are not given explicitely in *bins*. Defaults to the minimum and maximum values along each dimension.

Returns **statistic** : ndarray, shape(nx1, nx2, nx3,...)

The values of the selected statistic in each two-dimensional bin

bin_edges : list of ndarrays

A list of D arrays describing the (nxi + 1) bin edges for each dimension

binnumber : 1-D ndarray of ints

This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as values.

See also:

`np.histogramdd`, `binned_statistic`, `binned_statistic_2d`

Notes

New in version 0.11.0.

`obrientransform`(*args)	Computes the O'Brien transform on input data (any number of arrays).
`signaltonoise`(*args, **kwds)	`signaltonoise` is deprecated!
`bayes_mvs`(data[, alpha])	Bayesian confidence intervals for the mean, var, and std.
`mvsdist`(data)	'Frozen' distributions for mean, variance, and standard deviation of data.
`sem`(a[, axis, ddof])	Calculates the standard error of the mean (or standard error of measurement) of the values in th
`zmap`(scores, compare[, axis, ddof])	Calculates the relative z-scores.
`zscore`(a[, axis, ddof])	Calculates the z score of each value in the sample, relative to the sample mean and standard de

`scipy.stats.`**`obrientransform`**(**args*)

Computes the O'Brien transform on input data (any number of arrays).

Used to test for homogeneity of variance prior to running one-way stats. Each array in `*args` is one level of a factor. If `f_oneway` is run on the transformed data and found significant, the variances are unequal. From Maxwell and Delaney [R353], p.112.

Parameters **args** : tuple of array_like

Any number of arrays.

Returns **obrientransform** : ndarray

Transformed data for use in an ANOVA. The first dimension of the result corresponds to the sequence of transformed arrays. If the arrays given are all 1-D of the same length, the return value is a 2-D array; otherwise it is a 1-D array of type object, with each element being an ndarray.

References

[R353]

Examples

We'll test the following data sets for differences in their variance.

```
>>> x = [10, 11, 13, 9, 7, 12, 12, 9, 10]
>>> y = [13, 21, 5, 10, 8, 14, 10, 12, 7, 15]
```

Apply the O'Brien transform to the data.

```
>>> from scipy.stats import obrientransform
>>> tx, ty = obrientransform(x, y)
```

Use `scipy.stats.f_oneway` to apply a one-way ANOVA test to the transformed data.

```
>>> from scipy.stats import f_oneway
>>> F, p = f_oneway(tx, ty)
>>> p
0.1314139477040335
```

If we require that `p < 0.05` for significance, we cannot conclude that the variances are different.

`scipy.stats.`**`signaltonoise`**`(`**args*, ***kwds*`)`

`signaltonoise` is deprecated! scipy.stats.signaltonoise is deprecated in scipy 0.16.0

The signal-to-noise ratio of the input data.
Returns the signal-to-noise ratio of *a*, here defined as the mean divided by the standard deviation.

Parameters **a** : array_like

An array_like object containing the sample data.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Degrees of freedom correction for standard deviation. Default is 0.

Returns **s2n** : ndarray

The mean to standard deviation ratio(s) along *axis*, or 0 where the standard deviation is 0.

`scipy.stats.`**`bayes_mvs`**`(`*data*, *alpha=0.9*`)`

Bayesian confidence intervals for the mean, var, and std.

Parameters **data** : array_like

Input data, if multi-dimensional it is flattened to 1-D by `bayes_mvs`. Requires 2 or more data points.

alpha : float, optional

Probability that the returned confidence interval contains the true parameter.

Returns **mean_cntr, var_cntr, std_cntr** : tuple

The three results are for the mean, variance and standard deviation, respectively. Each result is a tuple of the form:

```
(center, (lower, upper))
```

with *center* the mean of the conditional pdf of the value given the data, and *(lower, upper)* a confidence interval, centered on the median, containing the estimate to a probability `alpha`.

Notes

Each tuple of mean, variance, and standard deviation estimates represent the (center, (lower, upper)) with center the mean of the conditional pdf of the value given the data and (lower, upper) is a confidence interval centered on the median, containing the estimate to a probability `alpha`.

Converts data to 1-D and assumes all data has the same mean and variance. Uses Jeffrey's prior for variance and std.

Equivalent to `tuple((x.mean(), x.interval(alpha)) for x in mvsdist(dat))`

References

T.E. Oliphant, "A Bayesian perspective on estimating mean, variance, and standard-deviation from data", http://hdl.handle.net/1877/438, 2006.

`scipy.stats.`**`mvsdist`**`(`*data*`)`

'Frozen' distributions for mean, variance, and standard deviation of data.

Parameters **data** : array_like

Input array. Converted to 1-D using ravel. Requires 2 or more data-points.

Returns **mdist** : "frozen" distribution object

Distribution object representing the mean of the data

vdist : "frozen" distribution object

Distribution object representing the variance of the data

sdist : "frozen" distribution object

Distribution object representing the standard deviation of the data

Notes

The return values from bayes_mvs(data) is equivalent to `tuple((x.mean(), x.interval(0.90)) for x in mvsdist(data))`.

In other words, calling `<dist>.mean()` and `<dist>.interval(0.90)` on the three distribution objects returned from this function will give the same results that are returned from `bayes_mvs`.

Examples

```
>>> from scipy import stats
>>> data = [6, 9, 12, 7, 8, 8, 13]
>>> mean, var, std = stats.mvsdist(data)
```

We now have frozen distribution objects "mean", "var" and "std" that we can examine:

```
>>> mean.mean()
9.0
>>> mean.interval(0.95)
(6.6120585482655692, 11.387941451734431)
>>> mean.std()
1.1952286093343936
```

`scipy.stats.`**`sem`**`(`*a*, *axis=0*, *ddof=1*`)`

Calculates the standard error of the mean (or standard error of measurement) of the values in the input array.

Parameters **a** : array_like

An array containing the values for which the standard error is returned.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof : int, optional

Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.

Returns **s** : ndarray or float

The standard error of the mean in the sample(s), along the input axis.

Notes

The default value for *ddof* is different to the default (0) used by other ddof containing routines, such as np.std nd stats.nanstd.

Examples

Find standard error along the first axis:

```
>>> from scipy import stats
>>> a = np.arange(20).reshape(5,4)
>>> stats.sem(a)
array([ 2.8284,  2.8284,  2.8284,  2.8284])
```

Find standard error across the whole array, using n degrees of freedom:

```
>>> stats.sem(a, axis=None, ddof=0)
1.2893796958227628
```

`scipy.stats.`**`zmap`**(*scores*, *compare*, *axis=0*, *ddof=0*)

Calculates the relative z-scores.

Returns an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters **scores** : array_like

The input for which z-scores are calculated.

compare : array_like

The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as *scores*.

axis : int or None, optional

Axis over which mean and variance of *compare* are calculated. Default is 0. If None, compute over the whole array *scores*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns **zscore** : array_like

Z-scores, in the same shape as *scores*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017,  0.        ,  0.35355339,  0.70710678])
```

`scipy.stats.`**`zscore`**(*a*, *axis=0*, *ddof=0*)

Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters

a : array_like

An array like object containing the sample data.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns

zscore : array_like

The z-scores, standardized by mean and standard deviation of input array *a*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> a = np.array([ 0.7972,  0.0767,  0.4383,  0.7866,  0.8091,  0.1954,
...                0.6307, 0.6599,  0.1065,  0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552,  1.0923,  1.1664, -0.8559,  0.5786,
        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148,  0.0478,  0.6243,  0.4608],
...               [ 0.7149,  0.0775,  0.6072,  0.9656],
...               [ 0.6341,  0.1403,  0.9759,  0.4064],
...               [ 0.5918,  0.6948,  0.904 ,  0.3721],
...               [ 0.0921,  0.2481,  0.1188,  0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119,  1.07259584,  0.40420358],
       [ 0.33048416, -1.37380874,  0.04251374,  1.00081084],
       [ 0.26796377, -1.12598418,  1.23283094, -0.37481053],
       [-0.22095197,  0.24468594,  1.19042819, -1.21416216],
       [-0.82780366,  1.4457416 , -0.43867764, -0.1792603 ]])
```

`sigmaclip`(a[, low, high])	Iterative sigma-clipping of array elements.
`threshold`(a[, threshmin, threshmax, newval])	Clip array to a given value.
`trimboth`(a, proportiontocut[, axis])	Slices off a proportion of items from both ends of an array.
`trim1`(a, proportiontocut[, tail])	Slices off a proportion of items from ONE end of the passed array distribution.

`scipy.stats.`**`sigmaclip`**(*a*, *low=4.0*, *high=4.0*)

Iterative sigma-clipping of array elements.

The output array contains only those elements of the input array *c* that satisfy the conditions

```
mean(c) - std(c)*low < c < mean(c) + std(c)*high
```

Starting from the full sample, all elements outside the critical range are removed. The iteration continues with a new critical range until no elements are outside the range.

Parameters

a : array_like
  Data array, will be raveled if not 1-D.

low : float, optional
  Lower bound factor of sigma clipping. Default is 4.

high : float, optional
  Upper bound factor of sigma clipping. Default is 4.

Returns

clipped : ndarray
  Input array with clipped elements removed.

lower : float
  Lower threshold value use for clipping.

upper : float
  Upper threshold value use for clipping.

Examples

```
>>> from scipy.stats import sigmaclip
>>> a = np.concatenate((np.linspace(9.5, 10.5, 31),
...                     np.linspace(0, 20, 5)))
>>> fact = 1.5
>>> c, low, upp = sigmaclip(a, fact, fact)
>>> c
array([  9.96666667,  10.        ,  10.03333333,  10.        ])
>>> c.var(), c.std()
(0.00055555555555555165, 0.023570226039551501)
>>> low, c.mean() - fact*c.std(), c.min()
(9.9646446609406727, 9.9646446609406727, 9.9666666666666668)
>>> upp, c.mean() + fact*c.std(), c.max()
(10.035355339059327, 10.035355339059327, 10.033333333333333)
```

```
>>> a = np.concatenate((np.linspace(9.5, 10.5, 11),
...                     np.linspace(-100, -50, 3)))
>>> c, low, upp = sigmaclip(a, 1.8, 1.8)
>>> (c == np.linspace(9.5, 10.5, 11)).all()
True
```

`scipy.stats.`**`threshold`**(*a*, *threshmin=None*, *threshmax=None*, *newval=0*)

Clip array to a given value.

Similar to numpy.clip(), except that values less than *threshmin* or greater than *threshmax* are replaced by *newval*, instead of by *threshmin* and *threshmax* respectively.

Parameters

a : array_like
  Data to threshold.

threshmin : float, int or None, optional
  Minimum threshold, defaults to None.

threshmax : float, int or None, optional
  Maximum threshold, defaults to None.

newval : float or int, optional
  Value to put in place of values in *a* outside of bounds. Defaults to 0.

Returns

out : ndarray
  The clipped input array, with values less than *threshmin* or greater than *threshmax* replaced with *newval*.

Examples

```
>>> a = np.array([9, 9, 6, 3, 1, 6, 1, 0, 0, 8])
>>> from scipy import stats
>>> stats.threshold(a, threshmin=2, threshmax=8, newval=-1)
array([-1, -1,  6,  3, -1,  6, -1, -1, -1,  8])
```

`scipy.stats.`**`trimboth`**(*a*, *proportiontocut*, *axis=0*)

Slices off a proportion of items from both ends of an array.

Slices off the passed proportion of items from both ends of the passed array (i.e., with *proportiontocut* = 0.1, slices leftmost 10% **and** rightmost 10% of scores). You must pre-sort the array if you want ‘proper’ trimming. Slices off less if proportion results in a non-integer slice index (i.e., conservatively slices off *proportiontocut*).

Parameters

a : array_like

Data to trim.

proportiontocut : float

Proportion (in range 0-1) of total data set to trim of each end.

axis : int or None, optional

Axis along which to trim data. Default is 0. If None, compute over the whole array *a*.

Returns

out : ndarray

Trimmed version of array *a*.

See also:

`trim_mean`

Examples

```
>>> from scipy import stats
>>> a = np.arange(20)
>>> b = stats.trimboth(a, 0.1)
>>> b.shape
(16,)
```

`scipy.stats.`**`trim1`**(*a*, *proportiontocut*, *tail='right'*)

Slices off a proportion of items from ONE end of the passed array distribution.

If *proportiontocut* = 0.1, slices off ‘leftmost’ or ‘rightmost’ 10% of scores. Slices off LESS if proportion results in a non-integer slice index (i.e., conservatively slices off *proportiontocut*).

Parameters

a : array_like

Input array

proportiontocut : float

Fraction to cut off of ‘left’ or ‘right’ of distribution

tail : {‘left’, ‘right’}, optional

Defaults to ‘right’.

Returns

trim1 : ndarray

Trimmed version of array *a*

`f_oneway`(*args)	Performs a 1-way ANOVA.
`pearsonr`(x, y)	Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.
`spearmanr`(a[, b, axis])	Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correl
`pointbiserialr`(x, y)	Calculates a point biserial correlation coefficient and the associated p-value.
`kendalltau`(x, y[, initial_lexsort])	Calculates Kendall’s tau, a correlation measure for ordinal data.
`linregress`(x[, y])	Calculate a regression line
`theilslopes`(y[, x, alpha])	Computes the Theil-Sen estimator for a set of points (x, y).

`scipy.stats.`**`f_oneway`**`(*args)`

Performs a 1-way ANOVA.

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. The test is applied to samples from two or more groups, possibly with differing sizes.

Parameters	**sample1, sample2, ...** : array_like The sample measurements for each group.
Returns	**statistic** : float The computed F-value of the test. **pvalue** : float The associated p-value from the F-distribution.

Notes

The ANOVA test has important assumptions that must be satisfied in order for the associated p-value to be valid.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. The population standard deviations of the groups are all equal. This property is known as homoscedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (`scipy.stats.kruskal`) although with some loss of power.

The algorithm is from Heiman[2], pp.394-7.

References

[R314], [R315]

`scipy.stats.`**`pearsonr`**`(x, y)`

Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.

The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson's correlation requires that each dataset be normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters	**x** : (N,) array_like Input **y** : (N,) array_like Input
Returns	(Pearson's correlation coefficient, 2-tailed p-value)

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

`scipy.stats.`**`spearmanr`**`(a, b=None, axis=0)`

Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the monotonicity of the relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact monotonic relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters **a, b** : 1D or 2D array_like, b is optional

One or two 1-D or 2-D arrays containing multiple variables and observations. Each column of *a* and *b* represents a variable, and each row entry a single observation of those variables. See also *axis*. Both arrays need to have the same length in the *axis* dimension.

axis : int or None, optional

If axis=0 (default), then each column represents a variable, with observations in the rows. If axis=0, the relationship is transposed: each row represents a variable, while the columns contain observations. If axis=None, then both arrays will be raveled.

Returns **correlation** : float or ndarray (2-D square)

Spearman correlation matrix or correlation coefficient (if only 2 variables are given as parameters. Correlation matrix is square with length equal to total number of variables (columns or rows) in a and b combined.

pvalue : float

The two-sided p-value for a hypothesis test whose null hypothesis is that two sets of data are uncorrelated, has same dimension as rho.

Notes

Changes in scipy 0.8.0: rewrite to add tie-handling, and axis.

References

[R363]

Examples

```
>>> from scipy import stats
>>> stats.spearmanr([1,2,3,4,5], [5,6,7,8,7])
(0.82078268166812329, 0.088587005313543798)
>>> np.random.seed(1234321)
>>> x2n = np.random.randn(100, 2)
>>> y2n = np.random.randn(100, 2)
>>> stats.spearmanr(x2n)
(0.059969996999699973, 0.55338590803773591)
>>> stats.spearmanr(x2n[:,0], x2n[:,1])
(0.059969996999699973, 0.55338590803773591)
>>> rho, pval = stats.spearmanr(x2n, y2n)
>>> rho
array([[ 1.        ,  0.05997   ,  0.18569457,  0.06258626],
       [ 0.05997   ,  1.        ,  0.110003  ,  0.02534653],
       [ 0.18569457,  0.110003  ,  1.        ,  0.03488749],
       [ 0.06258626,  0.02534653,  0.03488749,  1.        ]])
>>> pval
array([[ 0.        ,  0.55338591,  0.06435364,  0.53617935],
       [ 0.55338591,  0.        ,  0.27592895,  0.80234077],
       [ 0.06435364,  0.27592895,  0.        ,  0.73039992],
       [ 0.53617935,  0.80234077,  0.73039992,  0.        ]])
>>> rho, pval = stats.spearmanr(x2n.T, y2n.T, axis=1)
>>> rho
array([[ 1.        ,  0.05997   ,  0.18569457,  0.06258626],
       [ 0.05997   ,  1.        ,  0.110003  ,  0.02534653],
       [ 0.18569457,  0.110003  ,  1.        ,  0.03488749],
```

```
       [ 0.06258626,  0.02534653,  0.03488749,  1.        ]])
>>> stats.spearmanr(x2n, y2n, axis=None)
(0.10816770419260482, 0.1273562188027364)
>>> stats.spearmanr(x2n.ravel(), y2n.ravel())
(0.10816770419260482, 0.1273562188027364)
```

```
>>> xint = np.random.randint(10, size=(100, 2))
>>> stats.spearmanr(xint)
(0.052760927029710199, 0.60213045837062351)
```

`scipy.stats.`**`pointbiserialr`**`(`*x*, *y*`)`

Calculates a point biserial correlation coefficient and the associated p-value.

The point biserial correlation is used to measure the relationship between a binary variable, x, and a continuous variable, y. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a determinative relationship.

This function uses a shortcut formula but produces the same result as `pearsonr`.

Parameters

x : array_like of bools

Input array.

y : array_like

Input array.

Returns

correlation : float

R value

pvalue : float

2-tailed p-value

References

http://en.wikipedia.org/wiki/Point-biserial_correlation_coefficient

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)
>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)
>>> np.corrcoef(a, b)
array([[ 1.       ,  0.8660254],
       [ 0.8660254,  1.       ]])
```

`scipy.stats.`**`kendalltau`**`(`*x*, *y*, *initial_lexsort=True*`)`

Calculates Kendall's tau, a correlation measure for ordinal data.

Kendall's tau is a measure of the correspondence between two rankings. Values close to 1 indicate strong agreement, values close to -1 indicate strong disagreement. This is the tau-b version of Kendall's tau which accounts for ties.

Parameters

x, y : array_like

Arrays of rankings, of the same shape. If arrays are not 1-D, they will be flattened to 1-D.

initial_lexsort : bool, optional

Whether to use lexsort or quicksort as the sorting method for the initial sort of the inputs. Default is lexsort (True), for which `kendalltau` is of complexity O(n log(n)). If False, the complexity is O(n^2), but with a smaller pre-factor (so quicksort may be faster for small arrays).

Returns **correlation** : float

The tau statistic.

pvalue : float

The two-sided p-value for a hypothesis test whose null hypothesis is an absence of association, tau = 0.

Notes

The definition of Kendall's tau that is used is:

```
tau = (P - Q) / sqrt((P + Q + T) * (P + Q + U))
```

where P is the number of concordant pairs, Q the number of discordant pairs, T the number of ties only in *x*, and U the number of ties only in *y*. If a tie occurs for the same pair in both *x* and *y*, it is not added to either T or U.

References

W.R. Knight, "A Computer Method for Calculating Kendall's Tau with Ungrouped Data", Journal of the American Statistical Association, Vol. 61, No. 314, Part 1, pp. 436-439, 1966.

Examples

```
>>> from scipy import stats
>>> x1 = [12, 2, 1, 12, 2]
>>> x2 = [1, 4, 7, 1, 0]
>>> tau, p_value = stats.kendalltau(x1, x2)
>>> tau
-0.47140452079103173
>>> p_value
0.24821309157521476
```

`scipy.stats.`**`linregress`**`(`*x*, *y=None*`)`

Calculate a regression line

This computes a least-squares regression for two sets of measurements.

Parameters **x, y** : array_like

two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.

Returns **slope** : float

slope of the regression line

intercept : float

intercept of the regression line

rvalue : float

correlation coefficient

pvalue : float

two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero.

stderr : float

Standard error of the estimate

Examples

```
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x,y)
```

To get coefficient of determination (r_squared)

```
>>> print("r-squared:", r_value**2)
r-squared: 0.15286643777
```

`scipy.stats.`**`theilslopes`**`(`*y*, *x=None*, *alpha=0.95*`)`

Computes the Theil-Sen estimator for a set of points (x, y).

`theilslopes` implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

y : array_like

Dependent variable.

x : array_like or None, optional

Independent variable. If None, use `arange(len(y))` instead.

alpha : float, optional

Confidence degree between 0 and 1. Default is 95% confidence. Note that `alpha` is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as "find the 90% confidence interval".

Returns

medslope : float

Theil slope.

medintercept : float

Intercept of the Theil line, as `median(y) - medslope*median(x)`.

lo_slope : float

Lower bound of the confidence interval on *medslope*.

up_slope : float

Upper bound of the confidence interval on *medslope*.

Notes

The implementation of `theilslopes` follows [R364]. The intercept is not defined in [R364], and here it is defined as `median(y) - medslope*median(x)`, which is given in [R366]. Other definitions of the intercept exist in the literature. A confidence interval for the intercept is not given as this question is not addressed in [R364].

References

[R364], [R365], [R366]

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

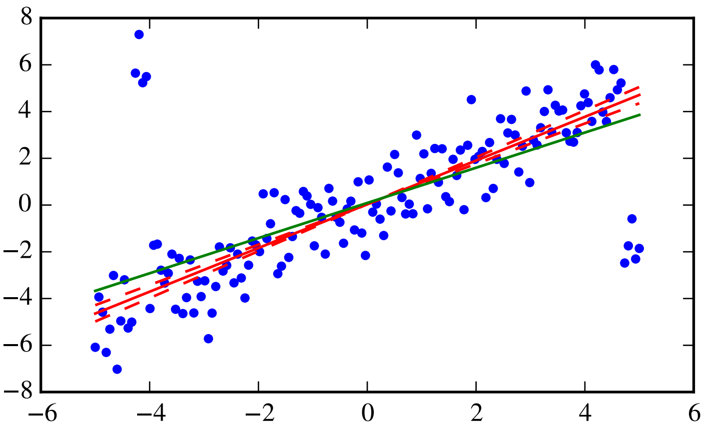
```
>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7
```

Compute the slope, intercept and 90% confidence interval. For comparison, also compute the least-squares fit with `linregress`:

```
>>> res = stats.theilslopes(y, x, 0.90)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Theil-Sen regression line is shown in red, with the dashed red lines illustrating the confidence interval of the slope (note that the dashed red lines are not the confidence interval of the regression as the confidence interval of the intercept is not included). The green line shows the least-squares fit for comparison.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.')
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, res[1] + res[2] * x, 'r--')
>>> ax.plot(x, res[1] + res[3] * x, 'r--')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```



`ttest_1samp`(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
`ttest_ind`(a, b[, axis, equal_var])	Calculates the T-test for the means of TWO INDEPENDENT samples of sco
`ttest_ind_from_stats`(mean1, std1, nobs1, ...)	T-test for means of two independent samples from descriptive statistics.
`ttest_rel`(a, b[, axis])	Calculates the T-test on TWO RELATED samples of scores, a and b.
`kstest`(rvs, cdf[, args, N, alternative, mode])	Perform the Kolmogorov-Smirnov test for goodness of fit.
`chisquare`(f_obs[, f_exp, ddof, axis])	Calculates a one-way chi square test.
`power_divergence`(f_obs[, f_exp, ddof, axis, ...])	Cressie-Read power divergence statistic and goodness of fit test.
`ks_2samp`(data1, data2)	Computes the Kolmogorov-Smirnov statistic on 2 samples.
`mannwhitneyu`(x, y[, use_continuity])	Computes the Mann-Whitney rank test on samples x and y.
`tiecorrect`(rankvals)	Tie correction factor for ties in the Mann-Whitney U and Kruskal-Wallis H te
`rankdata`(a[, method])	Assign ranks to data, dealing with ties appropriately.
`ranksums`(x, y)	Compute the Wilcoxon rank-sum statistic for two samples.
`wilcoxon`(x[, y, zero_method, correction])	Calculate the Wilcoxon signed-rank test.
`kruskal`(*args)	Compute the Kruskal-Wallis H-test for independent samples
`friedmanchisquare`(*args)	Computes the Friedman test for repeated measurements

Continued

Table 5.261 – continued from previous page

`combine_pvalues`(pvalues[, method, weights])	Methods for combining the p-values of independent tests bearing upon the sa

`scipy.stats.`**`ttest_1samp`**(*a*, *popmean*, *axis=0*)

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters **a** : array_like

sample observation

popmean : float or array_like

expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole array *a*.

Returns **statistic** : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`scipy.stats.`**`ttest_ind`**(*a*, *b*, *axis=0*, *equal_var=True*)

Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters **a, b** : array_like

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var : bool, optional

If True (default), perform a standard independent 2 sample test that assumes equal population variances [R368]. If False, perform Welch's t-test, which does not assume equal population variance [R369]. .. versionadded:: 0.11.0

Returns **statistic** : float or array

The calculated t-statistic.

pvalue : float or array

The two-tailed p-value.

Notes

We can use this test, if we observe two independent samples from the same or different population, e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average (expected) value differs significantly across samples. If we observe a large p-value, for example larger than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References

[R368], [R369]

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678)
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1,rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```

`ttest_ind` underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)
(-0.46580283298287162, 0.64149646246569292)
```

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)
(-0.94365973617132992, 0.34744170334794122)
```

`scipy.stats.`**`ttest_ind_from_stats`**(*mean1*, *std1*, *nobs1*, *mean2*, *std2*, *nobs2*, *equal_var=True*)

T-test for means of two independent samples from descriptive statistics.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values.

Parameters

mean1 : array_like
  The mean(s) of sample 1.

std1 : array_like
  The standard deviation(s) of sample 1.

nobs1 : array_like
  The number(s) of observations of sample 1.

mean2 : array_like
  The mean(s) of sample 2

std2 : array_like
  The standard deviations(s) of sample 2.

nobs2 : array_like
  The number(s) of observations of sample 2.

equal_var : bool, optional
  If True (default), perform a standard independent 2 sample test that assumes equal population variances [R370]. If False, perform Welch's t-test, which does not assume equal population variance [R371].

Returns

statistic : float or array
  The calculated t-statistics

pvalue : float or array
  The two-tailed p-value.

See also:

`scipy.stats.ttest_ind`

Notes

New in version 0.16.0.

References

[R370], [R371]

`scipy.stats.`**`ttest_rel`**(*a*, *b*, *axis=0*)

Calculates the T-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters

a, b : array_like
  The arrays must have the same shape.

axis : int or None, optional
  Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

Returns

statistic : float or array
  t-statistic

pvalue : float or array
  two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

http://en.wikipedia.org/wiki/T-test#Dependent_t-test

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678) # fix random seed to get same numbers
```

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = (stats.norm.rvs(loc=5,scale=10,size=500) +
...          stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs2)
(0.24101764965300962, 0.80964043445811562)
>>> rvs3 = (stats.norm.rvs(loc=8,scale=10,size=500) +
...          stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs3)
(-3.9995108708727933, 7.3082402191726459e-005)
```

`scipy.stats.`**`kstest`**(*rvs*, *cdf*, *args=()*, *N=20*, *alternative='two-sided'*, *mode='approx'*)

Perform the Kolmogorov-Smirnov test for goodness of fit.

This performs a test of the distribution G(x) of an observed random variable against a given distribution F(x). Under the null hypothesis the two distributions are identical, G(x)=F(x). The alternative hypothesis can be either 'two-sided' (default), 'less' or 'greater'. The KS test is only valid for continuous distributions.

Parameters

rvs : str, array or callable

If a string, it should be the name of a distribution in `scipy.stats`. If an array, it should be a 1-D array of observations of random variables. If a callable, it should be a function to generate random variables; it is required to have a keyword argument *size*.

cdf : str or callable

If a string, it should be the name of a distribution in `scipy.stats`. If *rvs* is a string then *cdf* can be False or the same as *rvs*. If a callable, that callable is used to calculate the cdf.

args : tuple, sequence, optional

Distribution parameters, used if *rvs* or *cdf* are strings.

N : int, optional

Sample size if *rvs* is string or callable. Default is 20.

alternative : {'two-sided', 'less','greater'}, optional

Defines the alternative hypothesis (see explanation above). Default is 'two-sided'.

mode : 'approx' (default) or 'asymp', optional

Defines the distribution used for calculating the p-value.

- 'approx' : use approximation to exact distribution of test statistic
- 'asymp' : use asymptotic distribution of test statistic

Returns

statistic : float

KS test statistic, either D, D+ or D-.

pvalue : float

One-tailed or two-tailed p-value.

Notes

In the one-sided test, the alternative is that the empirical cumulative distribution function of the random variable is "less" or "greater" than the cumulative distribution function F(x) of the hypothesis, `G(x)<=F(x)`, resp. `G(x)>=F(x)`.

Examples

```
>>> from scipy import stats
```

```
>>> x = np.linspace(-15, 15, 9)
>>> stats.kstest(x, 'norm')
(0.44435602715924361, 0.038850142705171065)
```

```
>>> np.random.seed(987654321) # set random seed to get the same result
>>> stats.kstest('norm', False, N=100)
(0.058352892479417884, 0.88531190944151261)
```

The above lines are equivalent to:

```
>>> np.random.seed(987654321)
>>> stats.kstest(stats.norm.rvs(size=100), 'norm')
(0.058352892479417884, 0.88531190944151261)
```

Test against one-sided alternative hypothesis

Shift distribution to larger values, so that `cdf_dgp(x) < norm.cdf(x)`:

```
>>> np.random.seed(987654321)
>>> x = stats.norm.rvs(loc=0.2, size=100)
>>> stats.kstest(x,'norm', alternative = 'less')
(0.12464329735846891, 0.040989164077641749)
```

Reject equal distribution against alternative hypothesis: less

```
>>> stats.kstest(x,'norm', alternative = 'greater')
(0.0072115233216311081, 0.98531158590396395)
```

Don't reject equal distribution against alternative hypothesis: greater

```
>>> stats.kstest(x,'norm', mode='asymp')
(0.12464329735846891, 0.08944488871182088)
```

Testing t distributed random variables against normal distribution

With 100 degrees of freedom the t distribution looks close to the normal distribution, and the K-S test does not reject the hypothesis that the sample came from the normal distribution:

```
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(100,size=100),'norm')
(0.072018929165471257, 0.67630062862479168)
```

With 3 degrees of freedom the t distribution looks sufficiently different from the normal distribution, that we can reject the hypothesis that the sample came from the normal distribution at the 10% level:

```
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(3,size=100),'norm')
(0.131016895759829, 0.058826222555312224)
```

`scipy.stats.`**`chisquare`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculates a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

f_obs : array_like

Observed frequencies in each category.

f_exp : array_like, optional

Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

"Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis : int or None, optional

The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq : float or ndarray

The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p : float or ndarray

The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

`power_divergence`, `mstats.chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References

[R307], [R308]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`scipy.stats.`**`power_divergence`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*, *lambda_=None*)

Cressie-Read power divergence statistic and goodness of fit test.

This function tests the null hypothesis that the categorical data has the given frequencies, using the Cressie-Read power divergence statistic.

Parameters

f_obs : array_like

Observed frequencies in each category.

f_exp : array_like, optional

Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

"Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis : int or None, optional

The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

lambda_ : float or str, optional

*lambda_* gives the power in the Cressie-Read power divergence statistic. The default is 1. For convenience, *lambda_* may be assigned one of the following strings, in which case the corresponding numerical value is used:

```
String              Value   Description
"pearson"             1     Pearson's chi-squared statistic.
                            In this case, the function is
                            equivalent to `stats.chisquare`.
"log-likelihood"      0     Log-likelihood ratio. Also known as
                            the G-test [R356]_.
"freeman-tukey"      -1/2   Freeman-Tukey statistic.
"mod-log-likelihood" -1     Modified log-likelihood ratio.
"neyman"             -2     Neyman's statistic.
"cressie-read"        2/3   The power recommended in [R358]_.
```

Returns **statistic** : float or ndarray

The Cressie-Read power divergence test statistic. The value is a float if *axis* is None or if‘ *f_obs* and *f_exp* are 1-D.

pvalue : float or ndarray

The p-value of the test. The value is a float if *ddof* and the return value `stat` are scalars.

See also:

`chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

When *lambda_* is less than zero, the formula for the statistic involves dividing by *f_obs*, so a warning or error may be generated if any value in *f_obs* is 0.

Similarly, a warning or error may be generated if any value in *f_exp* is zero when *lambda_* >= 0.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

This function handles masked arrays. If an element of *f_obs* or *f_exp* is masked, then data at that position is ignored, and does not count towards the size of the data set.

New in version 0.13.0.

References

[R354], [R355], [R356], [R357], [R358]

Examples

(See `chisquare` for more examples.)

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies. Here we perform a G-test (i.e. use the log-likelihood ratio statistic):

```
>>> from scipy.stats import power_divergence
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood')
(2.006573162632538, 0.84823476779463769)
```

The expected frequencies can be given with the *f_exp* argument:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[16, 16, 16, 16, 16, 8],
...                  lambda_='log-likelihood')
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> power_divergence(obs, lambda_="log-likelihood")
(array([ 2.00657316,  6.77634498]), array([ 0.84823477,  0.23781225]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> power_divergence(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> power_divergence(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the test statistic with *ddof*.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we must use `axis=1`:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[[16, 16, 16, 16, 16, 8],
...                         [8, 20, 20, 16, 12, 12]],
...                  axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`scipy.stats.`**`ks_2samp`**`(`*data1*, *data2*`)`

Computes the Kolmogorov-Smirnov statistic on 2 samples.

This is a two-sided test for the null hypothesis that 2 independent samples are drawn from the same continuous distribution.

Parameters **data1, data2** : sequence of 1-D ndarrays

two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different

Returns **statistic** : float

KS statistic

pvalue : float

two-tailed p-value

Notes

This tests whether 2 samples are drawn from the same distribution. Note that, like in the case of the one-sample K-S test, the distribution is assumed to be continuous.

This is the two-sided test, one-sided tests are not implemented. The test uses the two-sided asymptotic Kolmogorov-Smirnov distribution.

If the K-S statistic is small or the p-value is high, then we cannot reject the hypothesis that the distributions of the two samples are the same.

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678)  #fix random seed to get the same result
>>> n1 = 200  # size of first sample
>>> n2 = 300  # size of second sample
```

For a different distribution, we can reject the null hypothesis since the pvalue is below 1%:

```
>>> rvs1 = stats.norm.rvs(size=n1, loc=0., scale=1)
>>> rvs2 = stats.norm.rvs(size=n2, loc=0.5, scale=1.5)
>>> stats.ks_2samp(rvs1, rvs2)
(0.20833333333333337, 4.6674975515806989e-005)
```

For a slightly different distribution, we cannot reject the null hypothesis at a 10% or lower alpha since the p-value at 0.144 is higher than 10%

```
>>> rvs3 = stats.norm.rvs(size=n2, loc=0.01, scale=1.0)
>>> stats.ks_2samp(rvs1, rvs3)
(0.10333333333333333, 0.14498781825751686)
```

For an identical distribution, we cannot reject the null hypothesis since the p-value is high, 41%:

```
>>> rvs4 = stats.norm.rvs(size=n2, loc=0.0, scale=1.0)
>>> stats.ks_2samp(rvs1, rvs4)
(0.07999999999999996, 0.41126949729859719)
```

`scipy.stats.`**`mannwhitneyu`**(*x*, *y*, *use_continuity=True*)

Computes the Mann-Whitney rank test on samples x and y.

Parameters **x, y** : array_like

Array of samples, should be one-dimensional.

use_continuity : bool, optional

Whether a continuity correction (1/2.) should be taken into account. Default is True.

Returns **statistic** : float

The Mann-Whitney statistics.

pvalue : float

One-sided p-value assuming a asymptotic normal distribution.

Notes

Use only when the number of observation in each sample is > 20 and you have 2 independent samples of ranks. Mann-Whitney U is significant if the u-obtained is LESS THAN or equal to the critical value of U.

This test corrects for ties and by default uses a continuity correction. The reported p-value is for a one-sided hypothesis, to get the two-sided p-value multiply the returned p-value by 2.

`scipy.stats.`**`tiecorrect`**(*rankvals*)

Tie correction factor for ties in the Mann-Whitney U and Kruskal-Wallis H tests.

Parameters	**rankvals** : array_like A 1-D sequence of ranks. Typically this will be the array returned by `stats.rankdata`.
Returns	**factor** : float Correction factor for U or H.

See also:

`rankdata`	Assign ranks to the data
`mannwhitneyu`	Mann-Whitney rank test
`kruskal`	Kruskal-Wallis H test

References

[R367]

Examples

```
>>> from scipy.stats import tiecorrect, rankdata
>>> tiecorrect([1, 2.5, 2.5, 4])
0.9
>>> ranks = rankdata([1, 3, 2, 4, 5, 7, 2, 8, 4])
>>> ranks
array([ 1. ,  4. ,  2.5,  5.5,  7. ,  8. ,  2.5,  9. ,  5.5])
>>> tiecorrect(ranks)
0.98333333333333333
```

`scipy.stats.`**`rankdata`**(*a*, *method='average'*)

Assign ranks to data, dealing with ties appropriately.

Ranks begin at 1. The *method* argument controls how ranks are assigned to equal values. See [R359] for further discussion of ranking methods.

Parameters **a** : array_like

The array of values to be ranked. The array is first flattened.

method : str, optional

The method used to assign ranks to tied elements. The options are 'average', 'min', 'max', 'dense' and 'ordinal'.

'average':	The average of the ranks that would have been assigned to all the tied values is assigned to each value.
'min':	The minimum of the ranks that would have been assigned to all the tied values is assigned to each value. (This is also referred to as "competition" ranking.)
'max':	The maximum of the ranks that would have been assigned to all the tied values is assigned to each value.
'dense':	Like 'min', but the rank of the next highest element is assigned the rank immediately after those assigned to the tied elements.
'ordinal':	All values are given a distinct rank, corresponding to the order that the values occur in *a*.

The default is 'average'.

Returns **ranks** : ndarray

An array of length equal to the size of *a*, containing rank scores.

Notes

All floating point types are converted to numpy.float64 before ranking. This may result in spurious ties if an input array of floats has a wider data type than numpy.float64 (e.g. numpy.float128).

References

[R359]

Examples

```
>>> from scipy.stats import rankdata
>>> rankdata([0, 2, 3, 2])
array([ 1. ,  2.5,  4. ,  2.5])
>>> rankdata([0, 2, 3, 2], method='min')
array([ 1.,  2.,  4.,  2.])
>>> rankdata([0, 2, 3, 2], method='max')
array([ 1.,  3.,  4.,  3.])
>>> rankdata([0, 2, 3, 2], method='dense')
array([ 1.,  2.,  3.,  2.])
>>> rankdata([0, 2, 3, 2], method='ordinal')
array([ 1.,  2.,  4.,  3.])
```

`scipy.stats.`**`ranksums`**(*x*, *y*)

Compute the Wilcoxon rank-sum statistic for two samples.

The Wilcoxon rank-sum test tests the null hypothesis that two sets of measurements are drawn from the same distribution. The alternative hypothesis is that values in one sample are more likely to be larger than the values in the other sample.

This test should be used to compare two samples from continuous distributions. It does not handle ties between measurements in x and y. For tie-handling and an optional continuity correction see `scipy.stats.mannwhitneyu`.

Parameters **x,y** : array_like

The data from the two samples

Returns **statistic** : float

The test statistic under the large-sample approximation that the rank sum statistic is normally distributed

pvalue : float

The two-sided p-value of the test

References

[R360]

`scipy.stats.`**`wilcoxon`**(*x*, *y=None*, *zero_method='wilcox'*, *correction=False*)

Calculate the Wilcoxon signed-rank test.

The Wilcoxon signed-rank test tests the null hypothesis that two related paired samples come from the same distribution. In particular, it tests whether the distribution of the differences x - y is symmetric about zero. It is a non-parametric version of the paired T-test.

Parameters **x** : array_like

The first set of measurements.

y : array_like, optional

The second set of measurements. If *y* is not given, then the *x* array is considered to be the differences between the two sets of measurements.

zero_method : string, {"pratt", "wilcox", "zsplit"}, optional

"pratt": Pratt treatment: includes zero-differences in the ranking process (more conservative)

"wilcox": Wilcox treatment: discards all zero-differences

"zsplit": Zero rank split: just like Pratt, but spliting the zero rank between positive and negative ones

correction : bool, optional

If True, apply continuity correction by adjusting the Wilcoxon rank statistic by 0.5 towards the mean value when computing the z-statistic. Default is False.

Returns **statistic** : float

The sum of the ranks of the differences above or below zero, whichever is smaller.

pvalue : float

The two-sided p-value for the test.

Notes

Because the normal approximation is used for the calculations, the samples used should be large. A typical rule is to require that n > 20.

References

[R373]

`scipy.stats.`**`kruskal`**`(`*`*args`*`)`

Compute the Kruskal-Wallis H-test for independent samples

The Kruskal-Wallis H-test tests the null hypothesis that the population median of all of the groups are equal. It is a non-parametric version of ANOVA. The test works on 2 or more independent samples, which may have different sizes. Note that rejecting the null hypothesis does not indicate which of the groups differs. Post-hoc comparisons between groups are required to determine which groups are different.

Parameters **sample1, sample2, ...** : array_like

Two or more arrays with the sample measurements can be given as arguments.

Returns **statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

pvalue : float

The p-value for the test using the assumption that H has a chi square distribution

Notes

Due to the assumption that H has a chi square distribution, the number of samples in each group must not be too small. A typical rule is that each sample must have at least 5 measurements.

References

[R328]

`scipy.stats.`**`friedmanchisquare`**`(`*`*args`*`)`

Computes the Friedman test for repeated measurements

The Friedman test tests the null hypothesis that repeated measurements of the same individuals have the same distribution. It is often used to test for consistency among measurements obtained in different ways. For example, if two measurement techniques are used on the same set of individuals, the Friedman test can be used to determine if the two measurement techniques are consistent.

Parameters **measurements1, measurements2, measurements3...** : array_like

Arrays of measurements. All of the arrays must have the same number of elements. At least 3 sets of measurements must be given.

Returns **statistic** : float

the test statistic, correcting for ties

pvalue : float

the associated p-value assuming that the test statistic has a chi squared distribution

Notes

Due to the assumption that the test statistic has a chi squared distribution, the p-value is only reliable for n > 10 and more than 6 repeated measurements.

References

[R319]

`scipy.stats.`**`combine_pvalues`**(*pvalues*, *method='fisher'*, *weights=None*)

Methods for combining the p-values of independent tests bearing upon the same hypothesis.

Parameters **pvalues** : array_like, 1-D

Array of p-values assumed to come from independent tests.

method : {'fisher', 'stouffer'}, optional

Name of method to use to combine p-values. The following methods are available: - "fisher": Fisher's method (Fisher's combined probability test), the default.

- "stouffer": Stouffer's Z-score method.

weights : array_like, 1-D, optional

Optional array of weights used only for Stouffer's Z-score method.

Returns statistic: float

The statistic calculated by the specified method: - "fisher": The chi-squared statistic - "stouffer": The Z-score

pval: float

The combined p-value.

Notes

Fisher's method (also known as Fisher's combined probability test) [R309] uses a chi-squared statistic to compute a combined p-value. The closely related Stouffer's Z-score method [R310] uses Z-scores rather than p-values. The advantage of Stouffer's method is that it is straightforward to introduce weights, which can make Stouffer's method more powerful than Fisher's method when the p-values are from studies of different size [R311] [R312].

Fisher's method may be extended to combine p-values from dependent tests [R313]. Extensions such as Brown's method and Kost's method are not currently implemented.

New in version 0.15.0.

References

[R309], [R310], [R311], [R312], [R313]

`ansari`(x, y)	Perform the Ansari-Bradley test for equal scale parameters
`bartlett`(*args)	Perform Bartlett's test for equal variances
`levene`(*args, **kwds)	Perform Levene test for equal variances.
`shapiro`(x[, a, reta])	Perform the Shapiro-Wilk test for normality.

Continued on next page

Table 5.262 – continued from previous page

`anderson`(x[, dist])	Anderson-Darling test for data coming from a particular distribution
`anderson_ksamp`(samples[, midrank])	The Anderson-Darling test for k-samples.
`binom_test`(x[, n, p])	Perform a test that the probability of success is p.
`fligner`(*args, **kwds)	Perform Fligner's test for equal variances.
`median_test`(*args, **kwds)	Mood's median test.
`mood`(x, y[, axis])	Perform Mood's test for equal scale parameters.

`scipy.stats.`**`ansari`**(*x*, *y*)

Perform the Ansari-Bradley test for equal scale parameters

The Ansari-Bradley test is a non-parametric test for the equality of the scale parameter of the distributions from which two samples were drawn.

Parameters **x, y** : array_like

arrays of sample data

Returns **statistic** : float

The Ansari-Bradley test statistic

pvalue : float

The p-value of the hypothesis test

See also:

`fligner`	A non-parametric test for the equality of k variances
`mood`	A non-parametric test for the equality of two scale parameters

Notes

The p-value given is exact when the sample sizes are both less than 55 and there are no ties, otherwise a normal approximation for the p-value is used.

References

[R300]

`scipy.stats.`**`bartlett`**(**args*)

Perform Bartlett's test for equal variances

Bartlett's test tests the null hypothesis that all input samples are from populations with equal variances. For samples from significantly non-normal populations, Levene's test `levene` is more robust.

Parameters **sample1, sample2,...** : array_like

arrays of sample data. May be different lengths.

Returns **statistic** : float

The test statistic.

pvalue : float

The p-value of the test.

References

[R301], [R302]

`scipy.stats.`**`levene`**(**args*, ***kwds*)

Perform Levene test for equal variances.

The Levene test tests the null hypothesis that all input samples are from populations with equal variances. Levene's test is an alternative to Bartlett's test `bartlett` in the case where there are significant deviations from normality.

Parameters **sample1, sample2, ...** : array_like

The sample data, possibly with different lengths

center : {'mean', 'median', 'trimmed'}, optional
Which function of the data to use in the test. The default is 'median'.

proportiontocut : float, optional
When *center* is 'trimmed', this gives the proportion of data points to cut from each end. (See `scipy.stats.trim_mean`.) Default is 0.05.

Returns **statistic** : float
The test statistic.

pvalue : float
The p-value for the test.

Notes

Three variations of Levene's test are possible. The possibilities and their recommended usages are:

- 'median' : Recommended for skewed (non-normal) distributions>
- 'mean' : Recommended for symmetric, moderate-tailed distributions.
- 'trimmed' : Recommended for heavy-tailed distributions.

References

[R330], [R331], [R332]

`scipy.stats.`**`shapiro`**(*x*, *a=None*, *reta=False*)

Perform the Shapiro-Wilk test for normality.

The Shapiro-Wilk test tests the null hypothesis that the data was drawn from a normal distribution.

Parameters **x** : array_like
Array of sample data.

a : array_like, optional
Array of internal parameters used in the calculation. If these are not given, they will be computed internally. If x has length n, then a must have length n/2.

reta : bool, optional
Whether or not to return the internally computed a values. The default is False.

Returns **W** : float
The test statistic.

p-value : float
The p-value for the hypothesis test.

a : array_like, optional
If *reta* is True, then these are the internally computed "a" values that may be passed into this function on future calls.

See also:

`anderson` The Anderson-Darling test for normality

References

[R361]

`scipy.stats.`**`anderson`**(*x*, *dist='norm'*)

Anderson-Darling test for data coming from a particular distribution

The Anderson-Darling test is a modification of the Kolmogorov- Smirnov test `kstest` for the null hypothesis that a sample is drawn from a population that follows a particular distribution. For the Anderson-Darling test, the critical values depend on which distribution is being tested against. This function works for normal, exponential, logistic, or Gumbel (Extreme Value Type I) distributions.

Parameters **x** : array_like
array of sample data

	dist : {'norm','expon','logistic','gumbel','extreme1'}, optional the type of distribution to test against. The default is 'norm' and 'extreme1' is a synonym for 'gumbel'
Returns	**statistic** : float The Anderson-Darling test statistic **critical_values** : list The critical values for this distribution **significance_level** : list The significance levels for the corresponding critical values in percents. The function returns critical values for a differing set of significance levels depending on the distribution that is being tested against.

Notes

Critical values provided are for the following significance levels:

normal/exponenential	15%, 10%, 5%, 2.5%, 1%
logistic	25%, 10%, 5%, 2.5%, 1%, 0.5%
Gumbel	25%, 10%, 5%, 2.5%, 1%

If A2 is larger than these critical values then for the corresponding significance level, the null hypothesis that the data come from the chosen distribution can be rejected.

References

[R293], [R294], [R295], [R296], [R297], [R298]

`scipy.stats.`**`anderson_ksamp`**(*samples*, *midrank=True*)

The Anderson-Darling test for k-samples.

The k-sample Anderson-Darling test is a modification of the one-sample Anderson-Darling test. It tests the null hypothesis that k-samples are drawn from the same population without having to specify the distribution function of that population. The critical values depend on the number of samples.

Parameters	**samples** : sequence of 1-D array_like Array of sample data in arrays. **midrank** : bool, optional Type of Anderson-Darling test which is computed. Default (True) is the midrank test applicable to continuous and discrete populations. If False, the right side empirical distribution is used.
Returns	**statistic** : float Normalized k-sample Anderson-Darling test statistic. **critical_values** : array The critical values for significance levels 25%, 10%, 5%, 2.5%, 1%. **significance_level** : float An approximate significance level at which the null hypothesis for the provided samples can be rejected.
Raises	**ValueError** If less than 2 samples are provided, a sample is empty, or no distinct observations are in the samples.

See also:

`ks_2samp`	2 sample Kolmogorov-Smirnov test
`anderson`	1 sample Anderson-Darling test

Notes

[R299] Defines three versions of the k-sample Anderson-Darling test: one for continuous distributions and two for discrete distributions, in which ties between samples may occur. The default of this routine is to compute the version based on the midrank empirical distribution function. This test is applicable to continuous and discrete data. If midrank is set to False, the right side empirical distribution is used for a test for discrete data. According to [R299], the two discrete test statistics differ only slightly if a few collisions due to round-off errors occur in the test not adjusted for ties between samples.

New in version 0.14.0.

References

[R299]

Examples

```
>>> from scipy import stats
>>> np.random.seed(314159)
```

The null hypothesis that the two random samples come from the same distribution can be rejected at the 5% level because the returned test value is greater than the critical value for 5% (1.961) but not at the 2.5% level. The interpolation gives an approximate significance level of 3.1%:

```
>>> stats.anderson_ksamp([np.random.normal(size=50),
... np.random.normal(loc=0.5, size=30)])
(2.4615796189876105,
  array([ 0.325,  1.226,  1.961,  2.718,  3.752]),
  0.03134990135800783)
```

The null hypothesis cannot be rejected for three samples from an identical distribution. The approximate p-value (87%) has to be computed by extrapolation and may not be very accurate:

```
>>> stats.anderson_ksamp([np.random.normal(size=50),
... np.random.normal(size=30), np.random.normal(size=20)])
(-0.73091722665244196,
  array([ 0.44925884,  1.3052767 ,  1.9434184 ,  2.57696569,  3.41634856]),
  0.8789283903979661)
```

`scipy.stats.`**`binom_test`**(*x*, *n=None*, *p=0.5*)

Perform a test that the probability of success is p.

This is an exact, two-sided test of the null hypothesis that the probability of success in a Bernoulli experiment is *p*.

Parameters	**x** : integer or array_like the number of successes, or if x has length 2, it is the number of successes and the number of failures. **n** : integer the number of trials. This is ignored if x gives both the number of successes and failures **p** : float, optional The hypothesized probability of success. 0 <= p <= 1. The default value is p = 0.5
Returns	**p-value** : float The p-value of the hypothesis test

References

[R303]

`scipy.stats.`**`fligner`**(**args*, ***kwds*)

Perform Fligner's test for equal variances.

Fligner's test tests the null hypothesis that all input samples are from populations with equal variances. Fligner's test is non-parametric in contrast to Bartlett's test `bartlett` and Levene's test `levene`.

Parameters

sample1, sample2, ... : array_like
    Arrays of sample data. Need not be the same length.

center : {'mean', 'median', 'trimmed'}, optional
    Keyword argument controlling which function of the data is used in computing the test statistic. The default is 'median'.

proportiontocut : float, optional
    When *center* is 'trimmed', this gives the proportion of data points to cut from each end. (See `scipy.stats.trim_mean`.) Default is 0.05.

Returns

Xsq : float
    The test statistic.

p-value : float
    The p-value for the hypothesis test.

Notes

As with Levene's test there are three variants of Fligner's test that differ by the measure of central tendency used in the test. See `levene` for more information.

References

[R317], [R318]

`scipy.stats.`**`median_test`**`(*args, **kwds)`

Mood's median test.

Test that two or more samples come from populations with the same median.

Let `n = len(args)` be the number of samples. The "grand median" of all the data is computed, and a contingency table is formed by classifying the values in each sample as being above or below the grand median. The contingency table, along with *correction* and *lambda_*, are passed to `scipy.stats.chi2_contingency` to compute the test statistic and p-value.

Parameters

sample1, sample2, ... : array_like
    The set of samples. There must be at least two samples. Each sample must be a one-dimensional sequence containing at least one value. The samples are not required to have the same length.

ties : str, optional
    Determines how values equal to the grand median are classified in the contingency table. The string must be one of:

```
"below":
    Values equal to the grand median are counted as "below".
"above":
    Values equal to the grand median are counted as "above".
"ignore":
    Values equal to the grand median are not counted.
```

    The default is "below".

correction : bool, optional
    If True, *and* there are just two samples, apply Yates' correction for continuity when computing the test statistic associated with the contingency table. Default is True.

lambda_ : float or str, optional.
    By default, the statistic computed in this test is Pearson's chi-squared statistic. *lambda_* allows a statistic from the Cressie-Read power divergence

family to be used instead. See `power_divergence` for details. Default is 1 (Pearson's chi-squared statistic).

Returns **stat** : float

The test statistic. The statistic that is returned is determined by *lambda_*. The default is Pearson's chi-squared statistic.

p : float

The p-value of the test.

m : float

The grand median.

table : ndarray

The contingency table. The shape of the table is (2, n), where n is the number of samples. The first row holds the counts of the values above the grand median, and the second row holds the counts of the values below the grand median. The table allows further analysis with, for example, `scipy.stats.chi2_contingency`, or with `scipy.stats.fisher_exact` if there are two samples, without having to recompute the table.

See also:

`kruskal`	Compute the Kruskal-Wallis H-test for independent samples.
`mannwhitneyu`	Computes the Mann-Whitney rank test on samples x and y.

Notes

New in version 0.15.0.

References

[R334], [R335]

Examples

A biologist runs an experiment in which there are three groups of plants. Group 1 has 16 plants, group 2 has 15 plants, and group 3 has 17 plants. Each plant produces a number of seeds. The seed counts for each group are:

```
Group 1: 10 14 14 18 20 22 24 25 31 31 32 39 43 43 48 49
Group 2: 28 30 31 33 34 35 36 40 44 55 57 61 91 92 99
Group 3:  0  3  9 22 23 25 25 33 34 34 40 45 46 48 62 67 84
```

The following code applies Mood's median test to these samples.

```
>>> g1 = [10, 14, 14, 18, 20, 22, 24, 25, 31, 31, 32, 39, 43, 43, 48, 49]
>>> g2 = [28, 30, 31, 33, 34, 35, 36, 40, 44, 55, 57, 61, 91, 92, 99]
>>> g3 = [0, 3, 9, 22, 23, 25, 25, 33, 34, 34, 40, 45, 46, 48, 62, 67, 84]
>>> from scipy.stats import median_test
>>> stat, p, med, tbl = median_test(g1, g2, g3)
```

The median is

```
>>> med
34.0
```

and the contingency table is

```
>>> tbl
array([[ 5, 10,  7],
       [11,  5, 10]])
```

p is too large to conclude that the medians are not the same:

```
>>> p
0.12609082774093244
```

The "G-test" can be performed by passing `lambda_="log-likelihood"` to `median_test`.

```
>>> g, p, med, tbl = median_test(g1, g2, g3, lambda_="log-likelihood")
>>> p
0.12224779737117837
```

The median occurs several times in the data, so we'll get a different result if, for example, `ties="above"` is used:

```
>>> stat, p, med, tbl = median_test(g1, g2, g3, ties="above")
>>> p
0.063873276069553273
```

```
>>> tbl
array([[ 5, 11,  9],
       [11,  4,  8]])
```

This example demonstrates that if the data set is not large and there are values equal to the median, the p-value can be sensitive to the choice of *ties*.

`scipy.stats.`**`mood`**(*x*, *y*, *axis=0*)

Perform Mood's test for equal scale parameters.

Mood's two-sample test for scale parameters is a non-parametric test for the null hypothesis that two samples are drawn from the same distribution with the same scale parameter.

Parameters

x, y : array_like

Arrays of sample data.

axis : int, optional

The axis along which the samples are tested. *x* and *y* can be of different length along *axis*. If *axis* is None, *x* and *y* are flattened and the test is done on all values in the flattened arrays.

Returns

z : scalar or ndarray

The z-score for the hypothesis test. For 1-D inputs a scalar is returned.

p-value : scalar ndarray

The p-value for the hypothesis test.

See also:

`fligner`	A non-parametric test for the equality of k variances
`ansari`	A non-parametric test for the equality of 2 variances
`bartlett`	A parametric test for equality of k variances in normal samples
`levene`	A parametric test for equality of k variances

Notes

The data are assumed to be drawn from probability distributions `f(x)` and `f(x/s) / s` respectively, for some probability density function f. The null hypothesis is that `s == 1`.

For multi-dimensional arrays, if the inputs are of shapes `(n0, n1, n2, n3)` and `(n0, m1, n2, n3)`, then if `axis=1`, the resulting z and p values will have shape `(n0, n2, n3)`. Note that `n1` and `m1` don't have to be equal, but the other dimensions do.

Examples

```
>>> from scipy import stats
>>> x2 = np.random.randn(2, 45, 6, 7)
>>> x1 = np.random.randn(2, 30, 6, 7)
>>> z, p = stats.mood(x1, x2, axis=1)
>>> p.shape
(2, 6, 7)
```

Find the number of points where the difference in scale is not significant:

```
>>> (p > 0.1).sum()
74
```

Perform the test with different scales:

```
>>> x1 = np.random.randn(2, 30)
>>> x2 = np.random.randn(2, 35) * 10.0
>>> stats.mood(x1, x2, axis=1)
(array([-5.84332354, -5.6840814 ]), array([5.11694980e-09, 1.31517628e-08]))
```

`boxcox`(x[, lmbda, alpha])	Return a positive dataset transformed by a Box-Cox power transformation.
`boxcox_normmax`(x[, brack, method])	Compute optimal Box-Cox transform parameter for input data.
`boxcox_llf`(lmb, data)	The boxcox log-likelihood function.
`entropy`(pk[, qk, base])	Calculate the entropy of a distribution for given probability values.

`scipy.stats.`**`boxcox`**(*x*, *lmbda=None*, *alpha=None*)

Return a positive dataset transformed by a Box-Cox power transformation.

Parameters

x : ndarray

Input array. Should be 1-dimensional.

lmbda : {None, scalar}, optional

If *lmbda* is not None, do the transformation for that value.

If *lmbda* is None, find the lambda that maximizes the log-likelihood function and return it as the second output argument.

alpha : {None, float}, optional

If `alpha` is not None, return the `100 * (1-alpha)%` confidence interval for *lmbda* as the third output argument. Must be between 0.0 and 1.0.

Returns

boxcox : ndarray

Box-Cox power transformed array.

maxlog : float, optional

If the *lmbda* parameter is None, the second returned argument is the lambda that maximizes the log-likelihood function.

(min_ci, max_ci) : tuple of float, optional

If *lmbda* parameter is None and `alpha` is not None, this returned tuple of floats represents the minimum and maximum confidence limits given `alpha`.

See also:

`probplot`, `boxcox_normplot`, `boxcox_normmax`, `boxcox_llf`

Notes

The Box-Cox transform is given by:

```
y = (x**lmbda - 1) / lmbda,  for lmbda > 0
    log(x),                  for lmbda = 0
```

`boxcox` requires the input data to be positive. Sometimes a Box-Cox transformation provides a shift parameter to achieve this; `boxcox` does not. Such a shift parameter is equivalent to adding a positive constant to x before calling `boxcox`.

The confidence limits returned when `alpha` is provided give the interval where:

$$llf(\hat{\lambda}) - llf(\lambda) < \frac{1}{2}\chi^2(1 - \alpha, 1),$$

with `llf` the log-likelihood function and χ^2 the chi-squared function.

References

G.E.P. Box and D.R. Cox, “An Analysis of Transformations”, Journal of the Royal Statistical Society B, 26, 211-252 (1964).

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

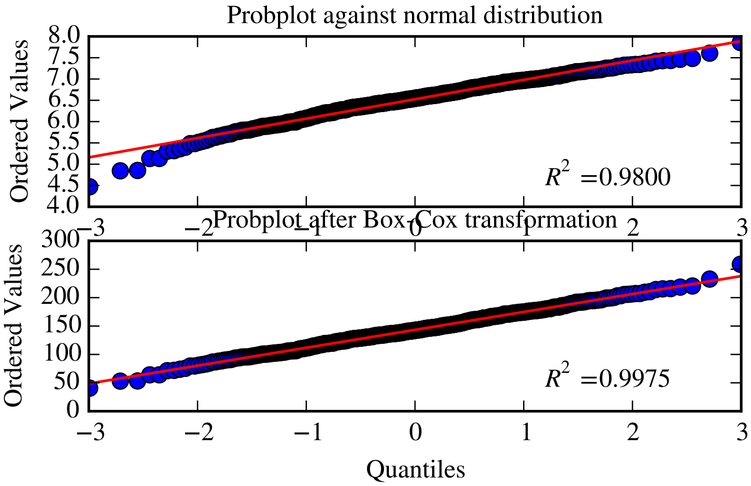
We generate some random variates from a non-normal distribution and make a probability plot for it, to show it is non-normal in the tails:

```
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> stats.probplot(x, dist=stats.norm, plot=ax1)
>>> ax1.set_xlabel('')
>>> ax1.set_title('Probplot against normal distribution')
```

We now use `boxcox` to transform the data so it’s closest to normal:

```
>>> ax2 = fig.add_subplot(212)
>>> xt, _ = stats.boxcox(x)
>>> stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Box-Cox transformation')
```

```
>>> plt.show()
```



`scipy.stats.`**`boxcox_normmax`**(*x*, *brack=(-2.0, 2.0)*, *method='pearsonr'*)

Compute optimal Box-Cox transform parameter for input data.

Parameters **x** : array_like

Input array.

brack : 2-tuple, optional

The starting interval for a downhill bracket search with *optimize.brent*. Note that this is in most cases not critical; the final result is allowed to be outside this bracket.

method : str, optional

The method to determine the optimal transform parameter (`boxcox` `lmbda` parameter). Options are:

'pearsonr' (default)

Maximizes the Pearson correlation coefficient between `y = boxcox(x)` and the expected values for `y` if *x* would be normally-distributed.

'mle' Minimizes the log-likelihood `boxcox_llf`. This is the method used in `boxcox`.

'all' Use all optimization methods available, and return all results. Useful to compare different methods.

Returns **maxlog** : float or ndarray

The optimal transform parameter found. An array instead of a scalar for `method='all'`.

See also:

`boxcox`, `boxcox_llf`, `boxcox_normplot`

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234)  # make this example reproducible
```

Generate some data and determine optimal `lmbda` in various ways:

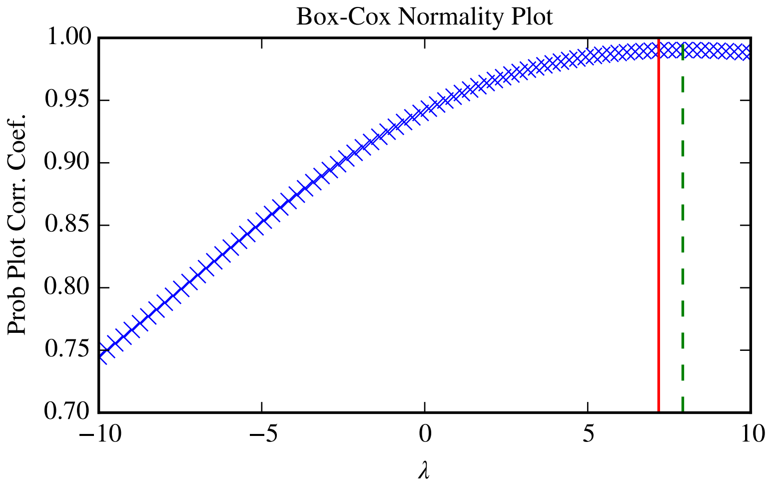
```
>>> x = stats.loggamma.rvs(5, size=30) + 5
>>> y, lmax_mle = stats.boxcox(x)
```

```
>>> lmax_pearsonr = stats.boxcox_normmax(x)
```

```
>>> lmax_mle
7.177...
>>> lmax_pearsonr
7.916...
>>> stats.boxcox_normmax(x, method='all')
array([ 7.91667384,  7.17718692])
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> stats.boxcox_normplot(x, -10, 10, plot=ax)
>>> ax.axvline(lmax_mle, color='r')
>>> ax.axvline(lmax_pearsonr, color='g', ls='--')
```

```
>>> plt.show()
```



scipy.stats.**boxcox_llf**(*lmb*, *data*)

The boxcox log-likelihood function.

Parameters **lmb** : scalar

Parameter for Box-Cox transformation. See `boxcox` for details.

data : array_like

Data to calculate Box-Cox log-likelihood for. If *data* is multi-dimensional, the log-likelihood is calculated along the first axis.

Returns **llf** : float or ndarray

Box-Cox log-likelihood of *data* given *lmb*. A float for 1-D *data*, an array otherwise.

See also:

`boxcox`, `probplot`, `boxcox_normplot`, `boxcox_normmax`

Notes

The Box-Cox log-likelihood function is defined here as

$$llf = (\lambda - 1)\sum_i(\log(x_i)) - N/2\log(\sum_i(y_i - \bar{y})^2/N),$$

where `y` is the Box-Cox transformed input data `x`.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.axes_grid1.inset_locator import inset_axes
>>> np.random.seed(1245)
```

Generate some random variates and calculate Box-Cox log-likelihood values for them for a range of `lmbda` values:

```
>>> x = stats.loggamma.rvs(5, loc=10, size=1000)
>>> lmbdas = np.linspace(-2, 10)
>>> llf = np.zeros(lmbdas.shape, dtype=np.float)
>>> for ii, lmbda in enumerate(lmbdas):
...     llf[ii] = stats.boxcox_llf(lmbda, x)
```

Also find the optimal lmbda value with `boxcox`:

```
>>> x_most_normal, lmbda_optimal = stats.boxcox(x)
```

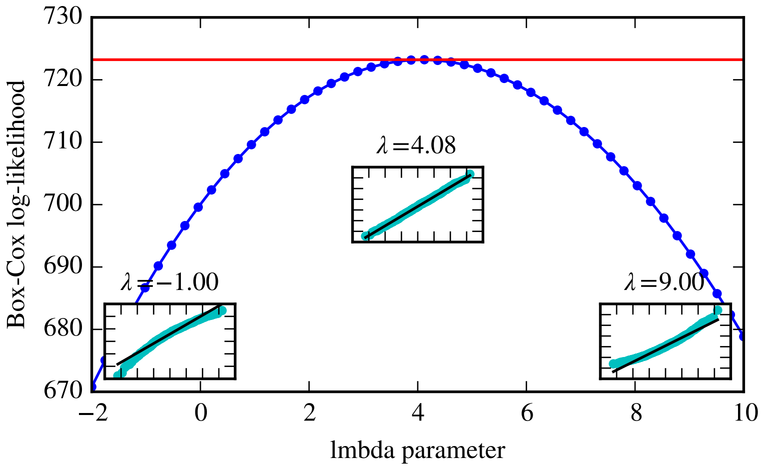
Plot the log-likelihood as function of lmbda. Add the optimal lmbda as a horizontal line to check that that's really the optimum:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(lmbdas, llf, 'b.-')
>>> ax.axhline(stats.boxcox_llf(lmbda_optimal, x), color='r')
>>> ax.set_xlabel('lmbda parameter')
>>> ax.set_ylabel('Box-Cox log-likelihood')
```

Now add some probability plots to show that where the log-likelihood is maximized the data transformed with `boxcox` looks closest to normal:

```
>>> locs = [3, 10, 4]  # 'lower left', 'center', 'lower right'
>>> for lmbda, loc in zip([-1, lmbda_optimal, 9], locs):
...     xt = stats.boxcox(x, lmbda=lmbda)
...     (osm, osr), (slope, intercept, r_sq) = stats.probplot(xt)
...     ax_inset = inset_axes(ax, width="20%", height="20%", loc=loc)
...     ax_inset.plot(osm, osr, 'c.', osm, slope*osm + intercept, 'k-')
...     ax_inset.set_xticklabels([])
...     ax_inset.set_yticklabels([])
...     ax_inset.set_title('$\lambda=%1.2f$' % lmbda)
```

```
>>> plt.show()
```



`scipy.stats.`**`entropy`**(*pk*, *qk=None*, *base=None*)

Calculate the entropy of a distribution for given probability values.

If only probabilities *pk* are given, the entropy is calculated as `S = -sum(pk * log(pk), axis=0)`.

If *qk* is not None, then compute the Kullback-Leibler divergence `S = sum(pk * log(pk / qk), axis=0)`.

This routine will normalize *pk* and *qk* if they don't sum to 1.

Parameters **pk** : sequence

Defines the (discrete) distribution. `pk[i]` is the (possibly unnormalized) probability of event `i`.

qk : sequence, optional

Sequence against which the relative entropy is computed. Should be in the same format as *pk*.

base : float, optional

The logarithmic base to use, defaults to `e` (natural logarithm).

Returns **S** : float

The calculated entropy.

5.34.5 Circular statistical functions

`circmean`(samples[, high, low, axis])	Compute the circular mean for samples in a range.
`circvar`(samples[, high, low, axis])	Compute the circular variance for samples assumed to be in a range
`circstd`(samples[, high, low, axis])	Compute the circular standard deviation for samples assumed to be in the range [low to high

`scipy.stats.`**`circmean`**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*)

Compute the circular mean for samples in a range.

Parameters **samples** : array_like

Input array.

high : float or int, optional

High boundary for circular mean range. Default is `2*pi`.

low : float or int, optional

Low boundary for circular mean range. Default is 0.

axis : int, optional
Axis along which means are computed. The default is to compute the mean of the flattened array.

Returns **circmean** : float
Circular mean.

`scipy.stats.`**`circvar`**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*)

Compute the circular variance for samples assumed to be in a range

Parameters **samples** : array_like
Input array.

low : float or int, optional
Low boundary for circular variance range. Default is 0.

high : float or int, optional
High boundary for circular variance range. Default is `2*pi`.

axis : int, optional
Axis along which variances are computed. The default is to compute the variance of the flattened array.

Returns **circvar** : float
Circular variance.

Notes

This uses a definition of circular variance that in the limit of small angles returns a number close to the 'linear' variance.

`scipy.stats.`**`circstd`**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*)

Compute the circular standard deviation for samples assumed to be in the range [low to high].

Parameters **samples** : array_like
Input array.

low : float or int, optional
Low boundary for circular standard deviation range. Default is 0.

high : float or int, optional
High boundary for circular standard deviation range. Default is `2*pi`.

axis : int, optional
Axis along which standard deviations are computed. The default is to compute the standard deviation of the flattened array.

Returns **circstd** : float
Circular standard deviation.

Notes

This uses a definition of circular standard deviation that in the limit of small angles returns a number close to the 'linear' standard deviation.

5.34.6 Contingency table functions

`chi2_contingency`(observed[, correction, **lambda_**])	Chi-square test of independence of variables in a contingency table.
`contingency.expected_freq`(observed)	Compute the expected frequencies from a contingency table.
`contingency.margins`(a)	Return a list of the marginal sums of the array *a*.
`fisher_exact`(table[, alternative])	Performs a Fisher exact test on a 2x2 contingency table.

`scipy.stats.`**`chi2_contingency`**(*observed*, *correction=True*, *lambda_=None*)

Chi-square test of independence of variables in a contingency table.

This function computes the chi-square statistic and p-value for the hypothesis test of independence of the observed frequencies in the contingency table [R304] *observed*. The expected frequencies are computed based on the marginal sums under the assumption of independence; see `scipy.stats.contingency.expected_freq`. The number of degrees of freedom is (expressed using numpy functions and attributes):

```
dof = observed.size - sum(observed.shape) + observed.ndim - 1
```

Parameters

observed : array_like
    The contingency table. The table contains the observed frequencies (i.e. number of occurrences) in each category. In the two-dimensional case, the table is often described as an "R x C table".

correction : bool, optional
    If True, *and* the degrees of freedom is 1, apply Yates' correction for continuity. The effect of the correction is to adjust each observed value by 0.5 towards the corresponding expected value.

lambda_ : float or str, optional.
    By default, the statistic computed in this test is Pearson's chi-squared statistic [R305]. *lambda_* allows a statistic from the Cressie-Read power divergence family [R306] to be used instead. See `power_divergence` for details.

Returns

chi2 : float
    The test statistic.

p : float
    The p-value of the test

dof : int
    Degrees of freedom

expected : ndarray, same shape as *observed*
    The expected frequencies, based on the marginal sums of the table.

See also:

`contingency.expected_freq`, `fisher_exact`, `chisquare`, `power_divergence`

Notes

An often quoted guideline for the validity of this calculation is that the test should be used only if the observed and expected frequency in each cell is at least 5.

This is a test for the independence of different categories of a population. The test is only meaningful when the dimension of *observed* is two or more. Applying the test to a one-dimensional table will always result in *expected* equal to *observed* and a chi-square statistic equal to 0.

This function does not handle masked arrays, because the calculation does not make sense with missing values.

Like stats.chisquare, this function computes a chi-square statistic; the convenience this function provides is to figure out the expected frequencies and degrees of freedom from the given contingency table. If these were already known, and if the Yates' correction was not required, one could use stats.chisquare. That is, if one calls:

```
chi2, p, dof, ex = chi2_contingency(obs, correction=False)
```

then the following is true:

```
(chi2, p) == stats.chisquare(obs.ravel(), f_exp=ex.ravel(),
                             ddof=obs.size - 1 - dof)
```

The *lambda_* argument was added in version 0.13.0 of scipy.

References

[R304], [R305], [R306]

Examples

A two-way example (2 x 3):

```
>>> from scipy.stats import chi2_contingency
>>> obs = np.array([[10, 10, 20], [20, 20, 20]])
>>> chi2_contingency(obs)
(2.7777777777777777,
 0.24935220877729619,
 2,
 array([[ 12.,  12.,  16.],
        [ 18.,  18.,  24.]]))
```

Perform the test using the log-likelihood ratio (i.e. the “G-test”) instead of Pearson’s chi-squared statistic.

```
>>> g, p, dof, expctd = chi2_contingency(obs, lambda_="log-likelihood")
>>> g, p
(2.7688587616781319, 0.25046668010954165)
```

A four-way example (2 x 2 x 2 x 2):

```
>>> obs = np.array(
...     [[[[12, 17],
...        [11, 16]],
...       [[11, 12],
...        [15, 16]]],
...      [[[23, 15],
...        [30, 22]],
...       [[14, 17],
...        [15, 16]]]])
>>> chi2_contingency(obs)
(8.7584514426741897,
 0.64417725029295503,
 11,
 array([[[[ 14.15462386,  14.15462386],
          [ 16.49423111,  16.49423111]],
         [[ 11.2461395 ,  11.2461395 ],
          [ 13.10500554,  13.10500554]]],
        [[[ 19.5591166 ,  19.5591166 ],
          [ 22.79202844,  22.79202844]],
         [[ 15.54012004,  15.54012004],
          [ 18.10873492,  18.10873492]]]]))
```

`scipy.stats.contingency.`**`expected_freq`**`(`*observed*`)`

Compute the expected frequencies from a contingency table.

Given an n-dimensional contingency table of observed frequencies, compute the expected frequencies for the table based on the marginal sums under the assumption that the groups associated with each dimension are independent.

Parameters **observed** : array_like

The table of observed frequencies. (While this function can handle a 1-D array, that case is trivial. Generally *observed* is at least 2-D.)

Returns **expected** : ndarray of float64

The expected frequencies, based on the marginal sums of the table. Same shape as *observed*.

Examples

```
>>> observed = np.array([[10, 10, 20],[20, 20, 20]])
>>> from scipy.stats import expected_freq
>>> expected_freq(observed)
array([[ 12.,  12.,  16.],
       [ 18.,  18.,  24.]])
```

`scipy.stats.contingency.`**`margins`**(*a*)

Return a list of the marginal sums of the array *a*.

Parameters **a** : ndarray

The array for which to compute the marginal sums.

Returns **margsums** : list of ndarrays

A list of length *a.ndim*. *margsums[k]* is the result of summing *a* over all axes except *k*; it has the same number of dimensions as *a*, but the length of each axis except axis *k* will be 1.

Examples

```
>>> a = np.arange(12).reshape(2, 6)
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11]])
>>> m0, m1 = margins(a)
>>> m0
array([[15],
       [51]])
>>> m1
array([[ 6,  8, 10, 12, 14, 16]])
```

```
>>> b = np.arange(24).reshape(2,3,4)
>>> m0, m1, m2 = margins(b)
>>> m0
array([[[ 66]],
       [[210]]])
>>> m1
array([[[ 60],
        [ 92],
        [124]]])
>>> m2
array([[[60, 66, 72, 78]]])
```

`scipy.stats.`**`fisher_exact`**(*table*, *alternative='two-sided'*)

Performs a Fisher exact test on a 2x2 contingency table.

Parameters **table** : array_like of ints

A 2x2 contingency table. Elements should be non-negative integers.

alternative : {'two-sided', 'less', 'greater'}, optional

Which alternative hypothesis to the null hypothesis the test uses. Default is 'two-sided'.

Returns **oddsratio** : float

This is prior odds ratio and not a posterior estimate.

p_value : float

P-value, the probability of obtaining a distribution at least as extreme as the one that was actually observed, assuming that the null hypothesis is true.

See also:

chi2_contingency Chi-square test of independence of variables in a contingency table.

Notes

The calculated odds ratio is different from the one R uses. This scipy implementation returns the (more common) "unconditional Maximum Likelihood Estimate", while R uses the "conditional Maximum Likelihood Estimate".

For tables with large numbers, the (inexact) chi-square test implemented in the function `chi2_contingency` can also be used.

Examples

Say we spend a few days counting whales and sharks in the Atlantic and Indian oceans. In the Atlantic ocean we find 8 whales and 1 shark, in the Indian ocean 2 whales and 5 sharks. Then our contingency table is:

```
        Atlantic  Indian
whales     8        2
sharks     1        5
```

We use this table to find the p-value:

```
>>> import scipy.stats as stats
>>> oddsratio, pvalue = stats.fisher_exact([[8, 2], [1, 5]])
>>> pvalue
0.0349...
```

The probability that we would observe this or an even more imbalanced ratio by chance is about 3.5%. A commonly used significance level is 5%–if we adopt that, we can therefore conclude that our observed imbalance is statistically significant; whales prefer the Atlantic while sharks prefer the Indian ocean.

5.34.7 Plot-tests

`ppcc_max`(x[, brack, dist])	Returns the shape parameter that maximizes the probability plot correlation coefficient fo
`ppcc_plot`(x, a, b[, dist, plot, N])	Calculate and optionally plot probability plot correlation coefficient.
`probplot`(x[, sparams, dist, fit, plot])	Calculate quantiles for a probability plot, and optionally show the plot.
`boxcox_normplot`(x, la, lb[, plot, N])	Compute parameters for a Box-Cox normality plot, optionally show it.

`scipy.stats.`**`ppcc_max`** (*x*, *brack=(0.0, 1.0)*, *dist='tukeylambda'*)

Returns the shape parameter that maximizes the probability plot correlation coefficient for the given data to a one-parameter family of distributions.

See also ppcc_plot

`scipy.stats.`**`ppcc_plot`** (*x*, *a*, *b*, *dist='tukeylambda'*, *plot=None*, *N=80*)

Calculate and optionally plot probability plot correlation coefficient.

The probability plot correlation coefficient (PPCC) plot can be used to determine the optimal shape parameter for a one-parameter family of distributions. It cannot be used for distributions without shape parameters (like the normal distribution) or with multiple shape parameters.

By default a Tukey-Lambda distribution (*stats.tukeylambda*) is used. A Tukey-Lambda PPCC plot interpolates from long-tailed to short-tailed distributions via an approximately normal one, and is therefore particularly useful in practice.

Parameters

x : array_like
  Input array.

a, b: scalar
  Lower and upper bounds of the shape parameter to use.

dist : str or stats.distributions instance, optional
  Distribution or distribution function name. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted. The default is `'tukeylambda'`.

plot : object, optional
  If given, plots PPCC against the shape parameter. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

N : int, optional
  Number of points on the horizontal axis (equally distributed from *a* to *b*).

Returns

svals : ndarray
  The shape values for which *ppcc* was calculated.

ppcc : ndarray
  The calculated probability plot correlation coefficient values.

See also:

`ppcc_max`, `probplot`, `boxcox_normplot`, `tukeylambda`

References

J.J. Filliben, "The Probability Plot Correlation Coefficient Test for Normality", Technometrics, Vol. 17, pp. 111-117, 1975.

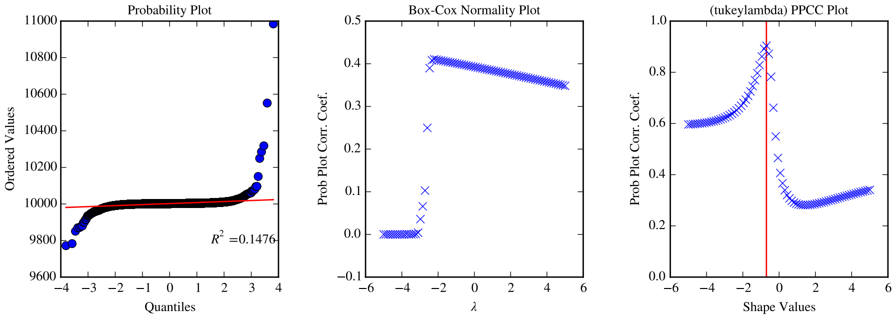
Examples

First we generate some random data from a Tukey-Lambda distribution, with shape parameter -0.7:

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234567)
>>> x = stats.tukeylambda.rvs(-0.7, loc=2, scale=0.5, size=10000) + 1e4
```

Now we explore this data with a PPCC plot as well as the related probability plot and Box-Cox normplot. A red line is drawn where we expect the PPCC value to be maximal (at the shape parameter -0.7 used above):

```
>>> fig = plt.figure(figsize=(12, 4))
>>> ax1 = fig.add_subplot(131)
>>> ax2 = fig.add_subplot(132)
>>> ax3 = fig.add_subplot(133)
>>> stats.probplot(x, plot=ax1)
>>> stats.boxcox_normplot(x, -5, 5, plot=ax2)
>>> stats.ppcc_plot(x, -5, 5, plot=ax3)
>>> ax3.vlines(-0.7, 0, 1, colors='r', label='Expected shape value')
>>> plt.show()
```



`scipy.stats.`**`probplot`**(*x*, *sparams=()*, *dist='norm'*, *fit=True*, *plot=None*)

Calculate quantiles for a probability plot, and optionally show the plot.

Generates a probability plot of sample data against the quantiles of a specified theoretical distribution (the normal distribution by default). `probplot` optionally calculates a best-fit line for the data and plots the results using Matplotlib or a given plot function.

Parameters

x : array_like
    Sample/response data from which `probplot` creates the plot.

sparams : tuple, optional
    Distribution-specific shape parameters (shape parameters plus location and scale).

dist : str or stats.distributions instance, optional
    Distribution or distribution function name. The default is 'norm' for a normal probability plot. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted.

fit : bool, optional
    Fit a least-squares regression (best-fit) line to the sample data if True (default).

plot : object, optional
    If given, plots the quantiles and least squares fit. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

Returns

(osm, osr) : tuple of ndarrays
    Tuple of theoretical quantiles (osm, or order statistic medians) and ordered responses (osr). *osr* is simply sorted input *x*. For details on how *osm* is calculated see the Notes section.

(slope, intercept, r) : tuple of floats, optional
    Tuple containing the result of the least-squares fit, if that is performed by `probplot`. *r* is the square root of the coefficient of determination. If `fit=False` and `plot=None`, this tuple is not returned.

Notes

Even if *plot* is given, the figure is not shown or saved by `probplot`; `plt.show()` or `plt.savefig('figname.png')` should be used after calling `probplot`.

`probplot` generates a probability plot, which should not be confused with a Q-Q or a P-P plot. Statsmodels has more extensive functionality of this type, see `statsmodels.api.ProbPlot`.

The formula used for the theoretical quantiles (horizontal axis of the probability plot) is Filliben's estimate:

```
quantiles = dist.ppf(val), for

        0.5**(1/n),                  for i = n
  val = (i - 0.3175) / (n + 0.365),  for i = 2, ..., n-1
        1 - 0.5**(1/n),              for i = 1
```

where `i` indicates the i-th ordered value and `n` is the total number of values.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> nsample = 100
>>> np.random.seed(7654321)
```

A t distribution with small degrees of freedom:

```
>>> ax1 = plt.subplot(221)
>>> x = stats.t.rvs(3, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

A t distribution with larger degrees of freedom:

```
>>> ax2 = plt.subplot(222)
>>> x = stats.t.rvs(25, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

A mixture of two normal distributions with broadcasting:

```
>>> ax3 = plt.subplot(223)
>>> x = stats.norm.rvs(loc=[0,5], scale=[1,1.5],
...                     size=(nsample/2.,2)).ravel()
>>> res = stats.probplot(x, plot=plt)
```

A standard normal distribution:

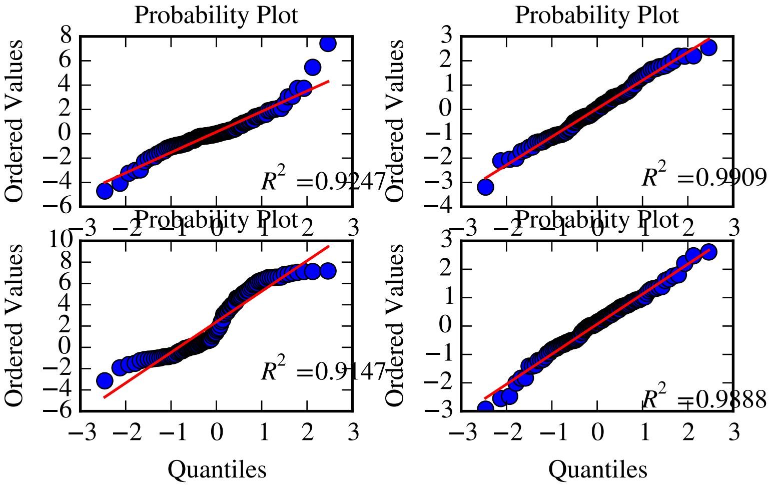
```
>>> ax4 = plt.subplot(224)
>>> x = stats.norm.rvs(loc=0, scale=1, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

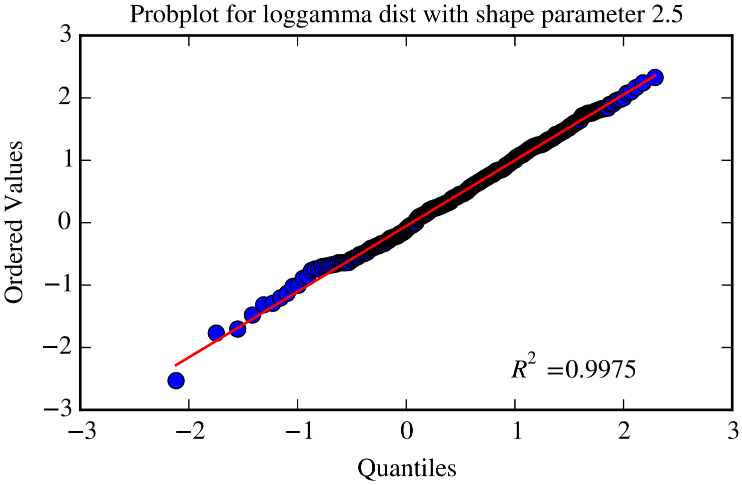
Produce a new figure with a loggamma distribution, using the `dist` and `sparams` keywords:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> x = stats.loggamma.rvs(c=2.5, size=500)
>>> stats.probplot(x, dist=stats.loggamma, sparams=(2.5,), plot=ax)
>>> ax.set_title("Probplot for loggamma dist with shape parameter 2.5")
```

Show the results with Matplotlib:

```
>>> plt.show()
```





`scipy.stats.`**`boxcox_normplot`** (*x*, *la*, *lb*, *plot=None*, *N=80*)

Compute parameters for a Box-Cox normality plot, optionally show it.

A Box-Cox normality plot shows graphically what the best transformation parameter is to use in `boxcox` to obtain a distribution that is close to normal.

Parameters **x** : array_like

Input array.

la, lb : scalar

The lower and upper bounds for the `lmbda` values to pass to `boxcox` for Box-Cox transformations. These are also the limits of the horizontal axis of the plot if that is generated.

plot : object, optional

If given, plots the quantiles and least squares fit. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

N : int, optional

Number of points on the horizontal axis (equally distributed from *la* to *lb*).

Returns **lmbdas** : ndarray

The `lmbda` values for which a Box-Cox transform was done.

ppcc : ndarray

Probability Plot Correlelation Coefficient, as obtained from `probplot` when fitting the Box-Cox transformed input *x* against a normal distribution.

See also:

`probplot`, `boxcox`, `boxcox_normmax`, `boxcox_llf`, `ppcc_max`

Notes

Even if *plot* is given, the figure is not shown or saved by `boxcox_normplot`; `plt.show()` or `plt.savefig('figname.png')` should be used after calling `probplot`.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

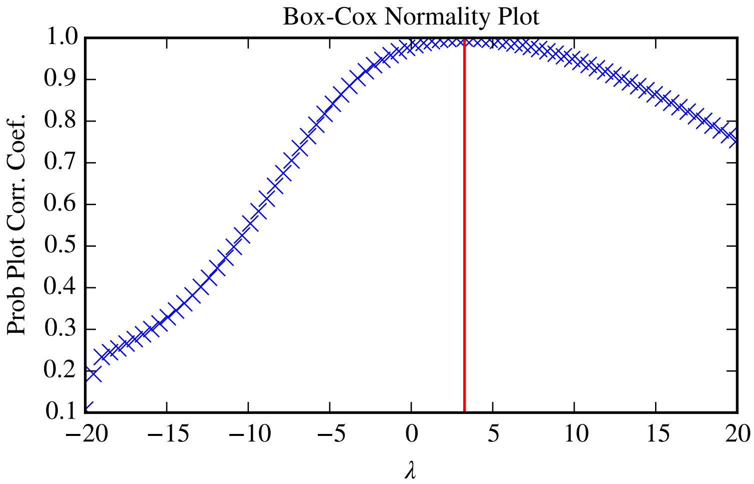
Generate some non-normally distributed data, and create a Box-Cox plot:

```
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> stats.boxcox_normplot(x, -20, 20, plot=ax)
```

Determine and plot the optimal `lmbda` to transform `x` and plot it in the same plot:

```
>>> _, maxlog = stats.boxcox(x)
>>> ax.axvline(maxlog, color='r')
```

```
>>> plt.show()
```



5.34.8 Masked statistics functions

Statistical functions for masked arrays (`scipy.stats.mstats`)

This module contains a large number of statistical functions that can be used with masked arrays.

Most of these functions are similar to those in scipy.stats but might have small differences in the API or in the algorithm used. Since this is a relatively new package, some API changes are still possible.

`argstoarray`(*args)	Constructs a 2D array from a group of sequences.
`betai`(a, b, x)	Returns the incomplete beta function.
`chisquare`(f_obs[, f_exp, ddof, axis])	Calculates a one-way chi square test.
`count_tied_groups`(x[, use_missing])	Counts the number of tied values.
`describe`(a[, axis, ddof])	Computes several descriptive statistics of the passed array.
`f_oneway`(*args)	Performs a 1-way ANOVA, returning an F-value and probability given a
`f_value_wilks_lambda`(ER, EF, dfnum, dfden, a, b)	Calculation of Wilks lambda F-statistic for multivariate data, per Maxwe
`find_repeats`(arr)	Find repeats in arr and return a tuple (repeats, repeat_count).
`friedmanchisquare`(*args)	Friedman Chi-Square is a non-parametric, one-way within-subjects AN
`kendalltau`(x, y[, use_ties, use_missing])	Computes Kendall's rank correlation tau on two variables *x* and *y*.
`kendalltau_seasonal`(x)	Computes a multivariate Kendall's rank correlation tau, for seasonal data
`kruskalwallis`(*args)	Compute the Kruskal-Wallis H-test for independent samples
`ks_twosamp`(data1, data2[, alternative])	Computes the Kolmogorov-Smirnov test on two samples.
`kurtosis`(a[, axis, fisher, bias])	Computes the kurtosis (Fisher or Pearson) of a dataset.
`kurtosistest`(a[, axis])	Tests whether a dataset has normal kurtosis
`linregress`(*args)	Calculate a regression line
`mannwhitneyu`(x, y[, use_continuity])	Computes the Mann-Whitney statistic
`plotting_positions`(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
`mode`(a[, axis])	Returns an array of the modal (most common) value in the passed array.
`moment`(a[, moment, axis])	Calculates the nth moment about the mean for a sample.
`mquantiles`(a[, prob, alphap, betap, axis, limit])	Computes empirical quantiles for a data array.
`msign`(x)	Returns the sign of x, or 0 if x is masked.
`normaltest`(a[, axis])	Tests whether a sample differs from a normal distribution.
`obrientransform`(*args)	Computes a transform on input data (any number of columns).
`pearsonr`(x, y)	Calculates a Pearson correlation coefficient and the p-value for testing n
`plotting_positions`(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
`pointbiserialr`(x, y)	Calculates a point biserial correlation coefficient and the associated p-va
`rankdata`(data[, axis, use_missing])	Returns the rank (also known as order statistics) of each data point along
`scoreatpercentile`(data, per[, limit, ...])	Calculate the score at the given 'per' percentile of the sequence a.
`sem`(a[, axis, ddof])	Calculates the standard error of the mean of the input array.
`signaltonoise`(*args, **kwds)	`signaltonoise` is deprecated!
`skew`(a[, axis, bias])	Computes the skewness of a data set.
`skewtest`(a[, axis])	Tests whether the skew is different from the normal distribution.
`spearmanr`(x, y[, use_ties])	Calculates a Spearman rank-order correlation coefficient and the p-value
`theilslopes`(y[, x, alpha])	Computes the Theil-Sen estimator for a set of points (x, y).
`threshold`(a[, threshmin, threshmax, newval])	Clip array to a given value.
`tmax`(a, upperlimit[, axis, inclusive])	Compute the trimmed maximum
`tmean`(a[, limits, inclusive])	Compute the trimmed mean.
`tmin`(a[, lowerlimit, axis, inclusive])	Compute the trimmed minimum
`trim`(a[, limits, inclusive, relative, axis])	Trims an array by masking the data outside some given limits.
`trima`(a[, limits, inclusive])	Trims an array by masking the data outside some given limits.
`trimboth`(data[, proportiontocut, inclusive, ...])	Trims the smallest and largest data values.
`trimmed_stde`(a[, limits, inclusive, axis])	Returns the standard error of the trimmed mean along the given axis.

Table 5.267 – continued from previous page

`trimr`(a[, limits, inclusive, axis])	Trims an array by masking some proportion of the data on each end.
`trimtail`(data[, proportiontocut, tail, ...])	Trims the data by masking values from one tail.
`tsem`(a[, limits, inclusive])	Compute the trimmed standard error of the mean.
`ttest_onesamp`(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
`ttest_ind`(a, b[, axis])	Calculates the T-test for the means of TWO INDEPENDENT samples o
`ttest_onesamp`(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
`ttest_rel`(a, b[, axis])	Calculates the T-test on TWO RELATED samples of scores, a and b.
`tvar`(a[, limits, inclusive])	Compute the trimmed variance
`variation`(a[, axis])	Computes the coefficient of variation, the ratio of the biased standard de
`winsorize`(a[, limits, inclusive, inplace, axis])	Returns a Winsorized version of the input array.
`zmap`(scores, compare[, axis, ddof])	Calculates the relative z-scores.
`zscore`(a[, axis, ddof])	Calculates the z score of each value in the sample, relative to the sample

`scipy.stats.mstats.`**`argstoarray`**(**args*)

Constructs a 2D array from a group of sequences.

Sequences are filled with missing values to match the length of the longest sequence.

Parameters **args** : sequences

Group of sequences.

Returns **argstoarray** : MaskedArray

A (m x n) masked array, where m is the number of arguments and n the length of the longest argument.

Notes

`numpy.ma.row_stack` has identical behavior, but is called with a sequence of sequences.

`scipy.stats.mstats.`**`betai`**(*a*, *b*, *x*)

Returns the incomplete beta function.

I_x(a,b) = 1/B(a,b)*(Integral(0,x) of t^(a-1)(1-t)^(b-1) dt)

where a,b>0 and B(a,b) = G(a)*G(b)/(G(a+b)) where G(a) is the gamma function of a.

The standard broadcasting rules apply to a, b, and x.

Parameters **a** : array_like or float > 0

b : array_like or float > 0

x : array_like or float

x will be clipped to be no greater than 1.0 .

Returns **betai** : ndarray

Incomplete beta function.

`scipy.stats.mstats.`**`chisquare`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculates a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters **f_obs** : array_like

Observed frequencies in each category.

f_exp : array_like, optional

Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

"Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis : int or None, optional

The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq : float or ndarray

The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p : float or ndarray

The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

`power_divergence`, `mstats.chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References

[R336], [R337]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`scipy.stats.mstats.`**`count_tied_groups`**(*x*, *use_missing=False*)

Counts the number of tied values.

Parameters	**x** : sequence Sequence of data on which to counts the ties **use_missing** : bool, optional Whether to consider missing values as tied.
Returns	**count_tied_groups** : dict Returns a dictionary (nb of ties: nb of groups).

Examples

```
>>> from scipy.stats import mstats
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> mstats.count_tied_groups(z)
{2: 1, 3: 2}
```

In the above example, the ties were 0 (3x), 2 (3x) and 3 (2x).

```
>>> z = np.ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> mstats.count_tied_groups(z)
{2: 2, 3: 1}
>>> z[[1,-1]] = np.ma.masked
>>> mstats.count_tied_groups(z, use_missing=True)
{2: 2, 3: 1}
```

`scipy.stats.mstats.`**`describe`**(*a*, *axis=0*, *ddof=0*)

Computes several descriptive statistics of the passed array.

Parameters	**a** : array_like Data array **axis** : int or None, optional Axis along which to calculate statistics. Default 0. If None, compute over the whole array *a*. **ddof** : int, optional degree of freedom (default 0); note that default ddof is different from the same routine in stats.describe
Returns	**nobs** : int (size of the data (discarding missing values)

minmax : (int, int)
min, max

mean : float
arithmetic mean

variance : float
unbiased variance

skewness : float
biased skewness

kurtosis : float
biased kurtosis

Examples

```
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])
>>> describe(ma)
(array(3),
 (0, 2),
 1.0,
 1.0,
 masked_array(data = 0.0,
              mask = False,
        fill_value = 1e+20)
,
 -1.5)
```

`scipy.stats.mstats.`**`f_oneway`**`(`*`*args`*`)`

Performs a 1-way ANOVA, returning an F-value and probability given any number of groups. From Heiman, pp.394-7.

Usage: `f_oneway(*args)`, where `*args` is 2 or more arrays, one per treatment group.

Returns **statistic** : float
The computed F-value of the test.

pvalue : float
The associated p-value from the F-distribution.

`scipy.stats.mstats.`**`f_value_wilks_lambda`**`(`*ER*, *EF*, *dfnum*, *dfden*, *a*, *b*`)`

Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell & Delaney p.657.

`scipy.stats.mstats.`**`find_repeats`**`(`*arr*`)`

Find repeats in arr and return a tuple (repeats, repeat_count). Masked values are discarded.

Parameters **arr** : sequence
Input array. The array is flattened if it is not 1D.

Returns **repeats** : ndarray
Array of repeated values.

counts : ndarray
Array of counts.

`scipy.stats.mstats.`**`friedmanchisquare`**`(`*`*args`*`)`

Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA. This function calculates the Friedman Chi-square test for repeated measures and returns the result, along with the associated probability value.

Each input is considered a given group. Ideally, the number of treatments among each group should be equal. If this is not the case, only the first n treatments are taken into account, where n is the number of treatments of the smallest group. If a group has some missing values, the corresponding treatments are masked in the other groups. The test statistic is corrected for ties.

Masked values in one group are propagated to the other groups.

Returns **statistic** : float

the test statistic.

pvalue : float

the associated p-value.

`scipy.stats.mstats.`**`kendalltau`**(*x*, *y*, *use_ties=True*, *use_missing=False*)

Computes Kendall's rank correlation tau on two variables *x* and *y*.

Parameters **x** : sequence

First data list (for example, time).

y : sequence

Second data list.

use_ties : {True, False}, optional

Whether ties correction should be performed.

use_missing : {False, True}, optional

Whether missing data should be allocated a rank of 0 (False) or the average rank (True)

Returns **correlation** : float

Kendall tau

pvalue : float

Approximate 2-side p-value.

`scipy.stats.mstats.`**`kendalltau_seasonal`**(*x*)

Computes a multivariate Kendall's rank correlation tau, for seasonal data.

Parameters **x** : 2-D ndarray

Array of seasonal data, with seasons in columns.

`scipy.stats.mstats.`**`kruskalwallis`**(**args*)

Compute the Kruskal-Wallis H-test for independent samples

The Kruskal-Wallis H-test tests the null hypothesis that the population median of all of the groups are equal. It is a non-parametric version of ANOVA. The test works on 2 or more independent samples, which may have different sizes. Note that rejecting the null hypothesis does not indicate which of the groups differs. Post-hoc comparisons between groups are required to determine which groups are different.

Parameters **sample1, sample2, ...** : array_like

Two or more arrays with the sample measurements can be given as arguments.

Returns **statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

pvalue : float

The p-value for the test using the assumption that H has a chi square distribution

Notes

Due to the assumption that H has a chi square distribution, the number of samples in each group must not be too small. A typical rule is that each sample must have at least 5 measurements.

References

[R338]

`scipy.stats.mstats.`**`ks_twosamp`**(*data1*, *data2*, *alternative='two-sided'*)

Computes the Kolmogorov-Smirnov test on two samples.

Missing values are discarded.

Parameters **data1** : array_like

First data set

data2 : array_like

Second data set

alternative : {'two-sided', 'less', 'greater'}, optional

Indicates the alternative hypothesis. Default is 'two-sided'.

Returns **d** : float

Value of the Kolmogorov Smirnov test

p : float

Corresponding p-value.

`scipy.stats.mstats.`**`kurtosis`**(*a*, *axis=0*, *fisher=True*, *bias=True*)

Computes the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use `kurtosistest` to see if result is close enough to normal.

Parameters **a** : array

data for which the kurtosis is calculated

axis : int or None, optional

Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.

fisher : bool, optional

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias : bool, optional

If False, then the calculations are corrected for statistical bias.

Returns **kurtosis** : array

The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[R339]

`scipy.stats.mstats.`**`kurtosistest`**(*a*, *axis=0*)

Tests whether a dataset has normal kurtosis

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: `kurtosis = 3(n-1)/(n+1)`.

Parameters **a** : array

array of the sample data

axis : int or None, optional

Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns **statistic** : float

The computed z-score for this test.

pvalue : float

The 2-sided p-value for the hypothesis test

Notes

Valid only for n>20. The Z-score is set to 0 for bad entries.

`scipy.stats.mstats.`**`linregress`**(**args*)

Calculate a regression line

This computes a least-squares regression for two sets of measurements.

Parameters	**x, y** : array_like two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.
Returns	**slope** : float slope of the regression line **intercept** : float intercept of the regression line **rvalue** : float correlation coefficient **pvalue** : float two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero. **stderr** : float Standard error of the estimate

Notes

Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

Examples

```
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x,y)
```

To get coefficient of determination (r_squared)

```
>>> print("r-squared:", r_value**2)
r-squared: 0.15286643777
```

`scipy.stats.mstats.`**`mannwhitneyu`**(*x*, *y*, *use_continuity=True*)

Computes the Mann-Whitney statistic

Missing values in *x* and/or *y* are discarded.

Parameters	**x** : sequence Input **y** : sequence Input **use_continuity** : {True, False}, optional Whether a continuity correction (1/2.) should be taken into account.
Returns	**statistic** : float The Mann-Whitney statistics **pvalue** : float Approximate p-value assuming a normal distribution.

`scipy.stats.mstats.`**`plotting_positions`**(*data*, *alpha=0.4*, *beta=0.4*)

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as **`(i-alpha)/(n+1-alpha-beta)`*****, where:***

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for* alpha *and* beta *are:

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters

data : array_like

Input data, as a sequence or array of dimension at most 2.

alpha : float, optional

Plotting positions parameter. Default is 0.4.

beta : float, optional

Plotting positions parameter. Default is 0.4.

Returns

positions : MaskedArray

The calculated plotting positions.

`scipy.stats.mstats.`**`mode`**`(`*a*, *axis=0*`)`

Returns an array of the modal (most common) value in the passed array.

If there is more than one such value, only the first is returned. The bin-count for the modal bins is also returned.

Parameters

a : array_like

n-dimensional array of which to find mode(s).

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

Returns

mode : ndarray

Array of modal values.

count : ndarray

Array of counts for each mode.

Examples

```
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 7],
...               [8, 1, 8, 4],
...               [5, 3, 0, 5],
...               [4, 7, 5, 9]])
>>> from scipy import stats
>>> stats.mode(a)
(array([[3, 1, 0, 0]]), array([[1, 1, 1, 1]]))
```

To get mode of whole array, specify `axis=None`:

```
>>> stats.mode(a, axis=None)
(array([3]), array([3]))
```

`scipy.stats.mstats.`**`moment`**`(`*a*, *moment=1*, *axis=0*`)`

Calculates the nth moment about the mean for a sample.

Generally used to calculate coefficients of skewness and kurtosis.

Parameters **a** : array_like

data

moment : int, optional

order of central moment that is returned

axis : int or None, optional

Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

Returns **n-th central moment** : ndarray or float

The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

`scipy.stats.mstats.`**`mquantiles`**`(`*a, prob=[0.25, 0.5, 0.75], alphap=0.4, betap=0.4, axis=None, limit=()*`)`

Computes empirical quantiles for a data array.

Samples quantile are defined by `Q(p) = (1-gamma)*x[j] + gamma*x[j+1]`, where `x[j]` is the j-th order statistic, and gamma is a function of `j = floor(n*p + m)`, `m = alphap + p*(1 - alphap - betap)` and `g = n*p + m - j`.

Reinterpreting the above equations to compare to **R** lead to the equation: `p(k) = (k - alphap)/(n + 1 - alphap - betap)`

Typical values of (alphap,betap) are:

- (0,1) : `p(k) = k/n` : linear interpolation of cdf (**R** type 4)
- (.5,.5) : `p(k) = (k - 1/2.)/n` : piecewise linear function (**R** type 5)
- (0,0) : `p(k) = k/(n+1)` : (**R** type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`: p(k) = mode[F(x[k])]. (**R** type 7, **R** default)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`: Then p(k) ~ median[F(x[k])]. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (**R** type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`: Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (**R** type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM

Parameters **a** : array_like

Input data, as a sequence or array of dimension at most 2.

prob : array_like, optional

List of quantiles to compute.

alphap : float, optional

Plotting positions parameter, default is 0.4.

betap : float, optional

Plotting positions parameter, default is 0.4.

axis : int, optional

Axis along which to perform the trimming. If None (default), the input array is first flattened.

limit : tuple, optional

Tuple of (lower, upper) values. Values of *a* outside this open interval are ignored.

Returns **mquantiles** : MaskedArray

An array containing the calculated quantiles.

Notes

This formulation is very similar to **R** except the calculation of `m` from `alphap` and `betap`, where in **R** `m` is defined with each type.

References

[R340], [R341]

Examples

```
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6., 47., 49., 15., 42., 41., 7., 39., 43., 40., 36.])
>>> mquantiles(a)
array([ 19.2,  40. ,  42.8])
```

Using a 2D array, specifying axis and limit.

```
>>> data = np.array([[   6.,    7.,    1.],
                     [  47.,   15.,    2.],
                     [  49.,   36.,    3.],
                     [  15.,   39.,    4.],
                     [  42.,   40., -999.],
                     [  41.,   41., -999.],
                     [   7., -999., -999.],
                     [  39., -999., -999.],
                     [  43., -999., -999.],
                     [  40., -999., -999.],
                     [  36., -999., -999.]])
>>> mquantiles(data, axis=0, limit=(0, 50))
array([[ 19.2 ,  14.6 ,   1.45],
       [ 40.  ,  37.5 ,   2.5 ],
       [ 42.8 ,  40.05,   3.55]])
```

```
>>> data[:, 2] = -999.
>>> mquantiles(data, axis=0, limit=(0, 50))
masked_array(data =
 [[19.2 14.6 --]
 [40.0 37.5 --]
 [42.8 40.05 --]],
             mask =
 [[False False  True]
  [False False  True]
  [False False  True]],
       fill_value = 1e+20)
```

`scipy.stats.mstats.`**`msign`**(*x*)

Returns the sign of x, or 0 if x is masked.

`scipy.stats.mstats.`**`normaltest`**(*a*, *axis=0*)

Tests whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's [R342], [R343] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters **a** : array_like

The array containing the data to be tested.

axis : int or None, optional

Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns **statistic** : float or array

s^2 + k^2, where *s* is the z-score returned by `skewtest` and *k* is the z-score returned by `kurtosistest`.

pvalue : float or array

A 2-sided chi squared probability for the hypothesis test.

References

[R342], [R343]

`scipy.stats.mstats.`**`obrientransform`**`(`**args*`)`

Computes a transform on input data (any number of columns). Used to test for homogeneity of variance prior to running one-way stats. Each array in `*args` is one level of a factor. If an *f_oneway()* run on the transformed data and found significant, variances are unequal. From Maxwell and Delaney, p.112.

Returns: transformed data for use in an ANOVA

`scipy.stats.mstats.`**`pearsonr`**`(`*x*, *y*`)`

Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.

The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson's correlation requires that each dataset be normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters **x** : 1-D array_like

Input

y : 1-D array_like

Input

Returns **pearsonr** : float

Pearson's correlation coefficient, 2-tailed p-value.

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

`scipy.stats.mstats.`**`plotting_positions`**`(`*data*, *alpha=0.4*, *beta=0.4*`)`

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as **`(i-alpha)/(n+1-alpha-beta)`*****, where:***

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for **alpha** ***and*** **beta** ***are:***

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)

- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters	**data** : array_like Input data, as a sequence or array of dimension at most 2. **alpha** : float, optional Plotting positions parameter. Default is 0.4. **beta** : float, optional Plotting positions parameter. Default is 0.4.
Returns	**positions** : MaskedArray The calculated plotting positions.

`scipy.stats.mstats.`**`pointbiserialr`**(*x*, *y*)

Calculates a point biserial correlation coefficient and the associated p-value.

The point biserial correlation is used to measure the relationship between a binary variable, x, and a continuous variable, y. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a determinative relationship.

This function uses a shortcut formula but produces the same result as `pearsonr`.

Parameters	**x** : array_like of bools Input array. **y** : array_like Input array.
Returns	**correlation** : float R value **pvalue** : float 2-tailed p-value

Notes

Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

References

http://en.wikipedia.org/wiki/Point-biserial_correlation_coefficient

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)
>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)
>>> np.corrcoef(a, b)
array([[ 1.       ,  0.8660254],
       [ 0.8660254,  1.       ]])
```

`scipy.stats.mstats.`**`rankdata`**(*data*, *axis=None*, *use_missing=False*)

Returns the rank (also known as order statistics) of each data point along the given axis.

If some values are tied, their rank is averaged. If some values are masked, their rank is set to 0 if use_missing is False, or set to the average rank of the unmasked values if use_missing is True.

Parameters **data** : sequence

Input data. The data is transformed to a masked array

axis : {None,int}, optional

Axis along which to perform the ranking. If None, the array is first flattened. An exception is raised if the axis is specified for arrays with a dimension larger than 2

use_missing : bool, optional

Whether the masked values have a rank of 0 (False) or equal to the average rank of the unmasked values (True).

`scipy.stats.mstats.`**`scoreatpercentile`**`(`*data*, *per*, *limit=()*, *alphap=0.4*, *betap=0.4*`)`

Calculate the score at the given 'per' percentile of the sequence a. For example, the score at per=50 is the median.

This function is a shortcut to mquantile

`scipy.stats.mstats.`**`sem`**`(`*a*, *axis=0*, *ddof=1*`)`

Calculates the standard error of the mean of the input array.

Also sometimes called standard error of measurement.

Parameters **a** : array_like

An array containing the values for which the standard error is returned.

axis : int or None, optional

If axis is None, ravel *a* first. If axis is an integer, this will be the axis over which to operate. Defaults to 0.

ddof : int, optional

Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.

Returns **s** : ndarray or float

The standard error of the mean in the sample(s), along the input axis.

Notes

The default value for *ddof* changed in scipy 0.15.0 to be consistent with *stats.sem* as well as with the most common definition used (like in the R documentation).

Examples

Find standard error along the first axis:

```
>>> from scipy import stats
>>> a = np.arange(20).reshape(5,4)
>>> stats.sem(a)
array([ 2.8284,  2.8284,  2.8284,  2.8284])
```

Find standard error across the whole array, using n degrees of freedom:

```
>>> stats.sem(a, axis=None, ddof=0)
1.2893796958227628
```

`scipy.stats.mstats.`**`signaltonoise`**`(`**args*, ***kwds*`)`

`signaltonoise` is deprecated! mstats.signaltonoise is deprecated in scipy 0.16.0

Calculates the signal-to-noise ratio, as the ratio of the mean over

standard deviation along the given axis.

Parameters **data** : sequence

Input data

axis [{0, int}, optional] Axis along which to compute. If None, the computation is performed on a flat version of the array.

`scipy.stats.mstats.`**`skew`**(*a*, *axis=0*, *bias=True*)

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left tail of the distribution. The function `skewtest` can be used to determine if the skewness value is close enough to 0, statistically speaking.

Parameters

a : ndarray

data

axis : int or None, optional

Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.

bias : bool, optional

If False, then the calculations are corrected for statistical bias.

Returns

skewness : ndarray

The skewness of values along an axis, returning 0 where all values are equal.

References

[R344]

`scipy.stats.mstats.`**`skewtest`**(*a*, *axis=0*)

Tests whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters

a : array

The data to be tested

axis : int or None, optional

Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

Returns

statistic : float

The computed z-score for this test.

pvalue : float

a 2-sided p-value for the hypothesis test

Notes

The sample size must be at least 8.

`scipy.stats.mstats.`**`spearmanr`**(*x*, *y*, *use_ties=True*)

Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the linear relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

Missing values are discarded pair-wise: if a value is missing in *x*, the corresponding value in *y* is masked.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters

x : array_like

The length of *x* must be > 2.

y : array_like
The length of *y* must be > 2.

use_ties : bool, optional
Whether the correction for ties should be computed.

Returns **correlation** : float
Spearman correlation coefficient

pvalue : float
2-tailed p-value.

References

[CRCProbStat2000] section 14.7

`scipy.stats.mstats.`**`theilslopes`**`(`*y*, *x=None*, *alpha=0.95*`)`

Computes the Theil-Sen estimator for a set of points (x, y).

`theilslopes` implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters **y** : array_like
Dependent variable.

x : array_like or None, optional
Independent variable. If None, use `arange(len(y))` instead.

alpha : float, optional
Confidence degree between 0 and 1. Default is 95% confidence. Note that *alpha* is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as "find the 90% confidence interval".

Returns **medslope** : float
Theil slope.

medintercept : float
Intercept of the Theil line, as `median(y) - medslope*median(x)`.

lo_slope : float
Lower bound of the confidence interval on *medslope*.

up_slope : float
Upper bound of the confidence interval on *medslope*.

Notes

The implementation of `theilslopes` follows [R345]. The intercept is not defined in [R345], and here it is defined as `median(y) - medslope*median(x)`, which is given in [R347]. Other definitions of the intercept exist in the literature. A confidence interval for the intercept is not given as this question is not addressed in [R345].

References

[R345], [R346], [R347]

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

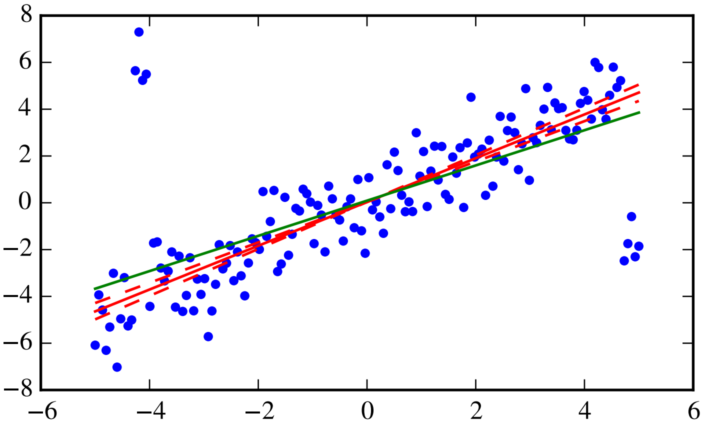
```
>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7
```

Compute the slope, intercept and 90% confidence interval. For comparison, also compute the least-squares fit with `linregress`:

```
>>> res = stats.theilslopes(y, x, 0.90)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Theil-Sen regression line is shown in red, with the dashed red lines illustrating the confidence interval of the slope (note that the dashed red lines are not the confidence interval of the regression as the confidence interval of the intercept is not included). The green line shows the least-squares fit for comparison.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.')
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, res[1] + res[2] * x, 'r--')
>>> ax.plot(x, res[1] + res[3] * x, 'r--')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```



`scipy.stats.mstats.`**`threshold`**`(`*a*, *threshmin=None*, *threshmax=None*, *newval=0*`)`

Clip array to a given value.

Similar to numpy.clip(), except that values less than *threshmin* or greater than *threshmax* are replaced by *newval*, instead of by *threshmin* and *threshmax* respectively.

Parameters **a** : ndarray

Input data

threshmin : {None, float}, optional

Lower threshold. If None, set to the minimum value.

threshmax : {None, float}, optional

Upper threshold. If None, set to the maximum value.

newval : {0, float}, optional

Value outside the thresholds.

Returns **threshold** : ndarray

Returns *a*, with values less then *threshmin* and values greater *threshmax* replaced with *newval*.

`scipy.stats.mstats.`**`tmax`**(*a*, *upperlimit*, *axis=0*, *inclusive=True*)

Compute the trimmed maximum

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters

a : array_like

array of values

upperlimit : None or float, optional

Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the upper limit are included. The default value is True.

Returns

tmax : float

`scipy.stats.mstats.`**`tmean`**(*a*, *limits=None*, *inclusive=(True*, *True)*)

Compute the trimmed mean.

This function finds the arithmetic mean of given values, ignoring values outside the given *limits*.

Parameters

a : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns

tmean : float

`scipy.stats.mstats.`**`tmin`**(*a*, *lowerlimit=None*, *axis=0*, *inclusive=True*)

Compute the trimmed minimum

This function finds the miminum value of an array *a* along the specified axis, but only considering values greater than a specified lower limit.

Parameters

a : array_like

array of values

lowerlimit : None or float, optional

Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the lower limit are included. The default value is True.

Returns

tmin : float

`scipy.stats.mstats.`**`trim`**(*a*, *limits=None*, *inclusive=(True*, *True)*, *relative=False*, *axis=None*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters **a** : sequence

Input array

limits : {None, tuple}, optional

If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.

If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.

Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.

If limits is None, no trimming is performed

inclusive : {(bool, bool) tuple}, optional

If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative : bool, optional

Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis : int, optional

Axis along which to trim.

Examples

```
>>> z = [ 1, 2, 3, 4, 5, 6, 7, 8, 9,10]
>>> trim(z,(3,8))
[--,--, 3, 4, 5, 6, 7, 8,--,--]
>>> trim(z,(0.1,0.2),relative=True)
[--, 2, 3, 4, 5, 6, 7, 8,--,--]
```

`scipy.stats.mstats.`**`trima`**(*a*, *limits=None*, *inclusive=(True*, *True)*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters **a** : array_like

Input array.

limits : {None, tuple}, optional

Tuple of (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit will be masked. A limit is None indicates an open interval.

inclusive : (bool, bool) tuple, optional

Tuple of (lower flag, upper flag), indicating whether values exactly equal to the lower (upper) limit are allowed.

`scipy.stats.mstats.`**`trimboth`**(*data*, *proportiontocut=0.2*, *inclusive=(True*, *True)*, *axis=None*)

Trims the smallest and largest data values.

Trims the *data* by masking the `int(proportiontocut * n)` smallest and `int(proportiontocut * n)` largest values of data along the given axis, where n is the number of unmasked values before trimming.

Parameters **data** : ndarray

Data to trim.

proportiontocut : float, optional

Percentage of trimming (as a float between 0 and 1). If n is the number of unmasked values before trimming, the number of values after trimming is `(1 - 2*proportiontocut) * n`. Default is 0.2.

inclusive : {(bool, bool) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis : int, optional

Axis along which to perform the trimming. If None, the input array is first flattened.

`scipy.stats.mstats.`**`trimmed_stde`**(*a*, *limits=(0.1*, *0.1)*, *inclusive=(1*, *1)*, *axis=None*)

Returns the standard error of the trimmed mean along the given axis.

Parameters

a : sequence

Input array

limits : {(0.1,0.1), tuple of float}, optional

tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.

If n is the number of unmasked data before trimming, the values smaller than `n * limits[0]` and the values larger than `n * 'limits[1]` are masked, and the total number of unmasked data after trimming is `n * (1.-sum(limits))`. In each case, the value of one limit can be set to None to indicate an open interval. If *limits* is None, no trimming is performed.

inclusive : {(bool, bool) tuple} optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis : int, optional

Axis along which to trim.

Returns

trimmed_stde : scalar or ndarray

`scipy.stats.mstats.`**`trimr`**(*a*, *limits=None*, *inclusive=(True*, *True)*, *axis=None*)

Trims an array by masking some proportion of the data on each end. Returns a masked version of the input array.

Parameters

a : sequence

Input array.

limits : {None, tuple}, optional

Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)). The value of one limit can be set to None to indicate an open interval.

inclusive : {(True,True) tuple}, optional

Tuple of flags indicating whether the number of data being masked on the left (right) end should be truncated (True) or rounded (False) to integers.

axis : {None,int}, optional

Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

`scipy.stats.mstats.`**`trimtail`**(*data*, *proportiontocut=0.2*, *tail='left'*, *inclusive=(True*, *True)*, *axis=None*)

Trims the data by masking values from one tail.

Parameters

data : array_like

Data to trim.

proportiontocut : float, optional

Percentage of trimming. If `n` is the number of unmasked values before trimming, the number of values after trimming is `(1 - proportiontocut) * n`. Default is 0.2.

tail : {'left','right'}, optional

If 'left' the *proportiontocut* lowest values will be masked. If 'right' the *proportiontocut* highest values will be masked. Default is 'left'.

inclusive : {(bool, bool) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False). Default is (True, True).

axis : int, optional

Axis along which to perform the trimming. If None, the input array is first flattened. Default is None.

Returns **trimtail** : ndarray

Returned array of same shape as *data* with masked tail values.

`scipy.stats.mstats.`**`tsem`**`(`*a*, *limits=None*, *inclusive=(True, True)*`)`

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given *limits*.

Parameters **a** : array_like

array of values

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tsem** : float

Notes

`tsem` uses unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.mstats.`**`ttest_onesamp`**`(`*a*, *popmean*, *axis=0*`)`

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters **a** : array_like

sample observation

popmean : float or array_like

expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole array *a*.

Returns **statistic** : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`scipy.stats.mstats.`**`ttest_ind`**(*a*, *b*, *axis=0*)

Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters

a, b : array_like

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var : bool, optional

If True (default), perform a standard independent 2 sample test that assumes equal population variances [R348]. If False, perform Welch's t-test, which does not assume equal population variance [R349]. .. versionadded:: 0.11.0

Returns

statistic : float or array

The calculated t-statistic.

pvalue : float or array

The two-tailed p-value.

Notes

We can use this test, if we observe two independent samples from the same or different population, e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average (expected) value differs significantly across samples. If we observe a large p-value, for example larger than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References

[R348], [R349]

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678)
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1,rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```

`ttest_ind` underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)
(-0.46580283298287162, 0.64149646246569292)
```

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)
(-0.94365973617132992, 0.34744170334794122)
```

`scipy.stats.mstats.`**`ttest_onesamp`**(*a*, *popmean*, *axis=0*)

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters

a : array_like

sample observation

popmean : float or array_like

expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole array *a*.

Returns

statistic : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`scipy.stats.mstats.`**`ttest_rel`**(*a*, *b*, *axis=0*)

Calculates the T-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters

a, b : array_like

The arrays must have the same shape.

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

Returns

statistic : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

http://en.wikipedia.org/wiki/T-test#Dependent_t-test

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678) # fix random seed to get same numbers
```

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = (stats.norm.rvs(loc=5,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs2)
(0.24101764965300962, 0.80964043445811562)
>>> rvs3 = (stats.norm.rvs(loc=8,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs3)
(-3.9995108708727933, 7.3082402191726459e-005)
```

`scipy.stats.mstats.`**`tvar`**`(`*a*, *limits=None*, *inclusive=(True, True)*`)`

Compute the trimmed variance

This function computes the sample variance of an array of values, while ignoring values which are outside of given *limits*.

Parameters **a** : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tvar** : float

Trimmed variance.

Notes

`tvar` computes the unbiased sample variance, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.mstats.`**`variation`**`(`*a*, *axis=0*`)`

Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters **a** : array_like

Input array.

axis : int or None, optional

Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array *a*.

References

[R350]

`scipy.stats.mstats.`**`winsorize`**`(`*a*, *limits=None*, *inclusive=(True, True)*, *inplace=False*, *axis=None*`)`

Returns a Winsorized version of the input array.

The (limits[0])th lowest values are set to the (limits[0])th percentile, and the (limits[1])th highest values are set to the (1 - limits[1])th percentile. Masked values are skipped.

Parameters **a** : sequence

Input array.

limits : {None, tuple of float}, optional

Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) The value of one limit can be set to None to indicate an open interval.

inclusive : {(True, True) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

inplace : {False, True}, optional

Whether to winsorize in place (True) or to use a copy (False)

axis : {None, int}, optional

Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

Notes

This function is applied to reduce the effect of possibly spurious outliers by limiting the extreme values.

`scipy.stats.mstats.`**`zmap`**(*scores*, *compare*, *axis=0*, *ddof=0*)

Calculates the relative z-scores.

Returns an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters

scores : array_like

The input for which z-scores are calculated.

compare : array_like

The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as *scores*.

axis : int or None, optional

Axis over which mean and variance of *compare* are calculated. Default is 0. If None, compute over the whole array *scores*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns

zscore : array_like

Z-scores, in the same shape as *scores*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017,  0.        ,  0.35355339,  0.70710678])
```

`scipy.stats.mstats.`**`zscore`**(*a*, *axis=0*, *ddof=0*)

Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters

a : array_like

An array like object containing the sample data.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns **zscore** : array_like

The z-scores, standardized by mean and standard deviation of input array *a*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> a = np.array([ 0.7972,  0.0767,  0.4383,  0.7866,  0.8091,  0.1954,
...                0.6307, 0.6599,  0.1065,  0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552,  1.0923,  1.1664, -0.8559,  0.5786,
        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148,  0.0478,  0.6243,  0.4608],
...               [ 0.7149,  0.0775,  0.6072,  0.9656],
...               [ 0.6341,  0.1403,  0.9759,  0.4064],
...               [ 0.5918,  0.6948,  0.904 ,  0.3721],
...               [ 0.0921,  0.2481,  0.1188,  0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119,  1.07259584,  0.40420358],
       [ 0.33048416, -1.37380874,  0.04251374,  1.00081084],
       [ 0.26796377, -1.12598418,  1.23283094, -0.37481053],
       [-0.22095197,  0.24468594,  1.19042819, -1.21416216],
       [-0.82780366,  1.4457416 , -0.43867764, -0.1792603 ]])
```

5.34.9 Univariate and multivariate kernel density estimation (`scipy.stats.kde`)

`gaussian_kde`(dataset[, bw_method])	Representation of a kernel-density estimate using Gaussian kernels.

class `scipy.stats.`**`gaussian_kde`**(*dataset*, *bw_method=None*)

Representation of a kernel-density estimate using Gaussian kernels.

Kernel density estimation is a way to estimate the probability density function (PDF) of a random variable in a non-parametric way. `gaussian_kde` works for both uni-variate and multi-variate data. It includes automatic bandwidth determination. The estimation works best for a unimodal distribution; bimodal or multi-modal distributions tend to be oversmoothed.

Parameters **dataset** : array_like

Datapoints to estimate from. In case of univariate data this is a 1-D array, otherwise a 2-D array with shape (# of dims, # of data).

bw_method : str, scalar or callable, optional

The method used to calculate the estimator bandwidth. This can be 'scott', 'silverman', a scalar constant or a callable. If a scalar, this will be used directly as *kde.factor*. If a callable, it should take a `gaussian_kde` instance as only parameter and return a scalar. If None (default), 'scott' is used. See Notes for more details.

Notes

Bandwidth selection strongly influences the estimate obtained from the KDE (much more so than the actual shape of the kernel). Bandwidth selection can be done by a "rule of thumb", by cross-validation, by "plug-in methods" or by other means; see [R322], [R323] for reviews. `gaussian_kde` uses a rule of thumb, the default is Scott's Rule.

Scott's Rule [R320], implemented as `scotts_factor`, is:

```
n**(-1./(d+4)),
```

with `n` the number of data points and `d` the number of dimensions. Silverman's Rule [R321], implemented as `silverman_factor`, is:

```
(n * (d + 2) / 4.)**(-1. / (d + 4)).
```

Good general descriptions of kernel density estimation can be found in [R320] and [R321], the mathematics for this multi-dimensional implementation can be found in [R320].

References

[R320], [R321], [R322], [R323]

Examples

Generate some random two-dimensional data:

```
>>> from scipy import stats
>>> def measure(n):
...     "Measurement model, return two coupled measurements."
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2
```

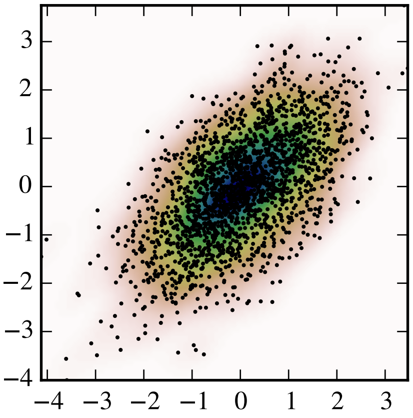
```
>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()
```

Perform a kernel density estimate on the data:

```
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel(positions).T, X.shape)
```

Plot the results:

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r,
...           extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)
>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])
>>> plt.show()
```



Attributes

dataset	(ndarray) The dataset with which `gaussian_kde` was initialized.
d	(int) Number of dimensions.
n	(int) Number of datapoints.
factor	(float) The bandwidth factor, obtained from *kde.covariance_factor*, with which the covariance matrix is multiplied.
covariance	(ndarray) The covariance matrix of *dataset*, scaled by the calculated bandwidth (*kde.factor*).
inv_cov	(ndarray) The inverse of *covariance*.

Methods

`evaluate`(points)	Evaluate the estimated pdf on a set of points.
`__call__`(points)	Evaluate the estimated pdf on a set of points.
`integrate_gaussian`(mean, cov)	Multiply estimated density by a multivariate Gaussian and integrate over
`integrate_box_1d`(low, high)	Computes the integral of a 1D pdf between two bounds.
`integrate_box`(low_bounds, high_bounds[, maxpts])	Computes the integral of a pdf over a rectangular interval.
`integrate_kde`(other)	Computes the integral of the product of this kernel density estimate with
`pdf`(x)	Evaluate the estimated pdf on a provided set of points.
`logpdf`(x)	Evaluate the log of the estimated pdf on a provided set of points.
`resample`([size])	Randomly sample a dataset from the estimated pdf.
`set_bandwidth`([bw_method])	Compute the estimator bandwidth with given method.
`covariance_factor`()	Computes the coefficient (*kde.factor*) that multiplies the data covariance

`gaussian_kde.`**`evaluate`**(*points*)

Evaluate the estimated pdf on a set of points.

Parameters	**points** : (# of dimensions, # of points)-array Alternatively, a (# of dimensions,) vector can be passed in and treated as a single point.
Returns	**values** : (# of points,)-array The values at each point.
Raises	**ValueError** : if the dimensionality of the input points is different than the dimensionality of the KDE.

`gaussian_kde.`**`__call__`**(*points*)

Evaluate the estimated pdf on a set of points.

Parameters	**points** : (# of dimensions, # of points)-array Alternatively, a (# of dimensions,) vector can be passed in and treated as a single point.
Returns	**values** : (# of points,)-array The values at each point.
Raises	**ValueError** : if the dimensionality of the input points is different than the dimensionality of the KDE.

`gaussian_kde.`**`integrate_gaussian`**(*mean*, *cov*)

Multiply estimated density by a multivariate Gaussian and integrate over the whole space.

Parameters	**mean** : aray_like A 1-D array, specifying the mean of the Gaussian. **cov** : array_like A 2-D array, specifying the covariance matrix of the Gaussian.
Returns	**result** : scalar The value of the integral.
Raises	**ValueError :** If the mean or covariance of the input Gaussian differs from the KDE's dimensionality.

`gaussian_kde.`**`integrate_box_1d`**(*low*, *high*)

Computes the integral of a 1D pdf between two bounds.

Parameters	**low** : scalar Lower bound of integration. **high** : scalar Upper bound of integration.
Returns	**value** : scalar The result of the integral.
Raises	**ValueError** If the KDE is over more than one dimension.

`gaussian_kde.`**`integrate_box`**(*low_bounds*, *high_bounds*, *maxpts=None*)

Computes the integral of a pdf over a rectangular interval.

Parameters	**low_bounds** : array_like A 1-D array containing the lower bounds of integration. **high_bounds** : array_like A 1-D array containing the upper bounds of integration. **maxpts** : int, optional The maximum number of points to use for integration.
Returns	**value** : scalar The result of the integral.

`gaussian_kde.`**`integrate_kde`**(*other*)

Computes the integral of the product of this kernel density estimate with another.

Parameters	**other** : gaussian_kde instance The other kde.

Returns **value** : scalar

The result of the integral.

Raises **ValueError**

If the KDEs have different dimensionality.

`gaussian_kde.`**`pdf`**`(`*x*`)`

Evaluate the estimated pdf on a provided set of points.

Notes

This is an alias for `gaussian_kde.evaluate`. See the `evaluate` docstring for more details.

`gaussian_kde.`**`logpdf`**`(`*x*`)`

Evaluate the log of the estimated pdf on a provided set of points.

Notes

See `gaussian_kde.evaluate` for more details; this method simply returns `np.log(gaussian_kde.evaluate(x))`.

`gaussian_kde.`**`resample`**`(`*size=None*`)`

Randomly sample a dataset from the estimated pdf.

Parameters **size** : int, optional

The number of samples to draw. If not provided, then the size is the same as the underlying dataset.

Returns **resample** : (self.d, *size*) ndarray

The sampled dataset.

`gaussian_kde.`**`set_bandwidth`**`(`*bw_method=None*`)`

Compute the estimator bandwidth with given method.

The new bandwidth calculated after a call to `set_bandwidth` is used for subsequent evaluations of the estimated density.

Parameters **bw_method** : str, scalar or callable, optional

The method used to calculate the estimator bandwidth. This can be 'scott', 'silverman', a scalar constant or a callable. If a scalar, this will be used directly as *kde.factor*. If a callable, it should take a `gaussian_kde` instance as only parameter and return a scalar. If None (default), nothing happens; the current *kde.covariance_factor* method is kept.

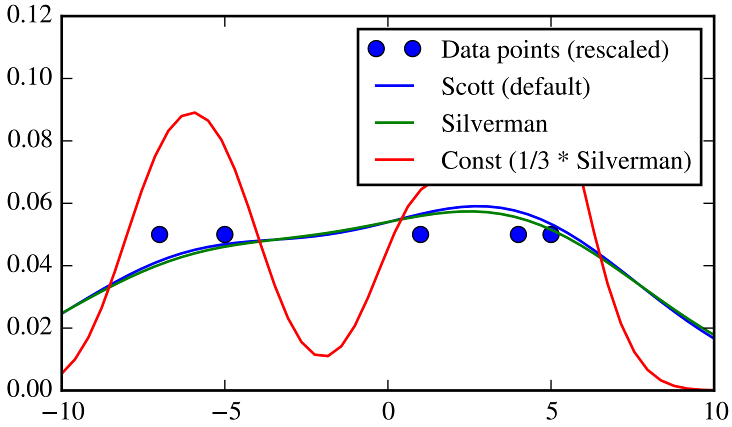
Notes

New in version 0.11.

Examples

```
>>> import scipy.stats as stats
>>> x1 = np.array([-7, -5, 1, 4, 5.])
>>> kde = stats.gaussian_kde(x1)
>>> xs = np.linspace(-10, 10, num=50)
>>> y1 = kde(xs)
>>> kde.set_bandwidth(bw_method='silverman')
>>> y2 = kde(xs)
>>> kde.set_bandwidth(bw_method=kde.factor / 3.)
>>> y3 = kde(xs)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.plot(x1, np.ones(x1.shape) / (4. * x1.size), 'bo',
...         label='Data points (rescaled)')
>>> ax.plot(xs, y1, label='Scott (default)')
>>> ax.plot(xs, y2, label='Silverman')
>>> ax.plot(xs, y3, label='Const (1/3 * Silverman)')
>>> ax.legend()
>>> plt.show()
```



gaussian_kde.**covariance_factor**()

Computes the coefficient (*kde.factor*) that multiplies the data covariance matrix to obtain the kernel covariance matrix. The default is `scotts_factor`. A subclass can overwrite this method to provide a different method, or set it through a call to *kde.set_bandwidth*.

For many more stat related functions install the software R and the interface package rpy.

5.35 Statistical functions for masked arrays (`scipy.stats.mstats`)

This module contains a large number of statistical functions that can be used with masked arrays.

Most of these functions are similar to those in scipy.stats but might have small differences in the API or in the algorithm used. Since this is a relatively new package, some API changes are still possible.

`argstoarray`(*args)	Constructs a 2D array from a group of sequences.
`betai`(a, b, x)	Returns the incomplete beta function.
`chisquare`(f_obs[, f_exp, ddof, axis])	Calculates a one-way chi square test.
`count_tied_groups`(x[, use_missing])	Counts the number of tied values.
`describe`(a[, axis, ddof])	Computes several descriptive statistics of the passed array.
`f_oneway`(*args)	Performs a 1-way ANOVA, returning an F-value and probability given a
`f_value_wilks_lambda`(ER, EF, dfnum, dfden, a, b)	Calculation of Wilks lambda F-statistic for multivariate data, per Maxwe
`find_repeats`(arr)	Find repeats in arr and return a tuple (repeats, repeat_count).
`friedmanchisquare`(*args)	Friedman Chi-Square is a non-parametric, one-way within-subjects ANC
`kendalltau`(x, y[, use_ties, use_missing])	Computes Kendall’s rank correlation tau on two variables *x* and *y*.

Table 5.270 – continued from previous page

`kendalltau_seasonal`(x)	Computes a multivariate Kendall's rank correlation tau, for seasonal data
`kruskalwallis`(*args)	Compute the Kruskal-Wallis H-test for independent samples
`ks_twosamp`(data1, data2[, alternative])	Computes the Kolmogorov-Smirnov test on two samples.
`kurtosis`(a[, axis, fisher, bias])	Computes the kurtosis (Fisher or Pearson) of a dataset.
`kurtosistest`(a[, axis])	Tests whether a dataset has normal kurtosis
`linregress`(*args)	Calculate a regression line
`mannwhitneyu`(x, y[, use_continuity])	Computes the Mann-Whitney statistic
`plotting_positions`(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
`mode`(a[, axis])	Returns an array of the modal (most common) value in the passed array.
`moment`(a[, moment, axis])	Calculates the nth moment about the mean for a sample.
`mquantiles`(a[, prob, alphap, betap, axis, limit])	Computes empirical quantiles for a data array.
`msign`(x)	Returns the sign of x, or 0 if x is masked.
`normaltest`(a[, axis])	Tests whether a sample differs from a normal distribution.
`obrientransform`(*args)	Computes a transform on input data (any number of columns).
`pearsonr`(x, y)	Calculates a Pearson correlation coefficient and the p-value for testing no
`plotting_positions`(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
`pointbiserialr`(x, y)	Calculates a point biserial correlation coefficient and the associated p-val
`rankdata`(data[, axis, use_missing])	Returns the rank (also known as order statistics) of each data point along
`scoreatpercentile`(data, per[, limit, ...])	Calculate the score at the given 'per' percentile of the sequence a.
`sem`(a[, axis, ddof])	Calculates the standard error of the mean of the input array.
`signaltonoise`(*args, **kwds)	`signaltonoise` is deprecated!
`skew`(a[, axis, bias])	Computes the skewness of a data set.
`skewtest`(a[, axis])	Tests whether the skew is different from the normal distribution.
`spearmanr`(x, y[, use_ties])	Calculates a Spearman rank-order correlation coefficient and the p-value
`theilslopes`(y[, x, alpha])	Computes the Theil-Sen estimator for a set of points (x, y).
`threshold`(a[, threshmin, threshmax, newval])	Clip array to a given value.
`tmax`(a, upperlimit[, axis, inclusive])	Compute the trimmed maximum
`tmean`(a[, limits, inclusive])	Compute the trimmed mean.
`tmin`(a[, lowerlimit, axis, inclusive])	Compute the trimmed minimum
`trim`(a[, limits, inclusive, relative, axis])	Trims an array by masking the data outside some given limits.
`trima`(a[, limits, inclusive])	Trims an array by masking the data outside some given limits.
`trimboth`(data[, proportiontocut, inclusive, ...])	Trims the smallest and largest data values.
`trimmed_stde`(a[, limits, inclusive, axis])	Returns the standard error of the trimmed mean along the given axis.
`trimr`(a[, limits, inclusive, axis])	Trims an array by masking some proportion of the data on each end.
`trimtail`(data[, proportiontocut, tail, ...])	Trims the data by masking values from one tail.
`tsem`(a[, limits, inclusive])	Compute the trimmed standard error of the mean.
`ttest_onesamp`(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
`ttest_ind`(a, b[, axis])	Calculates the T-test for the means of TWO INDEPENDENT samples of
`ttest_onesamp`(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
`ttest_rel`(a, b[, axis])	Calculates the T-test on TWO RELATED samples of scores, a and b.
`tvar`(a[, limits, inclusive])	Compute the trimmed variance
`variation`(a[, axis])	Computes the coefficient of variation, the ratio of the biased standard dev
`winsorize`(a[, limits, inclusive, inplace, axis])	Returns a Winsorized version of the input array.
`zmap`(scores, compare[, axis, ddof])	Calculates the relative z-scores.
`zscore`(a[, axis, ddof])	Calculates the z score of each value in the sample, relative to the sample

`scipy.stats.mstats.`**`argstoarray`**(**args*)

Constructs a 2D array from a group of sequences.

Sequences are filled with missing values to match the length of the longest sequence.

Parameters **args** : sequences

Group of sequences.

Returns **argstoarray** : MaskedArray

A (*m* x *n*) masked array, where *m* is the number of arguments and *n* the length of the longest argument.

Notes

`numpy.ma.row_stack` has identical behavior, but is called with a sequence of sequences.

`scipy.stats.mstats.`**`betai`**(*a*, *b*, *x*)

Returns the incomplete beta function.

I_x(a,b) = 1/B(a,b)*(Integral(0,x) of t^(a-1)(1-t)^(b-1) dt)

where a,b>0 and B(a,b) = G(a)*G(b)/(G(a+b)) where G(a) is the gamma function of a.

The standard broadcasting rules apply to a, b, and x.

Parameters **a** : array_like or float > 0

b : array_like or float > 0

x : array_like or float

x will be clipped to be no greater than 1.0 .

Returns **betai** : ndarray

Incomplete beta function.

`scipy.stats.mstats.`**`chisquare`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculates a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters **f_obs** : array_like

Observed frequencies in each category.

f_exp : array_like, optional

Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

“Delta degrees of freedom”: adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis : int or None, optional

The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns **chisq** : float or ndarray

The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p : float or ndarray

The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

`power_divergence`, `mstats.chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References

[R336], [R337]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`scipy.stats.mstats.`**`count_tied_groups`**(*x*, *use_missing=False*)

Counts the number of tied values.

Parameters **x** : sequence

Sequence of data on which to counts the ties

use_missing : bool, optional

Whether to consider missing values as tied.

Returns **count_tied_groups** : dict

Returns a dictionary (nb of ties: nb of groups).

Examples

```
>>> from scipy.stats import mstats
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> mstats.count_tied_groups(z)
{2: 1, 3: 2}
```

In the above example, the ties were 0 (3x), 2 (3x) and 3 (2x).

```
>>> z = np.ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> mstats.count_tied_groups(z)
{2: 2, 3: 1}
>>> z[[1,-1]] = np.ma.masked
>>> mstats.count_tied_groups(z, use_missing=True)
{2: 2, 3: 1}
```

`scipy.stats.mstats.`**`describe`**(*a*, *axis=0*, *ddof=0*)

Computes several descriptive statistics of the passed array.

Parameters **a** : array_like

Data array

axis : int or None, optional

Axis along which to calculate statistics. Default 0. If None, compute over the whole array *a*.

ddof : int, optional

degree of freedom (default 0); note that default ddof is different from the same routine in stats.describe

Returns **nobs** : int

(size of the data (discarding missing values)

minmax : (int, int)

min, max

mean : float

arithmetic mean

variance : float

unbiased variance

skewness : float

biased skewness

kurtosis : float

biased kurtosis

Examples

```
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])
>>> describe(ma)
(array(3),
 (0, 2),
 1.0,
```

```
 1.0,
 masked_array(data = 0.0,
             mask = False,
       fill_value = 1e+20)
,
 -1.5)
```

scipy.stats.mstats.**f_oneway**(**args*)

Performs a 1-way ANOVA, returning an F-value and probability given any number of groups. From Heiman, pp.394-7.

Usage: `f_oneway(*args)`, where `*args` is 2 or more arrays, one per treatment group.

Returns **statistic** : float

The computed F-value of the test.

pvalue : float

The associated p-value from the F-distribution.

scipy.stats.mstats.**f_value_wilks_lambda**(*ER*, *EF*, *dfnum*, *dfden*, *a*, *b*)

Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell & Delaney p.657.

scipy.stats.mstats.**find_repeats**(*arr*)

Find repeats in arr and return a tuple (repeats, repeat_count). Masked values are discarded.

Parameters **arr** : sequence

Input array. The array is flattened if it is not 1D.

Returns **repeats** : ndarray

Array of repeated values.

counts : ndarray

Array of counts.

scipy.stats.mstats.**friedmanchisquare**(**args*)

Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA. This function calculates the Friedman Chi-square test for repeated measures and returns the result, along with the associated probability value.

Each input is considered a given group. Ideally, the number of treatments among each group should be equal. If this is not the case, only the first n treatments are taken into account, where n is the number of treatments of the smallest group. If a group has some missing values, the corresponding treatments are masked in the other groups. The test statistic is corrected for ties.

Masked values in one group are propagated to the other groups.

Returns **statistic** : float

the test statistic.

pvalue : float

the associated p-value.

scipy.stats.mstats.**kendalltau**(*x*, *y*, *use_ties=True*, *use_missing=False*)

Computes Kendall's rank correlation tau on two variables *x* and *y*.

Parameters **x** : sequence

First data list (for example, time).

y : sequence

Second data list.

use_ties : {True, False}, optional

Whether ties correction should be performed.

use_missing : {False, True}, optional

Whether missing data should be allocated a rank of 0 (False) or the average rank (True)

Returns **correlation** : float

Kendall tau

pvalue : float

Approximate 2-side p-value.

`scipy.stats.mstats.`**`kendalltau_seasonal`**(*x*)

Computes a multivariate Kendall's rank correlation tau, for seasonal data.

Parameters **x** : 2-D ndarray

Array of seasonal data, with seasons in columns.

`scipy.stats.mstats.`**`kruskalwallis`**(**args*)

Compute the Kruskal-Wallis H-test for independent samples

The Kruskal-Wallis H-test tests the null hypothesis that the population median of all of the groups are equal. It is a non-parametric version of ANOVA. The test works on 2 or more independent samples, which may have different sizes. Note that rejecting the null hypothesis does not indicate which of the groups differs. Post-hoc comparisons between groups are required to determine which groups are different.

Parameters **sample1, sample2, ...** : array_like

Two or more arrays with the sample measurements can be given as arguments.

Returns **statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

pvalue : float

The p-value for the test using the assumption that H has a chi square distribution

Notes

Due to the assumption that H has a chi square distribution, the number of samples in each group must not be too small. A typical rule is that each sample must have at least 5 measurements.

References

[R338]

`scipy.stats.mstats.`**`ks_twosamp`**(*data1*, *data2*, *alternative='two-sided'*)

Computes the Kolmogorov-Smirnov test on two samples.

Missing values are discarded.

Parameters **data1** : array_like

First data set

data2 : array_like

Second data set

alternative : {'two-sided', 'less', 'greater'}, optional

Indicates the alternative hypothesis. Default is 'two-sided'.

Returns **d** : float

Value of the Kolmogorov Smirnov test

p : float

Corresponding p-value.

`scipy.stats.mstats.`**`kurtosis`**(*a*, *axis=0*, *fisher=True*, *bias=True*)

Computes the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use `kurtosistest` to see if result is close enough to normal.

Parameters	**a** : array data for which the kurtosis is calculated **axis** : int or None, optional Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*. **fisher** : bool, optional If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0). **bias** : bool, optional If False, then the calculations are corrected for statistical bias.
Returns	**kurtosis** : array The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[R339]

scipy.stats.mstats.**kurtosistest**(*a*, *axis=0*)

Tests whether a dataset has normal kurtosis

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: `kurtosis = 3(n-1)/(n+1)`.

Parameters	**a** : array array of the sample data **axis** : int or None, optional Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.
Returns	**statistic** : float The computed z-score for this test. **pvalue** : float The 2-sided p-value for the hypothesis test

Notes

Valid only for n>20. The Z-score is set to 0 for bad entries.

scipy.stats.mstats.**linregress**(**args*)

Calculate a regression line

This computes a least-squares regression for two sets of measurements.

Parameters	**x, y** : array_like two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.
Returns	**slope** : float slope of the regression line **intercept** : float intercept of the regression line **rvalue** : float correlation coefficient **pvalue** : float two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero. **stderr** : float Standard error of the estimate

Notes

Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

Examples

```
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x,y)
```

To get coefficient of determination (r_squared)

```
>>> print("r-squared:", r_value**2)
r-squared: 0.15286643777
```

`scipy.stats.mstats.`**`mannwhitneyu`**(*x*, *y*, *use_continuity=True*)

Computes the Mann-Whitney statistic

Missing values in *x* and/or *y* are discarded.

Parameters **x** : sequence

Input

y : sequence

Input

use_continuity : {True, False}, optional

Whether a continuity correction (1/2.) should be taken into account.

Returns **statistic** : float

The Mann-Whitney statistics

pvalue : float

Approximate p-value assuming a normal distribution.

`scipy.stats.mstats.`**`plotting_positions`**(*data*, *alpha=0.4*, *beta=0.4*)

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as `(i-alpha)/(n+1-alpha-beta)`, where:

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for* alpha *and* beta *are:

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters **data** : array_like

Input data, as a sequence or array of dimension at most 2.

alpha : float, optional

Plotting positions parameter. Default is 0.4.

beta : float, optional

Plotting positions parameter. Default is 0.4.

Returns **positions** : MaskedArray

The calculated plotting positions.

`scipy.stats.mstats.`**`mode`**(*a*, *axis=0*)

Returns an array of the modal (most common) value in the passed array.

If there is more than one such value, only the first is returned. The bin-count for the modal bins is also returned.

Parameters **a** : array_like

n-dimensional array of which to find mode(s).

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

Returns **mode** : ndarray

Array of modal values.

count : ndarray

Array of counts for each mode.

Examples

```
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 7],
...               [8, 1, 8, 4],
...               [5, 3, 0, 5],
...               [4, 7, 5, 9]])
>>> from scipy import stats
>>> stats.mode(a)
(array([[3, 1, 0, 0]]), array([[1, 1, 1, 1]]))
```

To get mode of whole array, specify `axis=None`:

```
>>> stats.mode(a, axis=None)
(array([3]), array([3]))
```

`scipy.stats.mstats.`**`moment`**(*a*, *moment=1*, *axis=0*)

Calculates the nth moment about the mean for a sample.

Generally used to calculate coefficients of skewness and kurtosis.

Parameters **a** : array_like

data

moment : int, optional

order of central moment that is returned

axis : int or None, optional

Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

Returns **n-th central moment** : ndarray or float

The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

`scipy.stats.mstats.`**`mquantiles`**(*a*, *prob=[0.25, 0.5, 0.75]*, *alphap=0.4*, *betap=0.4*, *axis=None*, *limit=()*)

Computes empirical quantiles for a data array.

Samples quantile are defined by `Q(p) = (1-gamma)*x[j] + gamma*x[j+1]`, where `x[j]` is the j-th order statistic, and gamma is a function of `j = floor(n*p + m)`, `m = alphap + p*(1 - alphap - betap)` and `g = n*p + m - j`.

Reinterpreting the above equations to compare to **R** lead to the equation: `p(k) = (k - alphap)/(n + 1 - alphap - betap)`

Typical values of (alphap,betap) are:

- (0,1) : `p(k) = k/n` : linear interpolation of cdf (**R** type 4)
- (.5,.5) : `p(k) = (k - 1/2.)/n` : piecewise linear function (**R** type 5)
- (0,0) : `p(k) = k/(n+1)` : (**R** type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`: p(k) = mode[F(x[k])]. (**R** type 7, **R** default)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`: Then p(k) ~ median[F(x[k])]. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (**R** type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`: Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (**R** type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM

Parameters

a : array_like

Input data, as a sequence or array of dimension at most 2.

prob : array_like, optional

List of quantiles to compute.

alphap : float, optional

Plotting positions parameter, default is 0.4.

betap : float, optional

Plotting positions parameter, default is 0.4.

axis : int, optional

Axis along which to perform the trimming. If None (default), the input array is first flattened.

limit : tuple, optional

Tuple of (lower, upper) values. Values of *a* outside this open interval are ignored.

Returns

mquantiles : MaskedArray

An array containing the calculated quantiles.

Notes

This formulation is very similar to **R** except the calculation of `m` from `alphap` and `betap`, where in **R** `m` is defined with each type.

References

[R340], [R341]

Examples

```
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6., 47., 49., 15., 42., 41., 7., 39., 43., 40., 36.])
>>> mquantiles(a)
array([ 19.2,  40. ,  42.8])
```

Using a 2D array, specifying axis and limit.

```
>>> data = np.array([[   6.,    7.,    1.],
                     [  47.,   15.,    2.],
                     [  49.,   36.,    3.],
                     [  15.,   39.,    4.],
                     [  42.,   40., -999.],
                     [  41.,   41., -999.],
                     [   7., -999., -999.],
                     [  39., -999., -999.],
                     [  43., -999., -999.],
                     [  40., -999., -999.],
                     [  36., -999., -999.]])
>>> mquantiles(data, axis=0, limit=(0, 50))
array([[ 19.2 ,  14.6 ,   1.45],
       [ 40.  ,  37.5 ,   2.5 ],
       [ 42.8 ,  40.05,   3.55]])
```

```
>>> data[:, 2] = -999.
>>> mquantiles(data, axis=0, limit=(0, 50))
masked_array(data =
 [[19.2 14.6 --]
 [40.0 37.5 --]
 [42.8 40.05 --]],
             mask =
 [[False False  True]
  [False False  True]
  [False False  True]],
       fill_value = 1e+20)
```

`scipy.stats.mstats.`**`msign`**`(`*x*`)`

Returns the sign of x, or 0 if x is masked.

`scipy.stats.mstats.`**`normaltest`**`(`*a*, *axis=0*`)`

Tests whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's [R342], [R343] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters **a** : array_like

The array containing the data to be tested.

axis : int or None, optional

Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns **statistic** : float or array

s^2 + *k*^2, where *s* is the z-score returned by `skewtest` and *k* is the z-score returned by `kurtosistest`.

pvalue : float or array

A 2-sided chi squared probability for the hypothesis test.

References

[R342], [R343]

`scipy.stats.mstats.`**`obrientransform`**`(`**args*`)`

Computes a transform on input data (any number of columns). Used to test for homogeneity of variance prior to running one-way stats. Each array in `*args` is one level of a factor. If an *f_oneway()* run on the transformed data and found significant, variances are unequal. From Maxwell and Delaney, p.112.

Returns: transformed data for use in an ANOVA `scipy.stats.mstats.`**`pearsonr`**(*x*, *y*)

Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.

The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson's correlation requires that each dataset be normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters **x** : 1-D array_like

Input

y : 1-D array_like

Input

Returns **pearsonr** : float

Pearson's correlation coefficient, 2-tailed p-value.

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

`scipy.stats.mstats.`**`plotting_positions`**(*data*, *alpha=0.4*, *beta=0.4*)

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as **`(i-alpha)/(n+1-alpha-beta)`*, where:***

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for **alpha** ***and*** **beta** ***are:***

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters **data** : array_like

Input data, as a sequence or array of dimension at most 2.

alpha : float, optional

Plotting positions parameter. Default is 0.4.

beta : float, optional

Plotting positions parameter. Default is 0.4.

Returns **positions** : MaskedArray

The calculated plotting positions.

`scipy.stats.mstats.`**`pointbiserialr`**(*x*, *y*)

Calculates a point biserial correlation coefficient and the associated p-value.

The point biserial correlation is used to measure the relationship between a binary variable, x, and a continuous variable, y. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a determinative relationship.

This function uses a shortcut formula but produces the same result as `pearsonr`.

Parameters

x : array_like of bools
  Input array.

y : array_like
  Input array.

Returns

correlation : float
  R value

pvalue : float
  2-tailed p-value

Notes

Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

References

http://en.wikipedia.org/wiki/Point-biserial_correlation_coefficient

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)
>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)
>>> np.corrcoef(a, b)
array([[ 1.       ,  0.8660254],
       [ 0.8660254,  1.       ]])
```

`scipy.stats.mstats.`**`rankdata`**(*data*, *axis=None*, *use_missing=False*)

Returns the rank (also known as order statistics) of each data point along the given axis.

If some values are tied, their rank is averaged. If some values are masked, their rank is set to 0 if use_missing is False, or set to the average rank of the unmasked values if use_missing is True.

Parameters

data : sequence
  Input data. The data is transformed to a masked array

axis : {None,int}, optional
  Axis along which to perform the ranking. If None, the array is first flattened. An exception is raised if the axis is specified for arrays with a dimension larger than 2

use_missing : bool, optional
  Whether the masked values have a rank of 0 (False) or equal to the average rank of the unmasked values (True).

`scipy.stats.mstats.`**`scoreatpercentile`**(*data*, *per*, *limit=()*, *alphap=0.4*, *betap=0.4*)

Calculate the score at the given 'per' percentile of the sequence a. For example, the score at per=50 is the median.

This function is a shortcut to mquantile `scipy.stats.mstats.`**`sem`**`(`*a*, *axis=0*, *ddof=1*`)`

Calculates the standard error of the mean of the input array.

Also sometimes called standard error of measurement.

Parameters **a** : array_like

An array containing the values for which the standard error is returned.

axis : int or None, optional

If axis is None, ravel *a* first. If axis is an integer, this will be the axis over which to operate. Defaults to 0.

ddof : int, optional

Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.

Returns **s** : ndarray or float

The standard error of the mean in the sample(s), along the input axis.

Notes

The default value for *ddof* changed in scipy 0.15.0 to be consistent with *stats.sem* as well as with the most common definition used (like in the R documentation).

Examples

Find standard error along the first axis:

```
>>> from scipy import stats
>>> a = np.arange(20).reshape(5,4)
>>> stats.sem(a)
array([ 2.8284,  2.8284,  2.8284,  2.8284])
```

Find standard error across the whole array, using n degrees of freedom:

```
>>> stats.sem(a, axis=None, ddof=0)
1.2893796958227628
```

`scipy.stats.mstats.`**`signaltonoise`**`(`**args*, ***kwds*`)`

`signaltonoise` is deprecated! mstats.signaltonoise is deprecated in scipy 0.16.0

Calculates the signal-to-noise ratio, as the ratio of the mean over

standard deviation along the given axis.

Parameters **data** : sequence

Input data

axis [{0, int}, optional] Axis along which to compute. If None, the computation is performed on a flat version of the array.

`scipy.stats.mstats.`**`skew`**`(`*a*, *axis=0*, *bias=True*`)`

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left tail of the distribution. The function `skewtest` can be used to determine if the skewness value is close enough to 0, statistically speaking.

Parameters **a** : ndarray

data

axis : int or None, optional

Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.

bias : bool, optional
If False, then the calculations are corrected for statistical bias.

Returns **skewness** : ndarray
The skewness of values along an axis, returning 0 where all values are equal.

References

[R344]

`scipy.stats.mstats.`**`skewtest`**(*a*, *axis=0*)

Tests whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters **a** : array
The data to be tested

axis : int or None, optional
Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

Returns **statistic** : float
The computed z-score for this test.

pvalue : float
a 2-sided p-value for the hypothesis test

Notes

The sample size must be at least 8.

`scipy.stats.mstats.`**`spearmanr`**(*x*, *y*, *use_ties=True*)

Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the linear relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

Missing values are discarded pair-wise: if a value is missing in *x*, the corresponding value in *y* is masked.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters **x** : array_like
The length of *x* must be > 2.

y : array_like
The length of *y* must be > 2.

use_ties : bool, optional
Whether the correction for ties should be computed.

Returns **correlation** : float
Spearman correlation coefficient

pvalue : float
2-tailed p-value.

References

[CRCProbStat2000] section 14.7

`scipy.stats.mstats.`**`theilslopes`**(*y*, *x=None*, *alpha=0.95*)

Computes the Theil-Sen estimator for a set of points (x, y).

`theilslopes` implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

y : array_like
  Dependent variable.

x : array_like or None, optional
  Independent variable. If None, use `arange(len(y))` instead.

alpha : float, optional
  Confidence degree between 0 and 1. Default is 95% confidence. Note that *alpha* is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as "find the 90% confidence interval".

Returns

medslope : float
  Theil slope.

medintercept : float
  Intercept of the Theil line, as `median(y) - medslope*median(x)`.

lo_slope : float
  Lower bound of the confidence interval on *medslope*.

up_slope : float
  Upper bound of the confidence interval on *medslope*.

Notes

The implementation of `theilslopes` follows [R345]. The intercept is not defined in [R345], and here it is defined as `median(y) - medslope*median(x)`, which is given in [R347]. Other definitions of the intercept exist in the literature. A confidence interval for the intercept is not given as this question is not addressed in [R345].

References

[R345], [R346], [R347]

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7
```

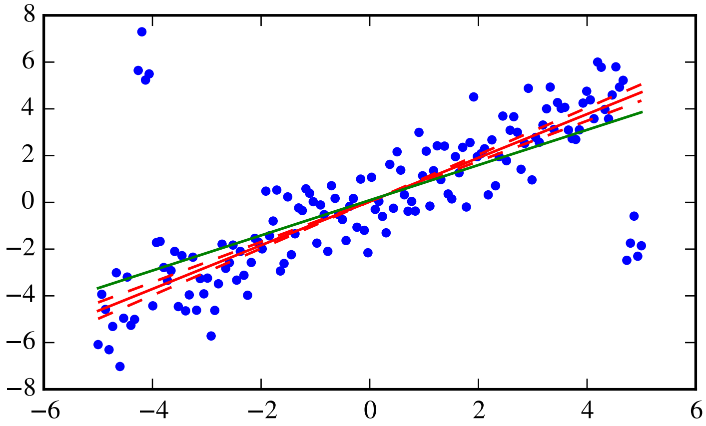
Compute the slope, intercept and 90% confidence interval. For comparison, also compute the least-squares fit with `linregress`:

```
>>> res = stats.theilslopes(y, x, 0.90)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Theil-Sen regression line is shown in red, with the dashed red lines illustrating the confidence interval of the slope (note that the dashed red lines are not the confidence interval of the regression as the confidence interval of the intercept is not included). The green line shows the least-squares fit for comparison.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.')
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, res[1] + res[2] * x, 'r--')
>>> ax.plot(x, res[1] + res[3] * x, 'r--')
```

```
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```



`scipy.stats.mstats.`**`threshold`**`(`*a*, *threshmin=None*, *threshmax=None*, *newval=0*`)`

Clip array to a given value.

Similar to numpy.clip(), except that values less than *threshmin* or greater than *threshmax* are replaced by *newval*, instead of by *threshmin* and *threshmax* respectively.

Parameters **a** : ndarray

Input data

threshmin : {None, float}, optional

Lower threshold. If None, set to the minimum value.

threshmax : {None, float}, optional

Upper threshold. If None, set to the maximum value.

newval : {0, float}, optional

Value outside the thresholds.

Returns **threshold** : ndarray

Returns *a*, with values less then *threshmin* and values greater *threshmax* replaced with *newval*.

`scipy.stats.mstats.`**`tmax`**`(`*a*, *upperlimit*, *axis=0*, *inclusive=True*`)`

Compute the trimmed maximum

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters **a** : array_like

array of values

upperlimit : None or float, optional

Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the upper limit are included. The default value is True.

Returns **tmax** : float

`scipy.stats.mstats.`**`tmean`**(*a*, *limits=None*, *inclusive=(True*, *True)*)

Compute the trimmed mean.

This function finds the arithmetic mean of given values, ignoring values outside the given *limits*.

Parameters

a : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns

tmean : float

`scipy.stats.mstats.`**`tmin`**(*a*, *lowerlimit=None*, *axis=0*, *inclusive=True*)

Compute the trimmed minimum

This function finds the miminum value of an array *a* along the specified axis, but only considering values greater than a specified lower limit.

Parameters

a : array_like

array of values

lowerlimit : None or float, optional

Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive : {True, False}, optional

This flag determines whether values exactly equal to the lower limit are included. The default value is True.

Returns

tmin : float

`scipy.stats.mstats.`**`trim`**(*a*, *limits=None*, *inclusive=(True*, *True)*, *relative=False*, *axis=None*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters

a : sequence

Input array

limits : {None, tuple}, optional

If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.

If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.

Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.

If limits is None, no trimming is performed

inclusive : {(bool, bool) tuple}, optional

If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative : bool, optional

Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis : int, optional

Axis along which to trim.

Examples

```
>>> z = [ 1, 2, 3, 4, 5, 6, 7, 8, 9,10]
>>> trim(z,(3,8))
[--,--, 3, 4, 5, 6, 7, 8,--,--]
>>> trim(z,(0.1,0.2),relative=True)
[--, 2, 3, 4, 5, 6, 7, 8,--,--]
```

`scipy.stats.mstats.`**`trima`**(*a*, *limits=None*, *inclusive=(True*, *True)*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters **a** : array_like

Input array.

limits : {None, tuple}, optional

Tuple of (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit will be masked. A limit is None indicates an open interval.

inclusive : (bool, bool) tuple, optional

Tuple of (lower flag, upper flag), indicating whether values exactly equal to the lower (upper) limit are allowed.

`scipy.stats.mstats.`**`trimboth`**(*data*, *proportiontocut=0.2*, *inclusive=(True*, *True)*, *axis=None*)

Trims the smallest and largest data values.

Trims the *data* by masking the `int(proportiontocut * n)` smallest and `int(proportiontocut * n)` largest values of data along the given axis, where n is the number of unmasked values before trimming.

Parameters **data** : ndarray

Data to trim.

proportiontocut : float, optional

Percentage of trimming (as a float between 0 and 1). If n is the number of unmasked values before trimming, the number of values after trimming is `(1 - 2*proportiontocut) * n`. Default is 0.2.

inclusive : {(bool, bool) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis : int, optional

Axis along which to perform the trimming. If None, the input array is first flattened.

`scipy.stats.mstats.`**`trimmed_stde`**(*a*, *limits=(0.1*, *0.1)*, *inclusive=(1*, *1)*, *axis=None*)

Returns the standard error of the trimmed mean along the given axis.

Parameters **a** : sequence

Input array

limits : {(0.1,0.1), tuple of float}, optional

tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.

If n is the number of unmasked data before trimming, the values smaller than `n * limits[0]` and the values larger than `n * `limits[1]` are masked, and the total number of unmasked data after trimming is `n * (1.-sum(limits))`. In each case, the value of one limit can be set to None to indicate an open interval. If *limits* is None, no trimming is performed.

inclusive : {(bool, bool) tuple} optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis : int, optional

Axis along which to trim.

Returns **trimmed_stde** : scalar or ndarray

`scipy.stats.mstats.`**`trimr`**(*a*, *limits=None*, *inclusive=(True*, *True)*, *axis=None*)

Trims an array by masking some proportion of the data on each end. Returns a masked version of the input array.

Parameters **a** : sequence

Input array.

limits : {None, tuple}, optional

Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)). The value of one limit can be set to None to indicate an open interval.

inclusive : {(True,True) tuple}, optional

Tuple of flags indicating whether the number of data being masked on the left (right) end should be truncated (True) or rounded (False) to integers.

axis : {None,int}, optional

Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

`scipy.stats.mstats.`**`trimtail`**(*data*, *proportiontocut=0.2*, *tail='left'*, *inclusive=(True*, *True)*, *axis=None*)

Trims the data by masking values from one tail.

Parameters **data** : array_like

Data to trim.

proportiontocut : float, optional

Percentage of trimming. If `n` is the number of unmasked values before trimming, the number of values after trimming is `(1 - proportiontocut) * n`. Default is 0.2.

tail : {'left','right'}, optional

If 'left' the *proportiontocut* lowest values will be masked. If 'right' the *proportiontocut* highest values will be masked. Default is 'left'.

inclusive : {(bool, bool) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False). Default is (True, True).

axis : int, optional

Axis along which to perform the trimming. If None, the input array is first flattened. Default is None.

Returns **trimtail** : ndarray

Returned array of same shape as *data* with masked tail values.

`scipy.stats.mstats.`**`tsem`**(*a*, *limits=None*, *inclusive=(True*, *True)*)

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given *limits*.

Parameters **a** : array_like

array of values

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tsem** : float

Notes

`tsem` uses unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.mstats.`**`ttest_onesamp`**`(`*a*, *popmean*, *axis=0*`)`

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters **a** : array_like

sample observation

popmean : float or array_like

expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole array *a*.

Returns **statistic** : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
```

```
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`scipy.stats.mstats.`**`ttest_ind`**`(`*a*, *b*, *axis=0*`)`

Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters

a, b : array_like

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var : bool, optional

If True (default), perform a standard independent 2 sample test that assumes equal population variances [R348]. If False, perform Welch's t-test, which does not assume equal population variance [R349]. .. versionadded:: 0.11.0

Returns

statistic : float or array

The calculated t-statistic.

pvalue : float or array

The two-tailed p-value.

Notes

We can use this test, if we observe two independent samples from the same or different population, e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average (expected) value differs significantly across samples. If we observe a large p-value, for example larger than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References

[R348], [R349]

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678)
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1,rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```

`ttest_ind` underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)
(-0.46580283298287162, 0.64149646246569292)
```

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)
(-0.94365973617132992, 0.34744170334794122)
```

`scipy.stats.mstats.`**`ttest_onesamp`**`(`*a*, *popmean*, *axis=0*`)`

Calculates the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters

a : array_like

sample observation

popmean : float or array_like

expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole array *a*.

Returns

statistic : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
```

```
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`scipy.stats.mstats.`**`ttest_rel`**(*a*, *b*, *axis=0*)

Calculates the T-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters **a, b** : array_like

The arrays must have the same shape.

axis : int or None, optional

Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

Returns **statistic** : float or array

t-statistic

pvalue : float or array

two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

http://en.wikipedia.org/wiki/T-test#Dependent_t-test

Examples

```
>>> from scipy import stats
>>> np.random.seed(12345678) # fix random seed to get same numbers
```

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = (stats.norm.rvs(loc=5,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs2)
(0.24101764965300962, 0.80964043445811562)
>>> rvs3 = (stats.norm.rvs(loc=8,scale=10,size=500) +
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs3)
(-3.9995108708727933, 7.3082402191726459e-005)
```

`scipy.stats.mstats.`**`tvar`**(*a*, *limits=None*, *inclusive=(True, True)*)

Compute the trimmed variance

This function computes the sample variance of an array of values, while ignoring values which are outside of given *limits*.

Parameters **a** : array_like

Array of values.

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns **tvar** : float

Trimmed variance.

Notes

`tvar` computes the unbiased sample variance, i.e. it uses a correction factor `n / (n - 1)`.

`scipy.stats.mstats.`**`variation`**`(`*a*, *axis=0*`)`

Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters **a** : array_like

Input array.

axis : int or None, optional

Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array *a*.

References

[R350]

`scipy.stats.mstats.`**`winsorize`**`(`*a*, *limits=None*, *inclusive=(True, True)*, *inplace=False*, *axis=None*`)`

Returns a Winsorized version of the input array.

The (limits[0])th lowest values are set to the (limits[0])th percentile, and the (limits[1])th highest values are set to the (1 - limits[1])th percentile. Masked values are skipped.

Parameters **a** : sequence

Input array.

limits : {None, tuple of float}, optional

Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) The value of one limit can be set to None to indicate an open interval.

inclusive : {(True, True) tuple}, optional

Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

inplace : {False, True}, optional

Whether to winsorize in place (True) or to use a copy (False)

axis : {None, int}, optional

Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

Notes

This function is applied to reduce the effect of possibly spurious outliers by limiting the extreme values.

`scipy.stats.mstats.`**`zmap`**`(`*scores*, *compare*, *axis=0*, *ddof=0*`)`

Calculates the relative z-scores.

Returns an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters **scores** : array_like

The input for which z-scores are calculated.

compare : array_like

The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as *scores*.

axis : int or None, optional

Axis over which mean and variance of *compare* are calculated. Default is 0. If None, compute over the whole array *scores*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns **zscore** : array_like

Z-scores, in the same shape as *scores*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017,  0.        ,  0.35355339,  0.70710678])
```

`scipy.stats.mstats.`**`zscore`**`(`*a, axis=0, ddof=0*`)`

Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters **a** : array_like

An array like object containing the sample data.

axis : int or None, optional

Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof : int, optional

Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns **zscore** : array_like

The z-scores, standardized by mean and standard deviation of input array *a*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> a = np.array([ 0.7972,  0.0767,  0.4383,  0.7866,  0.8091,  0.1954,
...                0.6307, 0.6599,  0.1065,  0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552,  1.0923,  1.1664, -0.8559,  0.5786,
        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148,  0.0478,  0.6243,  0.4608],
...               [ 0.7149,  0.0775,  0.6072,  0.9656],
...               [ 0.6341,  0.1403,  0.9759,  0.4064],
...               [ 0.5918,  0.6948,  0.904 ,  0.3721],
...               [ 0.0921,  0.2481,  0.1188,  0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119,  1.07259584,  0.40420358],
       [ 0.33048416, -1.37380874,  0.04251374,  1.00081084],
       [ 0.26796377, -1.12598418,  1.23283094, -0.37481053],
       [-0.22095197,  0.24468594,  1.19042819, -1.21416216],
       [-0.82780366,  1.4457416 , -0.43867764, -0.1792603 ]])
```

5.36 C/C++ integration (`scipy.weave`)

Warning: This documentation is work-in-progress and unorganized.

5.36.1 C/C++ integration

NOTE: this module is deprecated and will be removed from Scipy before the 1.0 release – use the standalone weave package (**'https://github.com/scipy/weave'_**) instead.

> inline – a function for including C/C++ code within Python blitz – a function for compiling Numeric expressions to C++ ext_tools – a module that helps construct C/C++ extension modules. accelerate – a module that inline accelerates Python functions

---

Note: On Linux one needs to have the Python development headers installed in order to be able to compile things with the *weave* module. Since this is a runtime dependency these headers (typically in a pythonX.Y-dev package) are not always installed when installing scipy.

`inline`(code[, arg_names, local_dict, ...])	Inline C/C++ code within Python scripts.
`blitz`(expr[, local_dict, global_dict, ...])	
`ext_tools`	
`accelerate`	

`scipy.weave.`**`inline`**(*code*, *arg_names=[]*, *local_dict=None*, *global_dict=None*, *force=0*, *compiler=''*, *verbose=0*, *support_code=None*, *headers=[]*, *customize=None*, *type_converters=None*, *auto_downcast=1*, *newarr_converter=0*, ***kw*)

Inline C/C++ code within Python scripts.

`inline()` compiles and executes C/C++ code on the fly. Variables in the local and global Python scope are also available in the C/C++ code. Values are passed to the C/C++ code by assignment much like variables passed are passed into a standard Python function. Values are returned from the C/C++ code through a special argument called return_val. Also, the contents of mutable objects can be changed within the C/C++ code and the changes remain after the C code exits and returns to Python.

inline has quite a few options as listed below. Also, the keyword arguments for distutils extension modules are accepted to specify extra information needed for compiling.

Parameters **code** : string

A string of valid C++ code. It should not specify a return statement. Instead it should assign results that need to be returned to Python in the *return_val*.

arg_names : [str], optional

A list of Python variable names that should be transferred from Python into the C/C++ code. It defaults to an empty string.

local_dict : dict, optional

If specified, it is a dictionary of values that should be used as the local scope for the C/C++ code. If local_dict is not specified the local dictionary of the calling function is used.

global_dict : dict, optional

If specified, it is a dictionary of values that should be used as the global scope for the C/C++ code. If *global_dict* is not specified, the global dictionary of the calling function is used.

force : {0, 1}, optional

If 1, the C++ code is compiled every time inline is called. This is really only useful for debugging, and probably only useful if your editing *support_code* a lot.

compiler : str, optional

The name of compiler to use when compiling. On windows, it understands 'msvc' and 'gcc' as well as all the compiler names understood by distutils. On Unix, it'll only understand the values understood by distutils. (I should add 'gcc' though to this).

On windows, the compiler defaults to the Microsoft C++ compiler. If this isn't available, it looks for mingw32 (the gcc compiler).

On Unix, it'll probably use the same compiler that was used when compiling Python. Cygwin's behavior should be similar.

verbose : {0,1,2}, optional

Specifies how much information is printed during the compile phase of inlining code. 0 is silent (except on windows with msvc where it still prints some garbage). 1 informs you when compiling starts, finishes, and how long it took. 2 prints out the command lines for the compilation process and can be useful if your having problems getting code to work. Its handy for finding the name of the .cpp file if you need to examine it. verbose has no effect if the compilation isn't necessary.

support_code : str, optional

A string of valid C++ code declaring extra code that might be needed by your compiled function. This could be declarations of functions, classes, or structures.

headers : [str], optional

A list of strings specifying header files to use when compiling the code. The list might look like `["<vector>","'my_header'"]`. Note that the header strings need to be in a form than can be pasted at the end of a `#include` statement in the C++ code.

customize : base_info.custom_info, optional

An alternative way to specify *support_code*, *headers*, etc. needed by the function. See `scipy.weave.base_info` for more details. (not sure this'll be used much).

type_converters : [type converters], optional

These guys are what convert Python data types to C/C++ data types. If you'd like to use a different set of type conversions than the default, specify them here. Look in the type conversions section of the main documentation for examples.

auto_downcast : {1,0}, optional

This only affects functions that have numpy arrays as input variables. Setting this to 1 will cause all floating point values to be cast as float instead of double if all the Numeric arrays are of type float. If even one of the arrays has type double or double complex, all variables maintain their standard types.

newarr_converter : int, optional

Unused.

Other Parameters

Relevant :mod:'distutils' keywords. These are duplicated from Greg Ward's :class:'distutils.extension.Extension' class for convenience:

sources : [string]

List of source filenames, relative to the distribution root (where the setup script lives), in Unix form (slash-separated) for portability. Source files may be C, C++, SWIG (.i), platform-specific resource files, or whatever else is recognized by the "build_ext" command as source for a Python extension.

Note: The *module_path* file is always appended to the front of this list

include_dirs : [string]

List of directories to search for C/C++ header files (in Unix form for portability).

define_macros : [(name

List of macros to define; each macro is defined using a 2-tuple, where 'value' is either the string to define it to or None to define it without a particular value (equivalent of "#define FOO" in source or -DFOO on Unix C compiler command line).

undef_macros : [string]

List of macros to undefine explicitly.

library_dirs : [string]

List of directories to search for C/C++ libraries at link time.

libraries : [string]

List of library names (not filenames or paths) to link against.

runtime_library_dirs : [string]

List of directories to search for C/C++ libraries at run time (for shared extensions, this is when the extension is loaded).

extra_objects : [string]

List of extra files to link with (e.g. object files not implied by 'sources', static libraries that must be explicitly specified, binary resource files, etc.)

extra_compile_args : [string]

Any extra platform- and compiler-specific information to use when compiling the source files in 'sources'. For platforms and compilers where "command line" makes sense, this is typically a list of command-line arguments, but for other platforms it could be anything.

extra_link_args : [string]

Any extra platform- and compiler-specific information to use when linking object files together to create the extension (or to create a new static Python interpreter). Similar interpretation as for 'extra_compile_args'.

export_symbols : [string]

List of symbols to be exported from a shared extension. Not used on all platforms, and not generally necessary for Python extensions, which typically export exactly one symbol: "init" + extension_name.

swig_opts : [string]

Any extra options to pass to SWIG if a source file has the .i extension.

depends : [string]

List of files that the extension depends on.

language : string
Extension language (i.e. "c", "c++", "objc"). Will be detected from the source extensions if not provided.

See also:

`distutils.extension.Extension`
Describes additional parameters.

`scipy.weave.`**`blitz`**(*expr*, *local_dict=None*, *global_dict=None*, *check_size=1*, *verbose=0*, ***kw*)

Functions

`assign_variable_types`(variables[, ...])	
`downcast`(var_specs)	Cast python scalars down to most common type of arrays used.
`format_error_msg`(errors)	
`generate_file_name`(module_name, module_location)	
`generate_module`(module_string, module_file)	generate the source code file. Only overwrite
`indent`(st, spaces)	

Classes

`ext_function`(name, code_block, args[, ...])	***Methods***
`ext_function_from_specs`(name, code_block, ...)	***Methods***
`ext_module`(name[, compiler])	***Methods***

[WPR] http://en.wikipedia.org/wiki/Romberg’s_method

[NPT] http://docs.scipy.org/doc/numpy/reference/generated/numpy.trapz.html

[KK] D.A. Knoll and D.E. Keyes, “Jacobian-free Newton-Krylov methods”, J. Comp. Phys. 193, 357 (2003).

[PP] PETSc http://www.mcs.anl.gov/petsc/ and its Python bindings http://code.google.com/p/petsc4py/

[AMG] PyAMG (algebraic multigrid preconditioners/solvers) http://code.google.com/p/pyamg/

[CT65] Cooley, James W., and John W. Tukey, 1965, “An algorithm for the machine calculation of complex Fourier series,” *Math. Comput.* 19: 297-301.

[NR] Press, W., Teukolsky, S., Vetterline, W.T., and Flannery, B.P., 2007, *Numerical Recipes: The Art of Scientific Computing*, ch. 12-13. Cambridge Univ. Press, Cambridge, UK.

[Mak] J. Makhoul, 1980, ‘A Fast Cosine Transform in One and Two Dimensions’, *IEEE Transactions on acoustics, speech and signal processing* vol. 28(1), pp. 27-34, http://dx.doi.org/10.1109/TASSP.1980.1163351

[WPW] http://en.wikipedia.org/wiki/Window_function

[WPC] http://en.wikipedia.org/wiki/Discrete_cosine_transform

[WPS] http://en.wikipedia.org/wiki/Discrete_sine_transform

[R1] “Statistics toolbox.” API Reference Documentation. The MathWorks. http://www.mathworks.com/access/helpdesk/help/toolbox/stats/. Accessed October 1, 2007.

[R2] “Hierarchical clustering.” API Reference Documentation. The Wolfram Research, Inc. http://reference.wolfram.com/mathematica/HierarchicalClustering/tutorial/ HierarchicalClustering.html. Accessed October 1, 2007.

[R3] Gower, JC and Ross, GJS. “Minimum Spanning Trees and Single Linkage Cluster Analysis.” Applied Statistics. 18(1): pp. 54–64. 1969.

[R4] Ward Jr, JH. “Hierarchical grouping to optimize an objective function.” Journal of the American Statistical Association. 58(301): pp. 236–44. 1963.

[R5] Johnson, SC. “Hierarchical clustering schemes.” Psychometrika. 32(2): pp. 241–54. 1966.

[R6] Sneath, PH and Sokal, RR. “Numerical taxonomy.” Nature. 193: pp. 855–60. 1962.

[R7] Batagelj, V. “Comparing resemblance measures.” Journal of Classification. 12: pp. 73–90. 1995.

[R8] Sokal, RR and Michener, CD. “A statistical method for evaluating systematic relationships.” Scientific Bulletins. 38(22): pp. 1409–38. 1958.

[R9] Edelbrock, C. “Mixture model tests of hierarchical clustering algorithms: the problem of classifying everybody.” Multivariate Behavioral Research. 14: pp. 367–84. 1979.

[CODATA2010] CODATA Recommended Values of the Fundamental Physical Constants 2010.

http://physics.nist.gov/cuu/Constants/index.html

[R36] 'A Fast Cosine Transform in One and Two Dimensions', by J. Makhoul, *IEEE Transactions on acoustics, speech and signal processing* vol. 28(1), pp. 27-34, http://dx.doi.org/10.1109/TASSP.1980.1163351 (1980).

[R37] Wikipedia, "Discrete cosine transform", http://en.wikipedia.org/wiki/Discrete_cosine_transform

[R38] Wikipedia, "Discrete sine transform", http://en.wikipedia.org/wiki/Discrete_sine_transform

[R39] 'Romberg's method' http://en.wikipedia.org/wiki/Romberg%27s_method

[HNW93] E. Hairer, S.P. Norsett and G. Wanner, Solving Ordinary Differential Equations i. Nonstiff Problems. 2nd edition. Springer Series in Computational Mathematics, Springer-Verlag (1993)

[R44] Krogh, "Efficient Algorithms for Polynomial Interpolation and Numerical Differentiation", 1970.

[R40] http://en.wikipedia.org/wiki/Bernstein_polynomial

[R41] Kenneth I. Joy, Bernstein polynomials, http://www.idav.ucdavis.edu/education/CAGDNotes/Bernstein-Polynomials.pdf

[R42] E. H. Doha, A. H. Bhrawy, and M. A. Saker, Boundary Value Problems, vol 2011, article ID 829546, doi:10.1155/2011/829543

[R45] http://www.qhull.org/

[R43] http://www.qhull.org/

[CT] See, for example, P. Alfeld, ''A trivariate Clough-Tocher scheme for tetrahedral data''. Computer Aided Geometric Design, 1, 169 (1984); G. Farin, ''Triangular Bernstein-Bezier patches''. Computer Aided Geometric Design, 3, 83 (1986).

[Nielson83] G. Nielson, ''A method for interpolating scattered data based upon a minimum norm network''. Math. Comp., 40, 253 (1983).

[Renka84] R. J. Renka and A. K. Cline. ''A Triangle-based C1 interpolation method.'', Rocky Mountain J. Math., 14, 223 (1984).

[R46] Python package *regulargrid* by Johannes Buchner, see https://pypi.python.org/pypi/regulargrid/

[R47] Trilinear interpolation. (2013, January 17). In Wikipedia, The Free Encyclopedia. Retrieved 27 Feb 2013 01:28. http://en.wikipedia.org/w/index.php?title=Trilinear_interpolation&oldid=533448871

[R48] Weiser, Alan, and Sergio E. Zarantonello. "A note on piecewise linear and multilinear table interpolation in many dimensions." MATH. COMPUT. 50.181 (1988): 189-196. http://www.ams.org/journals/mcom/1988-50-181/S0025-5718-1988-0917826-0/S0025-5718-1988-0917826-0.pdf

[R66] P. Dierckx, "An algorithm for smoothing, differentiation and integration of experimental data using spline functions", J.Comp.Appl.Maths 1 (1975) 165-184.

[R67] P. Dierckx, "A fast algorithm for smoothing data on a rectangular grid while using spline functions", SIAM J.Numer.Anal. 19 (1982) 1286-1304.

[R68] P. Dierckx, "An improved algorithm for curve fitting with spline functions", report tw54, Dept. Computer Science,K.U. Leuven, 1981.

[R69] P. Dierckx, "Curve and surface fitting with splines", Monographs on Numerical Analysis, Oxford University Press, 1993.

[R63] P. Dierckx, "Algorithms for smoothing data with periodic and parametric splines, Computer Graphics and Image Processing", 20 (1982) 171-184.

[R64] P. Dierckx, "Algorithms for smoothing data with periodic and parametric splines", report tw55, Dept. Computer Science, K.U.Leuven, 1981.

[R65] P. Dierckx, "Curve and surface fitting with splines", Monographs on Numerical Analysis, Oxford University Press, 1993.

[R58] C. de Boor, "On calculating with b-splines", J. Approximation Theory, 6, p.50-62, 1972.

[R59] M.G. Cox, "The numerical evaluation of b-splines", J. Inst. Maths Applics, 10, p.134-149, 1972.

[R60] P. Dierckx, "Curve and surface fitting with splines", Monographs on Numerical Analysis, Oxford University Press, 1993.

[R61] P.W. Gaffney, The calculation of indefinite integrals of b-splines", J. Inst. Maths Applics, 17, p.37-41, 1976.

[R62] P. Dierckx, "Curve and surface fitting with splines", Monographs on Numerical Analysis, Oxford University Press, 1993.

[R70] C. de Boor, "On calculating with b-splines", J. Approximation Theory, 6, p.50-62, 1972.

[R71] M.G. Cox, "The numerical evaluation of b-splines", J. Inst. Maths Applics, 10, p.134-149, 1972.

[R72] P. Dierckx, "Curve and surface fitting with splines", Monographs on Numerical Analysis, Oxford University Press, 1993.

[R55] de Boor C : On calculating with b-splines, J. Approximation Theory 6 (1972) 50-62.

[R56] Cox M.G. : The numerical evaluation of b-splines, J. Inst. Maths applics 10 (1972) 134-149.

[R57] Dierckx P. : Curve and surface fitting with splines, Monographs on Numerical Analysis, Oxford University Press, 1993.

[R52] Dierckx P.:An algorithm for surface fitting with spline functions Ima J. Numer. Anal. 1 (1981) 267-283.

[R53] Dierckx P.:An algorithm for surface fitting with spline functions report tw50, Dept. Computer Science,K.U.Leuven, 1980.

[R54] Dierckx P.:Curve and surface fitting with splines, Monographs on Numerical Analysis, Oxford University Press, 1993.

[R49] Dierckx P. : An algorithm for surface fitting with spline functions Ima J. Numer. Anal. 1 (1981) 267-283.

[R50] Dierckx P. : An algorithm for surface fitting with spline functions report tw50, Dept. Computer Science,K.U.Leuven, 1980.

[R51] Dierckx P. : Curve and surface fitting with splines, Monographs on Numerical Analysis, Oxford University Press, 1993.

[R86] G. H. Golub and C. F. Van Loan, *Matrix Computations*, Baltimore, MD, Johns Hopkins University Press, 1985, pg. 15

[R87] Peter H. Schonemann, "A generalized solution of the orthogonal Procrustes problem", Psychometrica – Vol. 31, No. 1, March, 1996.

[R88] R. A. Horn and C. R. Johnson, "Matrix Analysis", Cambridge University Press, 1985.

[R89] N. J. Higham, "Functions of Matrices: Theory and Computation", SIAM, 2008.

[R96] Golub, G. H. & Van Loan, C. F. Matrix Computations, 3rd Ed. (Johns Hopkins University Press, 1996).

[R97] Daniel, J. W., Gragg, W. B., Kaufman, L. & Stewart, G. W. Reorthogonalization and stable algorithms for updating the Gram-Schmidt QR factorization. Math. Comput. 30, 772-795 (1976).

[R98] Reichel, L. & Gragg, W. B. Algorithm 686: FORTRAN Subroutines for Updating the QR Decomposition. ACM Trans. Math. Softw. 16, 369-377 (1990).

[R90] Golub, G. H. & Van Loan, C. F. Matrix Computations, 3rd Ed. (Johns Hopkins University Press, 1996).

[R91] Daniel, J. W., Gragg, W. B., Kaufman, L. & Stewart, G. W. Reorthogonalization and stable algorithms for updating the Gram-Schmidt QR factorization. Math. Comput. 30, 772-795 (1976).

[R92] Reichel, L. & Gragg, W. B. Algorithm 686: FORTRAN Subroutines for Updating the QR Decomposition. ACM Trans. Math. Softw. 16, 369-377 (1990).

[R93] Golub, G. H. & Van Loan, C. F. Matrix Computations, 3rd Ed. (Johns Hopkins University Press, 1996).

[R94] Daniel, J. W., Gragg, W. B., Kaufman, L. & Stewart, G. W. Reorthogonalization and stable algorithms for updating the Gram-Schmidt QR factorization. Math. Comput. 30, 772-795 (1976).

[R95] Reichel, L. & Gragg, W. B. Algorithm 686: FORTRAN Subroutines for Updating the QR Decomposition. ACM Trans. Math. Softw. 16, 369-377 (1990).

[R75] Awad H. Al-Mohy and Nicholas J. Higham (2009) “A New Scaling and Squaring Algorithm for the Matrix Exponential.” SIAM Journal on Matrix Analysis and Applications. 31 (3). pp. 970-989. ISSN 1095-7162

[R83] Awad H. Al-Mohy and Nicholas J. Higham (2012) “Improved Inverse Scaling and Squaring Algorithms for the Matrix Logarithm.” SIAM Journal on Scientific Computing, 34 (4). C152-C169. ISSN 1095-7197

[R84] Nicholas J. Higham (2008) “Functions of Matrices: Theory and Computation” ISBN 978-0-898716-46-7

[R85] Nicholas J. Higham and Lijing lin (2011) “A Schur-Pade Algorithm for Fractional Powers of a Matrix.” SIAM Journal on Matrix Analysis and Applications, 32 (3). pp. 1056-1078. ISSN 0895-4798

[R101] Edvin Deadman, Nicholas J. Higham, Rui Ralha (2013) “Blocked Schur Algorithms for Computing the Matrix Square Root, Lecture Notes in Computer Science, 7782. pp. 171-182.

[R78] Gene H. Golub, Charles F. van Loan, Matrix Computations 4th ed.

[R76] Awad H. Al-Mohy and Nicholas J. Higham (2009) Computing the Frechet Derivative of the Matrix Exponential, with an application to Condition Number Estimation. SIAM Journal On Matrix Analysis and Applications., 30 (4). pp. 1639-1657. ISSN 1095-7162

[R77] Nicholas J. Higham and Lijing lin (2011) “A Schur-Pade Algorithm for Fractional Powers of a Matrix.” SIAM Journal on Matrix Analysis and Applications, 32 (3). pp. 1056-1078. ISSN 0895-4798

[R99] Hamilton, James D. Time Series Analysis, Princeton: Princeton University Press, 1994. 265. Print. http://www.scribd.com/doc/20577138/Hamilton-1994-Time-Series-Analysis

[R100] Gajic, Z., and M.T.J. Qureshi. 2008. Lyapunov Matrix Equation in System Stability and Control. Dover Books on Engineering Series. Dover Publications.

[R73] R. A. Horn & C. R. Johnson, *Matrix Analysis*. Cambridge, UK: Cambridge University Press, 1999, pp. 146-7.

[R74] “DFT matrix”, http://en.wikipedia.org/wiki/DFT_matrix

[R81] P. H. Leslie, On the use of matrices in certain population mathematics, Biometrika, Vol. 33, No. 3, 183–212 (Nov. 1945)

[R82] P. H. Leslie, Some further notes on the use of matrices in population mathematics, Biometrika, Vol. 35, No. 3/4, 213–245 (Dec. 1948)

[R79] “Pascal matrix”, http://en.wikipedia.org/wiki/Pascal_matrix

[R80] Cohen, A. M., “The inverse of a Pascal matrix”, Mathematical Gazette, 59(408), pp. 111-112, 1975.

[R439] P.G. Martinsson, V. Rokhlin, Y. Shkolnisky, M. Tygert. “ID: a software package for low-rank approximation of matrices via interpolative decompositions, version 0.2.” http://cims.nyu.edu/~tygert/id_doc.pdf.

[R440] H. Cheng, Z. Gimbutas, P.G. Martinsson, V. Rokhlin. “On the compression of low rank matrices.” *SIAM J. Sci. Comput.* 26 (4): 1389–1404, 2005. doi:10.1137/030602678.

[R441] E. Liberty, F. Woolfe, P.G. Martinsson, V. Rokhlin, M. Tygert. “Randomized algorithms for the low-rank approximation of matrices.” *Proc. Natl. Acad. Sci. U.S.A.* 104 (51): 20167–20172, 2007. doi:10.1073/pnas.0709640104.

[R442] P.G. Martinsson, V. Rokhlin, M. Tygert. “A randomized algorithm for the decomposition of matrices.” *Appl. Comput. Harmon. Anal.* 30 (1): 47–68, 2011. doi:10.1016/j.acha.2010.02.003.

[R443] F. Woolfe, E. Liberty, V. Rokhlin, M. Tygert. “A fast randomized algorithm for the approximation of matrices.” *Appl. Comput. Harmon. Anal.* 25 (3): 335–366, 2008. doi:10.1016/j.acha.2007.12.002.

[R102] http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.42.2777

[R103] http://www.richardhartersworld.com/cri/2001/slidingmin.html

[R104] http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.42.2777

[R105] http://www.richardhartersworld.com/cri/2001/slidingmin.html

[R106] A.X. Falcao, J. Stolfi and R. de Alencar Lotufo, “The image foresting transform: theory, algorithms, and applications”, Pattern Analysis and Machine Intelligence, vol. 26, pp. 19-29, 2004.

[R107] http://en.wikipedia.org/wiki/Closing_%28morphology%29

[R108] http://en.wikipedia.org/wiki/Mathematical_morphology

[R109] http://en.wikipedia.org/wiki/Dilation_%28morphology%29

[R110] http://en.wikipedia.org/wiki/Mathematical_morphology

[R111] http://en.wikipedia.org/wiki/Erosion_%28morphology%29

[R112] http://en.wikipedia.org/wiki/Mathematical_morphology

[R113] http://en.wikipedia.org/wiki/Mathematical_morphology

[R114] http://en.wikipedia.org/wiki/Hit-or-miss_transform

[R115] http://en.wikipedia.org/wiki/Opening_%28morphology%29

[R116] http://en.wikipedia.org/wiki/Mathematical_morphology

[R117] http://cmm.ensmp.fr/~serra/cours/pdf/en/ch6en.pdf, slide 15.

[R118] http://www.qi.tnw.tudelft.nl/Courses/FIP/noframes/fip-Morpholo.html#Heading102

[R119] http://en.wikipedia.org/wiki/Mathematical_morphology

[R120] http://en.wikipedia.org/wiki/Dilation_%28morphology%29

[R121] http://en.wikipedia.org/wiki/Mathematical_morphology

[R122] http://en.wikipedia.org/wiki/Erosion_%28morphology%29

[R123] http://en.wikipedia.org/wiki/Mathematical_morphology

[R124] http://en.wikipedia.org/wiki/Mathematical_morphology

[R125] http://en.wikipedia.org/wiki/Mathematical_morphology

[R468] P. T. Boggs and J. E. Rogers, “Orthogonal Distance Regression,” in “Statistical analysis of measurement error models and applications: proceedings of the AMS-IMS-SIAM joint summer research conference held June 10-16, 1989,” Contemporary Mathematics, vol. 112, pg. 186, 1990.

[R142] Nelder, J A, and R Mead. 1965. A Simplex Method for Function Minimization. The Computer Journal 7: 308-13.

[R143] Wright M H. 1996. Direct search methods: Once scorned, now respectable, in Numerical Analysis 1995: Proceedings of the 1995 Dundee Biennial Conference in Numerical Analysis (Eds. D F Griffiths and G A Watson). Addison Wesley Longman, Harlow, UK. 191-208.

[R144] Powell, M J D. 1964. An efficient method for finding the minimum of a function of several variables without calculating derivatives. The Computer Journal 7: 155-162.

[R145] Press W, S A Teukolsky, W T Vetterling and B P Flannery. Numerical Recipes (any edition), Cambridge University Press.

[R146] Nocedal, J, and S J Wright. 2006. Numerical Optimization. Springer New York.

[R147] Byrd, R H and P Lu and J. Nocedal. 1995. A Limited Memory Algorithm for Bound Constrained Optimization. SIAM Journal on Scientific and Statistical Computing 16 (5): 1190-1208.

[R148] Zhu, C and R H Byrd and J Nocedal. 1997. L-BFGS-B: Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization. ACM Transactions on Mathematical Software 23 (4): 550-560.

[R149] Nash, S G. Newton-Type Minimization Via the Lanczos Method. 1984. SIAM Journal of Numerical Analysis 21: 770-778.

[R150] Powell, M J D. A direct search optimization method that models the objective and constraint functions by linear interpolation. 1994. Advances in Optimization and Numerical Analysis, eds. S. Gomez and J-P Hennart, Kluwer Academic (Dordrecht), 51-67.

[R136] Nelder, J.A. and Mead, R. (1965), "A simplex method for function minimization", The Computer Journal, 7, pp. 308-313

[R137] Wright, M.H. (1996), "Direct Search Methods: Once Scorned, Now Respectable", in Numerical Analysis 1995, Proceedings of the 1995 Dundee Biennial Conference in Numerical Analysis, D.F. Griffiths and G.A. Watson (Eds.), Addison Wesley Longman, Harlow, UK, pp. 191-208.

[R138] Wright & Nocedal, "Numerical Optimization", 1999, pp. 120-122.

[R133] Storn, R and Price, K, Differential Evolution - a Simple and Efficient Heuristic for Global Optimization over Continuous Spaces, Journal of Global Optimization, 1997, 11, 341 - 359.

[R134] http://www1.icsi.berkeley.edu/~storn/code.html

[R135] http://en.wikipedia.org/wiki/Differential_evolution

[R127] Wales, David J. 2003, Energy Landscapes, Cambridge University Press, Cambridge, UK.

[R128] Wales, D J, and Doye J P K, Global Optimization by Basin-Hopping and the Lowest Energy Structures of Lennard-Jones Clusters Containing up to 110 Atoms. Journal of Physical Chemistry A, 1997, 101, 5111.

[R129] Li, Z. and Scheraga, H. A., Monte Carlo-minimization approach to the multiple-minima problem in protein folding, Proc. Natl. Acad. Sci. USA, 1987, 84, 6611.

[R130] Wales, D. J. and Scheraga, H. A., Global optimization of clusters, crystals, and biomolecules, Science, 1999, 285, 1368.

[R133] Storn, R and Price, K, Differential Evolution - a Simple and Efficient Heuristic for Global Optimization over Continuous Spaces, Journal of Global Optimization, 1997, 11, 341 - 359.

[R134] http://www1.icsi.berkeley.edu/~storn/code.html

[R135] http://en.wikipedia.org/wiki/Differential_evolution

[Brent1973] Brent, R. P., *Algorithms for Minimization Without Derivatives*. Englewood Cliffs, NJ: Prentice-Hall, 1973. Ch. 3-4.

[PressEtal1992] Press, W. H.; Flannery, B. P.; Teukolsky, S. A.; and Vetterling, W. T. *Numerical Recipes in FORTRAN: The Art of Scientific Computing*, 2nd ed. Cambridge, England: Cambridge University Press, pp. 352-355, 1992. Section 9.3: "Van Wijngaarden-Dekker-Brent Method."

[Ridders1979] Ridders, C. F. J. "A New Algorithm for Computing a Single Root of a Real Continuous Function." IEEE Trans. Circuits Systems 26, 979-980, 1979.

[R153] More, Jorge J., Burton S. Garbow, and Kenneth E. Hillstrom. 1980. User Guide for MINPACK-1.

[R154] C. T. Kelley. 1995. Iterative Methods for Linear and Nonlinear Equations. Society for Industrial and Applied Mathematics. <http://www.siam.org/books/kelley/>

[R155] 23. La Cruz, J.M. Martinez, M. Raydan. Math. Comp. 75, 1429 (2006).

[R131] B.A. van der Rotten, PhD thesis, "A limited memory Broyden method to solve high-dimensional systems of nonlinear equations". Mathematisch Instituut, Universiteit Leiden, The Netherlands (2003).

http://www.math.leidenuniv.nl/scripties/Rotten.pdf

[R132] B.A. van der Rotten, PhD thesis, "A limited memory Broyden method to solve high-dimensional systems of nonlinear equations". Mathematisch Instituut, Universiteit Leiden, The Netherlands (2003).

http://www.math.leidenuniv.nl/scripties/Rotten.pdf

[R509] "Spectral residual method without gradient information for solving large-scale nonlinear systems of equations." W. La Cruz, J.M. Martinez, M. Raydan. Math. Comp. **75**, 1429 (2006).

[R510] 23. La Cruz, Opt. Meth. Software, 29, 24 (2014).

[R511] 23. Cheng, D.-H. Li. IMA J. Numer. Anal. **29**, 814 (2009).

[R151] D.A. Knoll and D.E. Keyes, J. Comp. Phys. 193, 357 (2003).

[R152] A.H. Baker and E.R. Jessup and T. Manteuffel, SIAM J. Matrix Anal. Appl. 26, 962 (2005).

[Ey] 22. Eyert, J. Comp. Phys., 124, 271 (1996).

[R139] Dantzig, George B., Linear programming and extensions. Rand Corporation Research Study Princeton Univ. Press, Princeton, NJ, 1963

[R140] Hillier, S.H. and Lieberman, G.J. (1995), "Introduction to Mathematical Programming", McGraw-Hill, Chapter 4.

[R141] Bland, Robert G. New finite pivoting rules for the simplex method. Mathematics of Operations Research (2), 1977: pp. 103-107.

[R502] Dantzig, George B., Linear programming and extensions. Rand Corporation Research Study Princeton Univ. Press, Princeton, NJ, 1963

[R503] Hillier, S.H. and Lieberman, G.J. (1995), "Introduction to Mathematical Programming", McGraw-Hill, Chapter 4.

[R504] Bland, Robert G. New finite pivoting rules for the simplex method. Mathematics of Operations Research (2), 1977: pp. 103-107.

[R126] Nocedal, Jorge. "Updating quasi-Newton matrices with limited storage." Mathematics of computation 35.151 (1980): 773-782.

[R173] F. Gustaffson, "Determining the initial states in forward-backward filtering", Transactions on Signal Processing, Vol. 46, pp. 988-992, 1996.

[R186] Wikipedia, "Analytic signal". http://en.wikipedia.org/wiki/Analytic_signal

[R187] Wikipedia, "Analytic signal", http://en.wikipedia.org/wiki/Analytic_signal

[R175] Oppenheim, A. V. and Schafer, R. W., "Discrete-Time Signal Processing", Prentice-Hall, Englewood Cliffs, New Jersey (1989). (See, for example, Section 7.4.)

[R176] Smith, Steven W., "The Scientist and Engineer's Guide to Digital Signal Processing", Ch. 17. http://www.dspguide.com/ch17/1.htm

[R177] Richard G. Lyons, "Understanding Digital Signal Processing, 3rd edition", p. 830.

[R196] J. H. McClellan and T. W. Parks, "A unified approach to the design of optimum FIR linear phase digital filters", IEEE Trans. Circuit Theory, vol. CT-20, pp. 697-701, 1973.

[R197] J. H. McClellan, T. W. Parks and L. R. Rabiner, "A Computer Program for Designing Optimum FIR Linear Phase Digital Filters", IEEE Trans. Audio Electroacoust., vol. AU-21, pp. 506-525, 1973.

[R168] http://en.wikipedia.org/wiki/Discretization#Discretization_of_linear_state_space_models

[R169] http://techteach.no/publications/discretetime_signals_systems/discrete.pdf

[R170] G. Zhang, X. Chen, and T. Chen, Digital redesign via the generalized bilinear transformation, Int. J. Control, vol. 82, no. 4, pp. 741-754, 2009. (http://www.ece.ualberta.ca/~gfzhang/research/ZCC07_preprint.pdf)

[R194] J. Kautsky, N.K. Nichols and P. van Dooren, "Robust pole assignment in linear state feedback", International Journal of Control, Vol. 41 pp. 1129-1155, 1985.

[R195] A.L. Tits and Y. Yang, "Globally convergent algorithms for robust pole assignment by state feedback, IEEE Transactions on Automatic Control, Vol. 41, pp. 1432-1452, 1996.

[R156] M.S. Bartlett, "Periodogram Analysis and Continuous Spectra", Biometrika 37, 1-16, 1950.

[R157] E.R. Kanasewich, "Time Sequence Analysis in Geophysics", The University of Alberta Press, 1975, pp. 109-110.

[R158] A.V. Oppenheim and R.W. Schafer, "Discrete-Time Signal Processing", Prentice-Hall, 1999, pp. 468-471.

[R159] Wikipedia, "Window function", http://en.wikipedia.org/wiki/Window_function

[R160] W.H. Press, B.P. Flannery, S.A. Teukolsky, and W.T. Vetterling, "Numerical Recipes", Cambridge University Press, 1986, page 429.

[R161] Blackman, R.B. and Tukey, J.W., (1958) The measurement of power spectra, Dover Publications, New York.

[R162] Oppenheim, A.V., and R.W. Schafer. Discrete-Time Signal Processing. Upper Saddle River, NJ: Prentice-Hall, 1999, pp. 468-471.

[R163] C. Dolph, "A current distribution for broadside arrays which optimizes the relationship between beam width and side-lobe level", Proceedings of the IEEE, Vol. 34, Issue 6

[R164] Peter Lynch, "The Dolph-Chebyshev Window: A Simple Optimal Filter", American Meteorological Society (April 1997) http://mathsci.ucd.ie/~plynch/Publications/Dolph.pdf

[R165] F. J. Harris, "On the use of windows for harmonic analysis with the discrete Fourier transforms", Proceedings of the IEEE, Vol. 66, No. 1, January 1978

[R178] Blackman, R.B. and Tukey, J.W., (1958) The measurement of power spectra, Dover Publications, New York.

[R179] E.R. Kanasewich, "Time Sequence Analysis in Geophysics", The University of Alberta Press, 1975, pp. 109-110.

[R180] Wikipedia, "Window function", http://en.wikipedia.org/wiki/Window_function

[R181] W.H. Press, B.P. Flannery, S.A. Teukolsky, and W.T. Vetterling, "Numerical Recipes", Cambridge University Press, 1986, page 425.

[R182] Blackman, R.B. and Tukey, J.W., (1958) The measurement of power spectra, Dover Publications, New York.

[R183] E.R. Kanasewich, "Time Sequence Analysis in Geophysics", The University of Alberta Press, 1975, pp. 106-108.

[R184] Wikipedia, "Window function", http://en.wikipedia.org/wiki/Window_function

[R185] W.H. Press, B.P. Flannery, S.A. Teukolsky, and W.T. Vetterling, "Numerical Recipes", Cambridge University Press, 1986, page 425.

[R188] J. F. Kaiser, "Digital Filters" - Ch 7 in "Systems analysis by digital computer", Editors: F.F. Kuo and J.F. Kaiser, p 218-285. John Wiley and Sons, New York, (1966).

[R189] E.R. Kanasewich, “Time Sequence Analysis in Geophysics”, The University of Alberta Press, 1975, pp. 177-178.

[R190] Wikipedia, “Window function”, http://en.wikipedia.org/wiki/Window_function

[R198] Harris, Fredric J. (Jan 1978). “On the use of Windows for Harmonic Analysis with the Discrete Fourier Transform”. Proceedings of the IEEE 66 (1): 51-83. doi:10.1109/PROC.1978.10837

[R199] Wikipedia, “Window function”, http://en.wikipedia.org/wiki/Window_function#Tukey_window

[R174] Bioinformatics (2006) 22 (17): 2059-2065. doi: 10.1093/bioinformatics/btl355 http://bioinformatics.oxfordjournals.org/content/22/17/2059.long

[R200] P. Welch, “The use of the fast Fourier transform for the estimation of power spectra: A method based on time averaging over short, modified periodograms”, IEEE Trans. Audio Electroacoust. vol. 15, pp. 70-73, 1967.

[R201] M.S. Bartlett, “Periodogram Analysis and Continuous Spectra”, Biometrika, vol. 37, pp. 1-16, 1950.

[R171] P. Welch, “The use of the fast Fourier transform for the estimation of power spectra: A method based on time averaging over short, modified periodograms”, IEEE Trans. Audio Electroacoust. vol. 15, pp. 70-73, 1967.

[R172] Rabiner, Lawrence R., and B. Gold. “Theory and Application of Digital Signal Processing” Prentice-Hall, pp. 414-419, 1975

[R166] P. Welch, “The use of the fast Fourier transform for the estimation of power spectra: A method based on time averaging over short, modified periodograms”, IEEE Trans. Audio Electroacoust. vol. 15, pp. 70-73, 1967.

[R167] Stoica, Petre, and Randolph Moses, “Spectral Analysis of Signals” Prentice Hall, 2005

[R191] N.R. Lomb “Least-squares frequency analysis of unequally spaced data”, Astrophysics and Space Science, vol 39, pp. 447-462, 1976

[R192] J.D. Scargle “Studies in astronomical time series analysis. II - Statistical aspects of spectral analysis of unevenly spaced data”, The Astrophysical Journal, vol 263, pp. 835-853, 1982

[R193] R.H.D. Townsend, “Fast calculation of the Lomb-Scargle periodogram using graphics processing units.”, The Astrophysical Journal Supplement Series, vol 191, pp. 247-253, 2010

[R13] D. J. Pearce, “An Improved Algorithm for Finding the Strongly Connected Components of a Directed Graph”, Technical Report, 2005

[R18] Awad H. Al-Mohy and Nicholas J. Higham (2009) “A New Scaling and Squaring Algorithm for the Matrix Exponential.” SIAM Journal on Matrix Analysis and Applications. 31 (3). pp. 970-989. ISSN 1095-7162

[R19] Awad H. Al-Mohy and Nicholas J. Higham (2011) “Computing the Action of the Matrix Exponential, with an Application to Exponential Integrators.” SIAM Journal on Scientific Computing, 33 (2). pp. 488-511. ISSN 1064-8275 http://eprints.ma.man.ac.uk/1591/

[R20] Nicholas J. Higham and Awad H. Al-Mohy (2010) “Computing Matrix Functions.” Acta Numerica, 19. 159-208. ISSN 0962-4929 http://eprints.ma.man.ac.uk/1451/

[R31] Nicholas J. Higham and Francoise Tisseur (2000), “A Block Algorithm for Matrix 1-Norm Estimation, with an Application to 1-Norm Pseudospectra.” SIAM J. Matrix Anal. Appl. Vol. 21, No. 4, pp. 1185-1201.

[R32] Awad H. Al-Mohy and Nicholas J. Higham (2009), “A new scaling and squaring algorithm for the matrix exponential.” SIAM J. Matrix Anal. Appl. Vol. 31, No. 3, pp. 970-989.

[R21] A.H. Baker and E.R. Jessup and T. Manteuffel, SIAM J. Matrix Anal. Appl. 26, 962 (2005).

[R22] A.H. Baker, PhD thesis, University of Colorado (2003). http://amath.colorado.edu/activities/thesis/allisonb/Thesis.ps

[R28] C. C. Paige and M. A. Saunders (1982a). “LSQR: An algorithm for sparse linear equations and sparse least squares”, ACM TOMS 8(1), 43-71.

[R29] C. C. Paige and M. A. Saunders (1982b). “Algorithm 583. LSQR: Sparse linear equations and least squares problems”, ACM TOMS 8(2), 195-209.

[R30] M. A. Saunders (1995). “Solution of sparse rectangular systems using LSQR and CRAIG”, BIT 35, 588-604.

[R26] D. C.-L. Fong and M. A. Saunders, “LSMR: An iterative algorithm for sparse least-squares problems”, SIAM J. Sci. Comput., vol. 33, pp. 2950-2971, 2011. http://arxiv.org/abs/1006.0758

[R27] LSMR Software, http://web.stanford.edu/group/SOL/software/lsmr/

[R14] ARPACK Software, http://www.caam.rice.edu/software/ARPACK/

[R15] R. B. Lehoucq, D. C. Sorensen, and C. Yang, ARPACK USERS GUIDE: Solution of Large Scale Eigenvalue Problems by Implicitly Restarted Arnoldi Methods. SIAM, Philadelphia, PA, 1998.

[R16] ARPACK Software, http://www.caam.rice.edu/software/ARPACK/

[R17] R. B. Lehoucq, D. C. Sorensen, and C. Yang, ARPACK USERS GUIDE: Solution of Large Scale Eigenvalue Problems by Implicitly Restarted Arnoldi Methods. SIAM, Philadelphia, PA, 1998.

[R23] A. V. Knyazev (2001), Toward the Optimal Preconditioned Eigensolver: Locally Optimal Block Preconditioned Conjugate Gradient Method. SIAM Journal on Scientific Computing 23, no. 2, pp. 517-541. http://dx.doi.org/10.1137/S1064827500366124

[R24] A. V. Knyazev, I. Lashuk, M. E. Argentati, and E. Ovchinnikov (2007), Block Locally Optimal Preconditioned Eigenvalue Xolvers (BLOPEX) in hypre and PETSc. http://arxiv.org/abs/0705.2626

[R25] A. V. Knyazev’s C and MATLAB implementations: http://www-math.cudenver.edu/~aknyazev/software/BLOPEX/

[R35] SuperLU http://crd.lbl.gov/~xiaoye/SuperLU/

[R254] Awad H. Al-Mohy and Nicholas J. Higham (2009) “A New Scaling and Squaring Algorithm for the Matrix Exponential.” SIAM Journal on Matrix Analysis and Applications. 31 (3). pp. 970-989. ISSN 1095-7162

[R255] Awad H. Al-Mohy and Nicholas J. Higham (2011) “Computing the Action of the Matrix Exponential, with an Application to Exponential Integrators.” SIAM Journal on Scientific Computing, 33 (2). pp. 488-511. ISSN 1064-8275 http://eprints.ma.man.ac.uk/1591/

[R256] Nicholas J. Higham and Awad H. Al-Mohy (2010) “Computing Matrix Functions.” Acta Numerica, 19. 159-208. ISSN 0962-4929 http://eprints.ma.man.ac.uk/1451/

[R267] Nicholas J. Higham and Francoise Tisseur (2000), “A Block Algorithm for Matrix 1-Norm Estimation, with an Application to 1-Norm Pseudospectra.” SIAM J. Matrix Anal. Appl. Vol. 21, No. 4, pp. 1185-1201.

[R268] Awad H. Al-Mohy and Nicholas J. Higham (2009), “A new scaling and squaring algorithm for the matrix exponential.” SIAM J. Matrix Anal. Appl. Vol. 31, No. 3, pp. 970-989.

[R257] A.H. Baker and E.R. Jessup and T. Manteuffel, SIAM J. Matrix Anal. Appl. 26, 962 (2005).

[R258] A.H. Baker, PhD thesis, University of Colorado (2003). http://amath.colorado.edu/activities/thesis/allisonb/Thesis.ps

[R264] C. C. Paige and M. A. Saunders (1982a). “LSQR: An algorithm for sparse linear equations and sparse least squares”, ACM TOMS 8(1), 43-71.

[R265] C. C. Paige and M. A. Saunders (1982b). “Algorithm 583. LSQR: Sparse linear equations and least squares problems”, ACM TOMS 8(2), 195-209.

[R266] M. A. Saunders (1995). “Solution of sparse rectangular systems using LSQR and CRAIG”, BIT 35, 588-604.

[R262] D. C.-L. Fong and M. A. Saunders, “LSMR: An iterative algorithm for sparse least-squares problems”, SIAM J. Sci. Comput., vol. 33, pp. 2950-2971, 2011. http://arxiv.org/abs/1006.0758

[R263] LSMR Software, http://web.stanford.edu/group/SOL/software/lsmr/

[R250] ARPACK Software, http://www.caam.rice.edu/software/ARPACK/

[R251] R. B. Lehoucq, D. C. Sorensen, and C. Yang, ARPACK USERS GUIDE: Solution of Large Scale Eigenvalue Problems by Implicitly Restarted Arnoldi Methods. SIAM, Philadelphia, PA, 1998.

[R252] ARPACK Software, http://www.caam.rice.edu/software/ARPACK/

[R253] R. B. Lehoucq, D. C. Sorensen, and C. Yang, ARPACK USERS GUIDE: Solution of Large Scale Eigenvalue Problems by Implicitly Restarted Arnoldi Methods. SIAM, Philadelphia, PA, 1998.

[R259] A. V. Knyazev (2001), Toward the Optimal Preconditioned Eigensolver: Locally Optimal Block Preconditioned Conjugate Gradient Method. SIAM Journal on Scientific Computing 23, no. 2, pp. 517-541. http://dx.doi.org/10.1137/S1064827500366124

[R260] A. V. Knyazev, I. Lashuk, M. E. Argentati, and E. Ovchinnikov (2007), Block Locally Optimal Preconditioned Eigenvalue Xolvers (BLOPEX) in hypre and PETSc. http://arxiv.org/abs/0705.2626

[R261] A. V. Knyazev's C and MATLAB implementations: http://www-math.cudenver.edu/~aknyazev/software/BLOPEX/

[R271] SuperLU http://crd.lbl.gov/~xiaoye/SuperLU/

[R204] D. J. Pearce, "An Improved Algorithm for Finding the Strongly Connected Components of a Directed Graph", Technical Report, 2005

[Qhull] http://www.qhull.org/

[R273] Krzanowski, W. J. (2000). "Principles of Multivariate analysis".

[R274] Gower, J. C. (1975). "Generalized procrustes analysis".

[R282] http://en.wikipedia.org/wiki/Error_function

[R283] Milton Abramowitz and Irene A. Stegun, eds. Handbook of Mathematical Functions with Formulas, Graphs, and Mathematical Tables. New York: Dover, 1972. http://www.math.sfu.ca/~cbm/aands/page_297.htm

[R284] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R285] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R286] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R287] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R292] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R277] Steven G. Johnson, Faddeeva W function implementation. http://ab-initio.mit.edu/Faddeeva

[R291] Digital Library of Mathematical Functions, 14.30. http://dlmf.nist.gov/14.30

[R275] NIST Digital Library of Mathematical Functions http://dlmf.nist.gov/14.21

[R290] NIST Digital Library of Mathematical Functions http://dlmf.nist.gov/14.3

[R278] Digital Libary of Mathematical Functions 29.12 http://dlmf.nist.gov/29.12

[R279] Bardhan and Knepley, "Computational science and re-discovery: open-source implementations of ellipsoidal harmonics for problems in potential theory", Comput. Sci. Disc. 5, 014006 (2012) doi:10.1088/1749-4699/5/1/014006

[R280] David J.and Dechambre P, "Computation of Ellipsoidal Gravity Field Harmonics for small solar system bodies" pp. 30-36, 2000

[R281] George Dassios, "Ellipsoidal Harmonics: Theory and Applications" pp. 418, 2012

[R288] http://en.wikipedia.org/wiki/Lambert_W_function

[R289] Corless et al, "On the Lambert W function", Adv. Comp. Math. 5 (1996) 329-359. http://www.apmaths.uwo.ca/~djeffrey/Offprints/W-adv-cm.pdf

[R316] “Birnbaum-Saunders distribution”, http://en.wikipedia.org/wiki/Birnbaum-Saunders_distribution

[R324] “Generalized normal distribution, Version 1”, https://en.wikipedia.org/wiki/Generalized_normal_distribution#Version_1

[R325] “Generalized normal distribution, Version 1”, https://en.wikipedia.org/wiki/Generalized_normal_distribution#Version_1

[R333] http://mathworld.wolfram.com/MaxwellDistribution.html

[R374] M.L. Eaton, “Multivariate Statistics: A Vector Space Approach”, Wiley, 1983.

[R375] W.B. Smith and R.R. Hocking, “Algorithm AS 53: Wishart Variate Generator”, Applied Statistics, vol. 21, pp. 341-345, 1972.

[R326] M.L. Eaton, “Multivariate Statistics: A Vector Space Approach”, Wiley, 1983.

[R327] M.C. Jones, “Generating Inverse Wishart Matrices”, Communications in Statistics - Simulation and Computation, vol. 14.2, pp.511-514, 1985.

[R329] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.

[R351] D’Agostino, R. B. (1971), “An omnibus test of normality for moderate and large sample size,” Biometrika, 58, 341-348

[R352] D’Agostino, R. and Pearson, E. S. (1973), “Testing for departures from normality,” Biometrika, 60, 613-622

[R362] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000. Section 2.2.24.1

[R372] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.

[R353] S. E. Maxwell and H. D. Delaney, “Designing Experiments and Analyzing Data: A Model Comparison Perspective”, Wadsworth, 1990.

[R314] Lowry, Richard. “Concepts and Applications of Inferential Statistics”. Chapter 14. http://faculty.vassar.edu/lowry/ch14pt1.html

[R315] Heiman, G.W. Research Methods in Statistics. 2002.

[R363] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000. Section 14.7

[R364] P.K. Sen, “Estimates of the regression coefficient based on Kendall’s tau”, J. Am. Stat. Assoc., Vol. 63, pp. 1379-1389, 1968.

[R365] H. Theil, “A rank-invariant method of linear and polynomial regression analysis I, II and III”, Nederl. Akad. Wetensch., Proc. 53:, pp. 386-392, pp. 521-525, pp. 1397-1412, 1950.

[R366] W.L. Conover, “Practical nonparametric statistics”, 2nd ed., John Wiley and Sons, New York, pp. 493.

[R368] http://en.wikipedia.org/wiki/T-test#Independent_two-sample_t-test

[R369] http://en.wikipedia.org/wiki/Welch%27s_t_test

[R370] http://en.wikipedia.org/wiki/T-test#Independent_two-sample_t-test

[R371] http://en.wikipedia.org/wiki/Welch%27s_t_test

[R307] Lowry, Richard. “Concepts and Applications of Inferential Statistics”. Chapter 8. http://faculty.vassar.edu/lowry/ch8pt1.html

[R308] “Chi-squared test”, http://en.wikipedia.org/wiki/Chi-squared_test

[R354] Lowry, Richard. “Concepts and Applications of Inferential Statistics”. Chapter 8. http://faculty.vassar.edu/lowry/ch8pt1.html

[R355] "Chi-squared test", http://en.wikipedia.org/wiki/Chi-squared_test

[R356] "G-test", http://en.wikipedia.org/wiki/G-test

[R357] Sokal, R. R. and Rohlf, F. J. "Biometry: the principles and practice of statistics in biological research", New York: Freeman (1981)

[R358] Cressie, N. and Read, T. R. C., "Multinomial Goodness-of-Fit Tests", J. Royal Stat. Soc. Series B, Vol. 46, No. 3 (1984), pp. 440-464.

[R367] Siegel, S. (1956) Nonparametric Statistics for the Behavioral Sciences. New York: McGraw-Hill.

[R359] "Ranking", http://en.wikipedia.org/wiki/Ranking

[R360] http://en.wikipedia.org/wiki/Wilcoxon_rank-sum_test

[R373] http://en.wikipedia.org/wiki/Wilcoxon_signed-rank_test

[R328] http://en.wikipedia.org/wiki/Kruskal-Wallis_one-way_analysis_of_variance

[R319] http://en.wikipedia.org/wiki/Friedman_test

[R309] https://en.wikipedia.org/wiki/Fisher%27s_method

[R310] http://en.wikipedia.org/wiki/Fisher's_method#Relation_to_Stouffer.27s_Z-score_method

[R311] Whitlock, M. C. "Combining probability from independent tests: the weighted Z-method is superior to Fisher's approach." Journal of Evolutionary Biology 18, no. 5 (2005): 1368-1373.

[R312] Zaykin, Dmitri V. "Optimally weighted Z-test is a powerful method for combining probabilities in meta-analysis." Journal of Evolutionary Biology 24, no. 8 (2011): 1836-1841.

[R313] https://en.wikipedia.org/wiki/Extensions_of_Fisher%27s_method

[R300] Sprent, Peter and N.C. Smeeton. Applied nonparametric statistical methods. 3rd ed. Chapman and Hall/CRC. 2001. Section 5.8.2.

[R301] http://www.itl.nist.gov/div898/handbook/eda/section3/eda357.htm

[R302] Snedecor, George W. and Cochran, William G. (1989), Statistical Methods, Eighth Edition, Iowa State University Press.

[R330] http://www.itl.nist.gov/div898/handbook/eda/section3/eda35a.htm

[R331] Levene, H. (1960). In Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling, I. Olkin et al. eds., Stanford University Press, pp. 278-292.

[R332] Brown, M. B. and Forsythe, A. B. (1974), Journal of the American Statistical Association, 69, 364-367

[R361] http://www.itl.nist.gov/div898/handbook/prc/section2/prc213.htm

[R293] http://www.itl.nist.gov/div898/handbook/prc/section2/prc213.htm

[R294] Stephens, M. A. (1974). EDF Statistics for Goodness of Fit and Some Comparisons, Journal of the American Statistical Association, Vol. 69, pp. 730-737.

[R295] Stephens, M. A. (1976). Asymptotic Results for Goodness-of-Fit Statistics with Unknown Parameters, Annals of Statistics, Vol. 4, pp. 357-369.

[R296] Stephens, M. A. (1977). Goodness of Fit for the Extreme Value Distribution, Biometrika, Vol. 64, pp. 583-588.

[R297] Stephens, M. A. (1977). Goodness of Fit with Special Reference to Tests for Exponentiality , Technical Report No. 262, Department of Statistics, Stanford University, Stanford, CA.

[R298] Stephens, M. A. (1979). Tests of Fit for the Logistic Distribution Based on the Empirical Distribution Function, Biometrika, Vol. 66, pp. 591-595.

[R299] Scholz, F. W and Stephens, M. A. (1987), K-Sample Anderson-Darling Tests, Journal of the American Statistical Association, Vol. 82, pp. 918-924.

[R303] http://en.wikipedia.org/wiki/Binomial_test

[R317] http://www.stat.psu.edu/~bgl/center/tr/TR993.ps

[R318] Fligner, M.A. and Killeen, T.J. (1976). Distribution-free two-sample tests for scale. 'Journal of the American Statistical Association.' 71(353), 210-213.

[R334] Mood, A. M., Introduction to the Theory of Statistics. McGraw-Hill (1950), pp. 394-399.

[R335] Zar, J. H., Biostatistical Analysis, 5th ed. Prentice Hall (2010). See Sections 8.12 and 10.15.

[R304] "Contingency table", http://en.wikipedia.org/wiki/Contingency_table

[R305] "Pearson's chi-squared test", http://en.wikipedia.org/wiki/Pearson%27s_chi-squared_test

[R306] Cressie, N. and Read, T. R. C., "Multinomial Goodness-of-Fit Tests", J. Royal Stat. Soc. Series B, Vol. 46, No. 3 (1984), pp. 440-464.

[R336] Lowry, Richard. "Concepts and Applications of Inferential Statistics". Chapter 8. http://faculty.vassar.edu/lowry/ch8pt1.html

[R337] "Chi-squared test", http://en.wikipedia.org/wiki/Chi-squared_test

[R338] http://en.wikipedia.org/wiki/Kruskal-Wallis_one-way_analysis_of_variance

[R339] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.

[R340] *R* statistical software: http://www.r-project.org/

[R341] *R* `quantile` function: http://stat.ethz.ch/R-manual/R-devel/library/stats/html/quantile.html

[R342] D'Agostino, R. B. (1971), "An omnibus test of normality for moderate and large sample size," Biometrika, 58, 341-348

[R343] D'Agostino, R. and Pearson, E. S. (1973), "Testing for departures from normality," Biometrika, 60, 613-622

[R344] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000. Section 2.2.24.1

[R345] P.K. Sen, "Estimates of the regression coefficient based on Kendall's tau", J. Am. Stat. Assoc., Vol. 63, pp. 1379-1389, 1968.

[R346] H. Theil, "A rank-invariant method of linear and polynomial regression analysis I, II and III", Nederl. Akad. Wetensch., Proc. 53:, pp. 386-392, pp. 521-525, pp. 1397-1412, 1950.

[R347] W.L. Conover, "Practical nonparametric statistics", 2nd ed., John Wiley and Sons, New York, pp. 493.

[R348] http://en.wikipedia.org/wiki/T-test#Independent_two-sample_t-test

[R349] http://en.wikipedia.org/wiki/Welch%27s_t_test

[R350] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.

[R320] D.W. Scott, "Multivariate Density Estimation: Theory, Practice, and Visualization", John Wiley & Sons, New York, Chicester, 1992.

[R321] B.W. Silverman, "Density Estimation for Statistics and Data Analysis", Vol. 26, Monographs on Statistics and Applied Probability, Chapman and Hall, London, 1986.

[R322] B.A. Turlach, "Bandwidth Selection in Kernel Density Estimation: A Review", CORE and Institut de Statistique, Vol. 19, pp. 1-33, 1993.

[R323] D.M. Bashtannyk and R.J. Hyndman, "Bandwidth selection for kernel conditional density estimation", Computational Statistics & Data Analysis, Vol. 36, pp. 279-298, 2001.

[R336] Lowry, Richard. "Concepts and Applications of Inferential Statistics". Chapter 8. http://faculty.vassar.edu/lowry/ch8pt1.html

[R337] "Chi-squared test", http://en.wikipedia.org/wiki/Chi-squared_test

[R338] http://en.wikipedia.org/wiki/Kruskal-Wallis_one-way_analysis_of_variance

[R339] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.

[R340] *R* statistical software: http://www.r-project.org/

[R341] *R* `quantile` function: http://stat.ethz.ch/R-manual/R-devel/library/stats/html/quantile.html

[R342] D'Agostino, R. B. (1971), "An omnibus test of normality for moderate and large sample size," Biometrika, 58, 341-348

[R343] D'Agostino, R. and Pearson, E. S. (1973), "Testing for departures from normality," Biometrika, 60, 613-622

[R344] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000. Section 2.2.24.1

[R345] P.K. Sen, "Estimates of the regression coefficient based on Kendall's tau", J. Am. Stat. Assoc., Vol. 63, pp. 1379-1389, 1968.

[R346] H. Theil, "A rank-invariant method of linear and polynomial regression analysis I, II and III", Nederl. Akad. Wetensch., Proc. 53:, pp. 386-392, pp. 521-525, pp. 1397-1412, 1950.

[R347] W.L. Conover, "Practical nonparametric statistics", 2nd ed., John Wiley and Sons, New York, pp. 493.

[R348] http://en.wikipedia.org/wiki/T-test#Independent_two-sample_t-test

[R349] http://en.wikipedia.org/wiki/Welch%27s_t_test

[R350] Zwillinger, D. and Kokoska, S. (2000). CRC Standard Probability and Statistics Tables and Formulae. Chapman & Hall: New York. 2000.