# SciPy Reference Guide

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**Written by the SciPy community**

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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 for Python. It adds significant power to the interactive Python session by exposing the user to high-level commands and classes for the manipulation and visualization of 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 power of using SciPy within Python, however, is that a powerful programming language is also available for use in developing sophisticated programs and specialized applications. Scientific applications written in 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 document provides a tutorial for the first-time user of SciPy to help get started with some of the features available in this powerful package. It is assumed that the user has already installed the package. Some general Python facility is also assumed such as could be acquired by working through the Tutorial in the Python distribution. 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 scipy as sp
>>> 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 |
| `maxentropy` | Maximum entropy methods |
| `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 HTML and PDF versions of their documentation available at http://docs.scipy.org/, which currently details 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 also provides the facility of documentation strings. The functions and classes available in SciPy use this method for on-line documentation. There are two methods for reading these messages and getting help. Python provides the 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. Running the command help with an object as the argument displays the calling signature, and the documentation string of the object.

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 scipy-specific help system is also available under the command `sp.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 `sp.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:

```
>>> sp.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 in Numpy (and top-level scipy)

**Contents**

### 1.2.1 Interaction with Numpy

To begin with, all of the Numpy functions have been subsumed into the `scipy` namespace so that all of those functions are available without additionally importing Numpy. In addition, the universal functions (addition, subtraction, division) have been altered to not raise exceptions if floating-point errors are encountered; instead, NaN's and Inf's are returned in the arrays. To assist in detection of these events, several functions (`sp.isnan`, `sp.isfinite`, `sp.isinf`) are available.

Finally, some of the basic functions like log, sqrt, and inverse trig functions have been modified to return complex numbers instead of NaN's where appropriate (*i.e.* `sp.sqrt(-1)` returns `1j`).

### 1.2.2 Top-level scipy routines

The purpose of the top level of scipy is to collect general-purpose routines that the other sub-packages can use and to provide a simple replacement for Numpy. Anytime you might think to import Numpy, you can import scipy instead and remove yourself from direct dependence on Numpy. These routines are divided into several files for organizational purposes, but they are all available under the numpy namespace (and the scipy namespace). There are routines for type handling and type checking, shape and matrix manipulation, polynomial processing, and other useful functions. 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.

#### Type handling

Note the difference between `sp.iscomplex`/`sp.isreal` and `sp.iscomplexobj`/`sp.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 `sp.real` and `sp.imag` . These functions succeed for anything that can be turned into a Numpy array. Consider also the function `sp.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 `sp.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 `sp.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, `sp.cast['f'](d)` returns an array of `sp.float32` from *d*. This function is also useful as an easy way to get a scalar of a certain type:

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

### 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 `sp.mgrid` , `sp.ogrid` , `sp.r_` , and `sp.c_` for quickly constructing arrays.

One familiar with MATLAB (R) may complain that it is difficult to construct arrays from the interactive session with Python. Suppose, for example that one wants to construct an array that begins with 3 followed by 5 zeros and then contains 10 numbers spanning the range -1 to 1 (inclusive on both ends). Before SciPy, you would need to enter 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.`

### Other useful functions

There are several other functions in the scipy_base package including most of the other functions that are also in the Numpy package. The reason for duplicating these functions is to allow SciPy to potentially alter their original interface and make it easier for users to know how to get access to functions

```
>>> from scipy import *
```

Functions which should be mentioned are `mod(x,y)` which can replace `x % y` when it is desired that the result take the sign of *y* instead of *x* . Also included is `fix` which always rounds to the nearest integer towards zero. For doing phase processing, the functions `angle`, and `unwrap` are also 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 new 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])
>>> select([x > 3, x >= 0],[0,x+2])
array([0, 0, 2, 3, 4])
```

## 1.2.3 Common functions

Some functions depend on sub-packages of SciPy but should be available from the top-level of SciPy due to their common use. These are functions that might have been placed in scipy_base except for their dependence on other sub-packages of SciPy. 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. The functions `rand` and `randn` are used so often that they warranted a place at the top level. There are convenience functions for the interactive use: `disp` (similar to print), and `who` (returns a list of defined variables and memory consumption–upper bounded). 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.

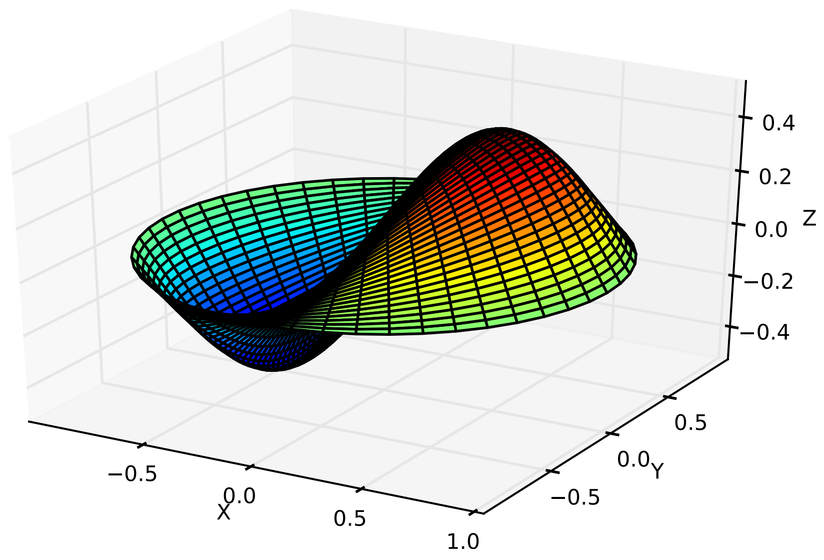
### 1.3.1 Bessel functions of real order(`jn`, `jn_zeros`)

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

>>> import pylab
>>> from mpl_toolkits.mplot3d import Axes3D
>>> from matplotlib import cm
>>> fig = pylab.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')
>>> pylab.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 $[0, 4.5]$.

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

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

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

where

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

is the Fresnel sine integral. Note that the numerically-computed integral is within $1.04\times10^{-11}$ of the exact result — well below the reported error bound.

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

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

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`. The mechanics of this for double and triple integration have been wrapped up into the functions `dblquad` and `tplquad`. The function, `dblquad` performs double integration. Use the help function to be sure that the arguments are defined in the correct order. In addition, the limits on all inner integrals are actually functions which can be constant 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)
```

### 1.4.2 Gaussian quadrature (integrate.gauss_quadtol)

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`).

### 1.4.3 Integrating using samples

There are three functions for computing integrals given only samples: `trapz` , `simps`, and `romb` . The first two functions use Newton-Coates formulas of order 1 and 2 respectively to perform integration. These two functions can handle, non-equally-spaced samples. 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.

If the samples are equally-spaced and the number of samples available is $2^k + 1$ for some integer $k$, then Romberg 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. (A different interface to Romberg integration useful when the function can be provided is also available as `romberg`).

### 1.4.4 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:

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

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]
```

## 1.5 Optimization (`scipy.optimize`)

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

The module contains:

1. Unconstrained and constrained minimization and least-squares algorithms (e.g., `fmin`: Nelder-Mead simplex, `fmin_bfgs`: BFGS, `fmin_ncg`: Newton Conjugate Gradient, `leastsq`: Levenberg-Marquardt, `fmin_cobyla`: COBYLA).
2. Global (brute-force) optimization routines (e.g., `anneal`)
3. Curve fitting (`curve_fit`)
4. Scalar function minimizers and root finders (e.g., Brent's method `fminbound`, and `newton`)
5. Multivariate equation system solvers (`fsolve`)
6. Large-scale multivariate equation system solvers (e.g. `newton_krylov`)

Below, several examples demonstrate their basic usage.

### 1.5.1 Nelder-Mead Simplex algorithm (`fmin`)

The simplex algorithm is probably the simplest way to minimize a fairly well-behaved function. The simplex algorithm 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. To demonstrate the minimization function consider the problem of minimizing the Rosenbrock function of $N$ variables:

$$f(\mathbf{x}) = \sum_{i=1}^{N-1} 100\left(x_i - x_{i-1}^2\right)^2 + \left(1 - x_{i-1}\right)^2.$$

The minimum value of this function is 0 which is achieved when $x_i = 1$. This minimum can be found using the `fmin` routine as shown in the example below:

```
>>> from scipy.optimize import fmin
>>> def rosen(x):
...     """The Rosenbrock function"""
...     return sum(100.0*(x[1:]-x[:-1]**2.0)**2.0 + (1-x[:-1])**2.0)

>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin(rosen, x0, xtol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 339
         Function evaluations: 571

>>> print xopt
[ 1.  1.  1.  1.  1.]
```

Another optimization algorithm that needs only function calls to find the minimum is Powell's method available as `fmin_powell`.

## 1.5.2 Broyden-Fletcher-Goldfarb-Shanno algorithm (`fmin_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 = 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
```

The calling signature for the BFGS minimization algorithm is similar to `fmin` with the addition of the *fprime* argument. An example usage of `fmin_bfgs` is shown in the following example which minimizes the Rosenbrock function.

```
>>> from scipy.optimize import fmin_bfgs
>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_bfgs(rosen, x0, fprime=rosen_der)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 53
         Function evaluations: 65
         Gradient evaluations: 65
>>> print xopt
[ 1.  1.  1.  1.  1.]
```

## 1.5.3 Newton-Conjugate-Gradient (`fmin_ncg`)

The method which requires the fewest function calls and is therefore often the fastest method to minimize functions of many variables is `fmin_ncg`. 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:

$$f(\mathbf{x}) \approx f(\mathbf{x}_0) + \nabla f(\mathbf{x}_0) \cdot (\mathbf{x} - \mathbf{x}_0) + \frac{1}{2}(\mathbf{x} - \mathbf{x}_0)^T \mathbf{H}(\mathbf{x}_0)(\mathbf{x} - \mathbf{x}_0).$$

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

$$\mathbf{x}_{\textrm{opt}} = \mathbf{x}_0 - \mathbf{H}^{-1}\nabla f.$$

The inverse of the Hessian is evaluted using the conjugate-gradient method. An example of employing this method to minimizing the Rosenbrock function is given below. To take full advantage of the NewtonCG method, a function which computes the Hessian must be provided. The Hessian matrix itself does not need to be constructed, only a vector which is the product of the Hessian with an arbitrary vector needs to be available to the minimization routine. As a result, the user can provide either a function to compute the Hessian matrix, or a function to compute the product of the Hessian with an arbitrary vector.

### Full Hessian example:

The Hessian of the Rosenbrock function is

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

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

$$\mathbf{H} = \left[\begin{array}{ccccc} 1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\ -400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\ 0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\ 0 & & -400x_2 & 202 + 1200x_3^2 - 400x_4 & -400x_3 \\ 0 & 0 & 0 & -400x_3 & 200 \end{array}\right].$$

The code which computes this Hessian along with the code to minimize the function using fmin_ncg is shown in the following example:

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

>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_ncg(rosen, x0, rosen_der, fhess=rosen_hess, avextol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 23
         Function evaluations: 26
         Gradient evaluations: 23
         Hessian evaluations: 23
>>> print xopt
[ 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 setting the *fhess_p* keyword to the desired function. The *fhess_p* function should take the minimization vector as the first argument and the arbitrary vector as the second argument. Any extra arguments passed to the function to be minimized will also be passed to this function. 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 $\mathbf{H}(\mathbf{x})\,\mathbf{p}$ has elements:

$$\mathbf{H}(\mathbf{x})\,\mathbf{p} = \left[\begin{array}{c} \left(1200x_0^2 - 400x_1 + 2\right) p_0 - 400x_0p_1 \\ \vdots \\ -400x_{i-1}p_{i-1} + \left(202 + 1200x_i^2 - 400x_{i+1}\right) p_i - 400x_ip_{i+1} \\ \vdots \\ -400x_{N-2}p_{N-2} + 200p_{N-1} \end{array}\right].$$

Code which makes use of the *fhess_p* keyword to minimize the Rosenbrock function using fmin_ncg follows:

```
>>> from scipy.optimize import fmin_ncg
>>> def rosen_hess_p(x,p):
...     x = asarray(x)
...     Hp = 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
```

```
>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_ncg(rosen, x0, rosen_der, fhess_p=rosen_hess_p, avextol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 22
         Function evaluations: 25
         Gradient evaluations: 22
         Hessian evaluations: 54
>>> print xopt
[ 1.  1.  1.  1.  1.]
```

### 1.5.4 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

$$e_i(\mathbf{p}, \mathbf{y}_i, \mathbf{x}_i) = \|\mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \mathbf{p})\|.$$

An objective function to pass to any of the previous minization algorithms to obtain a least-squares fit is.

$$J(\mathbf{p}) = \sum_{i=0}^{N-1} e_i^2(\mathbf{p}).$$

The `leastsq` algorithm performs this squaring and summing of the residuals automatically. It takes as an input argument the vector function $\mathbf{e}(\mathbf{p})$ 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

$$y_i = A\sin(2\pi k x_i + \theta)$$

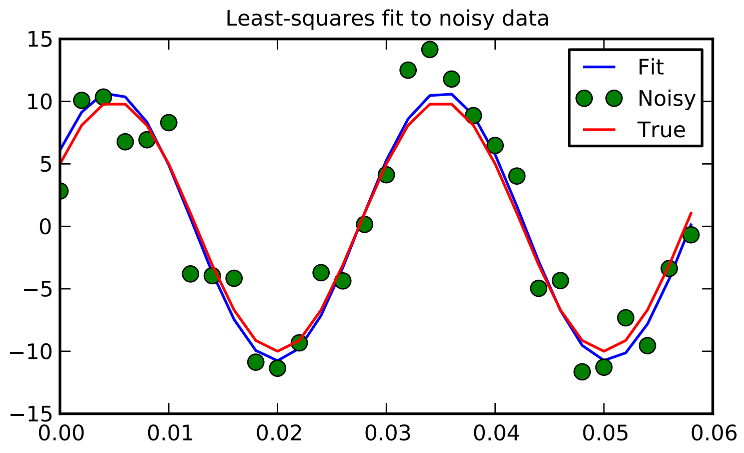
where the parameters $A$, $k$ , and $\theta$ are unknown. The residual vector is

$$e_i = |y_i - A\sin(2\pi k x_i + \theta)|.$$

By defining a function to compute the residuals and (selecting an appropriate starting position), the least-squares fit routine can be used to find the best-fit parameters $\hat{A}$, $\hat{k}$, $\hat{\theta}$. This is shown in the following example:

```
>>> from numpy import *
>>> 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()
```



### 1.5.5 Sequential Least-square fitting with constraints (`fmin_slsqp`)

This module implements the Sequential Least SQuares Programming optimization algorithm (SLSQP).

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

The following script shows examples for how constraints can be specified.

```
"""
This script tests fmin_slsqp using Example 14.4 from Numerical Methods for
Engineers by Steven Chapra and Raymond Canale.  This example maximizes the
function f(x) = 2*x0*x1 + 2*x0 - x0**2 - 2*x1**2, which has a maximum
at x0=2, x1=1.
"""
```

```
from scipy.optimize import fmin_slsqp
from numpy import array

def testfunc(x, *args):
    """
    Parameters
    ----------
    d : list
        A list of two elements, where d[0] represents x and
        d[1] represents y in the following equation.
    args : tuple
        First element of args is a multiplier for f.
        Since the objective function should be maximized, and the scipy
        optimizers can only minimize functions, it is nessessary to
        multiply the objective function by -1 to achieve the desired
        solution.
    Returns
    -------
    res : float
        The result, equal to ``2*x*y + 2*x - x**2 - 2*y**2``.

    """
    try:
        sign = args[0]
    except:
        sign = 1.0
    return sign*(2*x[0]*x[1] + 2*x[0] - x[0]**2 - 2*x[1]**2)

def testfunc_deriv(x,*args):
    """ This is the derivative of testfunc, returning a numpy array
    representing df/dx and df/dy """
    try:
        sign = args[0]
    except:
        sign = 1.0
    dfdx0 = sign*(-2*x[0] + 2*x[1] + 2)
    dfdx1 = sign*(2*x[0] - 4*x[1])
    return array([ dfdx0, dfdx1 ])

def test_eqcons(x,*args):
    """ Lefthandside of the equality constraint """
    return array([ x[0]**3-x[1] ])

def test_ieqcons(x,*args):
    """ Lefthandside of inequality constraint """
    return array([ x[1]-1 ])

def test_fprime_eqcons(x,*args):
    """ First derivative of equality constraint """
    return array([ 3.0*(x[0]**2.0), -1.0 ])

def test_fprime_ieqcons(x,*args):
    """ First derivative of inequality constraint """
    return array([ 0.0, 1.0 ])

from time import time

print "Unbounded optimization."
print "Derivatives of objective function approximated."
t0 = time()
result = fmin_slsqp(testfunc, [-1.0,1.0], args=(-1.0,), iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Unbounded optimization."
print "Derivatives of objective function provided."
t0 = time()
result = fmin_slsqp(testfunc, [-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Bound optimization (equality constraints)."
print "Constraints implemented via lambda function."
print "Derivatives of objective function approximated."
print "Derivatives of constraints approximated."
t0 = time()
result = fmin_slsqp(testfunc, [-1.0,1.0], args=(-1.0,),
               eqcons=[lambda x, args: x[0]-x[1] ], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Bound optimization (equality constraints)."
print "Constraints implemented via lambda."
print "Derivatives of objective function provided."
print "Derivatives of constraints approximated."
t0 = time()
result = fmin_slsqp(testfunc, [-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               eqcons=[lambda x, args: x[0]-x[1] ], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Bound optimization (equality and inequality constraints)."
print "Constraints implemented via lambda."
print "Derivatives of objective function provided."
print "Derivatives of constraints approximated."
t0 = time()
result = fmin_slsqp(testfunc,[-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               eqcons=[lambda x, args: x[0]-x[1] ],
               ieqcons=[lambda x, args: x[0]-.5], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Bound optimization (equality and inequality constraints)."
print "Constraints implemented via function."
print "Derivatives of objective function provided."
print "Derivatives of constraints approximated."
t0 = time()
result = fmin_slsqp(testfunc, [-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               f_eqcons=test_eqcons, f_ieqcons=test_ieqcons,
               iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"

print "Bound optimization (equality and inequality constraints)."
print "Constraints implemented via function."
print "All derivatives provided."
t0 = time()
result = fmin_slsqp(testfunc,[-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
                    f_eqcons=test_eqcons, fprime_eqcons=test_fprime_eqcons,
                    f_ieqcons=test_ieqcons, fprime_ieqcons=test_fprime_ieqcons,
                    iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results", result, "\n\n"
```

## 1.5.6 Scalar function minimizers

Often only the minimum of a scalar function is needed (a scalar function is one that takes a scalar as input and returns a scalar output). In these circumstances, other optimization techniques have been developed that can work faster.

### Unconstrained minimization (`brent`)

There are actually two methods that can be used to minimize a scalar function (`brent` and `golden`), but `golden` is included only for academic purposes and should rarely be used. The brent method uses Brent's algorithm for locating a minimum. Optimally a bracket 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).

### Bounded minimization (`fminbound`)

Thus far all of the minimization routines described have been unconstrained minimization routines. Very often, however, there are constraints that can be placed on the solution space before minimization occurs. The `fminbound` function 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.

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

```
>>> from scipy.special import j1
>>> from scipy.optimize import fminbound
>>> xmin = fminbound(j1, 4, 7)
>>> print xmin
5.33144184241
```

## 1.5.7 Root finding

### Sets of equations

To find the roots of a polynomial, the command `roots` is useful. To find a root of a set of non-linear equations, the command `fsolve` is needed. For example, the following example finds the roots of the single-variable transcendental equation

$$x + 2\cos(x) = 0,$$

and the set of non-linear equations

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

The results are $x = -1.0299$ and $x_0 = 6.5041,\ x_1 = 0.9084$ .

```
>>> def func(x):
...     return x + 2*cos(x)

>>> def func2(x):
...     out = [x[0]*cos(x[1]) - 4]
...     out.append(x[1]*x[0] - x[1] - 5)
...     return out

>>> from scipy.optimize import fsolve
>>> x0 = fsolve(func, 0.3)
>>> print x0
-1.02986652932

>>> x02 = fsolve(func2, [1, 1])
>>> print x02
[ 6.50409711  0.90841421]
```

### Scalar function root finding

If one has a single-variable equation, there are four different root finder algorithms that can be tried. Each of these root finding algorithms requires the endpoints of an interval where a root is suspected (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.

## 1.5.8 Root finding: Large problems

The `fsolve` function cannot deal with a very large number of variables (*N*), as it needs to calculate and invert a dense *N x N* Jacobian matrix on every Newton step. This becomes rather inefficent when *N* grows.

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

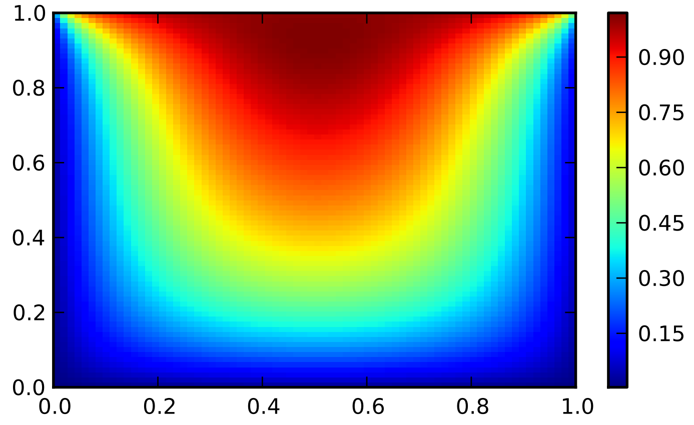
$$(\partial_x^2 + \partial_y^2)P + 5\left(\int_0^1 \int_0^1 \cosh(P)\,dx\,dy\right)^2 = 0$$

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, `fsolve` will take a long time to solve this problem. The solution can however be found using one of the large-scale solvers in `scipy.optimize`, for example `newton_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 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 + 5*cosh(P).mean()**2

# solve
guess = zeros((nx, ny), float)
sol = newton_krylov(residual, guess, verbose=1)
#sol = broyden2(residual, guess, max_rank=50, verbose=1)
#sol = anderson(residual, guess, M=10, verbose=1)
print 'Residual', 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()
```



### Still too slow? Preconditioning.

When looking for the zero of the functions $f_i(\mathbf{x}) = 0$, *i = 1, 2, ..., N*, the `newton_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 `newton_krylov` as the *inner_M* parameter. 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 newton_krylov
from scipy.sparse import spdiags, spkron
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 = spkron(Lx, eye(ny)) + spkron(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 = newton_krylov(residual, guess, verbose=1, inner_M=M)
    print 'Residual', abs(residual(sol)).max()
    print 'Evaluations', count[0]

    return sol

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**

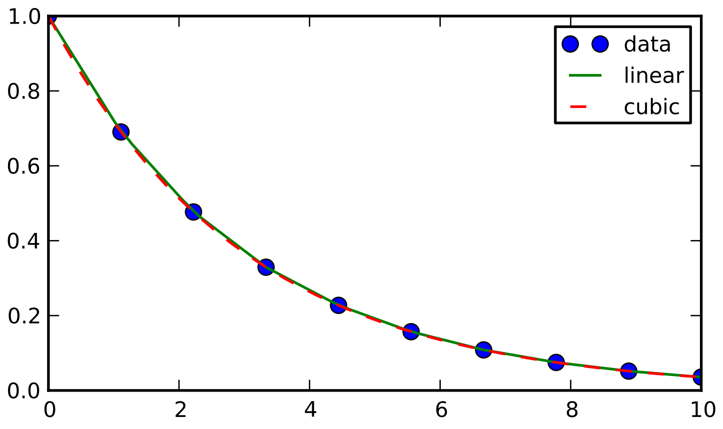
There are several general interpolation facilities available in SciPy, for data in 1, 2, and higher dimensions:

- 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, 10)
>>> y = np.exp(-x/3.0)
>>> f = interp1d(x, y)
>>> f2 = interp1d(x, y, kind='cubic')
>>> xnew = np.linspace(0, 10, 40)
>>> 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:

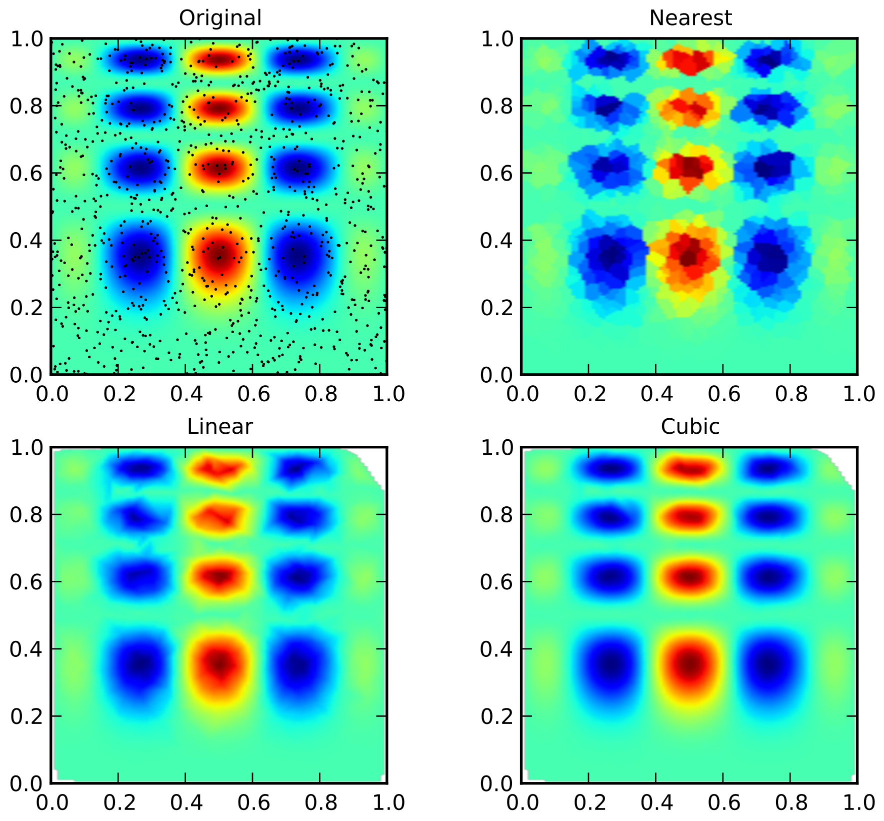
```
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```

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 $u$.

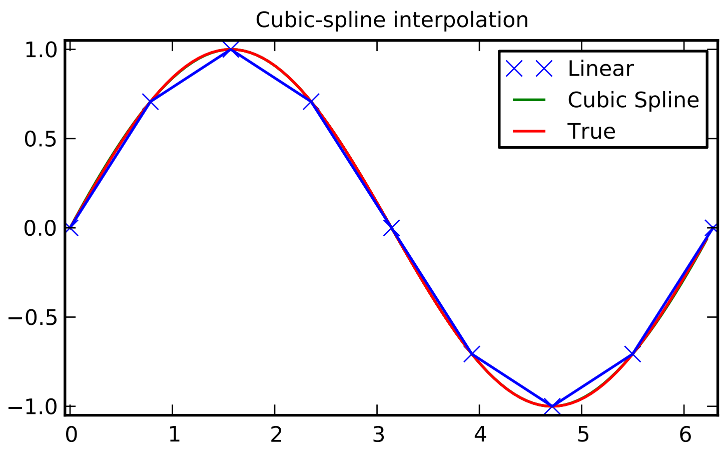
The keyword argument, $s$ , is used to specify the amount of smoothing to perform during the spline fit. The default value of $s$ is $s = m - \sqrt{2m}$ where $m$ is the number of data-points being fit. Therefore, **if no smoothing is desired a value of s $= 0$ should be passed to the routines.**

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
```

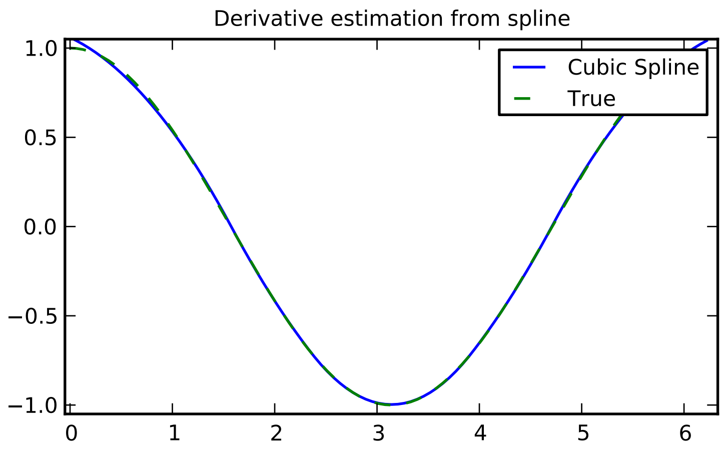
Cubic-spline

```
>>> 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()
```



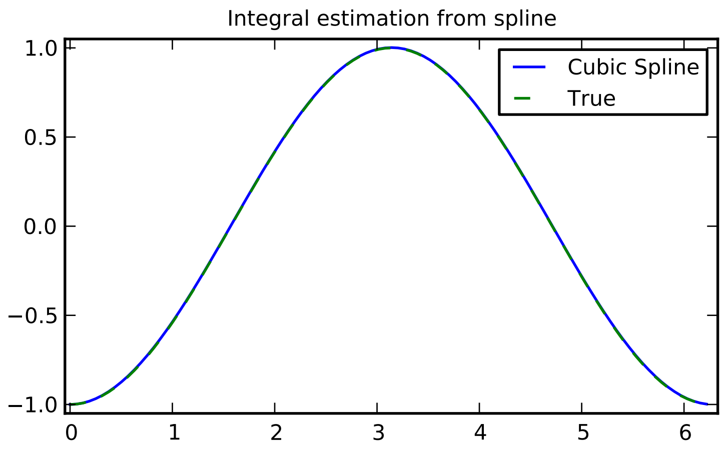
Derivative of spline

```
>>> 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()
```

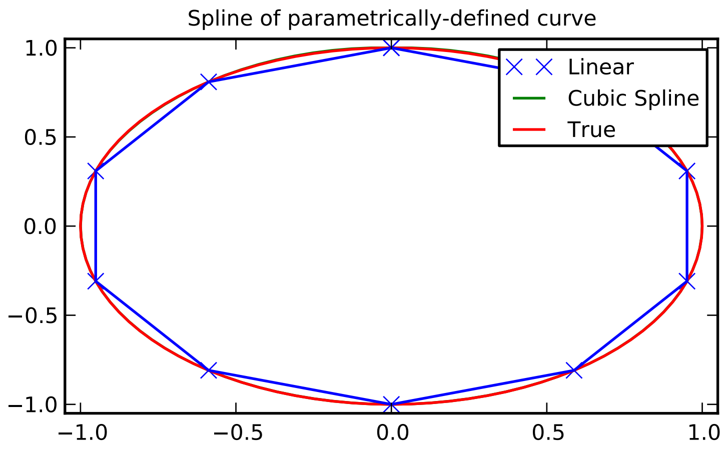


Roots of spline

```
>>> 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 methods `integral`, `derivatives`, and `roots` methods are also available on `UnivariateSpline` objects, allowing definite integrals, derivatives, and roots to be computed for the spline.

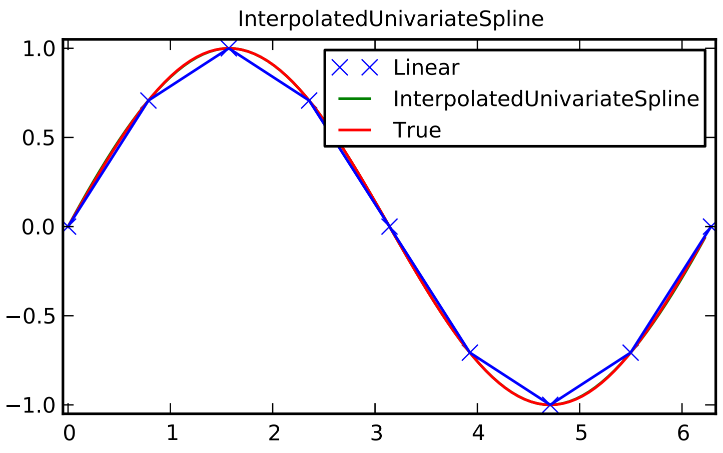
The UnivariateSpline class can also be used to smooth data by providing a non-zero value of the smoothing parameter *s*, with the same meaning as the *s* keyword of the `splrep` function described above. This results in a spline that has fewer knots than the number of data points, and hence is no longer 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 *LSQUnivarateSpline* is the other subclass of *UnivarateSpline*. It allows the user to specify the number and location of internal knots as 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
```

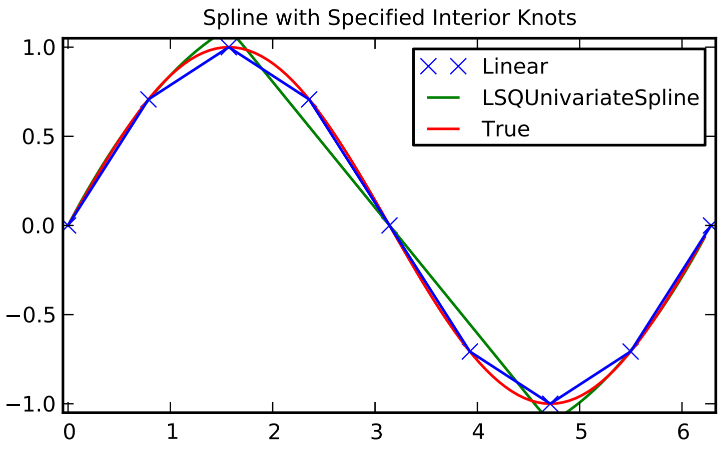
InterpolatedUnivariateSpline

```
>>> 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` .

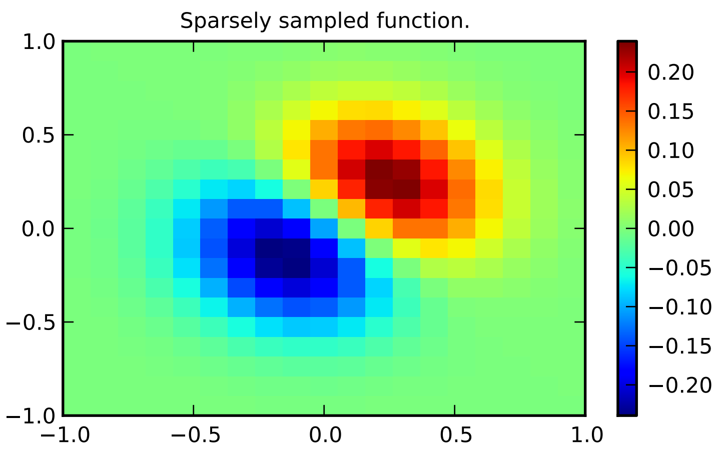
To evaluate the two-dimensional spline and it's partial derivatives (up to the order of the spline), the function `bisplev` is required. This function takes as the first two arguments **two 1-D arrays** whose cross-product specifies the domain over which to evaluate the spline. The third argument is 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 SciPy 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
```

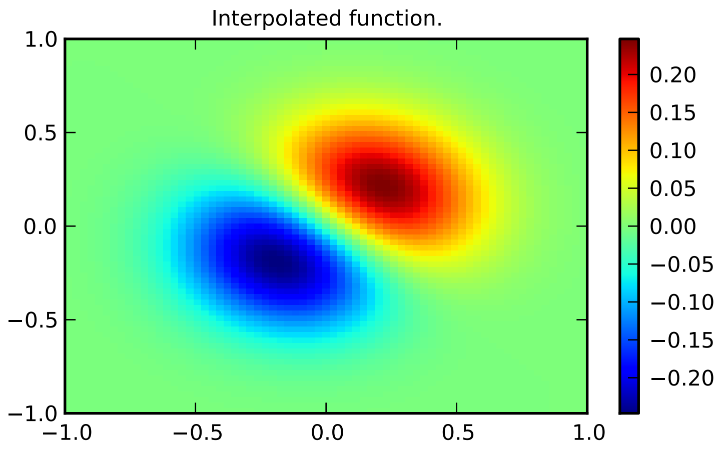
Define function over sparse 20x20 grid

```
>>> 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.

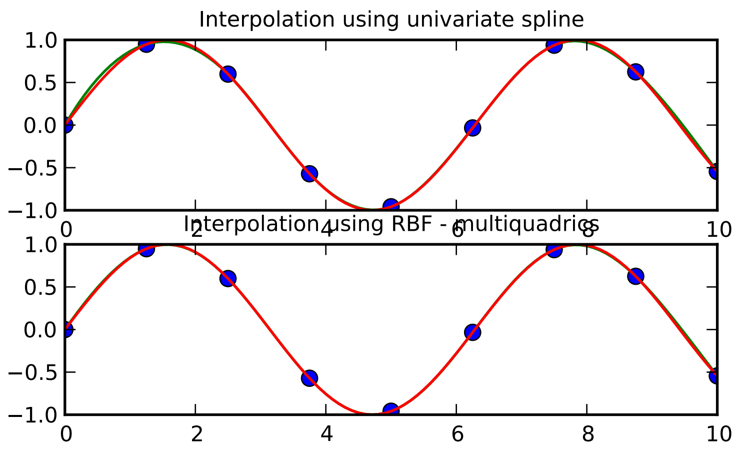
## 1.6.4 Using radial basis functions for smoothing/interpolation

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.

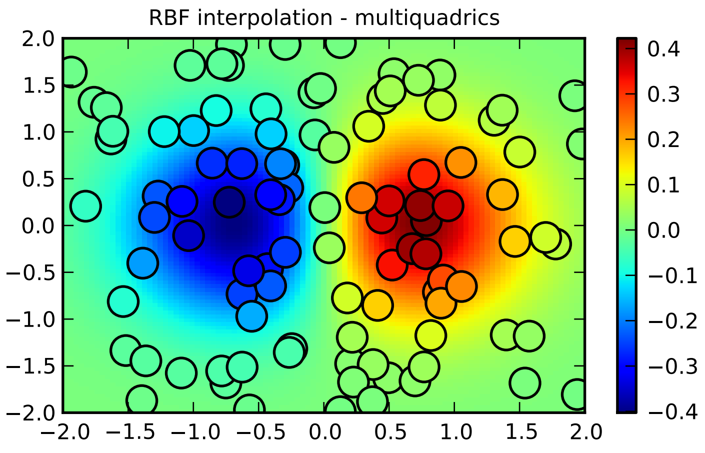
```
>>> import numpy as np
>>> from scipy.interpolate import Rbf, InterpolatedUnivariateSpline
>>> import matplotlib.pyplot as plt

>>> # 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`)

**Warning:** This is currently a stub page

**Contents**

Fourier analysis is fundamentally 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 [CT]. Press et al. [NR] provide an accessible introduction to Fourier analysis and its applications.

### 1.7.1 Fast Fourier transforms

### 1.7.2 One dimensional discrete Fourier transforms

fft, ifft, rfft, irfft

### 1.7.3 Two and n dimensional discrete Fourier transforms

fft in more than one dimension

### 1.7.4 Discrete Cosine Transforms

Return the Discrete Cosine Transform [Mak] of arbitrary type sequence `x`.

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

There are theoretically 8 types of the DCT [WP], 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`):

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

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

There are several definitions of the DCT-II; we use the following (for `norm=None`):

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

If `norm='ortho'`, $y_k$ is multiplied by a scaling factor $f$:

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

Which makes the corresponding matrix of coefficients orthonormal (*OO'* = *Id*).

#### type III

There are several definitions, we use the following (for `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'`:

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

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

### 1.7.5 FFT convolution

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

## 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 $\Delta x$ , then the B-spline approximation to a 1-dimensional function is the finite-basis expansion.

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

In two dimensions with knot-spacing $\Delta x$ and $\Delta y$ , the function representation is

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

In these expressions, $\beta^o(\cdot)$ 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

$$y''(x) = \frac{1}{\Delta x^2}\sum_j c_j \beta^{o''}\left(\frac{x}{\Delta x} - j\right).$$

Using the property of B-splines that

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

it can be seen that

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

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

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

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 (`signal.qspline1d`, `signal.qspline2d`, `signal.cspline1d`, `signal.cspline2d`). The package also supplies a function ( `signal.bspline` ) for evaluating the bspline basis function, $\beta^o(x)$ 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 $\sigma_o = (o+1)/12$ :

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

A function to compute this Gaussian for arbitrary $x$ and $o$ is also available ( `signal.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 `lena`. The command `signal.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 `signal.convolve2d` which convolves arbitrary two-dimensional filters and allows for choosing mirror-symmetric boundary conditions.

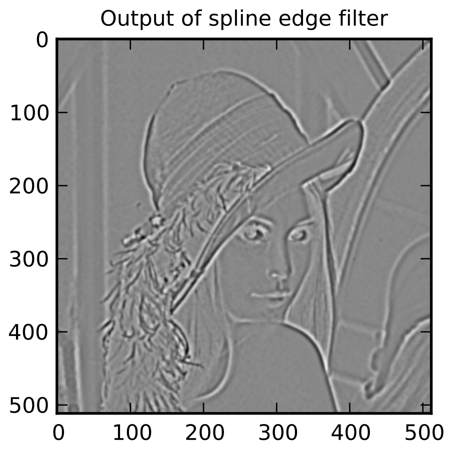
```
>>> from numpy import *
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

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

Alternatively we could have done:

```
laplacian = array([[0,1,0],[1,-4,1],[0,1,0]],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 $512 \times 512$ 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 256GB 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

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

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 `signal.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 largest 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.

This same function `signal.convolve` can actually take $N$ -dimensional arrays as inputs and will return the $N$ -dimensional convolution of the two arrays. The same input flags are available for that case as well.

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

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

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

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

Assuming again that $K\geq M$ this is

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

The SciPy function `signal.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 $w\left[M-K\right]$ to $w\left[0\right]$ inclusive.

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

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

Convolution is mainly used for filtering when one of the signals is much smaller than the other ( $K\gg M$ ), otherwise linear filtering is more easily accomplished in the frequency domain (see Fourier Transforms).

### Difference-equation filtering

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

$$\sum_{k=0}^{N}a_{k}y\left[n-k\right]=\sum_{k=0}^{M}b_{k}x\left[n-k\right]$$

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 $a_0 = 1$ ).

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

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 `signal.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 intial condition vector $z_0[-1]$ to $z_{K-1}[-1]$ given initial conditions on $y$ (and $x$ ). The command `signal.lfiltic` performs this function.

### 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 `signal.medfilt` . A specialized version that works only for two-dimensional arrays is available as `signal.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 `signal.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

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

where $m_x$ is the local estimate of the mean and $\sigma_x^2$ is the local estimate of the variance. The window for these estimates is an optional input parameter (default is $3 \times 3$ ). The parameter $\sigma^2$ is a threshold noise parameter. If $\sigma$ 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 $y = \text{hilbert}(x)$ 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.

## 1.8.3 Least-Squares Spectral Analysis (`spectral`)

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.

### Lomb-Scargle Periodograms (`spectral.lombscargle`)

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 $\tau$ 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

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

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 $\sim 2$ speed increase over the straightforward implementation.

### 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. There is a matrix class defined in Numpy, which you can initialize with an appropriate Numpy array in order to get objects for which multiplication is matrix-multiplication instead of the default, element-by-element multiplication.

[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

### 1.9.1 Matrix Class

The matrix class is initialized with the SciPy command `mat` which is just convenient short-hand for `matrix`. If you are going to be doing a lot of matrix-math, it is convenient to convert arrays into matrices using this command. One advantage of using the `mat` command is that you can enter two-dimensional matrices using MATLAB-like syntax with commas or spaces separating columns and semicolons separting rows as long as the matrix is placed in a string passed to `mat` .

### 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

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

The following example demonstrates this computation in SciPy

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> A
matrix([[1, 3, 5],
        [2, 5, 1],
        [2, 3, 8]])
>>> A.I
matrix([[-1.48,  0.36,  0.88],
        [ 0.56,  0.08, -0.36],
        [ 0.16, -0.12,  0.04]])
>>> from scipy import linalg
>>> linalg.inv(A)
array([[-1.48,  0.36,  0.88],
       [ 0.56,  0.08, -0.36],
       [ 0.16, -0.12,  0.04]])
```

#### 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:

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> b = mat('[10;8;3]')
>>> A.I*b
matrix([[-9.28],
        [ 5.16],
        [ 0.76]])
>>> linalg.solve(A,b)
array([[-9.28],
       [ 5.16],
       [ 0.76]])
```

### Finding Determinant

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

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

This is a recursive way to define the determinant where the base case is defined by accepting that the determinant of a $1\times1$ 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

$$\begin{aligned} \left|\mathbf{A}\right| & = & 1\left|\begin{array}{cc} 5 & 1\\ 3 & 8\end{array}\right|-3\left|\begin{array}{cc} 2 & 1\\ 2 & 8\end{array}\right|+5\left|\begin{array}{cc} 2 & 5\\ 2 & 3\end{array}\right|\\ & = & 1\left(5\cdot8-3\cdot1\right)-3\left(2\cdot8-2\cdot1\right)+5\left(2\cdot3-2\cdot5\right)=-25.\end{aligned}$$

In SciPy this is computed as shown in this example:

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> linalg.det(A)
-25.000000000000004
```

### 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

$$\|\mathbf{x}\|=\left\{\begin{array}{cc} \max\left|x_{i}\right| & \textrm{ord}=\textrm{inf}\\ \min\left|x_{i}\right| & \textrm{ord}=-\textrm{inf}\\ \left(\sum_{i}\left|x_{i}\right|^{\textrm{ord}}\right)^{1/\textrm{ord}} & \left|\textrm{ord}\right|<\infty.\end{array}\right.$$

For matrix $\mathbf{A}$ the only valid values for norm are $\pm2,\pm1,\pm$ inf, and 'fro' (or 'f') Thus,

$$\|\mathbf{A}\|=\left\{\begin{array}{cc} \max_{i}\sum_{j}\left|a_{ij}\right| & \textrm{ord}=\textrm{inf}\\ \min_{i}\sum_{j}\left|a_{ij}\right| & \textrm{ord}=-\textrm{inf}\\ \max_{j}\sum_{i}\left|a_{ij}\right| & \textrm{ord}=1\\ \min_{j}\sum_{i}\left|a_{ij}\right| & \textrm{ord}=-1\\ \max\sigma_{i} & \textrm{ord}=2\\ \min\sigma_{i} & \textrm{ord}=-2\\ \sqrt{\textrm{trace}\left(\mathbf{A}^{H}\mathbf{A}\right)} & \textrm{ord}=\textrm{'fro'}\end{array}\right.$$

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

## 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 $f_{j}\left(\mathbf{x}_{i}\right)$ via the model

$$y_{i}=\sum_{j}c_{j}f_{j}\left(\mathbf{x}_{i}\right)+\epsilon_{i}$$

where $\epsilon_{i}$ represents uncertainty in the data. The strategy of least squares is to pick the coefficients $c_{j}$ to minimize

$$J\left(\mathbf{c}\right)=\sum_{i}\left|y_{i}-\sum_{j}c_{j}f_{j}\left(x_{i}\right)\right|^{2}.$$

Theoretically, a global minimum will occur when

$$\frac{\partial J}{\partial c_{n}^{*}}=0=\sum_{i}\left(y_{i}-\sum_{j}c_{j}f_{j}\left(x_{i}\right)\right)\left(-f_{n}^{*}\left(x_{i}\right)\right)$$

or

$$\begin{aligned}\sum_{j}c_{j}\sum_{i}f_{j}\left(x_{i}\right)f_{n}^{*}\left(x_{i}\right) & = \sum_{i}y_{i}f_{n}^{*}\left(x_{i}\right)\\ \mathbf{A}^{H}\mathbf{Ac} & = \mathbf{A}^{H}\mathbf{y}\end{aligned}$$

where

$$\left\{\mathbf{A}\right\}_{ij}=f_{j}\left(x_{i}\right).$$

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

$$\mathbf{y}=\mathbf{Ac}+\boldsymbol{\epsilon}.$$

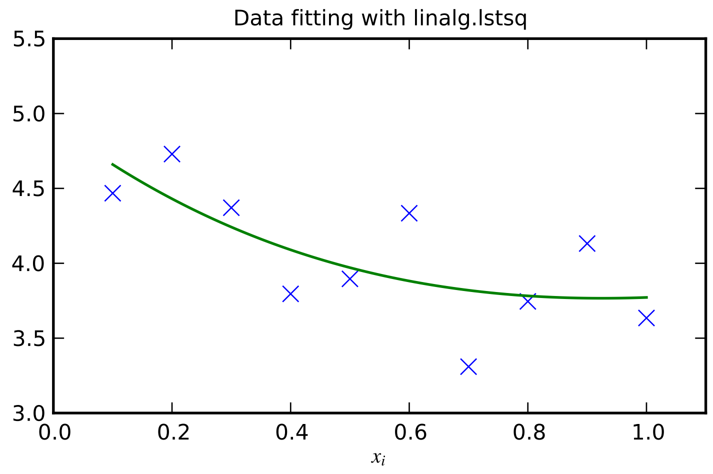
The command `linalg.lstsq` will solve the linear least squares problem for $\mathbf{c}$ given $\mathbf{A}$ and $\mathbf{y}$ . In addition `linalg.pinv` or `linalg.pinv2` (uses a different method based on singular value decomposition) will find $\mathbf{A}^{\dagger}$ given $\mathbf{A}$.

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.

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

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

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

>>> xi2 = r_[0.1:1.0:100j]
>>> yi2 = c[0]*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 $\lambda$ and corresponding vectors $\mathbf{v}$ such that

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

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 $\lambda$ and $\mathbf{v}$. However, it can also return $\mathbf{v}_L$ and just $\lambda$ by itself ( `linalg.eigvals` returns just $\lambda$ as well).

In addtion, `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

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

where $\mathbf{V}$ is the collection of eigenvectors into columns and $\boldsymbol{\Lambda}$ 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 $\left\Vert \mathbf{v}\right\Vert ^{2}=\sum_{i}v_{i}^{2}=1.$

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.

```
>>> from scipy import linalg
>>> A = mat('[1 5 2; 2 4 1; 3 6 2]')
>>> la,v = linalg.eig(A)
>>> l1,l2,l3 = la
>>> print l1, l2, l3
(7.95791620491+0j) (-1.25766470568+0j) (0.299748500767+0j)

>>> print v[:,0]
[-0.5297175  -0.44941741 -0.71932146]
>>> print v[:,1]
[-0.90730751  0.28662547  0.30763439]
>>> print v[:,2]
[ 0.28380519 -0.39012063  0.87593408]
>>> print sum(abs(v**2),axis=0)
[ 1.  1.  1.]

>>> v1 = mat(v[:,0]).T
>>> print max(ravel(abs(A*v1-l1*v1)))
8.881784197e-16
```

## Singular value decomposition

Singular Value Decompostion (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 addtion, 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 $\sigma_{i}^{2}$. 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 $\sigma_{i}$ 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`.

[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 $\mathbf{D}^{-1}=\mathbf{D}^{H}$.

```
>>> A = mat('[1 3 2; 1 2 3]')
>>> M,N = A.shape
>>> U,s,Vh = linalg.svd(A)
>>> Sig = mat(linalg.diagsvd(s,M,N))
>>> U, Vh = mat(U), mat(Vh)
>>> print U
[[-0.70710678 -0.70710678]
 [-0.70710678  0.70710678]]
>>> print Sig
[[ 5.19615242  0.          0.        ]
 [ 0.          1.          0.        ]]
>>> print Vh
[[ -2.72165527e-01  -6.80413817e-01  -6.80413817e-01]
 [ -6.18652536e-16  -7.07106781e-01   7.07106781e-01]
 [ -9.62250449e-01   1.92450090e-01   1.92450090e-01]]

>>> print A
[[1 3 2]
 [1 2 3]]
>>> print U*Sig*Vh
[[ 1.  3.  2.]
 [ 1.  2.  3.]]
```

### LU decomposition

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

$$\mathbf{A} = \mathbf{PLU}$$

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

$$\mathbf{PLU}\mathbf{x}_i = \mathbf{b}_i.$$

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 `linagl.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

$$\mathbf{A} = \mathbf{QR}.$$

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

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

implies that $\mathbf{Q} = \mathbf{U}$ and $\mathbf{R} = \mathbf{\Sigma V}^H$. 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

$$\mathbf{A} = \mathbf{ZTZ}^H$$

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 $2 \times 2$ 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]]
```

## 1.9.4 Matrix Functions

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

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

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

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

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.

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

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. |
| 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'` : Eigenvectors with largest magnitude (`eigs`, `eigsh`)

- `which = 'SM'` : Eigenvectors with smallest magnitude (`eigs`, `eigsh`)
- `which = 'LR'` : Eigenvectors with largest real part (`eigs`)
- `which = 'SR'` : Eigenvectors with smallest real part (`eigs`)
- `which = 'LI'` : Eigenvectors with largest imaginary part (`eigs`)
- `which = 'SI'` : Eigenvectors with smallest imaginary part (`eigs`)
- `which = 'LA'` : Eigenvectors with largest amplitude (`eigsh`)
- `which = 'SA'` : Eigenvectors with smallest amplitude (`eigsh`)
- `which = 'BE'` : Eigenvectors 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 $\lambda$ become large eigenvalues $\nu$.

```
>>> 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 $\nu \to \lambda$ 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 Statistics (`scipy.stats`)

### 1.11.1 Introduction

SciPy has a tremendous number of basic statistics routines with more 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 had using `info(stats)`.

#### 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 and 10 discrete random variables have been implemented using these classes. The list of the random variables available is in the docstring for the stats sub-package.

Note: The following is work in progress

### 1.11.2 Distributions

First some imports

```
>>> import numpy as np
>>> from scipy import stats
>>> import warnings
>>> warnings.simplefilter('ignore', DeprecationWarning)
```

We can obtain the list of available distribution through introspection:

```
>>> 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
```

Distributions can be used in one of two ways, either by passing all distribution parameters to each method call or by freezing the parameters for the instance of the distribution. As an example, we can get the median of the distribution by using the percent point function, ppf, which is the inverse of the cdf:

```
>>> print stats.nct.ppf(0.5, 10, 2.5)
2.56880722561
>>> my_nct = stats.nct(10, 2.5)
>>> print my_nct.ppf(0.5)
2.56880722561
```

`help(stats.nct)` prints the complete docstring of the distribution. Instead we can print just some basic information:

```
>>> print stats.nct.extradoc #contains the distribution specific docs
Non-central Student T distribution

                                 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, nc > 0.


>>> print 'number of arguments: %d, shape parameters: %s'% (stats.nct.numargs,
...                                                         stats.nct.shapes)
number of arguments: 2, shape parameters: df,nc
>>> print 'bounds of distribution lower: %s, upper: %s' % (stats.nct.a,
...                                                        stats.nct.b)
bounds of distribution lower: -1.#INF, upper: 1.#INF
```

We can list all methods and properties of the distribution with `dir(stats.nct)`. Some of the methods are private methods, that are not named as such, i.e. no leading underscore, for example veccdf or xa and xb are for internal calculation. The main methods we can see when we list the methods of the frozen distribution:

```
>>> print dir(my_nct) #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']
```

The main public methods 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

The main additional methods of the not frozen distribution are related to the estimation of distrition 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

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 location is the mean and scale is the standard deviation. The standardized distribution for a random variable *x* is obtained through `(x - loc) / scale`.

Discrete distribution have most of the same basic methods, 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 be used to shift the distribution.

The basic methods, pdf, cdf, sf, ppf, and isf are vectorized with `np.vectorize`, and the usual numpy broadcasting is applied. 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 is for 11 d.o.f., i.e. this is the same as

```
>>> 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 both, probabilities and degrees of freedom 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

```
>>> stats.t.isf([0.1, 0.05, 0.01], [10, 11, 12])
array([ 1.37218364,  1.79588482,  2.68099799])
```

### Performance and Remaining Issues

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, 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 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. 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.

The distributions in scipy.stats have recently been corrected and improved and gained a considerable test suite, however a few issues remain:

- skew and kurtosis, 3rd and 4th moments and entropy are not thoroughly tested and some coarse testing indicates that there are still some incorrect results left.
- 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.

The next example shows how to build our own discrete distribution, and more examples for the usage of the distributions are shown below together with the statistical tests.

### Example: discrete distribution rv_discrete

In the following we use stats.rv_discrete to generate a discrete distribution that has the probabilites of the truncated normal for the intervalls centered around the integers.

```
>>> 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
>>> grid = grid[:-1]
>>> probs = np.diff(stats.truncnorm.cdf(gridlimitsnorm, -normbound, normbound))
>>> gridint = grid
>>> normdiscrete = stats.rv_discrete(values = (gridint,
...              np.round(probs, decimals=7)), name='normdiscrete')
```

**From the docstring of rv_discrete:**

"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)."

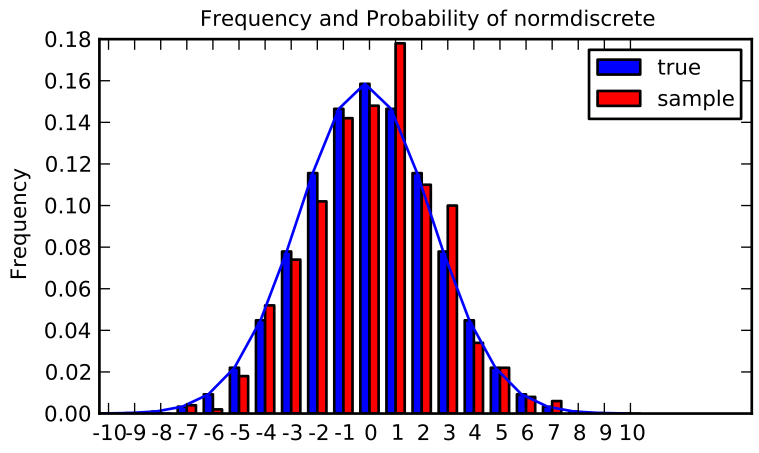
There are some requirements for this distribution to work. The keyword *name* is required. The support points of the distribution xk have to be integers. Also, I needed to limit the number of decimals. If the last two requirements are not satisfied an exception may be raised or the resulting numbers may be incorrect.

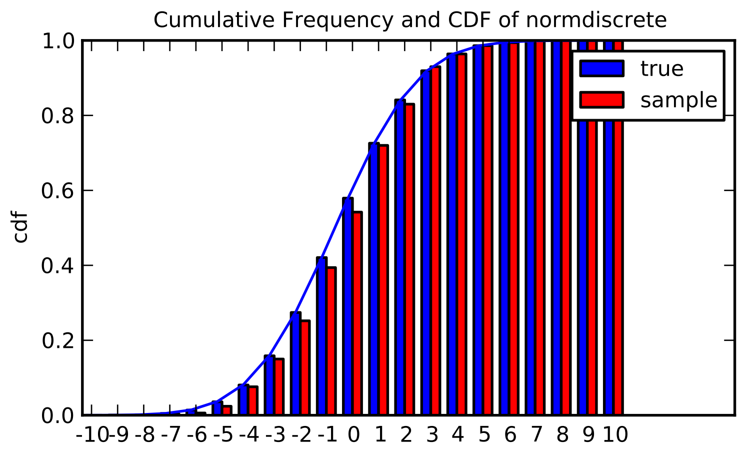
After defining the distribution, we obtain access to all methods of discrete distributions.

```
>>> 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'))
```

**Generate a random sample and compare observed frequencies with 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.

## 1.11.3 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=100 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.

### 1.11.4 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)
```

## 1.12 Multi-dimensional image processing (`scipy.ndimage`)

### 1.12.1 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 multi-dimensional 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.

### 1.12.2 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])
```

### 1.12.3 Filter functions

The functions described in this section all perform some type of spatial filtering of the 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 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 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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.

## 1.12.4 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 multi-dimensional spline filter.

**Note:** 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, 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 multi-dimensional 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.

## 1.12.5 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 multi-dimensional grey- scale erosion.
>
> The `grey_dilation` function calculates a multi-dimensional 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.

## 1.12.6 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.

---

## 1.12.7 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`.

## 1.12.8 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`.

### 1.12.9 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.

## 1.12.10 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.

## 1.13 File IO (scipy.io)

**See Also:**

*numpy-reference.routines.io* (in numpy)

### 1.13.1 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. |

Getting started:

```
>>> import scipy.io as sio
```

If you are using IPython, try tab completing on `sio`. You'll find:

```
sio.loadmat
sio.savemat
```

These are the high-level functions you will most likely use. You'll also find:

```
sio.matlab
```

This is the package from which `loadmat` and `savemat` are imported. Within `sio.matlab`, you will find the `mio` module - containing 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 / 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')
>>> print 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 3.2.3, 2010-05-30 02:13:40 UTC',
 '__globals__': []}
>>> oct_a = mat_contents['a']
>>> print oct_a
[[[  1.   4.   7.  10.]
  [  2.   5.   8.  11.]
  [  3.   6.   9.  12.]]]
>>> print oct_a.shape
(1, 3, 4)
```

Now let's try the other way round:

```
    >>> import numpy as np
    >>> vect = np.arange(10)
    >>> print vect.shape
    (10,)
    >>> sio.savemat('np_vector.mat', {'vect':vect})
    /Users/mb312/usr/local/lib/python2.6/site-packages/scipy/io/matlab/mio.py:196: FutureWarning: Us
```

oned_as=oned_as)

Then back to Octave:

```
octave:5> load np_vector.mat
octave:6> vect
vect =

  0
  1
  2
  3
  4
  5
  6
  7
  8
  9

octave:7> size(vect)
ans =

   10    1
```

Note the deprecation warning. The `oned_as` keyword determines the way in which one-dimensional vectors are stored. In the future, this will default to `row` instead of `column`:

```
>>> sio.savemat('np_vector.mat', {'vect':vect}, oned_as='row')
```

We can load this in Octave or MATLAB:

```
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
```

## 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')
>>> print mat_contents
{'my_struct': array([[([[1.0]], [[2.0]])]],
      dtype=[('field1', '|O8'), ('field2', '|O8')]), '__version__': '1.0', '__header__': 'MATLAB 5.0
>>> oct_struct = mat_contents['my_struct']
>>> print oct_struct.shape
(1, 1)
>>> val = oct_struct[0,0]
>>> print val
([[1.0]], [[2.0]])
>>> print val['field1']
[[ 1.]]
>>> print val['field2']
[[ 2.]]
>>> print val.dtype
[('field1', '|O8'), ('field2', '|O8')]
```

In this version of Scipy (0.8.0), 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 ar-rarys - 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 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'
>>> print type(oct_struct)
<class 'scipy.io.matlab.mio5_params.mat_struct'>
>>> print oct_struct.field1
1.0
```

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 =
{
  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)
>>> print arr
[(0.0, '') (0.0, '')]
>>> 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]
>>> print val
[[ 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'
>>> print obj_arr
[1 a string]
>>> 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
}
```

## 1.13.2 IDL files

| | |
|---|---|
| readsav(file_name[, idict, python_dict, ...]) | Read an IDL .sav file |

### 1.13.3 Matrix Market files

| | |
|---|---|
| mminfo(source) | Queries the contents of the Matrix Market file 'filename' to |
| 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 matrix A to a Matrix Market formatted file. |

### 1.13.4 Other

| | |
|---|---|
| save_as_module([file_name, data]) | Save the dictionary "data" into a module and shelf named save. |

### 1.13.5 Wav sound files (`scipy.io.wavfile`)

| | |
|---|---|
| read(file) | 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 |

### 1.13.6 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. |

### 1.13.7 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)

## 1.14 Weave (`scipy.weave`)

### 1.14.1 Outline

**Contents**

### 1.14.2 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.

### 1.14.3 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.

### 1.14.4 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.

### 1.14.5 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?

## 1.14.6 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 1.1: 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 1.2: 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.

### 1.14.7 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 speed up can be worth while – anywhwere 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 supress 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` preceeding 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 beacuse `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 simplier 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 acutually part of the compilers output that distutils does not supress. The name of the extension file, `sc_bighonkingnumber.cpp`, is generated from the md5 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
```

Everytime, 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.de
-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` truely 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 md5 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 "unkown 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 withing 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 1.3: 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 convserion 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 demostrate 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 has 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'])
```

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 there 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 generate 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 everytime 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 persistent 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 everytime 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 check sums 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 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 shelve 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.

## 1.14.8 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 arguements, 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. Futher, 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 mathematic 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 straight forward to write. (take a peak in 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., its 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 declaraions 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 name spaces are maintained in the C++ code to lessen the likelyhood 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 it 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.

## 1.14.9 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 md5 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 md5 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.

### 1.14.10 Customizing Type Conversions – Type Factories

not written

### 1.14.11 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

# 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.

## 2.1 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:

```
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.

## 2.2 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.maxentropy
- scipy.misc
- scipy.ndimage
- scipy.odr

- scipy.optimize
- scipy.signal
- scipy.sparse
  - linalg
- scipy.spatial
  - distance
- scipy.special
- scipy.stats
  - distributions
  - mstats
- scipy.weave

CHAPTER

THREE

# RELEASE NOTES

## 3.1 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.

### 3.1.1 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`.

#### 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)

### 3.1.2 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.

### 3.1.3 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``)
```

### 3.1.4 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.

### 3.1.5 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.

## 3.2 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.

### 3.2.1 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`.

### 3.2.2 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

### 3.2.3 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)).

### 3.2.4 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`)

### 3.2.5 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.

### 3.2.6 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

## 3.3 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.

### 3.3.1 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.

### 3.3.2 Major documentation improvements

SciPy documentation is greatly improved.

### 3.3.3 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.

### 3.3.4 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.

### 3.3.5 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.

## 3.4 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.

## 3.5 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

## 3.5.1 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 and the one for python 2.6 requires numpy 1.3.0 or above.

## 3.5.2 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.

## 3.6 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.

### 3.6.1 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.

### 3.6.2 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.

### 3.6.3 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.

### 3.6.4 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.

### 3.6.5 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.

### 3.6.6 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.

### 3.6.7 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.

## 3.6.8 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

## 3.6.9 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.

## 3.6.10 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.

### 3.6.11 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.

### 3.6.12 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.

### 3.6.13 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.

### 3.6.14 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).

### 3.6.15 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.

### 3.6.16 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.

### 3.6.17 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.

### 3.6.18 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

FOUR

# REFERENCE

## 4.1 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, computing distance matrices from observation vectors, calculating statistics on clusters, cutting linkages to generate flat clusters, and visualizing clusters with dendrograms.

## 4.2 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) | Normalize a group of observations on a per feature basis. |
| `vq`(obs, code_book) | 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, missing]) | Classify a set of observations into k clusters using the k-means algorithm. |

`scipy.cluster.vq.`**`whiten`**`(`*obs*`)`

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
```

**Returns**

**result** : ndarray

Contains the values in *obs* scaled by the standard devation of each column.

## Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import whiten
>>> features  = array([[  1.9,2.3,1.7],
...                     [  1.5,2.5,2.2],
...                     [  0.8,0.6,1.7,]])
>>> whiten(features)
array([[ 3.41250074,  2.20300046,  5.88897275],
       [ 2.69407953,  2.39456571,  7.62102355],
       [ 1.43684242,  0.57469577,  5.88897275]])
```

`scipy.cluster.vq.`**`vq`**`(`*obs*, *code_book*`)`

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 acheived 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 'N' x 'M' 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
```

**Returns**

**code** : ndarray

A length N array holding the code book index for each observation.

**dist** : ndarray

The distortion (distance) between the observation and its nearest code.

## Notes

This currently forces 32-bit math precision for speed. Anyone know of a situation where this undermines the accuracy of the algorithm?

### 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*)

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.

**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'*)
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

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

(not used yet)

**minit** : string

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.

**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.

### 4.2.1 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.

## 4.3 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 |
| `fclusterdata`(X, t[, criterion, metric, ...]) | Cluster observation data using a given metric. |
| `leaders`(Z, T) | (L, M) = leaders(Z, T): |

`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** : 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.

**method** : str, optional

The linkage method to use (single, complete, average, weighted, median centroid, ward). See `linkage` for more information. Default is "single".

**metric** : str, optional

The distance metric for calculating pairwise distances. See `distance.pdist` for descriptions and linkage to verify compatibility with the linkage method.

**t** : double, optional

The cut-off threshold for the cluster function or the maximum number of clusters (criterion='maxclust').

**depth** : int, optional

The maximum depth for the inconsistency calculation. See `inconsistent` for more information.

**R** : ndarray, optional

The inconsistency matrix. It will be computed if necessary if it is not passed.

**Returns**

**T** : 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*)

(L, M) = leaders(Z, T):

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**

**A tuple (L, M) with** :

**L** : ndarray

The leader linkage node id's stored as a k-element 1D 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 1D 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 complete/max/farthest point linkage on the condensed distance matrix `y`. |
| `average`(y) | Performs average/UPGMA linkage on the condensed distance matrix |
| `weighted`(y) | Performs weighted/WPGMA linkage on the condensed distance matrix |
| `centroid`(y) | Performs centroid/UPGMC linkage. See `linkage` for more |
| `median`(y) | Performs median/WPGMC linkage. See `linkage` for more |
| `ward`(y) | Performs Ward's linkage on a condensed or redundant distance |

`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. This is called UPGMA.

- 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 math:*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, optional

The distance metric to use. See the `distance.pdist` function for a list of valid distance metrics.

**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`. 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

The linkage matrix.

**See Also:**

**`linkage`**
for advanced creation of hierarchical clusterings.

`scipy.cluster.hierarchy.`**`complete`**`(y)`

Performs complete complete/max/farthest point linkage on the condensed distance matrix `y`. 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.

`scipy.cluster.hierarchy.`**`average`**`(y)`

Performs average/UPGMA linkage on the condensed distance matrix `y`. 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.`**`weighted`**`(`*y*`)`

Performs weighted/WPGMA linkage on the condensed distance matrix `y`. 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**

**Q** : 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**

**Q** : 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**

**Q** : 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 |
| from_mlab_linkage(Z) | Converts a linkage matrix generated by MATLAB(TM) to a new |
| 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 cluster for each 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 Z generated by the linkage function |

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**

**res** : tuple

A tuple (c, {d}):

- **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**

**d** : int

The number of links up to `d` levels below each non-singleton cluster.

**Z**

[ndarray] The $(n-1)$ by 4 matrix encoding the linkage (hierarchical clustering). See `linkage` documentation for more information on its form.

**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,

**rac{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 cluster for each non-singleton cluster.

**Parameters**

**Z** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

**Returns**

**MD** : 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** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

**R** : ndarray

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 `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**

**ZM** : ndarray

A linkage matrix compatible with MATLAB(TM)'s hierarchical clustering functions.

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*`)`

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 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 the $i$ th position 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'/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'/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_label_rotation** : double, optional

Specifies the angle (in degrees) to rotate the leaf labels. When unspecified, the rotation based on the number of nodes in the dendrogram. (Default=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

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** : lambda/function

When a callable function, 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]`.

**Returns**

**R** : dict

A dictionary of data structures computed to render the dendrogram. Its has the following keys:

- 'icoords': a list of lists `[I1, I2, ..., Ip]` where

  `Ik` is a list of 4 independent variable coordinates corresponding to the line that represents the k'th link painted.

- 'dcoords': a list of lists `[I2, I2, ..., Ip]` where

  `Ik` is a list of 4 independent variable coordinates corresponding to the line that represents the k'th link painted.

- 'ivl': a list of labels corresponding to the leaf nodes.
- 'leaves': for each i, `H[i] == j`, cluster node

  $j$ appears in the $i$ th position 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 (corresponding to observation vector index) as they appear in the tree from left to right. |
| `to_tree`(Z[, rd]) | Converts a hierarchical clustering encoded in the matrix `Z` (by |

**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**
**c** : 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 0x3846938>*)

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 (corresponding to observation vector index) as they appear in the tree from left to right. Z is a linkage matrix.

**Parameters**

**Z** : ndarray

The hierarchical clustering encoded as a matrix. See `linkage` for more information.

**Returns**

**L** : 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 `T1` and |
| `is_monotonic`(Z) | Returns `True` if the linkage passed is monotonic. The linkage |
| `correspond`(Z, Y) | Checks if a linkage matrix `Z` and condensed distance matrix |
| `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 nd-array (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`, $0 \leq \texttt{Z}[\texttt{i}, 0] \leq i+n-1$ 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 `T1` and `T2` are equivalent.

**Parameters**

**T1** : ndarray

An assignment of singleton cluster ids to flat cluster ids.

**T2** : ndarray

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 if a linkage matrix `Z` and condensed distance matrix `Y` could possibly correspond to one another.

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** : ndarray

The linkage matrix to check for correspondance.

**Y** : ndarray

The condensed distance matrix to check for correspondance.

**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)` | Changes the list of matplotlib color codes to use when coloring links with the dendrogram color_threshold feature. |

`scipy.cluster.hierarchy.`**`set_link_color_palette`**(*palette*)

Changes the list of matplotlib color codes to use when coloring links with the dendrogram color_threshold feature.

**Parameters**

**palette** : 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.

### 4.3.1 References

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## 4.4 Constants (`scipy.constants`)

Physical and mathematical constants and units.

### 4.4.1 Mathematical constants

| | |
|---|---|
| `pi` | Pi |
| `golden` | Golden ratio |

### 4.4.2 Physical constants

| | |
|---|---|
| `c` | speed of light in vacuum |
| `mu_0` | the magnetic constant $\mu_0$ |
| `epsilon_0` | the electric constant (vacuum permittivity), $\epsilon_0$ |
| `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 $\sigma$ |
| `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 |

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**Table 4.1 – continued from previous page**

| | |
|---|---|
| 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 |
| 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 |

Continued on next page

**Table 4.1 – continued from previous page**

| | |
|---|---|
| `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 |
| `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 |

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**Table 4.1 – continued from previous page**

| | |
|---|---|
| `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 |
| `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 |

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**Table 4.1 – continued from previous page**

| | |
|---|---|
| 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 |
| 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 |

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**Table 4.1 – continued from previous page**

| | |
|---|---|
| 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 |
| 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 |

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**Table 4.1 – continued from previous page**

| | |
|---|---|
| `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 |
| `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 |

Continued on next page

Table 4.1 – continued from previous page

| | |
|---|---|
| {220} lattice spacing of silicon | 1.920155714e-10 m |

### 4.4.3 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])
```

### 4.4.4 References

## 4.5 Discrete Fourier transforms (`scipy.fftpack`)

### 4.5.1 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 multi-dimensional discrete Fourier transform of x. |
| `ifftn`(x[, shape, axes, overwrite_x]) | Return inverse multi-dimensional discrete Fourier transform of |
| `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. |

`scipy.fftpack.`**`fft`**(*x*, *n=None*, *axis=-1*, *overwrite_x=0*)

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+1] contains the positive-frequency terms, and A[n/2+1:] 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].

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 is most efficient for n a power of two.

## 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=0*)

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.

`scipy.fftpack.`**`fft2`**(*x*, *shape=None*, *axes=(-2, -1)*, *overwrite_x=0*)

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=0*)

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=0*)

Return multi-dimensional discrete Fourier transform of x.

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

```
>>> 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=0*)

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=0*)

Discrete Fourier transform of a real sequence.

The returned real arrays 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()`.

**Parameters**

**x** : array_like, real-valued

The data to tranform.

**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.

**See Also:**

`fft`, `irfft`, `scipy.fftpack.basic`

### Notes

Within numerical accuracy, `y == rfft(irfft(y))`.

`scipy.fftpack.irfft`(*x*, *n=None*, *axis=-1*, *overwrite_x=0*) → y

Return inverse discrete Fourier transform of real sequence x. The contents of x is interpreted as the output of rfft(..) function.

**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 preceeding expression.

Optional input: see rfft.__doc__

`scipy.fftpack.dct`(*x*, *type=2*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=0*)

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.

**axis** : int, optional

Axis over which to compute the transform.

**norm** : {None, 'ortho'}, optional

Normalization mode (see Notes). Default is None.

**overwrite_x** : bool, optional

If True the contents of x can be destroyed. (default=False)

**Returns**

**y** : ndarray of real

The transformed input array.

**See Also:**

`idct`

## 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.

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

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`).

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(1/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

http://en.wikipedia.org/wiki/Discrete_cosine_transform

'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).

`scipy.fftpack.`**`idct`**(*x, type=2, n=None, axis=-1, norm=None, overwrite_x=0*)

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.

**axis** : int, optional

Axis over which to compute the transform.

**norm** : {None, 'ortho'}, optional

Normalization mode (see Notes). Default is None.

**overwrite_x** : bool, optional

If True the contents of x can be destroyed. (default=False)

**Returns**

**y** : ndarray of real

The transformed input array.

**See Also:**

`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`.

## 4.5.2 Differential and pseudo-differential operators

| | |
|---|---|
| `diff`((x[, order, period]) | Return k-th derivative (or integral) of a periodic sequence x. |
| `tilbert`((x, h[, period]) | Return h-Tilbert transform of a periodic sequence x. |
| `itilbert`((x, h[, period]) | Return inverse h-Tilbert transform of a periodic sequence x. |
| `hilbert`((x) -> y) | Return Hilbert transform of a periodic sequence x. |
| `ihilbert`((x) -> y) | Return inverse Hilbert transform of a periodic sequence x. |
| `cs_diff`((x, a, b[, period]) | Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence x. |
| `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]) | Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x. |
| `cc_diff`((x, a, b[, period]) | Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence x. |
| `shift`((x, a[, period]) | Shift periodic sequence x by a: y(u) = x(u+a). |

`scipy.fftpack.`**`diff`**`(`*x*, *order=1*, *period=2*pi*`)` $\rightarrow$ y

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.

**Optional input:**

**order**
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**
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=2*pi*) → y
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

**Input:**

**h**
Defines the parameter of the Tilbert transform.

**period**
The assumed period of the sequence. Default period is 2*pi.

**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=2*pi*) → y
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

Optional input: see tilbert.__doc__

`scipy.fftpack.`**`hilbert`**(*x*) → y
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*) → y

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=2*pi*) → y

Return (a,b)-cosh/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 = -sqrt(-1)*cosh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j y_0 = 0

**Input:**

**a,b**

Defines the parameters of the cosh/sinh pseudo-differential operator.

**period**

The period of the sequence. Default period is 2*pi.

**Notes:**

For even len(x), the Nyquist mode of x is taken 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=2*pi*) → y

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

**Input:**

**a,b**
Defines the parameters of the sinh/sinh pseudo-differential operator.

**period**
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=2*pi*) → y

Return (a,b)-cosh/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 = cosh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j

**Input:**

**a,b**
Defines the parameters of the sinh/sinh pseudo-differential operator.

**Optional input:**

**period**
The period of the sequence x. Default is 2*pi.

**Notes:**
cc_diff(cc_diff(x,a,b),b,a) == x

`scipy.fftpack.`**`shift`**(*x*, *a*, *period=2*pi*) → y

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

**Optional input:**

**period**
The period of the sequences x and y. Default period is 2*pi.

## 4.5.3 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 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, ..., 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

Sample spacing.

**Returns**

**out** : ndarray

The 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

### 4.5.4 Convolutions (`scipy.fftpack.convolve`)

| | |
|---|---|
| `convolve` | convolve - Function signature: |
| `convolve_z` | convolve_z - Function signature: |
| `init_convolution_kernel` | init_convolution_kernel - Function signature: |
| `destroy_convolve_cache` | destroy_convolve_cache - Function signature: |

`scipy.fftpack.convolve.`**`convolve`** **= <fortran object>**

**convolve - Function signature:**
y = convolve(x,omega,[swap_real_imag,overwrite_x])

**Required arguments:**
x : input rank-1 array('d') with bounds (n) omega : input rank-1 array('d') with bounds (n)

**Optional arguments:**
overwrite_x := 0 input int swap_real_imag := 0 input int

**Return objects:**
y : rank-1 array('d') with bounds (n) and x storage

`scipy.fftpack.convolve.`**`convolve_z`** **= <fortran object>**

**convolve_z - Function signature:**
y = convolve_z(x,omega_real,omega_imag,[overwrite_x])

**Required arguments:**
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)

**Optional arguments:**
overwrite_x := 0 input int

**Return objects:**
y : rank-1 array('d') with bounds (n) and x storage

`scipy.fftpack.convolve.`**`init_convolution_kernel`** **= <fortran object>**

**init_convolution_kernel - Function signature:**
omega = init_convolution_kernel(n,kernel_func,[d,zero_nyquist,kernel_func_extra_args])

**Required arguments:**
n : input int kernel_func : call-back function

**Optional arguments:**
d := 0 input int kernel_func_extra_args := () input tuple zero_nyquist := d%2 input int

**Return objects:**
omega : rank-1 array('d') with bounds (n)

**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>**
destroy_convolve_cache - Function signature: destroy_convolve_cache()

### 4.5.5 Other (`scipy.fftpack._fftpack`)

| | |
|---|---|
| `drfft` | drfft - Function signature: |
| `zfft` | zfft - Function signature: |
| `zrfft` | zrfft - Function signature: |
| `zfftnd` | zfftnd - Function signature: |
| `destroy_drfft_cache` | destroy_drfft_cache - Function signature: |
| `destroy_zfft_cache` | destroy_zfft_cache - Function signature: |
| `destroy_zfftnd_cache` | destroy_zfftnd_cache - Function signature: |

`scipy.fftpack._fftpack.`**`drfft`** **= <fortran object>**

**drfft - Function signature:**
y = drfft(x,[n,direction,normalize,overwrite_x])

**Required arguments:**
x : input rank-1 array('d') with bounds (*)

**Optional arguments:**
overwrite_x := 0 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

**Return objects:**
y : rank-1 array('d') with bounds (*) and x storage

`scipy.fftpack._fftpack.`**`zfft`** **= <fortran object>**

**zfft - Function signature:**
y = zfft(x,[n,direction,normalize,overwrite_x])

**Required arguments:**
x : input rank-1 array('D') with bounds (*)

**Optional arguments:**
overwrite_x := 0 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

**Return objects:**
y : rank-1 array('D') with bounds (*) and x storage

`scipy.fftpack._fftpack.`**`zrfft`** **= <fortran object>**

**zrfft - Function signature:**
y = zrfft(x,[n,direction,normalize,overwrite_x])

**Required arguments:**
x : input rank-1 array('D') with bounds (*)

**Optional arguments:**
overwrite_x := 1 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

**Return objects:**
y : rank-1 array('D') with bounds (*) and x storage

`scipy.fftpack._fftpack.`**`zfftnd`** = **<fortran object>**

**zfftnd - Function signature:**
y = zfftnd(x,[s,direction,normalize,overwrite_x])

**Required arguments:**
x : input rank-1 array('D') with bounds (*)

**Optional arguments:**
overwrite_x := 0 input int s := old_shape(x,j++) input rank-1 array('i') with bounds (r) direction := 1 input int normalize := (direction<0) input int

**Return objects:**
y : rank-1 array('D') with bounds (*) and x storage

`scipy.fftpack._fftpack.`**`destroy_drfft_cache`** = **<fortran object>**
destroy_drfft_cache - Function signature: destroy_drfft_cache()

`scipy.fftpack._fftpack.`**`destroy_zfft_cache`** = **<fortran object>**
destroy_zfft_cache - Function signature: destroy_zfft_cache()

`scipy.fftpack._fftpack.`**`destroy_zfftnd_cache`** = **<fortran object>**
destroy_zfftnd_cache - Function signature: destroy_zfftnd_cache()

## 4.6 Integration and ODEs (`scipy.integrate`)

### 4.6.1 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. |
| `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.

If func takes many arguments, it is integrated along the axis corresponding to the first argument. Use the keyword argument *args* to pass the other arguments.

Run scipy.integrate.quad_explain() for more information on the more esoteric inputs and outputs.

**Parameters**
**func** : function

A Python function or method to integrate.

**a** : float

Lower limit of integration (use -scipy.integrate.Inf for -infinity).

**b** : float

Upper limit of integration (use scipy.integrate.Inf for +infinity).

**args** : tuple, optional

extra arguments to pass to func

**full_output** : int

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 :** :

absolute error tolerance.

**epsrel :** :

relative error tolerance.

**limit :** :

an upper bound on the number of subintervals used in the adaptive algorithm.

**points :** :

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 :** :

string indicating weighting function.

**wvar :** :

variables for use with weighting functions.

**limlst :** :

Upper bound on the number of cylces (>=3) for use with a sinusoidal weighting and an infinite end-point.

**wopts :** :

Optional input for reusing Chebyshev moments.

**maxp1 :** :

An upper bound on the number of Chebyshev moments.

**See Also:**

dblquad, tplquad

**fixed_quad**
fixed-order Gaussian quadrature

**quadrature**
adaptive Gaussian quadrature

odeint, ode, simps, trapz, romb

**scipy.special**
for coefficients and roots of orthogonal polynomials

## 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
21.3333333333
```

Calculate $\int_0^\infty e^{-x} dx$

```
>>> invexp = lambda x: exp(-x)
>>> integrate.quad(invexp,0,inf)
(0.99999999999999989, 5.8426061711142159e-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
```

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)** : tuple

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 *func2d*.

**epsabs** : float, optional

Absolute tolerance passed directly to the inner 1-D quadrature integration. Default is 1.49e-8.

**epsrel** : float

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

**`fixed_quad`**
fixed-order Gaussian quadrature

**`quadrature`**
adaptive Gaussian quadrature

`odeint`, `ode`, `simps`, `trapz`, `romb`

**`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)** : tuple

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** : Arguments

Extra arguments to pass to func3d.

**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

`romb`
Integrators for sampled data

`trapz`
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.`**`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`, `tplquad`

**`romberg`**
adaptive Romberg quadrature

**`quadrature`**
adaptive Gaussian quadrature

`romb`, `simps`, `trapz`

**`cumtrapz`**
cumulative integration for sampled data

`ode`, `odeint`

`scipy.integrate.`**`quadrature`**(*func*, *a*, *b*, *args=()*, *tol=1.49e-08*, *rtol=1.49e-08*, *maxiter=50*, *vec_func=True*)

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, rol** : 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 number of iterations.

**vec_func** : bool, optional

True or False if func handles arrays as arguments (is a "vector" function). Default is True.

**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 |
| `trapz` | 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`, `tplquad`, `romb`, `simps`, `trapz`

**`cumtrapz`**
Cumulative integration for sampled data.

`ode`, `odeint`

## References

[R1]

### Examples

Integrate a gaussian from 0 to 1 and compare to the error function.

```
>>> from scipy.special import erf
>>> gaussian = lambda x: 1/np.sqrt(np.pi) * np.exp(-x**2)
>>> result = romberg(gaussian, 0, 1, show=True)
Romberg integration of <function vfunc at 0x101eceaa0> 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 2*result,erf(1)
0.84270079295 0.84270079295
```

## 4.6.2 Integrating functions, given fixed samples

| | |
|---|---|
| trapz(y[, x, dx, axis]) | Integrate along the given axis using the composite trapezoidal rule. |
| cumtrapz(y[, x, dx, axis]) | Cumulatively integrate y(x) using samples along the given axis and the composite trapezoidal rule. |
| simps(y[, x, dx, axis, even]) | Integrate y(x) using samples along the given axis and the composite |
| romb(y[, dx, axis, show]) | Romberg integration using samples of a function. |

scipy.integrate.**trapz**(*y*, *x=None*, *dx=1.0*, *axis=-1*)

Integrate along the given axis using the composite trapezoidal rule.

Integrate *y* (*x*) along given axis.

**Parameters**

**y** : array_like

Input array to integrate.

**x** : array_like, optional

If *x* is None, then spacing between all *y* elements is *dx*.

**dx** : scalar, optional

If *x* is None, spacing given by *dx* is assumed. Default is 1.

**axis** : int, optional

Specify the axis.

**Returns**

**out** : float

Definite integral as approximated by trapezoidal rule.

**See Also:**

sum, cumsum

### Notes

Image [R3] illustrates trapezoidal rule – y-axis locations of points will be taken from *y* array, by default x-axis distances between points will be 1.0, alternatively they can be provided with *x* array or with *dx* scalar. Return value will be equal to combined area under the red lines.

### References

[R2], [R3]

### Examples

```
>>> np.trapz([1,2,3])
4.0
>>> np.trapz([1,2,3], x=[4,6,8])
8.0
>>> np.trapz([1,2,3], dx=2)
8.0
>>> a = np.arange(6).reshape(2, 3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.trapz(a, axis=0)
array([ 1.5,  2.5,  3.5])
>>> np.trapz(a, axis=1)
array([ 2.,  8.])
```

`scipy.integrate.`**`cumtrapz`**(*y*, *x=None*, *dx=1.0*, *axis=-1*)

Cumulatively integrate y(x) using samples along the given axis and the composite trapezoidal rule. If x is None, spacing given by *dx* is assumed.

**Parameters**

**y** : array

**x** : array, optional

**dx** : int, optional

**axis** : int, optional

Specifies the axis to cumulate:

- -1 –> X axis
- 0 –> Z axis
- 1 –> Y 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

**`romb`**
integrators for sampled data

**`trapz`**
integrators for sampled data

**`cumtrapz`**
cumulative integration for sampled data

**`ode`**
ODE integrators

**`odeint`**
ODE integrators

`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

**`trapz`**
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** : array_like, optional

The sample spacing. Default is 1.

**axis** : array_like?, 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**

**ret** : array_like?

The integrated result for each axis.

**See Also:**

`quad`, `romberg`, `quadrature`, `fixed_quad`, `dblquad`, `tplquad`, `simps`, `trapz`, `cumtrapz`, `ode`, `odeint`

**See Also:**

`scipy.special` for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

### 4.6.3 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

Extra arguments to pass to function.

**Dfun** : callable(y, t0, ...)

Gradient (Jacobian) of func.

**col_deriv** : boolean

True if Dfun defines derivatives down columns (faster), otherwise Dfun should define derivatives across rows.

**full_output** : boolean

True if to return a dictionary of optional outputs as the second output

**printmessg** : boolean

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** : integer

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 columns contain the non-zero bands (starting with the lowest diagonal). Thus, the return matrix from Dfun should have shape `len(y0) * (ml + mu + 1) when ml >=0 or mu >=0`

**rtol, atol** : float

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** : array

Vector of critical points (e.g. singularities) where integration care should be taken.

**h0** : float, (0: solver-determined)

The step size to be attempted on the first step.

**hmax** : float, (0: solver-determined)

The maximum absolute step size allowed.

**hmin** : float, (0: solver-determined)

The minimum absolute step size allowed.

**ixpr** : boolean

Whether to generate extra printing at method switches.

**mxstep** : integer, (0: solver-determined)

Maximum number of (internally defined) steps allowed for each integration point in t.

**mxhnil** : integer, (0: solver-determined)

Maximum number of messages printed.

**mxordn** : integer, (0: solver-determined)

Maximum order to be allowed for the nonstiff (Adams) method.

**mxords** : integer, (0: solver-determined)

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)

**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)

**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
- rband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+rband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+lband, j] = jac[i,j].
- method: 'adams' or 'bdf' Which solver to use, Adams (non-stiff) or BDF (stiff)
- with_jacobian : bool Whether to use the 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).

"dopri5"

This is an explicit runge-kutta method of order (4)5 due to Dormand & Prince (with stepsize control and dense output).

Authors:

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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.

"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', with_jacobian=True)
>>> 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:
>>>     r.integrate(r.t+dt)
>>>     print r.t, r.y
```

## 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. |
| `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.`**`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** : 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. |
| `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.`**`successful`**()

Check if integration was successful.

## 4.7 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.

### 4.7.1 Univariate interpolation

| | |
|---|---|
| `interp1d`(x, y[, kind, axis, copy, ...]) | Interpolate a 1-D function. |
| `BarycentricInterpolator`(xi[, yi]) | The interpolating polynomial for a set of points |
| `KroghInterpolator`(xi, yi) | The interpolating polynomial for a set of points |
| `PiecewisePolynomial`(xi, yi[, orders, direction]) | Piecewise polynomial curve specified by points and derivatives |
| `barycentric_interpolate`(xi, yi, x) | Convenience function for polynomial interpolation |
| `krogh_interpolate`(xi, yi, x[, der]) | Convenience function for polynomial interpolation. |
| `piecewise_polynomial_interpolate`(xi, yi, x) | Convenience function for piecewise polynomial interpolation |

**class** `scipy.interpolate.`**`interp1d`**(*x*, *y*, *kind='linear'*, *axis=-1*, *copy=True*, *bounds_error=True*, *fill_value=np.nan*)

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** : array_like

A 1-D array of monotonically increasing real values.

**y** : 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') 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, an error is thrown 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.

**See Also:**

**`UnivariateSpline`**
A more recent wrapper of the FITPACK routines.

`splrep`, `splev`, `interp2d`

## Examples

```
>>> import scipy.interpolate
>>> x = np.arange(0, 10)
>>> y = np.exp(-x/3.0)
>>> f = sp.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, '-')
```

### Methods

| | |
|---|---|
| `__call__`(x_new) | Find interpolated y_new = f(x_new). |

`interp1d.__call__(x_new)`

Find interpolated y_new = f(x_new).

**Parameters**

**x_new** : number or array

New independent variable(s).

**Returns**

**y_new** : ndarray

Interpolated value(s) corresponding to x_new.

**class** `scipy.interpolate.BarycentricInterpolator(xi, yi=None)`

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.

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) | Update the y values to be interpolated |

`BarycentricInterpolator.__call__(x)`

Evaluate the interpolating polynomial at the points x

**Parameters**

**x** : scalar or array-like of length M

**Returns**

**y** : scalar or array-like of length R or length M or M by R

The shape of y depends on the shape of x and whether the interpolator is vector-valued or scalar-valued.

### Notes

Currently the code computes an outer product between x and the weights, that is, it constructs an intermediate array of size N by M, 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 of length N1

The x coordinates of the points the polynomial should pass through

**yi** : array_like N1 by R or None

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued. If None the y values will be supplied later. The yi should be specified if and only if the interpolator has y values specified.

`BarycentricInterpolator.`**`set_yi`**(*yi*)

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 N by R

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued. If None the y values will be supplied later.

**class** `scipy.interpolate.`**`KroghInterpolator`**(*xi*, *yi*)

The interpolating polynomial for a set of points

Constructs a polynomial that passes through a given set of points, optionally with specified derivatives at those points. 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.

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 [R4].

**Parameters**

**xi** : array-like, length N

Known x-coordinates

**yi** : array-like, N by R

Known y-coordinates, interpreted as vectors of length R, or scalars if R=1. When an xi occurs two or more times in a row, the corresponding yi's represent derivative values.

## References

[R4]

## Methods

| | |
|---|---|
| `__call__`(x) | Evaluate the polynomial at the point x |
| `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 polynomial at the point x

**Parameters**

**x** : scalar or array-like of length N

**Returns**

**y** : scalar, array of length R, array of length N, or array of length N by R

If x is a scalar, returns either a vector or a scalar depending on whether the interpolator is vector-valued or scalar-valued. If x is a vector, returns a vector of values.

`KroghInterpolator.`**`derivative`**`(`*x*, *der*`)`

Evaluate one derivative of the polynomial at the point x

**Parameters**

**x** : scalar or array_like of length N

Point or points at which to evaluate the derivatives

**der** : None or integer

Which derivative to extract. This number includes the function value as 0th derivative.

**Returns**

**d** : ndarray

If the interpolator's values are R-dimensional then the returned array will be N by R. If x is a scalar, the middle dimension will be dropped; if R is 1 then the last dimension will be dropped.

## 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** : scalar or array_like of length N

Point or points at which to evaluate the derivatives

**der** : None or integer

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

If the interpolator's values are R-dimensional then the returned array will be der by N by R. If x is a scalar, the middle dimension will be dropped; if R is 1 then the last dimension will be dropped.

## 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*`)`

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 very 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.

## Methods

| | |
|---|---|
| `__call__`(x) | Evaluate the piecewise polynomial |
| `append`(xi, yi[, order]) | Append a single point with derivatives to the PiecewisePolynomial |
| `derivative`(x, der) | Evaluate a derivative of the piecewise polynomial |
| `derivatives`(x, der) | Evaluate a derivative of the piecewise polynomial |
| `extend`(xi, yi[, orders]) | Extend the PiecewisePolynomial by a list of points |

`PiecewisePolynomial.`**`__call__`**(*x*)

Evaluate the piecewise polynomial

**Parameters**

**x** : scalar or array-like of length N

**Returns**

**y** : scalar or array-like of length R or length N or N by R

`PiecewisePolynomial.`**`append`**(*xi*, *yi*, *order=None*)

Append a single point with derivatives to the PiecewisePolynomial

**Parameters**

**xi** : float

**yi** : array_like

yi is the list of derivatives known at xi

**order** : integer or None

a polynomial order, or instructions to use the highest possible order

`PiecewisePolynomial.`**`derivative`**(*x*, *der*)

Evaluate a derivative of the piecewise polynomial

**Parameters**

**x** : scalar or array_like of length N

**der** : integer

which single derivative to extract

**Returns**

**y** : scalar or array_like of length R or length N or N by R

### Notes

This currently computes (using self.derivatives()) all derivatives of the curve segment containing each x but returns only one.

`PiecewisePolynomial.`**`derivatives`**(*x*, *der*)

Evaluate a derivative of the piecewise polynomial

**Parameters**

**x** : scalar or array_like of length N

**der** : integer

how many derivatives (including the function value as 0th derivative) to extract

**Returns**

**y** : array_like of shape der by R or der by N or der by N by R

`PiecewisePolynomial.`**`extend`**(*xi*, *yi*, *orders=None*)

Extend the PiecewisePolynomial by a list of points

**Parameters**

**xi** : array_like of length N1

a sorted list of x-coordinates

**yi** : list of lists of length N1

yi[i] is the list of derivatives known at xi[i]

**orders** : list of integers, or integer

a list of polynomial orders, or a single universal order

**direction** : {None, 1, -1}

indicates whether the xi are increasing or decreasing +1 indicates increasing -1 indicates decreasing None indicates that it should be deduced from the first two xi

`scipy.interpolate.`**`barycentric_interpolate`**(*xi*, *yi*, *x*)

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.

Based on Berrut and Trefethen 2004, "Barycentric Lagrange Interpolation".

**Parameters**

**xi** : array_like of length N

The x coordinates of the points the polynomial should pass through

**yi** : array_like N by R

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued.

**x** : scalar or array_like of length M

**Returns**

**y** : scalar or array_like of length R or length M or M by R

The shape of y depends on the shape of x and whether the interpolator is vector-valued or scalar-valued.

## 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*)

Convenience function for polynomial interpolation.

Constructs a polynomial that passes through a given set of points, optionally with specified derivatives at those points. Evaluates the polynomial or some of 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.

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 Krogh 1970, "Efficient Algorithms for Polynomial Interpolation and Numerical Differentiation"

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.

**Parameters**

**xi** : array_like, length N

known x-coordinates

**yi** : array_like, N by R

known y-coordinates, interpreted as vectors of length R, or scalars if R=1

**x** : scalar or array_like of length N

Point or points at which to evaluate the derivatives

**der** : integer or list

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.

**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.

## 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*)

Convenience function for piecewise polynomial interpolation

**Parameters**

**xi** : array_like

A sorted list of x-coordinates, of length N.

**yi** : list of lists

yi[i] is the list of derivatives known at xi[i]. Of length N.

**x** : scalar or array_like

Of length M.

**orders** : int or list of ints

a list of polynomial orders, or a single universal order

**der** : int

Which single derivative to extract.

**Returns**

**y** : scalar or array_like

The result, of length R or length M or M by R,

### 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).

## 4.7.2 Multivariate interpolation

Unstructured data:

| | |
|---|---|
| `griddata`(points, values, xi[, method, ...]) | Interpolate unstructured N-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-dimensional scattered data. |
| `interp2d`(x, y, z[, kind, copy, ...]) | Interpolate over a 2-D grid. |

`scipy.interpolate.`**`griddata`**(*points*, *values*, *xi*, *method='linear'*, *fill_value=nan*)

Interpolate unstructured N-dimensional data. New in version 0.9.

**Parameters**

**points** : ndarray of floats, shape (npoints, ndims)

Data point coordinates. Can either be a ndarray of size (npoints, ndim), or a tuple of *ndim* arrays.

**values** : ndarray of float or complex, shape (npoints, ...)

Data values.

**xi** : ndarray of float, shape (..., ndim)

Points where to interpolate data at.

**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 detemined 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.

## 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:

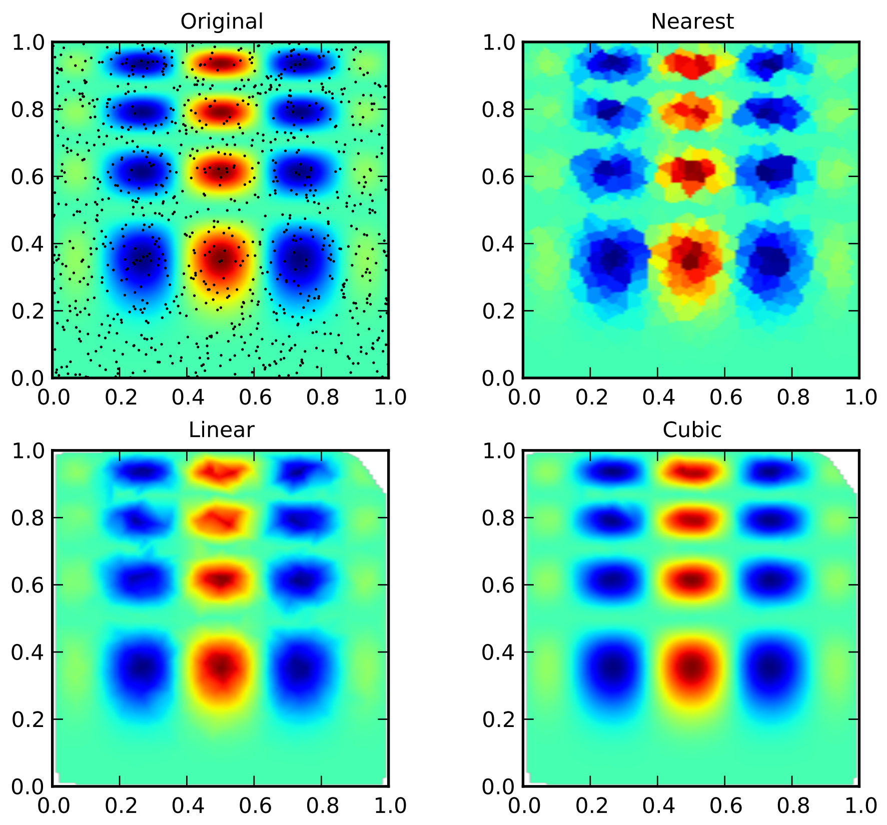
```
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```

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*)
Piecewise linear interpolant in N dimensions. New in version 0.9.

**Parameters**

**points** : ndarray of floats, shape (npoints, ndims)

Data point coordinates.

**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`.

## Notes

The interpolant is constructed by triangulating the input data with Qhull [Qhull], and on each triangle performing linear barycentric interpolation.

### References

[Qhull]

### 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**

**points** : ndarray of floats, shape (npoints, ndims)

Data point coordinates.

**values** : ndarray of float or complex, shape (npoints, ...)

Data values.

### 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)

Data point coordinates.

**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.

### Notes

The interpolant is constructed by triangulating the input data with Qhull [Qhull], 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

[Qhull], [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 (defult 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.

**Parameters**

**x, y** : 1-D ndarrays

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** : 1-D ndarray

The values of the function to interpolate at the data points. If *z* is a multi-dimensional array, it is flattened before use.

**kind** : {'linear', 'cubic', 'quintic'}, optional

The kind of spline interpolation to use. Default is 'linear'.

**copy** : bool, optional

If True, then data is copied, otherwise only a reference is held.

**bounds_error** : bool, optional

If True, when interpolated values are requested outside of the domain of the input data, an error 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. Defaults to NaN.

**See Also:**

`bisplrep`, `bisplev`

**`BivariateSpline`**
a more recent wrapper of the FITPACK routines

`interp1d`

## 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:

```
>>> 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 = sp.interpolate.interp2d(x, y, z, kind='cubic')
```

Now use the obtained interpolation function and plot the result:

```
>>> 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-')
```

## Methods

| | |
|---|---|
| `__call__`(x, y[, dx, dy]) | Interpolate the function. |

`interp2d.`**`__call__`**(*x*, *y*, *dx=0*, *dy=0*)
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.

**Returns**

**z** : 2D array with shape (len(y), len(x))

The interpolated values.

For data on a grid:

| | |
|---|---|
| `RectBivariateSpline`(x, y, z[, bbox, kx, ky, s]) | Bivariate spline approximation over a rectangular mesh. |

**See Also:**

`scipy.ndimage.map_coordinates`

## 4.7.3 1-D Splines

| | |
|---|---|
| `UnivariateSpline`(x, y[, w, bbox, k, s]) | One-dimensional smoothing spline fit to a given set of data points. |
| `InterpolatedUnivariateSpline`(x, y[, w, bbox, k]) | 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*)

One-dimensional smoothing spline fit to a given set of data points.

Fits a spline y=s(x) of degree *k* to the provided *x*, *y* data. *s* specifies the number of knots by specifying a smoothing condition.

**Parameters**

**x** : array_like

1-D array of independent input data. Must be increasing.

**y** : array_like

1-D array of dependent input data, of the same length as *x*.

**w** : array_like, optional

Weights for spline fitting. Must be positive. If None (default), weights are all equal.

**bbox** : 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.

**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]-s(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.

**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*.

### Examples

```
>>> from numpy import linspace,exp
>>> from numpy.random import randn
>>> from scipy.interpolate import UnivariateSpline
>>> x = linspace(-3, 3, 100)
>>> y = exp(-x**2) + randn(100)/10
>>> s = UnivariateSpline(x, y, s=1)
>>> xs = linspace(-3, 3, 1000)
>>> ys = s(xs)
```

xs,ys is now a smoothed, super-sampled version of the noisy gaussian x,y.

### Methods

| | |
|---|---|
| __call__(x[, nu]) | Evaluate spline (or its nu-th derivative) at positions x. |
| derivatives(x) | Return all derivatives of the spline at the point x. |
| get_coeffs() | Return spline coefficients. |
| get_knots() | Return the positions of (boundary and interior) |
| get_residual() | Return weighted sum of squared residuals of the spline |
| integral(a, b) | Return definite integral of the spline between two |
| roots() | Return the zeros of the spline. |
| set_smoothing_factor(s) | Continue spline computation with the given smoothing |

UnivariateSpline.**__call__**(*x*, *nu=0*)
Evaluate spline (or its nu-th derivative) at positions x. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

UnivariateSpline.**derivatives**(*x*)
Return all derivatives of the spline at the point x.

UnivariateSpline.**get_coeffs**()
Return spline coefficients.

UnivariateSpline.**get_knots**()
Return the positions of (boundary and interior) knots of the spline.

UnivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

UnivariateSpline.**integral**(*a*, *b*)
Return definite integral of the spline between two given points.

`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.

**class** `scipy.interpolate.`**`InterpolatedUnivariateSpline`**`(`*x, y, w=None, bbox=[None, None], k=3*`)`

One-dimensional interpolating spline for a given set of data points.

Fits a spline y=s(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** : array_like

input dimension of data points – must be increasing

**y** : array_like

input dimension of data points

**w** : array_like, optional

Weights for spline fitting. Must be positive. If None (default), weights are all equal.

**bbox** : 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.

**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

```
>>> from numpy import linspace,exp
>>> from numpy.random import randn
>>> from scipy.interpolate import UnivariateSpline
>>> x = linspace(-3, 3, 100)
>>> y = exp(-x**2) + randn(100)/10
>>> s = UnivariateSpline(x, y, s=1)
>>> xs = linspace(-3, 3, 1000)
>>> ys = s(xs)
```

xs,ys is now a smoothed, super-sampled version of the noisy gaussian x,y

### Methods

| | |
|---|---|
| `__call__`(x[, nu]) | Evaluate spline (or its nu-th derivative) at positions x. |
| `derivatives`(x) | Return all derivatives of the spline at the point x. |
| `get_coeffs`() | Return spline coefficients. |
| `get_knots`() | Return the positions of (boundary and interior) |
| `get_residual`() | Return weighted sum of squared residuals of the spline |
| `integral`(a, b) | Return definite integral of the spline between two |
| `roots`() | Return the zeros of the spline. |
| `set_smoothing_factor`(s) | Continue spline computation with the given smoothing |

`InterpolatedUnivariateSpline.`**`__call__`**(*x*, *nu=0*)

Evaluate spline (or its nu-th derivative) at positions x. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

`InterpolatedUnivariateSpline.`**`derivatives`**(*x*)

Return all derivatives of the spline at the point x.

`InterpolatedUnivariateSpline.`**`get_coeffs`**()

Return spline coefficients.

`InterpolatedUnivariateSpline.`**`get_knots`**()

Return the positions of (boundary and interior) knots of the spline.

`InterpolatedUnivariateSpline.`**`get_residual`**()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

`InterpolatedUnivariateSpline.`**`integral`**(*a*, *b*)

Return definite integral of the spline between two given points.

`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.

**class** `scipy.interpolate.`**`LSQUnivariateSpline`**(*x, y, t, w=None, bbox=[None, None], k=3*)

One-dimensional spline with explicit internal knots.

Fits a spline y=s(x) of degree *k* to the provided *x*, *y* data. *t* specifies the internal knots of the spline

**Parameters**

**x** : array_like

input dimension of data points – must be increasing

**y** : array_like

input dimension of data points

**t: array_like** :

interior knots of the spline. Must be in ascending order and bbox[0]<t[0]<...<t[-1]<bbox[-1]

**w** : array_like, optional

weights for spline fitting. Must be positive. If None (default), weights are all equal.

**bbox** : 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.

**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*.

## Examples

```
>>> from numpy import linspace,exp
>>> from numpy.random import randn
>>> from scipy.interpolate import LSQUnivariateSpline
>>> x = linspace(-3,3,100)
>>> y = exp(-x**2) + randn(100)/10
>>> t = [-1,0,1]
>>> s = LSQUnivariateSpline(x,y,t)
>>> xs = linspace(-3,3,1000)
>>> ys = s(xs)
```

xs,ys is now a smoothed, super-sampled version of the noisy gaussian x,y with knots [-3,-1,0,1,3]

## Methods

| | |
|---|---|
| `__call__`(x[, nu]) | Evaluate spline (or its nu-th derivative) at positions x. |
| `derivatives`(x) | Return all derivatives of the spline at the point x. |
| `get_coeffs`() | Return spline coefficients. |
| `get_knots`() | Return the positions of (boundary and interior) |
| `get_residual`() | Return weighted sum of squared residuals of the spline |
| `integral`(a, b) | Return definite integral of the spline between two |
| `roots`() | Return the zeros of the spline. |
| `set_smoothing_factor`(s) | Continue spline computation with the given smoothing |

`LSQUnivariateSpline.`**`__call__`**(*x*, *nu=0*)
Evaluate spline (or its nu-th derivative) at positions x. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

`LSQUnivariateSpline.`**`derivatives`**(*x*)
Return all derivatives of the spline at the point x.

`LSQUnivariateSpline.`**`get_coeffs`**()
Return spline coefficients.

`LSQUnivariateSpline.`**`get_knots`**()
Return the positions of (boundary and interior) knots of the spline.

`LSQUnivariateSpline.`**`get_residual`**()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

`LSQUnivariateSpline.`**`integral`**(*a*, *b*)
Return definite integral of the spline between two given points.

`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.

The above univariate spline classes have the following methods:

| | |
|---|---|
| `UnivariateSpline.__call__`(x[, nu]) | Evaluate spline (or its nu-th derivative) at positions x. |
| `UnivariateSpline.derivatives`(x) | Return all derivatives of the spline at the point x. |
| `UnivariateSpline.integral`(a, b) | Return definite integral of the spline between two |
| `UnivariateSpline.roots`() | Return the zeros of the spline. |
| `UnivariateSpline.get_coeffs`() | Return spline coefficients. |
| `UnivariateSpline.get_knots`() | Return the positions of (boundary and interior) |
| `UnivariateSpline.get_residual`() | Return weighted sum of squared residuals of the spline |
| `UnivariateSpline.set_smoothing_factor`(s) | Continue spline computation with the given smoothing |

Low-level 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. |
| `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.`**`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. The coefficients, c, and the knot points, t, are returned. Uses the FORTRAN routine curfit from FITPACK.

**Parameters**

**x, y** : array_like

The data points defining a curve y = f(x).

**w** : array_like

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

The interval to fit. If None, these default to x[0] and x[-1] respectively.

**k** : int

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}

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

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** : int

The knots needed for task=-1. If given then task is automatically set to -1.

**full_output** : bool

If non-zero, then return optional outputs.

**per** : bool

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

Non-zero to suppress messages.

**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.

## References

Based on algorithms described in [1], [2], [3], and [4]:

[R22], [R23], [R24], [R25]

## Examples

```
>>> x = linspace(0, 10, 10)
>>> y = sin(x)
>>> tck = splrep(x, y)
>>> x2 = linspace(0, 10, 200)
>>> y2 = splev(x2, tck)
>>> plot(x, y, 'o', x2, y2)
```

`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.

**u** : array_like, optional

An array of parameter values. If not given, these values are calculated automatically as `M = len(x[0])`:

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.

**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.

## References

[R19], [R20], [R21]

`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

A 1-D 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

The order of derivative of the spline to compute (must be less than or equal to k).

**ext** : int

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

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 splrep, then this is a list of arrays representing the curve in N-dimensional space.

**See Also:**

`splprep`, `splrep`, `sproot`, `spalde`, `splint`, `bisplrep`, `bisplev`

## References

[R14], [R15], [R16]

`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

### References

[R17], [R18]

`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. The knots must be a montonically increasing sequence.

**mest** : int

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

[R26], [R27], [R28]

`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**

**tck** : tuple

A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.

**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*.

**Returns**

**results** : array_like

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

[R11], [R12], [R13]

`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.

**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

[R8], [R9], [R10]

`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

[R5], [R6], [R7]

## 4.7.4 2-D Splines

For data on a grid:

| | |
|---|---|
| `RectBivariateSpline`(x, y, z[, bbox, kx, ky, s]) | Bivariate spline approximation over a rectangular mesh. |

**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`, `bisplev`

**`UnivariateSpline`**
a similar class for univariate spline interpolation

## Methods

| | |
|---|---|
| `__call__`(x, y[, mth]) | Evaluate spline at positions x,y. |
| `ev`(xi, yi) | Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1 |
| `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-variable, respectively. |
| `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='array'*)
Evaluate spline at positions x,y.

`RectBivariateSpline.`**`ev`**(*xi*, *yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

`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.

For unstructured data:

| | |
|---|---|
| `BivariateSpline` | Bivariate spline s(x,y) of degrees kx and ky on the rectangle [xb,xe] x [yb, ye] calculated from a given set of data points (x,y,z). |
| `SmoothBivariateSpline`(x, y, z[, w, bbox, ...]) | Smooth bivariate spline approximation. |
| `LSQBivariateSpline`(x, y, z, tx, ty[, w, ...]) | Weighted least-squares bivariate spline approximation. |

**class** `scipy.interpolate.`**`BivariateSpline`**

Bivariate spline s(x,y) of degrees kx and ky on the rectangle [xb,xe] x [yb, ye] calculated from a given set of data points (x,y,z).

**See Also:**

`bisplrep`, `bisplev`

**`UnivariateSpline`**
a similar class for univariate spline interpolation

**`SmoothUnivariateSpline`**
to create a BivariateSpline through the given points

**`LSQUnivariateSpline`**
to create a BivariateSpline using weighted least-squares fitting

## Methods

| | |
|---|---|
| `__call__`(x, y[, mth]) | Evaluate spline at positions x,y. |
| `ev`(xi, yi) | Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1 |
| `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-variable, respectively. |
| `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='array'*)
Evaluate spline at positions x,y.

`BivariateSpline.`**`ev`**(*xi*, *yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

`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_lie, optional

Positive 1-D sequence of weights.

**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`, `bisplev`

**`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]) | Evaluate spline at positions x,y. |
| `ev`(xi, yi) | Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1 |
| `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-variable, respectively. |
| `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='array'*)
Evaluate spline at positions x,y.

`SmoothBivariateSpline.`**`ev`**(*xi*, *yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

`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.`**`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_lie, optional

Positive 1-D sequence of weights.

**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`, `bisplev`

**`UnivariateSpline`**
a similar class for univariate spline interpolation

**`SmoothUnivariateSpline`**
To create a BivariateSpline through the given points

## Notes

The length of *x*, *y* and *z* should be at least `(kx+1) * (ky+1)`.

## Methods

| | |
|---|---|
| `__call__`(x, y[, mth]) | Evaluate spline at positions x,y. |
| `ev`(xi, yi) | Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1 |
| `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-variable, respectively. |
| `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='array'*)
Evaluate spline at positions x,y.

`LSQBivariateSpline.`**`ev`**(*xi*, *yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

`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.

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.

**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

[R8], [R9], [R10]

`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

[R5], [R6], [R7]

## 4.7.5 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*).

`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

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.map_coordinates`, `scipy.ndimage.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`.

## 4.8 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)

### 4.8.1 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. |

`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.

**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=None*)

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** : {'column', 'row', None}, optional

If 'column', write 1-D numpy arrays as column vectors. If 'row', write 1-D numpy arrays as row vectors. If None (the default), the behavior depends on the value of *format* (see Notes below).

**See Also:**

`mio4.MatFile4Writer`, `mio5.MatFile5Writer`

### Notes

If `format == '4'`, *mio4.MatFile4Writer* is called, which sets *oned_as* to 'row' if it had been None. If `format == '5'`, *mio5.MatFile5Writer* is called, which sets *oned_as* to 'column' if it had been None, but first it executes:

```
warnings.warn("Using oned_as default value ('column')" +
    " This will change to 'row' in future versions",        FutureWarning,
    stacklevel=2)
```

without being more specific as to precisely when the change will take place.

## 4.8.2 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.

## 4.8.3 Matrix Market files

| | |
|---|---|
| `mminfo`(source) | Queries the contents of the Matrix Market file 'filename' to |
| `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 matrix 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** : {'coordinate', 'array'}

**field** : {'real', 'complex', 'pattern', 'integer'}

**symm** : {'general', 'symmetric', 'skew-symmetric', '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 matrix A to a Matrix Market formatted file.

**Parameters**

**target** : file

Matrix Market filename (extension .mtx) or open file object

**a** : array like

Sparse or full matrix

**comment** : str

comments to be prepended to the Matrix Market file

**field** : {'real', 'complex', 'pattern', 'integer'}, optional

**precision :** :

Number of digits to display for real or complex values.

## 4.8.4 Other

| | |
|---|---|
| save_as_module([file_name, data]) | Save the dictionary "data" into a module and shelf named save. |

`scipy.io.save_as_module(file_name=None, data=None)`

Save the dictionary "data" into a module and shelf named save.

**Parameters**

**file_name** : str, optional

File name of the module to save.

**data** : dict, optional

The dictionary to store in the module.

## 4.8.5 Wav sound files (`scipy.io.wavfile`)

| | |
|---|---|
| read(file) | 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(file)`

Return the sample rate (in samples/sec) and data from a WAV file

**Parameters**

**file** : file

Input wav file.

**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.

`scipy.io.wavfile.`**`write`**(*filename*, *rate*, *data*)

Write a numpy array as a WAV file

**Parameters**

**filename** : file

The name of the file to write (will be over-written).

**rate** : int

The sample rate (in samples/sec).

**data** : ndarray

A 1-D or 2-D numpy array of integer data-type.

### Notes

- 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).

## 4.8.6 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.

## 4.8.7 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'}, optional

read-write 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

**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.

### 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 the dimensions it uses. |
| `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).

## 4.9 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.

### 4.9.1 Basics

| | |
|---|---|
| `inv`(a[, overwrite_a]) | 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, 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_triangular`(a, b[, trans, lower, ...]) | Solve the equation *a x = b* for *x*, assuming a is a triangular matrix. |
| `det`(a[, overwrite_a]) | Compute the determinant of a matrix |
| `norm`(a[, ord]) | Matrix or vector norm. |
| `lstsq`(a, b[, cond, overwrite_a, overwrite_b]) | Compute least-squares solution to equation Ax = b. |
| `pinv`(a[, cond, rcond]) | Compute the (Moore-Penrose) pseudo-inverse of a matrix. |
| `pinv2`(a[, cond, rcond]) | Compute the (Moore-Penrose) pseudo-inverse of a matrix. |
| `kron`(a, b) | Kronecker product of a and b. |
| `tril`(m[, k]) | Construct a copy of a matrix with elements above the k-th diagonal zeroed. |
| `triu`(m[, k]) | Construct a copy of a matrix with elements below the k-th diagonal zeroed. |

`scipy.linalg.`**`inv`**(*a*, *overwrite_a=False*)

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.

**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

```
>>> a = np.array([[1., 2.], [3., 4.]])
>>> sp.linalg.inv(a)
array([[-2. ,  1. ],
       [ 1.5, -0.5]])
>>> np.dot(a, sp.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*)

Solve the equation a x = b for x

**Parameters**

**a** : array, shape (M, M)

**b** : array, shape (M,) or (M, N)

**sym_pos** : boolean

Assume a is symmetric and positive definite

**lower** : boolean

Use only data contained in the lower triangle of a, if sym_pos is true. Default is to use upper triangle.

**overwrite_a** : boolean

Allow overwriting data in a (may enhance performance)

**overwrite_b** : boolean

Allow overwriting data in b (may enhance performance)

**Returns**

**x** : array, shape (M,) or (M, N) depending on b

Solution to the system a x = b

**Raises LinAlgError if a is singular** :

`scipy.linalg.solve_banded`(*(l, u)*, *ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *debug=False*)

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** : array, shape (l+u+1, M)

Banded matrix

**b** : array, shape (M,) or (M, K)

Right-hand side

**overwrite_ab** : boolean

Discard data in ab (may enhance performance)

**overwrite_b** : boolean

Discard data in b (may enhance performance)

**Returns**

**x** : array, shape (M,) or (M, K)

The solution to the system a x = b

`scipy.linalg.`**`solveh_banded`**(*ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *lower=False*)

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** : array, shape (u + 1, M)

Banded matrix

**b** : array, shape (M,) or (M, K)

Right-hand side

**overwrite_ab** : boolean

Discard data in ab (may enhance performance)

**overwrite_b** : boolean

Discard data in b (may enhance performance)

**lower** : boolean

Is the matrix in the lower form. (Default is upper form)

**Returns**

**x** : array, shape (M,) or (M, K)

The solution to the system a x = b

`scipy.linalg.`**`solve_triangular`**(*a*, *b*, *trans=0*, *lower=False*, *unit_diagonal=False*, *overwrite_b=False*, *debug=False*)

Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.

**Parameters**

**a** : array, shape (M, M)

**b** : array, shape (M,) or (M, N)

**lower** : boolean

Use only data contained in the lower triangle of a. Default is to use upper triangle.

**trans** : {0, 1, 2, 'N', 'T', 'C'}

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** : boolean

If True, diagonal elements of A are assumed to be 1 and will not be referenced.

**overwrite_b** : boolean

Allow overwriting data in b (may enhance performance)

**Returns**

**x** : array, shape (M,) or (M, N) depending on b

Solution to the system a x = b

**Raises**

**LinAlgError** :

If a is singular

## Notes

New in version 0.9.0.

`scipy.linalg.`**`det`**`(`*a*, *overwrite_a=False*`)`

Compute the determinant of a matrix

**Parameters**

**a** : array, shape (M, M)

**Returns**

**det** : float or complex

Determinant of a

## Notes

The determinant is computed via LU factorization, LAPACK routine z/dgetrf.

`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**

**x** : array_like, shape (M,) or (M, N)

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**

**n** : 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 [R32]:

$$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$$

### References

[R32]

### Examples

```
>>> from numpy import linalg as LA
>>> 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]])

>>> LA.norm(a)
7.745966692414834
>>> LA.norm(b)
7.745966692414834
>>> LA.norm(b, 'fro')
7.745966692414834
>>> LA.norm(a, np.inf)
4
>>> LA.norm(b, np.inf)
9
>>> LA.norm(a, -np.inf)
0
>>> LA.norm(b, -np.inf)
2

>>> LA.norm(a, 1)
20
>>> LA.norm(b, 1)
7
>>> LA.norm(a, -1)
```

```
-4.6566128774142013e-010
>>> LA.norm(b, -1)
6
>>> LA.norm(a, 2)
7.745966692414834
>>> LA.norm(b, 2)
7.3484692283495345

>>> LA.norm(a, -2)
nan
>>> LA.norm(b, -2)
1.8570331885190563e-016
>>> LA.norm(a, 3)
5.8480354764257312
>>> LA.norm(a, -3)
nan
```

`scipy.linalg.`**`lstsq`**(*a*, *b*, *cond=None*, *overwrite_a=False*, *overwrite_b=False*)

Compute least-squares solution to equation Ax = b.

Compute a vector x such that the 2-norm `|b - A x|` is minimized.

**Parameters**

**a** : array, shape (M, N)

Left hand side matrix (2-D array).

**b** : array, shape (M,) or (M, K)

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.

**Returns**

**x** : array, shape (N,) or (N, K) depending on shape of b

Least-squares solution.

**residues** : ndarray, shape () or (1,) or (K,)

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** : array, shape (min(M,N),)

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*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using a least-squares solver.

**Parameters**

**a** : array, shape (M, N)

Matrix to be pseudo-inverted

**cond, rcond** : float

Cutoff for 'small' singular values in the least-squares solver. Singular values smaller than rcond*largest_singular_value are considered zero.

**Returns**

**B** : array, shape (N, M)

**Raises LinAlgError if computation does not converge** :

## Examples

```
>>> from numpy import *
>>> a = random.randn(9, 6)
>>> B = linalg.pinv(a)
>>> allclose(a, dot(a, dot(B, a)))
True
>>> allclose(B, dot(B, dot(a, B)))
True
```

`scipy.linalg.`**`pinv2`**(*a*, *cond=None*, *rcond=None*)

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** : array, shape (M, N)

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.

**Returns**

**B** : array, shape (N, M)

**Raises LinAlgError if SVD computation does not converge** :

### Examples

```
>>> from numpy import *
>>> a = random.randn(9, 6)
>>> B = linalg.pinv2(a)
>>> allclose(a, dot(a, dot(B, a)))
True
>>> allclose(B, dot(B, dot(a, B)))
True
```

`scipy.linalg.kron(a, b)`

Kronecker product of a and b.

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** : array, shape (M, N)

**b** : array, shape (P, Q)

**Returns**

**A** : array, shape (M*P, N*Q)

Kronecker product of a and b

### Examples

```
>>> from scipy import kron, array
>>> 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)`

Construct a copy of a matrix with elements above the k-th diagonal zeroed.

**Parameters**

**m** : array

Matrix whose elements to return

**k** : integer

Diagonal above which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

**Returns**

**A** : array, shape m.shape, dtype m.dtype

### 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*`)`

Construct a copy of a matrix with elements below the k-th diagonal zeroed.

**Parameters**

**m** : array

Matrix whose elements to return

**k** : integer

Diagonal below which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

**Returns**

**A** : array, shape m.shape, dtype m.dtype

### Examples

```
>>> from scipy.linalg import tril
>>> 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]])
```

## 4.9.2 Eigenvalue Problems

| | |
|---|---|
| `eig`(a[, b, left, right, overwrite_a, ...]) | Solve an ordinary or generalized eigenvalue problem of a square matrix. |
| `eigvals`(a[, b, overwrite_a]) | 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 |
| `eigvalsh`(a[, b, lower, overwrite_a, ...]) | Solve an ordinary or generalized eigenvalue problem for a complex |
| `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*`)`

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 Hermitean conjugation.

**Parameters**

**a** : array, shape (M, M)

A complex or real matrix whose eigenvalues and eigenvectors will be computed.

**b** : array, shape (M, M)

Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

**left** : boolean

Whether to calculate and return left eigenvectors

**right** : boolean

Whether to calculate and return right eigenvectors

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**overwrite_b** : boolean

Whether to overwrite data in b (may improve performance)

**Returns**

**w** : double or complex array, shape (M,)

The eigenvalues, each repeated according to its multiplicity.

**(if left == True)** :

**vl** : double or complex array, shape (M, M)

The normalized left eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

**(if right == True)** :

**vr** : double or complex array, shape (M, M)

The normalized right eigenvector corresponding to the eigenvalue w[i] is the column vr[:,i].

**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*)

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** : array, shape (M, M)

A complex or real matrix whose eigenvalues and eigenvectors will be computed.

**b** : array, shape (M, M)

Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**Returns**

**w** : double or complex array, shape (M,)

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 Hemitiean arrays

**eig**
: eigenvalues and right eigenvectors of general arrays

**eigh**
: eigenvalues and eigenvectors of symmetric/Hermitean arrays.

`scipy.linalg.`**`eigh`**(*a*, *b=None*, *lower=True*, *eigvals_only=False*, *overwrite_a=False*, *overwrite_b=False*, *turbo=True*, *eigvals=None*, *type=1*)

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** : array, shape (M, M)

A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

**b** : array, shape (M, M)

A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

**lower** : boolean

Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

**eigvals_only** : boolean

Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)

**turbo** : boolean

Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

**eigvals** : tuple (lo, hi)

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: integer** :

**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** : boolean

Whether to overwrite data in a (may improve performance)

**overwrite_b** : boolean

Whether to overwrite data in b (may improve performance)

**Returns**

**w** : real array, shape (N,)

The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

**(if eigvals_only == False)** :

**v** : complex array, shape (M, N)

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*)

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** : array, shape (M, M)

A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

**b** : array, shape (M, M)

A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

**lower** : boolean

Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

**turbo** : boolean

Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

**eigvals** : tuple (lo, hi)

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: integer** :

**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** : boolean

Whether to overwrite data in a (may improve performance)

**overwrite_b** : boolean

Whether to overwrite data in b (may improve performance)

**Returns**

**w** : real array, shape (N,)

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*)

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 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**

**a_band** : array, shape (M, u+1)

Banded matrix whose eigenvalues to calculate

**lower** : boolean

Is the matrix in the lower form. (Default is upper form)

**eigvals_only** : boolean

Compute only the eigenvalues and no eigenvectors. (Default: calculate also eigenvectors)

**overwrite_a_band:** :

Discard data in a_band (may enhance performance)

**select: {'a', 'v', 'i'}** :

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)

Range of selected eigenvalues

**max_ev** : integer

For select=='v', maximum number of eigenvalues expected. For other values of select, has no meaning.

In doubt, leave this parameter untouched.

**Returns**

**w** : array, shape (M,)

The eigenvalues, in ascending order, each repeated according to its multiplicity.

**v** : double or complex double array, shape (M, M)

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*)

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 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**

**a_band** : array, shape (M, u+1)

Banded matrix whose eigenvalues to calculate

**lower** : boolean

Is the matrix in the lower form. (Default is upper form)

**overwrite_a_band:** :

Discard data in a_band (may enhance performance)

**select: {'a', 'v', 'i'}** :

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)

Range of selected eigenvalues

**Returns**

**w** : array, shape (M,)

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

### 4.9.3 Decompositions

| | |
|---|---|
| lu(a[, permute_l, overwrite_a]) | Compute pivoted LU decompostion of a matrix. |
| lu_factor(a[, overwrite_a]) | Compute pivoted LU decomposition of a matrix. |
| lu_solve((lu, piv), b[, trans, overwrite_b]) | Solve an equation system, a x = b, given the LU factorization of a |
| svd(a[, full_matrices, compute_uv, overwrite_a]) | Singular Value Decomposition. |
| svdvals(a[, overwrite_a]) | 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]) | Compute the Cholesky decomposition of a matrix. |
| cholesky_banded(ab[, overwrite_ab, lower]) | Cholesky decompose a banded Hermitian positive-definite matrix |
| cho_factor(a[, lower, overwrite_a]) | Compute the Cholesky decomposition of a matrix, to use in cho_solve |
| cho_solve((c, lower), b[, overwrite_b]) | Solve the linear equations A x = b, given the Cholesky factorization of A. |
| cho_solve_banded((cb, lower), b[, overwrite_b]) | Solve the linear equations A x = b, given the Cholesky factorization of A. |
| qr(a[, overwrite_a, lwork, mode, pivoting]) | Compute QR decomposition of a matrix. |
| schur(a[, output, lwork, overwrite_a, sort]) | Compute Schur decomposition of a matrix. |
| rsf2csf(T, Z) | 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*)

Compute pivoted LU decompostion 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** : array, shape (M, N)

Array to decompose

**permute_l** : boolean

Perform the multiplication P*L (Default: do not permute)

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**Returns**

**(If permute_l == False)** :

**p** : array, shape (M, M)

Permutation matrix

**l** : array, shape (M, K)

Lower triangular or trapezoidal matrix with unit diagonal. K = min(M, N)

**u** : array, shape (K, N)

Upper triangular or trapezoidal matrix

**(If permute_l == True)** :

**pl** : array, shape (M, K)

Permuted L matrix. K = min(M, N)

**u** : array, shape (K, N)

Upper triangular or trapezoidal matrix

## Notes

This is a LU factorization routine written for Scipy.

`scipy.linalg.lu_factor(a, overwrite_a=False)`

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** : array, shape (M, M)

Matrix to decompose

**overwrite_a** : boolean

Whether to overwrite data in A (may increase performance)

**Returns**

**lu** : array, shape (N, N)

Matrix containing U in its upper triangle, and L in its lower triangle. The unit diagonal elements of L are not stored.

**piv** : array, shape (N,)

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, piv), b, trans=0, overwrite_b=False)`

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}

Type of system to solve:

| trans | system |
|---|---|
| 0 | a x = b |
| 1 | a^T x = b |
| 2 | a^H x = b |

**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*)
Singular Value Decomposition.

Factorizes the matrix a into two unitary matrices U and Vh and an 1d-array s of singular values (real, non-negative) such that a == U S Vh if S is an suitably shaped matrix of zeros whose main diagonal is s.

**Parameters**

**a** : array, shape (M, N)

Matrix to decompose

**full_matrices** : boolean

If true, U, Vh are shaped (M,M), (N,N) If false, the shapes are (M,K), (K,N) where K = min(M,N)

**compute_uv** : boolean

Whether to compute also U, Vh in addition to s (Default: true)

**overwrite_a** : boolean

Whether data in a is overwritten (may improve performance)

**Returns**

**U: array, shape (M,M) or (M,K) depending on full_matrices** :

**s: array, shape (K,)** :

The singular values, sorted so that s[i] >= s[i+1]. K = min(M, N)

**Vh: array, 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`
return singular values of a matrix

`diagsvd`
return the Sigma matrix, given the vector s

### Examples

```
>>> from scipy import random, linalg, allclose, dot
>>> a = random.randn(9, 6) + 1j*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)
>>> allclose(a, dot(U, dot(S, Vh)))
True

>>> s2 = linalg.svd(a, compute_uv=False)
>>> allclose(s, s2)
True
```

`scipy.linalg.`**`svdvals`**(*a*, *overwrite_a=False*)

Compute singular values of a matrix.

**Parameters**

**a** : array, shape (M, N)

Matrix to decompose

**overwrite_a** : boolean

Whether data in a is overwritten (may improve performance)

**Returns**

**s: array, shape (K,)** :

The singular values, sorted so that s[i] >= s[i+1]. K = min(M, N)

**Raises LinAlgError if SVD computation does not converge** :

**See Also:**

**`svd`**
return the full singular value decomposition of a matrix

**`diagsvd`**
return the Sigma matrix, given the vector s

`scipy.linalg.`**`diagsvd`**(*s*, *M*, *N*)

Construct the sigma matrix in SVD from singular values and size M,N.

**Parameters**

**s** : array, shape (M,) or (N,)

Singular values

**M** : integer

**N** : integer

Size of the matrix whose singular values are s

**Returns**

**S** : array, shape (M, N)

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** : array, shape (M, N)

**Returns**

**Q** : array, shape (M, K)

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*`)`

Compute the Cholesky decomposition of a matrix.

Returns the Cholesky decomposition, **:lm:‘A = L L^*‘** or **:lm:‘A = U^* U‘** of a Hermitian positive-definite matrix **:lm:‘A‘**.

**Parameters**

**a** : array, shape (M, M)

Matrix to be decomposed

**lower** : boolean

Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**Returns**

**c** : array, shape (M, M)

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*`)`

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** : array, shape (u + 1, M)

Banded matrix

**overwrite_ab** : boolean

Discard data in ab (may enhance performance)

**lower** : boolean

Is the matrix in the lower form. (Default is upper form)

**Returns**

**c** : array, shape (u+1, M)

Cholesky factorization of a, in the same banded format as ab

`scipy.linalg.`**`cho_factor`**`(`*a*, *lower=False*, *overwrite_a=False*`)`

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** : array, shape (M, M)

Matrix to be decomposed

**lower** : boolean

Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**Returns**

**c** : array, shape (M, M)

Matrix whose upper or lower triangle contains the Cholesky factor of *a*. Other parts of the matrix contain random data.

**lower** : boolean

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, lower)*, *b*, *overwrite_b=False*`)`

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

**Returns**

**x** : array

The solution to the system A x = b

**See Also:**

`cho_factor`
Cholesky factorization of a matrix

`scipy.linalg.`**`cho_solve_banded`**`(`*(cb, lower)*, *b*, *overwrite_b=False*`)`

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

If True, the function will overwrite the values in *b*.

**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.`**`qr`**(*a*, *overwrite_a=False*, *lwork=None*, *mode='full'*, *pivoting=False*)

Compute QR decomposition of a matrix.

Calculate the decomposition **:lm:'A = Q R'** where Q is unitary/orthogonal and R upper triangular.

**Parameters**

**a** : array, shape (M, N)

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'}

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).

**pivoting** : bool, optional

Whether or not factorization should include pivoting for rank-revealing qr decomposition. If pivoting, compute the decomposition **:lm:'A P = Q R'** as above, but where P is chosen such that the diagonal of R is non-increasing.

**Returns**

**Q** : double or complex ndarray

Of shape (M, M), or (M, K) for `mode='economic'`. Not returned if `mode='r'`.

**R** : double or complex ndarray

Of shape (M, N), or (K, N) for `mode='economic'`. `K = min(M, N)`.

**P** : integer 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, 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.`**`schur`**(*a*, *output='real'*, *lwork=None*, *overwrite_a=False*, *sort=None*)

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** : array, shape (M, M)

Matrix to decompose

**output** : {'real', 'complex'}

Construct the real or complex Schur decomposition (for real matrices).

**lwork** : integer

Work array size. If None or -1, it is automatically computed.

**overwrite_a** : boolean

Whether to overwrite data in a (may improve performance)

**sort** : {None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}

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).

**Returns**

**T** : array, shape (M, M)

Schur form of A. It is real-valued for the real Schur decomposition.

**Z** : array, shape (M, M)

An unitary Schur transformation matrix for A. It is real-valued for the real Schur decomposition.

**sdim** : integer

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*)

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** : array, shape (M, M)

Real Schur form of the original matrix

**Z** : array, shape (M, M)

Schur transformation matrix

**Returns**

**T** : array, shape (M, M)

Complex Schur form of the original matrix

**Z** : array, shape (M, M)

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*)

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 subdiagonal.

**Parameters**

**a** : array, shape (M,M)

Matrix to bring into Hessenberg form

**calc_q** : boolean

Whether to compute the transformation matrix

**overwrite_a** : boolean

Whether to ovewrite data in a (may improve performance)

**Returns**

**H** : array, shape (M,M)

Hessenberg form of A

**(If calc_q == True)** :

**Q** : array, shape (M,M)

Unitary/orthogonal similarity transformation matrix s.t. A = Q H Q^H

## 4.9.4 Matrix Functions

| | |
|---|---|
| `expm`(A[, q]) | Compute the matrix exponential using Pade approximation. |
| `expm2`(A) | Compute the matrix exponential using eigenvalue decomposition. |
| `expm3`(A[, q]) | Compute the matrix exponential using Taylor series. |
| `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]) | Matrix square root. |
| `funm`(A, func[, disp]) | Evaluate a matrix function specified by a callable. |

`scipy.linalg.`**`expm`**(*A*, *q=7*)

Compute the matrix exponential using Pade approximation.

**Parameters**

**A** : array, shape(M,M)

Matrix to be exponentiated

**q** : integer

Order of the Pade approximation

**Returns**

**expA** : array, shape(M,M)

Matrix exponential of A

`scipy.linalg.`**`expm2`**`(`*A*`)`

Compute the matrix exponential using eigenvalue decomposition.

**Parameters**

**A** : array, shape(M,M)

Matrix to be exponentiated

**Returns**

**expA** : array, shape(M,M)

Matrix exponential of A

`scipy.linalg.`**`expm3`**`(`*A*, *q=20*`)`

Compute the matrix exponential using Taylor series.

**Parameters**

**A** : array, shape(M,M)

Matrix to be exponentiated

**q** : integer

Order of the Taylor series

**Returns**

**expA** : array, shape(M,M)

Matrix exponential of A

`scipy.linalg.`**`logm`**`(`*A*, *disp=True*`)`

Compute matrix logarithm.

The matrix logarithm is the inverse of expm: expm(logm(A)) == A

**Parameters**

**A** : array, shape(M,M)

Matrix whose logarithm to evaluate

**disp** : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

**Returns**

**logA** : array, shape(M,M)

Matrix logarithm of A

**(if disp == False)** :

**errest** : float

1-norm of the estimated error, ||err||_1 / ||A||_1

`scipy.linalg.`**`cosm`**`(`*A*`)`

Compute the matrix cosine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**cosA** : array, shape(M,M)

Matrix cosine of A

`scipy.linalg.`**`sinm`**`(`*A*`)`

Compute the matrix sine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**sinA** : array, shape(M,M)

Matrix cosine of A

`scipy.linalg.`**`tanm`**`(`*A*`)`

Compute the matrix tangent.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**tanA** : array, shape(M,M)

Matrix tangent of A

`scipy.linalg.`**`coshm`**`(`*A*`)`

Compute the hyperbolic matrix cosine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**coshA** : array, shape(M,M)

Hyperbolic matrix cosine of A

`scipy.linalg.`**`sinhm`**`(`*A*`)`

Compute the hyperbolic matrix sine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**sinhA** : array, shape(M,M)

Hyperbolic matrix sine of A

`scipy.linalg.`**`tanhm`**`(`*A*`)`

Compute the hyperbolic matrix tangent.

This routine uses expm to compute the matrix exponentials.

**Parameters**
**A** : array, shape(M,M)

**Returns**
**tanhA** : array, shape(M,M)

Hyperbolic matrix tangent of A

`scipy.linalg.`**`signm`**`(`*a*, *disp=True*`)`
Matrix sign function.

Extension of the scalar sign(x) to matrices.

**Parameters**
**A** : array, shape(M,M)

Matrix at which to evaluate the sign function

**disp** : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

**Returns**
**sgnA** : array, shape(M,M)

Value of the sign function at A

**(if disp == False)** :

**errest** : float

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*`)`
Matrix square root.

**Parameters**
**A** : array, shape(M,M)

Matrix whose square root to evaluate

**disp** : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

**Returns**
**sgnA** : array, shape(M,M)

Value of the sign function at A

**(if disp == False)** :

**errest** : float

Frobenius norm of the estimated error, ||err||_F / ||A||_F

#### Notes

Uses algorithm by Nicholas J. Higham

`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** : array, shape(M,M)

Matrix at which to evaluate the function

**func** : callable

Callable object that evaluates a scalar function f. Must be vectorized (eg. using vectorize).

**disp** : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

**Returns**
**fA** : array, shape(M,M)

Value of the matrix function specified by func evaluated at A

**(if disp == False)** :

**errest** : float

1-norm of the estimated error, ||err||_1 / ||A||_1

### 4.9.5 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. |
| `hadamard`(n[, dtype]) | Construct a Hadamard matrix. |
| `hankel`(c[, r]) | Construct a Hankel matrix. |
| `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. |
| `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.

## Examples

```
>>> 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** : array_like

1-D array, the first column of the matrix.

**Returns**

**A** : array, shape (len(c), len(c))

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 [R29] associated with the polynomial whose coefficients are given in *a*.

**Parameters**

**a** : 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** : ndarray

A square array of shape `(n-1, n-1)`, where *n* is the length of *a*. 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

[R29]

## Examples

```
>>> from scipy.linalg import companion
>>> companion([1, -10, 31, -30])
array([[ 10., -31.,  30.],
       [  1.,   0.,   0.],
       [  0.,   1.,   0.]])
```

scipy.linalg.**hadamard**(*n*, *dtype=<type 'int'>*)

Construct a Hadamard matrix.

*hadamard(n)* 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** : numpy dtype

The data type of the array to be constructed.

**Returns**

**H** : ndarray with shape (n, n)

The Hadamard matrix.

### Notes

New in version 0.8.0.

### Examples

```
>>> 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, 1D

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** : array, shape (len(c), len(r))

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.`**`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** : ndarray with shape (n, n)

The Hilber matrix.

## Notes

New in version 0.10.0.

## Examples

```
>>> 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*.

**Parameters**
**n** : int

The order of the Hilbert matrix.

**exact** : bool

If False, the data type of the array that is returned in np.float64, and the array is an approximation of the inverse. If True, the array is exact integer 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** : ndarray with shape (n, n)

The data type of the array is np.float64 is 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.

## Notes

New in version 0.10.0.

## Examples

```
>>> 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** : array_like

The "fecundity" coefficients, has to be 1-D.

**s** : 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** : ndarray

Returns a 2-D ndarray of shape `(n, n)`, where *n* is the length of *f*. 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 [R30] [R31]. 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

[R30], [R31]

## Examples

```
>>> 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.**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

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** : array, shape (len(c), len(r))

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** : integer

The size of the first dimension of the matrix.

**M** : integer or None

The size of the second dimension of the matrix. If $M$ is None, $M = N$ is assumed.

**k** : integer

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

Data type of the matrix.

**Returns**

**A** : array, shape (N, M)

### 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]])
```

## 4.10 Maximum entropy models (`scipy.maxentropy`)

**Warning:** This module is deprecated in scipy 0.10, and will be removed in 0.11. Do not use this module in your new code. For questions about this deprecation, please ask on the scipy-dev mailing list.

### 4.10.1 Package content

Models:

| | |
|---|---|
| `model`([f, samplespace]) | A maximum-entropy (exponential-form) model on a discrete sample space. |
| `bigmodel`() | A maximum-entropy (exponential-form) model on a large sample space. |
| `basemodel`() | A base class providing generic functionality for both small and large maximum entropy models. |
| `conditionalmodel`(F, counts, numcontexts) | A conditional maximum-entropy (exponential-form) model p(x\|w) on a discrete sample space. |

**class** `scipy.maxentropy.`**`model`**(*f=None*, *samplespace=None*)

A maximum-entropy (exponential-form) model on a discrete sample space.

## Methods

| | |
|---|---|
| beginlogging(filename[, freq]) | Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... |
| clearcache() | Clears the interim results of computations depending on the |
| crossentropy(fx[, log_prior_x, base]) | Returns the cross entropy H(q, p) of the empirical |
| dual([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| endlogging() | Stop logging param values whenever setparams() is called. |
| entropydual([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| expectations() | The vector E_p[f(X)] under the model p_params of the vector of |
| fit(K[, algorithm]) | Fit the maxent model p whose feature expectations are given |
| grad([params, ignorepenalty]) | Computes or estimates the gradient of the entropy dual. |
| log(params) | This method is called every iteration during the optimization process. |
| lognormconst() | Compute the log of the normalization constant (partition |
| logparams() | Saves the model parameters if logging has been |
| logpmf() | Returns an array indexed by integers representing the |
| normconst() | Returns the normalization constant, or partition function, for the current model. |
| pmf() | Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params). |
| pmf_function([f]) | Returns the pmf p_theta(x) as a function taking values on the model's sample space. |
| probdist() | Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params). |
| reset([numfeatures]) | Resets the parameters self.params to zero, clearing the cache variables dependent on them. |
| setcallback([callback, callback_dual, ...]) | Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. |
| setfeaturesandsamplespace(f, samplespace) | Creates a new matrix self.F of features f of all points in the |
| setparams(params) | Set the parameter vector to params, replacing the existing parameters. |
| setsmooth(sigma) | Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. |

model.**beginlogging**(*filename*, *freq=10*)
Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... each 'freq' iterations.

model.**clearcache**()
Clears the interim results of computations depending on the parameters and the sample.

model.**crossentropy**(*fx*, *log_prior_x=None*, *base=2.718281828459045*)
Returns the cross entropy H(q, p) of the empirical distribution q of the data (with the given feature matrix fx) with respect to the model p. For discrete distributions this is defined as:

H(q, p) = - n^{-1} sum_{j=1}^n log p(x_j)

where x_j are the data elements assumed drawn from q whose features are given by the matrix fx = {f(x_j)}, j=1,...,n.

The 'base' argument specifies the base of the logarithm, which defaults to e.

For continuous distributions this makes no sense!

`model.`**`dual`**(*params=None*, *ignorepenalty=False*, *ignoretest=False*)

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**
L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`model.`**`endlogging`**()

Stop logging param values whenever setparams() is called.

`model.`**`entropydual`**(*params=None*, *ignorepenalty=False*, *ignoretest=False*)

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**
L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`model.`**`expectations`**`()`

The vector E_p[f(X)] under the model p_params of the vector of feature functions f_i over the sample space.

`model.`**`fit`**`(`*K*, *algorithm='CG'*`)`

Fit the maxent model p whose feature expectations are given by the vector K.

Model expectations are computed either exactly or using Monte Carlo simulation, depending on the 'func' and 'grad' parameters passed to this function.

For 'model' instances, expectations are computed exactly, by summing over the given sample space. If the sample space is continuous or too large to iterate over, use the 'bigmodel' class instead.

For 'bigmodel' instances, the model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo simulation). Simulation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model. This instrumental distribution is specified by calling setsampleFgen() with a user-supplied generator function that yields a matrix of features of a random sample and its log pdf values.

The algorithm can be 'CG', 'BFGS', 'LBFGSB', 'Powell', or 'Nelder-Mead'.

The CG (conjugate gradients) method is the default; it is quite fast and requires only linear space in the number of parameters, (not quadratic, like Newton-based methods).

The BFGS (Broyden-Fletcher-Goldfarb-Shanno) algorithm is a variable metric Newton method. It is perhaps faster than the CG method but requires O(N^2) instead of O(N) memory, so it is infeasible for more than about 10^3 parameters.

The Powell algorithm doesn't require gradients. For small models it is slow but robust. For big models (where func and grad are simulated) with large variance in the function estimates, this may be less robust than the gradient-based algorithms.

`model.`**`grad`**`(`*params=None*, *ignorepenalty=False*`)`

Computes or estimates the gradient of the entropy dual.

`model.`**`log`**`(`*params*`)`

This method is called every iteration during the optimization process. It calls the user-supplied callback function (if any), logs the evolution of the entropy dual and gradient norm, and checks whether the process appears to be diverging, which would indicate inconsistent constraints (or, for bigmodel instances, too large a variance in the estimates).

`model.`**`lognormconst`**`()`

Compute the log of the normalization constant (partition function) Z=sum_{x in samplespace} p_0(x) exp(params . f(x)). The sample space must be discrete and finite.

`model.`**`logparams`**`()`

Saves the model parameters if logging has been enabled and the # of iterations since the last save has reached self.paramslogfreq.

`model.`**`logpmf`**`()`

Returns an array indexed by integers representing the logarithms of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

`model.`**`normconst`**`()`

Returns the normalization constant, or partition function, for the current model. Warning – this may be too large to represent; if so, this will result in numerical overflow. In this case use lognormconst() instead.

For 'bigmodel' instances, estimates the normalization term as Z = E_aux_dist [{exp (params.f(X))} / aux_dist(X)] using a sample from aux_dist.

`model.`**`pmf`**`()`

Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

Equivalent to exp(self.logpmf())

`model.`**`pmf_function`**`(`*f=None*`)`

Returns the pmf p_theta(x) as a function taking values on the model's sample space. The returned pmf is defined as:

> p_theta(x) = exp(theta.f(x) - log Z)

where theta is the current parameter vector self.params. The returned function p_theta also satisfies

> all([p(x) for x in self.samplespace] == pmf()).

The feature statistic f should be a list of functions [f1(),...,fn(x)]. This must be passed unless the model already contains an equivalent attribute 'model.f'.

Requires that the sample space be discrete and finite, and stored as self.samplespace as a list or array.

`model.`**`probdist`**`()`

Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

Equivalent to exp(self.logpmf())

`model.`**`reset`**`(`*numfeatures=None*`)`

Resets the parameters self.params to zero, clearing the cache variables dependent on them. Also resets the number of function and gradient evaluations to zero.

`model.`**`setcallback`**`(`*callback=None*, *callback_dual=None*, *callback_grad=None*`)`

Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. All callback functions are passed one argument, the current model object.

Note that line search algorithms in e.g. CG make potentially several function and gradient evaluations per iteration, some of which we expect to be poor.

`model.`**`setfeaturesandsamplespace`**`(`*f*, *samplespace*`)`

Creates a new matrix self.F of features f of all points in the sample space. f is a list of feature functions f_i mapping the sample space to real values. The parameter vector self.params is initialized to zero.

We also compute f(x) for each x in the sample space and store them as self.F. This uses lots of memory but is much faster.

This is only appropriate when the sample space is finite.

`model.`**`setparams`**`(`*params*`)`

Set the parameter vector to params, replacing the existing parameters. params must be a list or numpy array of the same length as the model's feature vector f.

`model.`**`setsmooth`**`(`*sigma*`)`

Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. This 'smooths' the model to account for noise in the target expectation values or to improve robustness when using simulation to fit models and when the sampling distribution has high variance. The smoothing mechanism is described in Chen and Rosenfeld, 'A Gaussian prior for smoothing maximum entropy models' (1999).

The parameter 'sigma' will be squared and stored as self.sigma2.

**class** `scipy.maxentropy.`**`bigmodel`**

A maximum-entropy (exponential-form) model on a large sample space.

The model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo estimation). Approximation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model.

## Methods

| | |
|---|---|
| `beginlogging`(filename[, freq]) | Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... |
| `clearcache`() | Clears the interim results of computations depending on the |
| `crossentropy`(fx[, log_prior_x, base]) | Returns the cross entropy H(q, p) of the empirical |
| `dual`([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| `endlogging`() | Stop logging param values whenever setparams() is called. |
| `entropydual`([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| `estimate`() | This function approximates both the feature expectation vector |
| `expectations`() | Estimates the feature expectations E_p[f(X)] under the current |
| `fit`(K[, algorithm]) | Fit the maxent model p whose feature expectations are given |
| `grad`([params, ignorepenalty]) | Computes or estimates the gradient of the entropy dual. |
| `log`(params) | This method is called every iteration during the optimization process. |
| `lognormconst`() | Estimate the normalization constant (partition function) using |
| `logparams`() | Saves the model parameters if logging has been |
| `logpdf`(fx[, log_prior_x]) | Returns the log of the estimated density p(x) = p_theta(x) at the point x. |
| `normconst`() | Returns the normalization constant, or partition function, for the current model. |
| `pdf`(fx) | Returns the estimated density p_theta(x) at the point x with feature statistic fx = f(x). |
| `pdf_function`() | Returns the estimated density p_theta(x) as a function p(f) taking a vector f = f(x) of feature statistics at any point x. |
| `resample`() | (Re)samples the matrix F of sample features. |
| `reset`([numfeatures]) | Resets the parameters self.params to zero, clearing the cache variables dependent on them. |
| `setcallback`([callback, callback_dual, ...]) | Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. |
| `setparams`(params) | Set the parameter vector to params, replacing the existing parameters. |
| `setsampleFgen`(sampler[, staticsample]) | Initializes the Monte Carlo sampler to use the supplied |
| `setsmooth`(sigma) | Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. |
| `settestsamples`(F_list, logprob_list[, ...]) | Requests that the model be tested every 'testevery' iterations |
| `stochapprox`(K) | Tries to fit the model to the feature expectations K using |
| `test`() | Estimate the dual and gradient on the external samples, keeping track of the parameters that yield the minimum such dual. |

`bigmodel.`**`beginlogging`**(*filename*, *freq=10*)

Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... each 'freq' iterations.

`bigmodel.`**`clearcache`**`()`

Clears the interim results of computations depending on the parameters and the sample.

`bigmodel.`**`crossentropy`**`(`*fx*, *log_prior_x=None*, *base=2.718281828459045*`)`

Returns the cross entropy H(q, p) of the empirical distribution q of the data (with the given feature matrix fx) with respect to the model p. For discrete distributions this is defined as:

H(q, p) = - n^{-1} sum_{j=1}^n log p(x_j)

where x_j are the data elements assumed drawn from q whose features are given by the matrix fx = {f(x_j)}, j=1,...,n.

The 'base' argument specifies the base of the logarithm, which defaults to e.

For continuous distributions this makes no sense!

`bigmodel.`**`dual`**`(`*params=None*, *ignorepenalty=False*, *ignoretest=False*`)`

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**

L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**

Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`bigmodel.`**`endlogging`**`()`

Stop logging param values whenever setparams() is called.

`bigmodel.`**`entropydual`**`(`*params=None*, *ignorepenalty=False*, *ignoretest=False*`)`

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**

L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample.

Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`bigmodel.estimate()`

This function approximates both the feature expectation vector E_p f(X) and the log of the normalization term Z with importance sampling.

It also computes the sample variance of the component estimates of the feature expectations as: varE = var(E_1, ..., E_T) where T is self.matrixtrials and E_t is the estimate of E_p f(X) approximated using the 't'th auxiliary feature matrix.

It doesn't return anything, but stores the member variables logZapprox, mu and varE. (This is done because some optimization algorithms retrieve the dual fn and gradient fn in separate function calls, but we can compute them more efficiently together.)

It uses a supplied generator sampleFgen whose .next() method returns features of random observations s_j generated according to an auxiliary distribution aux_dist. It uses these either in a matrix (with multiple runs) or with a sequential procedure, with more updating overhead but potentially stopping earlier (needing fewer samples). In the matrix case, the features F={f_i(s_j)} and vector [log_aux_dist(s_j)] of log probabilities are generated by calling resample().

**We use [Rosenfeld01Wholesentence]'s estimate of E_p[f_i] as:**

**{sum_j p(s_j)/aux_dist(s_j) f_i(s_j) }**
/ {sum_j p(s_j) / aux_dist(s_j)}.

Note that this is consistent but biased.

**This equals:**

**{sum_j p_dot(s_j)/aux_dist(s_j) f_i(s_j) }**
/ {sum_j p_dot(s_j) / aux_dist(s_j)}

**Compute the estimator E_p f_i(X) in log space as:**
num_i / denom,

**where**

**num_i = exp(logsumexp(theta.f(s_j) - log aux_dist(s_j)**

- log f_i(s_j)))

**and**
denom = [n * Zapprox]

where Zapprox = exp(self.lognormconst()).

**We can compute the denominator n*Zapprox directly as:**

exp(logsumexp(log p_dot(s_j) - log aux_dist(s_j)))

= exp(logsumexp(theta.f(s_j) - log aux_dist(s_j)))

bigmodel.**expectations**()

Estimates the feature expectations E_p[f(X)] under the current model p = p_theta using the given sample feature matrix. If self.staticsample is True, uses the current feature matrix self.sampleF. If self.staticsample is False or self.matrixtrials is > 1, draw one or more sample feature matrices F afresh using the generator function supplied to sampleFgen().

bigmodel.**fit**(*K*, *algorithm='CG'*)

Fit the maxent model p whose feature expectations are given by the vector K.

Model expectations are computed either exactly or using Monte Carlo simulation, depending on the 'func' and 'grad' parameters passed to this function.

For 'model' instances, expectations are computed exactly, by summing over the given sample space. If the sample space is continuous or too large to iterate over, use the 'bigmodel' class instead.

For 'bigmodel' instances, the model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo simulation). Simulation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model. This instrumental distribution is specified by calling setsampleFgen() with a user-supplied generator function that yields a matrix of features of a random sample and its log pdf values.

The algorithm can be 'CG', 'BFGS', 'LBFGSB', 'Powell', or 'Nelder-Mead'.

The CG (conjugate gradients) method is the default; it is quite fast and requires only linear space in the number of parameters, (not quadratic, like Newton-based methods).

The BFGS (Broyden-Fletcher-Goldfarb-Shanno) algorithm is a variable metric Newton method. It is perhaps faster than the CG method but requires O(N^2) instead of O(N) memory, so it is infeasible for more than about 10^3 parameters.

The Powell algorithm doesn't require gradients. For small models it is slow but robust. For big models (where func and grad are simulated) with large variance in the function estimates, this may be less robust than the gradient-based algorithms.

bigmodel.**grad**(*params=None*, *ignorepenalty=False*)

Computes or estimates the gradient of the entropy dual.

bigmodel.**log**(*params*)

This method is called every iteration during the optimization process. It calls the user-supplied callback function (if any), logs the evolution of the entropy dual and gradient norm, and checks whether the process appears to be diverging, which would indicate inconsistent constraints (or, for bigmodel instances, too large a variance in the estimates).

bigmodel.**lognormconst**()

Estimate the normalization constant (partition function) using the current sample matrix F.

bigmodel.**logparams**()

Saves the model parameters if logging has been enabled and the # of iterations since the last save has reached self.paramslogfreq.

`bigmodel.`**`logpdf`**`(`*fx*, *log_prior_x=None*`)`

Returns the log of the estimated density p(x) = p_theta(x) at the point x. If log_prior_x is None, this is defined as:

> log p(x) = theta.f(x) - log Z

where f(x) is given by the (m x 1) array fx.

If, instead, fx is a 2-d (m x n) array, this function interprets each of its rows j=0,...,n-1 as a feature vector f(x_j), and returns an array containing the log pdf value of each point x_j under the current model.

log Z is estimated using the sample provided with setsampleFgen().

The optional argument log_prior_x is the log of the prior density p_0 at the point x (or at each point x_j if fx is 2-dimensional). The log pdf of the model is then defined as

> log p(x) = log p0(x) + theta.f(x) - log Z

and p then represents the model of minimum KL divergence D(p||p0) instead of maximum entropy.

`bigmodel.`**`normconst`**`()`

Returns the normalization constant, or partition function, for the current model. Warning – this may be too large to represent; if so, this will result in numerical overflow. In this case use lognormconst() instead.

For 'bigmodel' instances, estimates the normalization term as Z = E_aux_dist [{exp (params.f(X))} / aux_dist(X)] using a sample from aux_dist.

`bigmodel.`**`pdf`**`(`*fx*`)`

Returns the estimated density p_theta(x) at the point x with feature statistic fx = f(x). This is defined as

> p_theta(x) = exp(theta.f(x)) / Z(theta),

where Z is the estimated value self.normconst() of the partition function.

`bigmodel.`**`pdf_function`**`()`

Returns the estimated density p_theta(x) as a function p(f) taking a vector f = f(x) of feature statistics at any point x. This is defined as:

> p_theta(x) = exp(theta.f(x)) / Z

`bigmodel.`**`resample`**`()`

(Re)samples the matrix F of sample features.

`bigmodel.`**`reset`**`(`*numfeatures=None*`)`

Resets the parameters self.params to zero, clearing the cache variables dependent on them. Also resets the number of function and gradient evaluations to zero.

`bigmodel.`**`setcallback`**`(`*callback=None*, *callback_dual=None*, *callback_grad=None*`)`

Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. All callback functions are passed one argument, the current model object.

Note that line search algorithms in e.g. CG make potentially several function and gradient evaluations per iteration, some of which we expect to be poor.

`bigmodel.`**`setparams`**`(`*params*`)`

Set the parameter vector to params, replacing the existing parameters. params must be a list or numpy array of the same length as the model's feature vector f.

`bigmodel.`**`setsampleFgen`**`(`*sampler*, *staticsample=True*`)`

Initializes the Monte Carlo sampler to use the supplied generator of samples' features and log probabilities. This is an alternative to defining a sampler in terms of a (fixed size) feature matrix sampleF and accompanying vector samplelogprobs of log probabilities.

Calling sampler.next() should generate tuples (F, lp), where F is an (m x n) matrix of features of the n sample points x_1,...,x_n, and lp is an array of length n containing the (natural) log probability density (pdf or pmf) of each point under the auxiliary sampling distribution.

The output of sampler.next() can optionally be a 3-tuple (F, lp, sample) instead of a 2-tuple (F, lp). In this case the value 'sample' is then stored as a class variable self.sample. This is useful for inspecting the output and understanding the model characteristics.

If matrixtrials > 1 and staticsample = True, (which is useful for estimating variance between the different feature estimates), sampler.next() will be called once for each trial (0,...,matrixtrials) for each iteration. This allows using a set of feature matrices, each of which stays constant over all iterations.

We now insist that sampleFgen.next() return the entire sample feature matrix to be used each iteration to avoid overhead in extra function calls and memory copying (and extra code).

An alternative was to supply a list of samplers, sampler=[sampler0, sampler1, ..., sampler_{m-1}, samplerZ], one for each feature and one for estimating the normalization constant Z. But this code was unmaintained, and has now been removed (but it's in Ed's CVS repository :).

Example use: >>> import spmatrix >>> model = bigmodel() >>> def sampler(): ... n = 0 ... while True: ... f = spmatrix.ll_mat(1,3) ... f[0,0] = n+1; f[0,1] = n+1; f[0,2] = n+1 ... yield f, 1.0 ... n += 1 ... >>> model.setsampleFgen(sampler()) >>> type(model.sampleFgen) <type 'generator'> >>> [model.sampleF[0,i] for i in range(3)] [1.0, 1.0, 1.0]

We now set matrixtrials as a class property instead, rather than passing it as an argument to this function, where it can be written over (perhaps with the default function argument by accident) when we re-call this func (e.g. to change the matrix size.)

`bigmodel.`**`setsmooth`**`(`*sigma*`)`

Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. This 'smooths' the model to account for noise in the target expectation values or to improve robustness when using simulation to fit models and when the sampling distribution has high variance. The smoothing mechanism is described in Chen and Rosenfeld, 'A Gaussian prior for smoothing maximum entropy models' (1999).

The parameter 'sigma' will be squared and stored as self.sigma2.

`bigmodel.`**`settestsamples`**`(`*F_list*, *logprob_list*, *testevery=1*, *priorlogprob_list=None*`)`

Requests that the model be tested every 'testevery' iterations during fitting using the provided list F_list of feature matrices, each representing a sample {x_j} from an auxiliary distribution q, together with the corresponding log probabiltiy mass or density values log {q(x_j)} in logprob_list. This is useful as an external check on the fitting process with sample path optimization, which could otherwise reflect the vagaries of the single sample being used for optimization, rather than the population as a whole.

If self.testevery > 1, only perform the test every self.testevery calls.

If priorlogprob_list is not None, it should be a list of arrays of log(p0(x_j)) values, j = 0,. ..., n - 1, specifying the prior distribution p0 for the sample points x_j for each of the test samples.

`bigmodel.`**`stochapprox`**`(`*K*`)`

Tries to fit the model to the feature expectations K using stochastic approximation, with the Robbins-Monro stochastic approximation algorithm: theta_{k+1} = theta_k + a_k g_k - a_k e_k where g_k is the gradient vector (= feature expectations E - K) evaluated at the point theta_k, a_k is the sequence a_k = a_0 / k, where a_0 is some step size parameter defined as self.a_0 in the model, and e_k is an unknown error term representing the uncertainty of the estimate of g_k. We assume e_k has nice enough properties for the algorithm to converge.

`bigmodel.`**`test`**`()`

Estimate the dual and gradient on the external samples, keeping track of the parameters that yield the minimum such dual. The vector of desired (target) feature expectations is stored as self.K.

**class** `scipy.maxentropy.basemodel`

A base class providing generic functionality for both small and large maximum entropy models. Cannot be instantiated.

## Methods

| | |
|---|---|
| `beginlogging`(filename[, freq]) | Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... |
| `clearcache`() | Clears the interim results of computations depending on the |
| `crossentropy`(fx[, log_prior_x, base]) | Returns the cross entropy H(q, p) of the empirical |
| `dual`([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| `endlogging`() | Stop logging param values whenever setparams() is called. |
| `entropydual`([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| `fit`(K[, algorithm]) | Fit the maxent model p whose feature expectations are given |
| `grad`([params, ignorepenalty]) | Computes or estimates the gradient of the entropy dual. |
| `log`(params) | This method is called every iteration during the optimization process. |
| `logparams`() | Saves the model parameters if logging has been |
| `normconst`() | Returns the normalization constant, or partition function, for the current model. |
| `reset`([numfeatures]) | Resets the parameters self.params to zero, clearing the cache variables dependent on them. |
| `setcallback`([callback, callback_dual, ...]) | Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. |
| `setparams`(params) | Set the parameter vector to params, replacing the existing parameters. |
| `setsmooth`(sigma) | Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. |

`basemodel.`**`beginlogging`**(*filename*, *freq=10*)

Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... each 'freq' iterations.

`basemodel.`**`clearcache`**()

Clears the interim results of computations depending on the parameters and the sample.

`basemodel.`**`crossentropy`**(*fx*, *log_prior_x=None*, *base=2.718281828459045*)

Returns the cross entropy H(q, p) of the empirical distribution q of the data (with the given feature matrix fx) with respect to the model p. For discrete distributions this is defined as:

H(q, p) = - n^{-1} sum_{j=1}^n log p(x_j)

where x_j are the data elements assumed drawn from q whose features are given by the matrix fx = {f(x_j)}, j=1,...,n.

The 'base' argument specifies the base of the logarithm, which defaults to e.

For continuous distributions this makes no sense!

`basemodel.`**`dual`**(*params=None*, *ignorepenalty=False*, *ignoretest=False*)

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**
L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`basemodel.`**`endlogging`**`()`
Stop logging param values whenever setparams() is called.

`basemodel.`**`entropydual`**`(`*params=None*, *ignorepenalty=False*, *ignoretest=False*`)`
Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**
L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`basemodel.`**`fit`**`(`*K*, *algorithm='CG'*`)`
Fit the maxent model p whose feature expectations are given by the vector K.

Model expectations are computed either exactly or using Monte Carlo simulation, depending on the 'func' and 'grad' parameters passed to this function.

For 'model' instances, expectations are computed exactly, by summing over the given sample space. If the sample space is continuous or too large to iterate over, use the 'bigmodel' class instead.

For 'bigmodel' instances, the model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo simulation). Simulation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model. This instrumental distribution is specified by calling setsampleFgen() with a user-supplied generator function that yields a matrix of features of a random sample and its log pdf values.

The algorithm can be 'CG', 'BFGS', 'LBFGSB', 'Powell', or 'Nelder-Mead'.

The CG (conjugate gradients) method is the default; it is quite fast and requires only linear space in the number of parameters, (not quadratic, like Newton-based methods).

The BFGS (Broyden-Fletcher-Goldfarb-Shanno) algorithm is a variable metric Newton method. It is perhaps faster than the CG method but requires O(N^2) instead of O(N) memory, so it is infeasible for more than about 10^3 parameters.

The Powell algorithm doesn't require gradients. For small models it is slow but robust. For big models (where func and grad are simulated) with large variance in the function estimates, this may be less robust than the gradient-based algorithms.

`basemodel.`**`grad`**`(`*params=None*, *ignorepenalty=False*`)`
Computes or estimates the gradient of the entropy dual.

`basemodel.`**`log`**`(`*params*`)`
This method is called every iteration during the optimization process. It calls the user-supplied callback function (if any), logs the evolution of the entropy dual and gradient norm, and checks whether the process appears to be diverging, which would indicate inconsistent constraints (or, for bigmodel instances, too large a variance in the estimates).

`basemodel.`**`logparams`**`()`
Saves the model parameters if logging has been enabled and the # of iterations since the last save has reached self.paramslogfreq.

`basemodel.`**`normconst`**`()`
Returns the normalization constant, or partition function, for the current model. Warning – this may be too large to represent; if so, this will result in numerical overflow. In this case use lognormconst() instead.

For 'bigmodel' instances, estimates the normalization term as Z = E_aux_dist [{exp (params.f(X))} / aux_dist(X)] using a sample from aux_dist.

`basemodel.`**`reset`**`(`*numfeatures=None*`)`
Resets the parameters self.params to zero, clearing the cache variables dependent on them. Also resets the number of function and gradient evaluations to zero.

`basemodel.`**`setcallback`**`(`*callback=None*, *callback_dual=None*, *callback_grad=None*`)`
Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. All callback functions are passed one argument, the current model object.

Note that line search algorithms in e.g. CG make potentially several function and gradient evaluations per iteration, some of which we expect to be poor.

`basemodel.`**`setparams`**`(`*params*`)`
Set the parameter vector to params, replacing the existing parameters. params must be a list or numpy array of the same length as the model's feature vector f.

`basemodel.`**`setsmooth`**`(`*sigma*`)`
Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. This 'smooths' the model to account for noise in the target expectation values

or to improve robustness when using simulation to fit models and when the sampling distribution has high variance. The smoothing mechanism is described in Chen and Rosenfeld, 'A Gaussian prior for smoothing maximum entropy models' (1999).

The parameter 'sigma' will be squared and stored as self.sigma2.

**class** `scipy.maxentropy.`**`conditionalmodel`**(*F*, *counts*, *numcontexts*)

A conditional maximum-entropy (exponential-form) model p(x|w) on a discrete sample space.

This is useful for classification problems: given the context w, what is the probability of each class x?

The form of such a model is:

```
p(x | w) = exp(theta . f(w, x)) / Z(w; theta)
```

where Z(w; theta) is a normalization term equal to:

```
Z(w; theta) = sum_x exp(theta . f(w, x)).
```

The sum is over all classes x in the set Y, which must be supplied to the constructor as the parameter 'samplespace'.

Such a model form arises from maximizing the entropy of a conditional model p(x | w) subject to the constraints:

```
K_i = E f_i(W, X)
```

where the expectation is with respect to the distribution:

```
q(w) p(x | w)
```

where q(w) is the empirical probability mass function derived from observations of the context w in a training set. Normally the vector K = {K_i} of expectations is set equal to the expectation of f_i(w, x) with respect to the empirical distribution.

This method minimizes the Lagrangian dual L of the entropy, which is defined for conditional models as:

```
L(theta) = sum_w q(w) log Z(w; theta)
           - sum_{w,x} q(w,x) [theta . f(w,x)]
```

Note that both sums are only over the training set {w,x}, not the entire sample space, since q(w,x) = 0 for all w,x not in the training set.

The partial derivatives of L are:

```
dL / dtheta_i = K_i - E f_i(X, Y)
```

where the expectation is as defined above.

## Methods

| | |
|---|---|
| beginlogging(filename[, freq]) | Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... |
| clearcache() | Clears the interim results of computations depending on the |
| crossentropy(fx[, log_prior_x, base]) | Returns the cross entropy H(q, p) of the empirical |
| dual([params, ignorepenalty]) | The entropy dual function is defined for conditional models as |
| endlogging() | Stop logging param values whenever setparams() is called. |
| entropydual([params, ignorepenalty, ignoretest]) | Computes the Lagrangian dual L(theta) of the entropy of the |
| expectations() | The vector of expectations of the features with respect to the |
| fit([algorithm]) | Fits the conditional maximum entropy model subject to the |
| grad([params, ignorepenalty]) | Computes or estimates the gradient of the entropy dual. |
| log(params) | This method is called every iteration during the optimization process. |
| lognormconst() | Compute the elementwise log of the normalization constant |
| logparams() | Saves the model parameters if logging has been |
| logpmf() | Returns a (sparse) row vector of logarithms of the conditional probability mass function (pmf) values p(x \| c) for all pairs (c, x), where c are contexts and x are points in the sample space. |
| normconst() | Returns the normalization constant, or partition function, for the current model. |
| pmf() | Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params). |
| pmf_function([f]) | Returns the pmf p_theta(x) as a function taking values on the model's sample space. |
| probdist() | Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params). |
| reset([numfeatures]) | Resets the parameters self.params to zero, clearing the cache variables dependent on them. |
| setcallback([callback, callback_dual, ...]) | Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. |
| setfeaturesandsamplespace(f, samplespace) | Creates a new matrix self.F of features f of all points in the |
| setparams(params) | Set the parameter vector to params, replacing the existing parameters. |
| setsmooth(sigma) | Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. |

conditionalmodel.**beginlogging**(*filename*, *freq=10*)

Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... each 'freq' iterations.

conditionalmodel.**clearcache**()

Clears the interim results of computations depending on the parameters and the sample.

conditionalmodel.**crossentropy**(*fx*, *log_prior_x=None*, *base=2.718281828459045*)

Returns the cross entropy H(q, p) of the empirical distribution q of the data (with the given feature matrix fx) with respect to the model p. For discrete distributions this is defined as:

H(q, p) = - n^{-1} sum_{j=1}^n log p(x_j)

where x_j are the data elements assumed drawn from q whose features are given by the matrix fx =

{f(x_j)}, j=1,...,n.

The 'base' argument specifies the base of the logarithm, which defaults to e.

For continuous distributions this makes no sense!

`conditionalmodel.`**`dual`**(*params=None*, *ignorepenalty=False*)

The entropy dual function is defined for conditional models as

**L(theta) = sum_w q(w) log Z(w; theta)**

- sum_{w,x} q(w,x) [theta . f(w,x)]

or equivalently as

L(theta) = sum_w q(w) log Z(w; theta) - (theta . k)

where K_i = sum_{w, x} q(w, x) f_i(w, x), and where q(w) is the empirical probability mass function derived from observations of the context w in a training set. Normally q(w, x) will be 1, unless the same class label is assigned to the same context more than once.

Note that both sums are only over the training set {w,x}, not the entire sample space, since q(w,x) = 0 for all w,x not in the training set.

The entropy dual function is proportional to the negative log likelihood.

**Compare to the entropy dual of an unconditional model:**
L(theta) = log(Z) - theta^T . K

`conditionalmodel.`**`endlogging`**()

Stop logging param values whenever setparams() is called.

`conditionalmodel.`**`entropydual`**(*params=None*, *ignorepenalty=False*, *ignoretest=False*)

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

**This function is computed as:**
L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

**where**
Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

`conditionalmodel.`**`expectations`**()

The vector of expectations of the features with respect to the distribution p_tilde(w) p(x | w), where p_tilde(w) is the empirical probability mass function value stored as self.p_tilde_context[w].

conditionalmodel.**fit**(*algorithm='CG'*)
Fits the conditional maximum entropy model subject to the constraints

sum_{w, x} p_tilde(w) p(x | w) f_i(w, x) = k_i

**for i=1,...,m, where k_i is the empirical expectation**
k_i = sum_{w, x} p_tilde(w, x) f_i(w, x).

conditionalmodel.**grad**(*params=None*, *ignorepenalty=False*)
Computes or estimates the gradient of the entropy dual.

conditionalmodel.**log**(*params*)
This method is called every iteration during the optimization process. It calls the user-supplied callback function (if any), logs the evolution of the entropy dual and gradient norm, and checks whether the process appears to be diverging, which would indicate inconsistent constraints (or, for bigmodel instances, too large a variance in the estimates).

conditionalmodel.**lognormconst**()
Compute the elementwise log of the normalization constant (partition function) Z(w)=sum_{y in Y(w)} exp(theta . f(w, y)). The sample space must be discrete and finite. This is a vector with one element for each context w.

conditionalmodel.**logparams**()
Saves the model parameters if logging has been enabled and the # of iterations since the last save has reached self.paramslogfreq.

conditionalmodel.**logpmf**()
Returns a (sparse) row vector of logarithms of the conditional probability mass function (pmf) values p(x | c) for all pairs (c, x), where c are contexts and x are points in the sample space. The order of these is log p(x | c) = logpmf()[c * numsamplepoints + x].

conditionalmodel.**normconst**()
Returns the normalization constant, or partition function, for the current model. Warning – this may be too large to represent; if so, this will result in numerical overflow. In this case use lognormconst() instead.

For 'bigmodel' instances, estimates the normalization term as Z = E_aux_dist [{exp (params.f(X))} / aux_dist(X)] using a sample from aux_dist.

conditionalmodel.**pmf**()
Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

Equivalent to exp(self.logpmf())

conditionalmodel.**pmf_function**(*f=None*)
Returns the pmf p_theta(x) as a function taking values on the model's sample space. The returned pmf is defined as:

p_theta(x) = exp(theta.f(x) - log Z)

where theta is the current parameter vector self.params. The returned function p_theta also satisfies

all([p(x) for x in self.samplespace] == pmf()).

The feature statistic f should be a list of functions [f1(),...,fn(x)]. This must be passed unless the model already contains an equivalent attribute 'model.f'.

Requires that the sample space be discrete and finite, and stored as self.samplespace as a list or array.

conditionalmodel.**probdist**()
Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

Equivalent to exp(self.logpmf())

`conditionalmodel.`**`reset`**`(`*numfeatures=None*`)`

Resets the parameters self.params to zero, clearing the cache variables dependent on them. Also resets the number of function and gradient evaluations to zero.

`conditionalmodel.`**`setcallback`**`(`*callback=None*, *callback_dual=None*, *callback_grad=None*`)`

Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. All callback functions are passed one argument, the current model object.

Note that line search algorithms in e.g. CG make potentially several function and gradient evaluations per iteration, some of which we expect to be poor.

`conditionalmodel.`**`setfeaturesandsamplespace`**`(`*f*, *samplespace*`)`

Creates a new matrix self.F of features f of all points in the sample space. f is a list of feature functions f_i mapping the sample space to real values. The parameter vector self.params is initialized to zero.

We also compute f(x) for each x in the sample space and store them as self.F. This uses lots of memory but is much faster.

This is only appropriate when the sample space is finite.

`conditionalmodel.`**`setparams`**`(`*params*`)`

Set the parameter vector to params, replacing the existing parameters. params must be a list or numpy array of the same length as the model's feature vector f.

`conditionalmodel.`**`setsmooth`**`(`*sigma*`)`

Specifies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. This 'smooths' the model to account for noise in the target expectation values or to improve robustness when using simulation to fit models and when the sampling distribution has high variance. The smoothing mechanism is described in Chen and Rosenfeld, 'A Gaussian prior for smoothing maximum entropy models' (1999).

The parameter 'sigma' will be squared and stored as self.sigma2.

Utilities:

| | |
|---|---|
| `arrayexp`(x) | Returns the elementwise antilog of the real array x. |
| `arrayexpcomplex` | |
| `columnmeans`(A) | This is a wrapper for general dense or sparse dot products. |
| `columnvariances`(A) | This is a wrapper for general dense or sparse dot products. |
| `densefeaturematrix` | |
| `densefeatures` | |
| `dotprod` | |
| `flatten`(a) | Flattens the sparse matrix or dense array/matrix 'a' into a |
| `innerprod`(A, v) | This is a wrapper around general dense or sparse dot products. |
| `innerprodtranspose`(A, v) | This is a wrapper around general dense or sparse dot products. |
| `logsumexp`(a) | Compute the log of the sum of exponentials of input elements. |
| `logsumexp_naive` | |
| `robustlog` | |
| `rowmeans` | |
| `sample_wr` | |
| `sparsefeaturematrix`(f, sample[, format]) | Returns an (m x n) sparse matrix of non-zero evaluations of the scalar or vector functions f_1,...,f_m in the list f at the points x_1,...,x_n in the sequence 'sample'. |
| `sparsefeatures` | |

`scipy.maxentropy.`**`arrayexp`**`(`*x*`)`

Returns the elementwise antilog of the real array x.

We try to exponentiate with numpy.exp() and, if that fails, with python's math.exp(). numpy.exp() is about 10 times faster but throws an OverflowError exception for numerical underflow (e.g. exp(-800), whereas python's math.exp() just returns zero, which is much more helpful.

`scipy.maxentropy.`**`columnmeans`**`(`*A*`)`

This is a wrapper for general dense or sparse dot products.

It is only necessary as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns a dense (1 x n) vector with the column averages of A, which can be an (m x n) sparse or dense matrix.

```
>>> a = numpy.array([[1,2],[3,4]],'d')
>>> columnmeans(a)
array([ 2.,  3.])
```

`scipy.maxentropy.`**`columnvariances`**`(`*A*`)`

This is a wrapper for general dense or sparse dot products.

It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns a dense (1 x n) vector with unbiased estimators for the column variances for each column of the (m x n) sparse or dense matrix A. (The normalization is by (m - 1).)

```
>>> a = numpy.array([[1,2], [3,4]], 'd')
>>> columnvariances(a)
array([ 2.,  2.])
```

`scipy.maxentropy.`**`flatten`**`(`*a*`)`

Flattens the sparse matrix or dense array/matrix 'a' into a 1-dimensional array

`scipy.maxentropy.`**`innerprod`**`(`*A, v*`)`

This is a wrapper around general dense or sparse dot products.

It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns the inner product of the (m x n) dense or sparse matrix A with the n-element dense array v. This is a wrapper for A.dot(v) for dense arrays and spmatrix objects, and for A.matvec(v, result) for PySparse matrices.

`scipy.maxentropy.`**`innerprodtranspose`**`(`*A, v*`)`

This is a wrapper around general dense or sparse dot products.

It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Computes A^T V, where A is a dense or sparse matrix and V is a numpy array. If A is sparse, V must be a rank-1 array, not a matrix. This function is efficient for large matrices A. This is a wrapper for u.T.dot(v) for dense arrays and spmatrix objects, and for u.matvec_transp(v, result) for pysparse matrices.

`scipy.maxentropy.`**`logsumexp`**`(`*a*`)`

Compute the log of the sum of exponentials of input elements.

**Parameters**

**a** : array_like

Input array.

**Returns**

**res** : ndarray

The result, `np.log(np.sum(np.exp(a)))` calculated in a numerically more stable way.

**See Also:**

`numpy.logaddexp`, `numpy.logaddexp2`

#### Notes

Numpy has a logaddexp function which is very similar to `logsumexp`.

`scipy.maxentropy.`**`sparsefeaturematrix`**(*f*, *sample*, *format='csc_matrix'*)

Returns an (m x n) sparse matrix of non-zero evaluations of the scalar or vector functions f_1,...,f_m in the list f at the points x_1,...,x_n in the sequence 'sample'.

If format='ll_mat', the PySparse module (or a symlink to it) must be available in the Python site-packages/ directory. A trimmed-down version, patched for NumPy compatibility, is available in the SciPy sandbox/pysparse directory.

### 4.10.2 Usage information

Contains two classes for fitting maximum entropy models (also known as "exponential family" models) subject to linear constraints on the expectations of arbitrary feature statistics. One class, "model", is for small discrete sample spaces, using explicit summation. The other, "bigmodel", is for sample spaces that are either continuous (and perhaps high-dimensional) or discrete but too large to sum over, and uses importance sampling. conditional Monte Carlo methods.

The maximum entropy model has exponential form

$$p\left(x\right)=\exp\left(\frac{\theta^{T}f\left(x\right)}{Z\left(\theta\right)}\right)$$

with a real parameter vector theta of the same length as the feature statistic f(x), For more background, see, for example, Cover and Thomas (1991), *Elements of Information Theory*.

See the file bergerexample.py for a walk-through of how to use these routines when the sample space is small enough to be enumerated.

See bergerexamplesimulated.py for a a similar walk-through using simulation.

## 4.11 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.

| | |
|---|---|
| `bytescale`(data[, cmin, cmax, high, low]) | Byte scales an array (image). |
| `central_diff_weights`(Np[, ndiv]) | Return weights for an Np-point central derivative of order ndiv |
| `comb`(N, k[, exact]) | 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 point x0. |
| `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 file from a filename. |
| `imresize`(arr, size[, interp, mode]) | Resize an image. |
| `imrotate`(arr, angle[, interp]) | Rotate an image counter-clockwise by angle degrees. |
| `imsave`(name, arr) | 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 |
| `pade`(an, m) | Given Taylor series coefficients in an, return a Pade approximation to |
| `radon`(arr[, theta]) | |
| `toimage`(arr[, high, low, cmin, cmax, pal, ...]) | Takes a numpy array and returns a PIL image. The mode of the |

`scipy.misc.`**`bytescale`**(*data*, *cmin=None*, *cmax=None*, *high=255*, *low=0*)

Byte scales an array (image).

**Parameters**

**data** : ndarray

PIL image data array.

**cmin** : Scalar

Bias scaling of small values, Default is data.min().

**cmax** : scalar

Bias scaling of large values, Default is data.max().

**high** : scalar

Scale max value to *high*.

**low** : scalar

Scale min value to *low*.

**Returns**

**img_array** : ndarray

Bytescaled 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 of order ndiv assuming 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)

### Notes

Can be inaccurate for large number of points.

`scipy.misc.`**`comb`**(*N*, *k*, *exact=0*)

The number of combinations of N things taken k at a time. This is often expressed as “N choose k”.

**Parameters**

**N** : int, array

Number of things.

**k** : int, array

Number of elements taken.

**exact** : int, optional

If exact is 0, then floating point precision is used, otherwise exact long integer is computed.

**Returns**

**val** : int, array

The total number of combinations.

### Notes

•Array arguments accepted only for exact=0 case.

•If k > N, N < 0, or k < 0, then a 0 is returned.

### Examples

```
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> sc.comb(n, k, exact=False)
array([ 120.,  210.])
>>> sc.comb(10, 3, exact=True)
120L
```

`scipy.misc.`**`derivative`**(*func*, *x0*, *dx=1.0*, *n=1*, *args=()*, *order=3*)

Find the n-th derivative of a function at point x0.

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 nth 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 x2(x):
...     return x*x
...
>>> derivative(x2, 2)
4.0
```

scipy.misc.**factorial**(*n*, *exact=0*)

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=0 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

```
>>> arr = np.array([3,4,5])
>>> sc.factorial(arr, exact=False)
array([   6.,   24.,  120.])
>>> sc.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

```
>>> factorial2(7, exact=False)
array(105.00000000000001)
>>> factorial2(7, exact=True)
105L
```

`scipy.misc.`**`factorialk`**`(`*n*, *k*, *exact=1*`)`

n(!!...!) = multifactorial of order k k times

**Parameters**

**n** : int, array_like

Calculate multifactorial. Arrays are only supported with exact set to False. If n < 0, the return value is 0.

**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

```
>>> sc.factorialk(5, 1, exact=True)
120L
>>> sc.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 file from a filename.

**Parameters**

**name** : str

The file name 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 *name*.

## 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** : nd_array

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

Interpolation to use for re-sizing ('nearest', 'bilinear', 'bicubic' or 'cubic').

**mode** : str

The PIL image mode ('P', 'L', etc.).

**Returns**

**imresize** : ndarray

The resized array of image.

`scipy.misc.`**`imrotate`**(*arr*, *angle*, *interp='bilinear'*)

Rotate an image counter-clockwise by angle degrees.

**Parameters**

**arr** : nd_array

Input array of image to be rotated.

**angle** : float

The angle of rotation.

**interp** : str, optional

Interpolation

**Returns**

**imrotate** : nd_array

The rotated array of image.

### Notes

**Interpolation methods can be:**

- 'nearest' : for nearest neighbor
- 'bilinear' : for bilinear
- 'cubic' : cubic
- 'bicubic' : for bicubic

`scipy.misc.`**`imsave`**(*name*, *arr*)

Save an array as an image.

**Parameters**

**filename** : str

Output filename.

**image** : 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.

## 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 0x2b52d7ab81e0>, 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** :

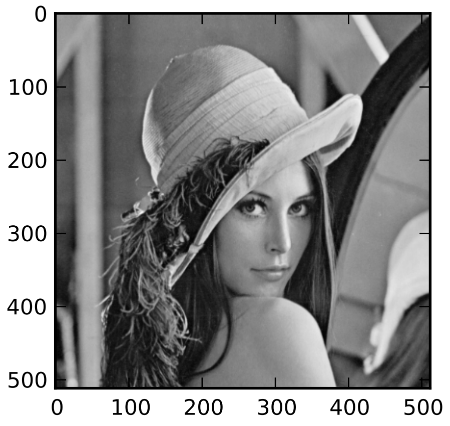
**Returns**

**lena** : ndarray

Lena image

### 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.`**`pade`**`(`*an*, *m*`)`

Given Taylor series coefficients in an, return a Pade approximation to the function as the ratio of two polynomials p / q where the order of q is m.

`scipy.misc.`**`radon`**`(`*arr*, *theta=None*`)`

`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, the pal keyword, and the mode keyword.

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

**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.

if the

The numpy array must be either 2 dimensional or 3 dimensional.

## 4.12 Multi-dimensional image processing (`scipy.ndimage`)

This package contains various functions for multi-dimensional image processing.

### 4.12.1 Filters `scipy.ndimage.filters`

| | |
|---|---|
| `convolve`(input, weights[, output, mode, ...]) | Multi-dimensional 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, ...]) | Multi-dimensional Gaussian filter. |
| `gaussian_filter1d`(input, sigma[, axis, ...]) | One-dimensional Gaussian filter. |
| `gaussian_gradient_magnitude`(input, sigma[, ...]) | Calculate a multidimensional gradient magnitude using gaussian derivatives. |
| `gaussian_laplace`(input, sigma[, output, ...]) | Calculate a 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) | Calculate a gradient magnitude using the provided function for the gradient. |
| `generic_laplace`(input, derivative2[, ...]) | Calculate a multidimensional laplace filter using the provided second derivative function. |
| `laplace`(input[, output, mode, cval]) | Calculate a multidimensional laplace filter using an estimation for the second derivative based on differences. |
| `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 multi-dimensional 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. |
| `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*)

Multi-dimensional 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** : scalar, 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** : integer, optional

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** :

`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** : integer, optional

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** :

`scipy.ndimage.filters.`**`gaussian_filter`**(*input*, *sigma*, *order=0*, *output=None*, *mode='reflect'*, *cval=0.0*)

Multi-dimensional 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

## Notes

The multi-dimensional 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*)

One-dimensional Gaussian filter.

**Parameters**

**input** : array-like

input array to filter

**sigma** : scalar

standard deviation for Gaussian kernel

**axis** : integer, optional

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

`scipy.ndimage.filters.`**`gaussian_gradient_magnitude`**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*)

Calculate a 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

`scipy.ndimage.filters.`**`gaussian_laplace`**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*)

Calculate a 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

`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** :

**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** : integer, optional

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** :

**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*)

Calculate a gradient magnitude using the provided function for the gradient.

**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*)

Calculate a multidimensional laplace filter using the 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*)

Calculate a multidimensional laplace filter using an estimation for the second derivative based on differences.

**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** :

`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 1D maximum

**axis** : integer, optional

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** :

`scipy.ndimage.filters.`**`median_filter`**(*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculates a multi-dimensional 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

`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** :

`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** : integer, optional

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** :

`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** :

`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** : integer, optional

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** : integer

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** :

`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** : integer, optional

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

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** :

## 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** : integer

length of uniform filter

**axis** : integer, optional

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** :

## 4.12.2 Fourier filters `scipy.ndimage.fourier`

| | |
|---|---|
| `fourier_ellipsoid`(input, size[, n, axis, output]) | Multi-dimensional ellipsoid fourier filter. |
| `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**

**return_value** : 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**

**return_value** : 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**

**return_value** : 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**

**return_value** : ndarray or None

The filtered input. If *output* is given as a parameter, None is returned.

## 4.12.3 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**

**return_value** : 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 arbitrary 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

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

```
>>> a = np.arange(12.).reshape((4, 3))
>>> def shift_func(output_coords):
...     return (output_coords[0] - 0.5, output_coords[1] - 0.5)
...
>>> sp.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**

**return_value** : 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**

**return_value** : 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**

**return_value** : 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**

**return_value** : 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**

**return_value** : ndarray or None

The zoomed input. If *output* is given as a parameter, None is returned.

## 4.12.4 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, along with their positions. |
| `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. |
| `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, |
| `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 |
| `watershed_ift`(input, markers[, structure, ...]) | Apply watershed from markers using a iterative forest 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.labels. 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.

**Returns**

**centerofmass** : tuple, or list of tuples

Co-ordinates of centers-of-masses.

### 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, 0.0), (1.0, 3.0), (3.0, 1.0)],
 [(1.0, 0.0), (2.0, 3.0), (3.0, 0.0)])
```

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.

**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 slices

A list of slices, one for the extent of each labeled object. 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]
```

`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*. *Labels* and *index* 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

**Returns**

**labeled_array** : array_like

An array-like object where each unique feature has a unique value

**num_features** : int

How many objects were found

**If 'output' is None or a data type, this function returns a tuple,** :

**('labeled_array', 'num_features').** :

**If 'output' is an array, 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 = 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.`**`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.

Labels must be None or an array of the same dimensions as the input.

Index must be None, a single label or sequence of labels. If none, all values where label is greater than zero are used.

`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**

**output** : 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.

Labels must be None or an array of the same dimensions as the input.

Index must be None, a single label or sequence of labels. If none, all values where label is greater than zero are used.

`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**

**std** : 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** : scalar or array_like, optional

A single label number or a sequence of label numbers of the objects to be measured.

**Returns**

**output** : list

A list of the sums of the values of *input* inside the regions defined by *labels*.

**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]
```

`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**

**vars** : 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 a iterative forest transform algorithm.

Negative markers are considered background markers which are processed after the other markers. A structuring element defining the connectivity of the object can be provided. If none is provided, an element is generated with a squared connectivity equal to one. An output array can optionally be provided.

## 4.12.5 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 footprint corresponding to a flat structuring element. |
| `grey_erosion`(input[, size, footprint, ...]) | Calculate a greyscale erosion, using either a structuring element, or a footprint corresponding to a flat structuring element. |
| `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**

**out** : 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* [R33] is a mathematical morphology operation [R34] 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

[R33], [R34]

## 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)

Value at the border in the output array.

**Returns**

**out** : 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 [R35] is a mathematical morphology operation [R36] 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

[R35], [R36]

## 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)** :

Value at the border in the output array.

**Returns**

**out: 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 [R37] is a mathematical morphology operation [R38] 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

[R37], [R38]

## 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

[R39]

## 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**

**output** : ndarray

Hit-or-miss transform of *input* with the given structuring element (*structure1*, *structure2*).

**See Also:**

ndimage.morphology, binary_erosion

### References

[R40]

### 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**

**out** : 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* [R41] is a mathematical morphology operation [R42] 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

[R41], [R42]

## 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

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

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.

**origin** : int or tuple of ints, optional

Placement of the filter, by default 0.

**Returns**

**ouput** : 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

[R43], [R44]

## 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.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

**See Also:**

`grey_opening`, `grey_closing`

### References

[R45], [R46]

`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). Three types of distance metric are supported: 'euclidean', 'taxicab' and '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.

This function employs a slow brute force algorithm, see also the function distance_transform_cdt for more efficient taxicab and chessboard algorithms.

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).

`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.

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 rank of the array. These choices correspond to the common interpretations of the taxicab and the chessboard distance metrics 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).

`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.

**distance** : 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**

**result** : ndarray or list of ndarray

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.rank(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* 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**

**output** : 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

[R47]

### 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* 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**

**output** : 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 [R48] is a *mathematical morphology* operation [R49].

## References

[R48], [R49]

## 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* 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 [R50] is a *mathematical morphology* operation [R51].

### References

[R50], [R51]

### 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* 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**

**output** : 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

[R52]

## 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**

**output: 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* 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**

**output** : 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

[R53]

### 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.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

`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.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

### 4.12.6 Utility

| | |
|---|---|
| `imread`(fname[, flatten]) | Load an image from file. |

`scipy.ndimage.`**`imread`**(*fname*, *flatten=False*)

Load an image from file.

**Parameters**

**fname** : str

Image file name, e.g. `test.jpg`.

**flatten** : bool, optional

If true, convert the output to grey-scale. Default is False.

**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.

## 4.13 Orthogonal distance regression (`scipy.odr`)

### 4.13.1 Package Content

| | |
|---|---|
| `odr`(fcn, beta0, y, x[, we, wd, fjacb, ...]) | |
| `ODR`(data, model[, beta0, delta0, ifixb, ...]) | The ODR class gathers all information and coordinates the running of the |
| `Data`(x[, y, we, wd, fix, meta]) | The Data class stores the data to fit. |
| `Model`(fcn[, fjacb, fjacd, extra_args, ...]) | The Model class stores information about the function you wish to fit. |
| `Output`(output) | The Output class stores the output of an ODR run. |
| `RealData`(x[, y, sx, sy, covx, covy, fix, meta]) | The RealData class stores the weightings as actual standard deviations |
| `odr_error` | |
| `odr_stop` | |

`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*)

**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

**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.

**output** : Output class instance

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.`**`Data`**(*x*, *y=None*, *we=None*, *wd=None*, *fix=None*, *meta={}*)
The Data class stores 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

Freeform 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.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 :

**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] = @f_l(X,B)/@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] = @f_l(X,B)/@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.`**`Output`**`(`*output*`)`
The Output class stores the output of an ODR run.

Takes one argument for initialization, the return value from the function `odr`.

### Notes

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.

**class** `scipy.odr.`**`RealData`**`(`*x, y=None, sx=None, sy=None, covx=None, covy=None, fix=None, meta={}*`)`
The RealData class stores the weightings as actual standard deviations and/or covariances.

The weights needed for ODRPACK are generated on-the-fly with __getattr__ trickery.

sx and sy are standard deviations of x and y and are converted to weights by dividing 1.0 by their squares.

E.g. 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.

**E.g. we[i] = numpy.linalg.inv(covy[i]) # i in range(len(covy))**
# if covy.shape == (n,q,q)

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.

**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 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.

### 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")

**exception** `scipy.odr.`**`odr_error`**

**exception** `scipy.odr.`**`odr_stop`**

## 4.13.2 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 [R157] 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.

odr provides two interfaces: a single function, and a set of high-level classes that wrap that function; please refer to their docstrings for more information. While the docstring of the function odr does not have a full explanation of its arguments, the classes do, and arguments of the same name usually have the same requirements. Furthermore, the user is urged to at least skim the ODRPACK User's Guide - "Know Thy Algorithm."

#### Use

See the docstrings of *odr.odrpack* and the functions and classes for usage instructions. The ODRPACK User's Guide (linked above) is also quite helpful.

#### References

## 4.14 Optimization and root finding (`scipy.optimize`)

### 4.14.1 Optimization

#### General-purpose

| | |
|---|---|
| `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. This 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. |
| `leastsq`(func, x0[, args, Dfun, full_output, ...]) | Minimize the sum of squares of a set of equations. |

`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

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.

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

Nelder, J.A. and Mead, R. (1965), "A simplex method for function minimization", The Computer Journal, 7, pp. 308-313 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.

`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

Extra arguments passed to func.

**callback** : callable

An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current parameter vector.

**direc** : ndarray

Initial direction set.

**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.

**Other Parameters**

**xtol** : float

Line-search error tolerance.

**ftol** : float

Relative error in `func(xopt)` acceptable for convergence.

**maxiter** : int

Maximum number of iterations to perform.

**maxfun** : int

Maximum number of function evaluations to make.

**full_output** : bool

If True, fopt, xi, direc, iter, funcalls, and warnflag are returned.

**disp** : bool

If True, print convergence messages.

**retall** : bool

If True, return a list of the solution at each iteration.

### 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.

**x0** : ndarray

Initial guess.

**fprime** : callable f'(x,*args)

Function which computes the gradient of f.

**args** : tuple

Extra arguments passed to f and fprime.

**gtol** : float

Stop when norm of gradient is less than gtol.

**norm** : float

Order of vector norm to use. -Inf is min, Inf is max.

**epsilon** : float or ndarray

If fprime is approximated, use this value for the step size (can be scalar or vector).

**callback** : callable

An optional user-supplied function, called after each iteration. Called as callback(xk), where xk is the current parameter vector.

**Returns**

**xopt** : ndarray

Parameters which minimize f, i.e. f(xopt) == fopt.

**fopt** : float

Minimum value found, f(xopt).

**func_calls** : int

The number of function_calls made.

**grad_calls** : int

The number of gradient calls made.

**warnflag** : int

1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing.

**allvecs** : ndarray

If retall is True (see other parameters below), then this vector containing the result at each iteration is returned.

**Other Parameters**

**maxiter** : int

Maximum number of iterations to perform.

**full_output** : bool

If True then return fopt, func_calls, grad_calls, and warnflag in addition to xopt.

**disp** : bool

Print convergence message if True.

**retall** : bool

Return a list of results at each iteration if True.

## Notes

Optimize the function, f, whose gradient is given by fprime using the nonlinear conjugate gradient algorithm of Polak and Ribiere. See Wright & Nocedal, 'Numerical Optimization', 1999, pg. 120-122.

`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)

Gradient of f.

**args** : tuple

Extra arguments passed to f and fprime.

**gtol** : float

Gradient norm must be less than gtol before succesful termination.

**norm** : float

Order of norm (Inf is max, -Inf is min)

**epsilon** : int or ndarray

If fprime is approximated, use this value for the step size.

**callback** : callable

An optional user-supplied function to call after each iteration. Called as callback(xk), where xk is the current parameter vector.

**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

Results at each iteration. Only returned if retall is True.

**Other Parameters**

**maxiter** : int

Maximum number of iterations to perform.

**full_output** : bool

If True,return fopt, func_calls, grad_calls, and warnflag in addition to xopt.

**disp** : bool

Print convergence message if True.

**retall** : bool

Return a list of results at each iteration if True.

## 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)

Function which computes the Hessian of f times an arbitrary vector, p.

**fhess** : callable fhess(x,*args)

Function to compute the Hessian matrix of f.

**args** : tuple

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

If fhess is approximated, use this value for the step size.

**callback** : callable

An optional user-supplied function which is called after each iteration. Called as callback(xk), where xk is the current parameter vector.

**Returns**

**xopt** : ndarray

Parameters which minimizer 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).

**Other Parameters**

**avextol** : float

Convergence is assumed when the average relative error in the minimizer falls below this amount.

**maxiter** : int

Maximum number of iterations to perform.

**full_output** : bool

If True, return the optional outputs.

**disp** : bool

If True, print convergence message.

**retall** : bool

If True, return a list of results at each iteration.

## 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 seperately.)

## References

Wright & Nocedal, 'Numerical Optimization', 1999, pg. 140.

`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=0.0*, *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.

**x0** : ndarray

The starting estimate for the minimization.

**args** : tuple

Any extra arguments to func are placed in this tuple.

**Dfun** : callable

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

non-zero to return all optional outputs.

**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.

**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.

**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.

**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 standard deviation 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
```

### Constrained (multivariate)

| | |
|---|---|
| `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 |
| `fmin_cobyla`(func, x0, cons[, args, ...]) | Minimize a function using the Constrained Optimization BY Linear |
| `fmin_slsqp`(func, x0[, eqcons, f_eqcons, ...]) | Minimize a function using Sequential Least SQuares Programming |
| `nnls`(A, b) | Solve `argmin_x || Ax - b ||_2` for `x>=0`. This is a wrapper |

`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*, *disp=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)

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

Arguments to pass to *func* and *fprime*.

**approx_grad** : bool

Whether to approximate the gradient numerically (in which case *func* returns only the function value).

**bounds** : list

`(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.

**m** : 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.

**pgtol** : float

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

Step size used when *approx_grad* is True, for numerically calculating the gradient

**iprint** : int

Controls the frequency of output. `iprint < 0` means no output.

**disp** : int, optional

If zero, then no output. If positive number, then this over-rides *iprint*.

**maxfun** : int

Maximum number of function evaluations.

**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,
  - 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.

### Notes

License of L-BFGS-B (Fortran code):

The version included here (in fortran code) is 2.1 (released in 1997). 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.

### 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, Vol 23, Num. 4, pp. 550 - 560.

`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*)

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 seperately as fprime 3. Return the function value and set approx_grad=True. If the function returns None, the minimization is aborted.

**x0** : list of floats

Initial estimate of minimum.

**fprime** : callable `fprime(x, *args)`

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

Arguments to pass to function.

**approx_grad** : bool

If true, approximate the gradient numerically.

**bounds** : list

(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** :

Used if approx_grad is True. The stepsize in a finite difference approximation for fprime.

**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 substract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

**messages :** :

Bit mask used to select messages display during minimization values defined in the MSGS dict. Defaults to MGS_ALL.

**disp** : int

Integer interface to messages. 0 = no message, 5 = all 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.

**maxfun** : int

Maximum number of function evaluation. if None, maxfun 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.

**fmin** : 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.

**pgtol** : float

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

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.

**Returns**

**x** : list of floats

The solution.

**nfeval** : int

The number of function evaluations.

**rc** : int

Return code as defined in the RCSTRINGS dict.

## 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.

### 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*)

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.

**args** : tuple

Extra arguments to pass to function.

**consargs** : tuple

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 :** :

Reasonable initial changes to the variables.

**rhoend :** :

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}

Controls the frequency of output; 0 implies no output. Deprecated.

**disp** : {0, 1, 2, 3}

Over-rides the iprint interface. Preferred.

**maxfun** : int

Maximum number of function evaluations.

**Returns**

**x** : ndarray

The argument that minimises *f*.

## 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]
...
>>> 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*)

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

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)

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

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)

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

A list of tuples specifying the lower and upper bound for each independent variable [(xl0, xu0),(xl1, xu1),...]

**fprime** : callable *f(x,*args)*

A function that evaluates the partial derivatives of func.

**fprime_eqcons** : callable *f(x,*args)*

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)*

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

Additional arguments passed to func and fprime.

**iter** : int

The maximum number of iterations.

**acc** : float

Requested accuracy.

**iprint** : int

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

Over-rides the iprint interface (preferred).

**full_output** : bool

If False, return only the minimizer of func (default). Otherwise, output final objective function and summary information.

**epsilon** : float

The step size for finite-difference derivative estimates.

**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.

## 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.`**`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

| | |
|---|---|
| `anneal`(func, x0[, args, schedule, ...]) | Minimize a function using simulated annealing. |
| `brute`(func, ranges[, args, Ns, full_output, ...]) | Minimize a function over a given range by brute force. |

`scipy.optimize.`**`anneal`** (*func*, *x0*, *args=()*, *schedule='fast'*, *full_output=0*, *T0=None*, *Tf=1e-12*, *maxeval=None*, *maxaccept=None*, *maxiter=400*, *boltzmann=1.0*, *learn_rate=0.5*, *feps=1e-06*, *quench=1.0*, *m=1.0*, *n=1.0*, *lower=-100*, *upper=100*, *dwell=50*)

Minimize a function using simulated annealing.

Schedule is a schedule class implementing the annealing schedule. Available ones are 'fast', 'cauchy', 'boltzmann'

**Parameters**

**func** : callable f(x, *args)

Function to be optimized.

**x0** : ndarray

Initial guess.

**args** : tuple

Extra parameters to *func*.

**schedule** : base_schedule

Annealing schedule to use (a class).

**full_output** : bool

Whether to return optional outputs.

**T0** : float

Initial Temperature (estimated as 1.2 times the largest cost-function deviation over random points in the range).

**Tf** : float

Final goal temperature.

**maxeval** : int

Maximum function evaluations.

**maxaccept** : int

Maximum changes to accept.

**maxiter** : int

Maximum cooling iterations.

**learn_rate** : float

Scale constant for adjusting guesses.

**boltzmann** : float

Boltzmann constant in acceptance test (increase for less stringent test at each temperature).

**feps** : float

Stopping relative error tolerance for the function value in last four coolings.

**quench, m, n** : float

Parameters to alter fast_sa schedule.

**lower, upper** : float or ndarray

Lower and upper bounds on *x*.

**dwell** : int

The number of times to search the space at each temperature.

**Returns**

**xmin** : ndarray

Point giving smallest value found.

**Jmin** : float

Minimum value of function found.

**T** : float

Final temperature.

**feval** : int

Number of function evaluations.

**iters** : int

Number of cooling iterations.

**accept** : int

Number of tests accepted.

**retval** : int

Flag indicating stopping condition:

```
0 : Points no longer changing
1 : Cooled to final temperature
2 : Maximum function evaluations
3 : Maximum cooling iterations reached
4 : Maximum accepted query locations reached
5 : Final point not the minimum amongst encountered points
```

## Notes

Simulated annealing is a random algorithm which uses no derivative information from the function being optimized. In practice it has been more useful in discrete optimization than continuous optimization, as there are usually better algorithms for continuous optimization problems.

Some experimentation by trying the difference temperature schedules and altering their parameters is likely required to obtain good performance.

The randomness in the algorithm comes from random sampling in numpy. To obtain the same results you can call numpy.random.seed with the same seed immediately before calling scipy.optimize.anneal.

We give a brief description of how the three temperature schedules generate new points and vary their temperature. Temperatures are only updated with iterations in the outer loop. The inner loop is over loop over xrange(dwell), and new points are generated for every iteration in the inner loop. (Though whether the proposed new points are accepted is probabilistic.)

For readability, let d denote the dimension of the inputs to func. Also, let x_old denote the previous state, and k denote the iteration number of the outer loop. All other variables not defined below are input variables to scipy.optimize.anneal itself.

In the 'fast' schedule the updates are

```
u ~ Uniform(0, 1, size=d)
y = sgn(u - 0.5) * T * ((1+ 1/T)**abs(2u-1) -1.0)
xc = y * (upper - lower)
x_new = x_old + xc

c = n * exp(-n * quench)
T_new = T0 * exp(-c * k**quench)
```

In the 'cauchy' schedule the updates are

```
u ~ Uniform(-pi/2, pi/2, size=d)
xc = learn_rate * T * tan(u)
x_new = x_old + xc

T_new = T0 / (1+k)
```

In the 'boltzmann' schedule the updates are

```
std = minimum( sqrt(T) * ones(d), (upper-lower) / (3*learn_rate) )
y ~ Normal(0, std, size=d)
x_new = x_old + learn_rate * y

T_new = T0 / log(1+k)
```

`scipy.optimize.`**`brute`**`(`*func*, *ranges*, *args=()*, *Ns=20*, *full_output=0*, *finish=<function fmin at 0x3a23f50>*`)`

Minimize a function over a given range by brute force.

**Parameters**

**func** : callable `f(x,*args)`

Objective function to be minimized.

**ranges** : tuple

Each element is a tuple of parameters or a slice object to be handed to `numpy.mgrid`.

**args** : tuple

Extra arguments passed to function.

**Ns** : int

Default number of samples, if those are not provided.

**full_output** : bool

If True, return the evaluation grid.

**finish** : callable, optional

An optimization function that is called with the result of brute force minimization as initial guess. *finish* should take the initial guess as positional argument, and take take *args*, *full_output* and *disp* as keyword arguments. See Notes for more details.

**Returns**

**x0** : ndarray

Value of arguments to *func*, giving minimum over the grid.

**fval** : int

Function value at minimum.

**grid** : tuple

Representation of the evaluation grid. It has the same length as x0.

**Jout** : ndarray

Function values over grid: `Jout = func(*grid)`.

### Notes

The range is respected by the brute force minimization, but if the *finish* keyword specifies another optimization function (including the default `fmin`), the returned value may still be (just) outside the range. In order to ensure the range is specified, use `finish=None`.

## Scalar function minimizers

| | |
|---|---|
| `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 minimum of the function isolated to a fractional precision of tol. |
| `golden`(func[, args, brack, tol, full_output]) | Given a function of one-variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol. |
| `bracket`(func[, xa, xb, args, grow_limit, ...]) | 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). |

`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

Extra arguments passed to function.

**xtol** : float

The convergence tolerance.

**maxfun** : int

Maximum number of function evaluations allowed.

**full_output** : bool

If True, return optional outputs.

**disp** : int

**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.

## 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** :

Additional arguments (if present).

**brack** : tuple

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.

**full_output** : bool

If True, return all output args (xmin, fval, iter, funcalls).

**Returns**

**xmin** : ndarray

Optimum point.

**fval** : float

Optimum value.

**iter** : int

Number of iterations.

**funcalls** : int

Number of objective function evaluations made.

### 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*)

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

Additional arguments (if present), passed to func.

**brack** : tuple

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

x tolerance stop criterion

**full_output** : bool

If True, return optional outputs.

### Notes

Uses analog of bisection method to decrease the bracketed interval.

`scipy.optimize.`**`bracket`**(*func*, *xa=0.0*, *xb=1.0*, *args=()*, *grow_limit=110.0*, *maxiter=1000*)

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

Bracketing interval.

**args** : tuple

Additional arguments (if present), passed to *func*.

**grow_limit** : float

Maximum grow limit.

**maxiter** : int

Maximum number of iterations to perform.

**Returns**

**xa, xb, xc** : float

Bracket.

**fa, fb, fc** : float

Objective function values in bracket.

**funcalls** : int

Number of function evaluations made.

### 4.14.2 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*, ***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 N-length sequence or an (k,N)-shaped array

for functions with k predictors. The independent variable where the data is measured.

**ydata** : N-length sequence

The dependent data — nominally f(xdata, ...)

**p0** : None, scalar, or M-length sequence

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 N-length sequence

If not None, it represents the standard-deviation of ydata. This vector, if given, will be used as weights in the least-squares problem.

**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.

**See Also:**

`leastsq`

### Notes

The algorithm uses the Levenburg-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

>>> x = np.linspace(0,4,50)
>>> y = func(x, 2.5, 1.3, 0.5)
>>> yn = y + 0.2*np.random.normal(size=len(x))

>>> popt, pcov = curve_fit(func, x, yn)
```

## 4.14.3 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 f in [a,b]. |
| `newton`(func, x0[, fprime, args, tol, maxiter]) | 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-Deker-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.

**maxiter** : number, optional

if convergence is not achieved in maxiter iterations, and 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**
`anneal`, `brute`

**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) can not 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.

**maxiter** : number, optional

if convergence is not achieved in maxiter iterations, and 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`, `anneal`, `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.

**maxiter** : number, optional

if convergence is not achieved in maxiter iterations, and 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 f in [a,b].

Basic bisection routine to find a zero of the function f between the arguments a and b. f(a) and f(b) can not 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.

**maxiter** : number, optional

if convergence is not achieved in maxiter iterations, and 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*)

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.

**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.

**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 while that of the secant method is somewhat less. This means that if the function is well behaved the actual error in the estimated zero is approximately the square 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 the point where func(x) == x |

`scipy.optimize.`**`fixed_point`**(*func*, *x0*, *args=()*, *xtol=1e-08*, *maxiter=500*)
Find the point where func(x) == x

Given a function of one or more variables and a starting point, find a fixed-point of the function: i.e. where func(x)=x.

Uses Steffensen's Method using Aitken's Del^2 convergence acceleration. See Burden, Faires, "Numerical Analysis", 5th edition, pg. 80

### Examples

```
>>> from numpy import sqrt, array
>>> from scipy.optimize import fixed_point
>>> def func(x, c1, c2):
        return sqrt(c1/(x+c2))
>>> c1 = array([10,12.])
>>> c2 = array([3, 5.])
>>> fixed_point(func, [1.2, 1.3], args=(c1,c2))
array([ 1.4920333 ,  1.37228132])
```

## Multidimensional

General nonlinear solvers:

| | |
|---|---|
| `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.`**`fsolve`**(*func*, *x0*, *args=()*, *fprime=None*, *full_output=0*, *col_deriv=0*, *xtol=1.49012e-08*, *maxfev=0*, *band=None*, *epsfcn=0.0*, *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

Any extra arguments to *func*.

**fprime** : callable(x)

A function to compute the Jacobian of *func* with derivatives across the rows. By default, the Jacobian will be estimated.

**full_output** : bool

If True, return optional outputs.

**col_deriv** : bool

Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

**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 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.

**Other Parameters**

**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`).

**epsfcn** : float

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

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.

## 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. Extra parameters:
  - `to_retain`': 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** : array-like

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

[vR]

`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. Extra parameters:
  - `to_retain`: 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** : array-like

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

[vR]

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,

```
>>> 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.

**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** : array-like

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 numerical differentiation:

$$Jv \approx (f(x + \omega * v/|v|) - f(x))/\omega$$

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 [KK], and for the LGMRES sparse inverse method, see [BJM].

### References

[KK], [BJM]

`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** : array-like

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** : array-like

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** : array-like

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** : array-like

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`

## 4.14.4 Utility Functions

| | |
|---|---|
| `line_search`(f, myfprime, xk, pk[, gfk, ...]) | Find alpha that satisfies strong Wolfe conditions. |
| `check_grad`(func, grad, x0, *args) | Check the correctness of a gradient function by comparing it against a finite-difference approximation of the gradient. |

`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 (can be None).

**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.

**Returns**

**alpha0** : float

Alpha for which `x_new = x0 + alpha * pk`.

**fc** : int

Number of function evaluations made.

**gc** : int

Number of gradient evaluations made.

### 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.`**`check_grad`**(*func*, *grad*, *x0*, **args*)

Check the correctness of a gradient function by comparing it against a 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 finite difference approximation of grad using func.

**args: optional** :

Extra arguments passed to func and grad

**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.

## 4.15 Nonlinear solvers

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.

### 4.15.1 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. |

### 4.15.2 Examples

#### 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.])
```

#### Large problem

Suppose that we needed to solve the following integrodifferential equation on the square $[0,1] \times [0,1]$:

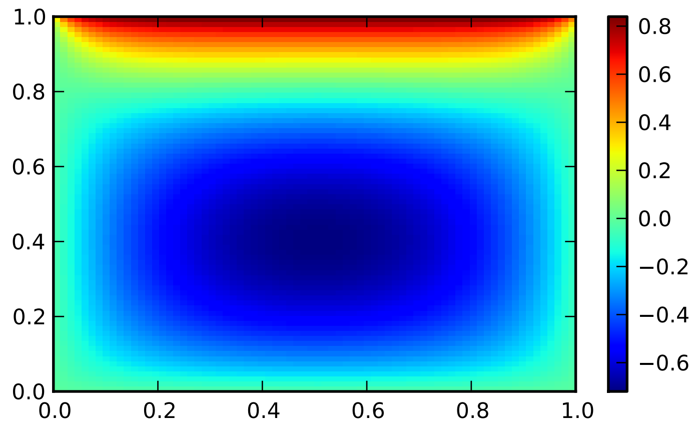
$$\nabla^2 P = 10 \left( \int_0^1 \int_0^1 \cosh(P)\, dx\, dy \right)^2$$

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', 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()
```



## 4.16 Signal processing (`scipy.signal`)

### 4.16.1 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. See convolve. |
| `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 output size determined by mode.

**Parameters**

**in1: array** :

first input.

**in2: array** :

second input. Should have the same number of dimensions as in1.

**mode: str {'valid', 'same', 'full'}** :

a string indicating the size of the output:

**`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.

**`full`**

[the output is the full discrete linear cross-correlation] of the inputs. (Default)

**Returns**

**out: array** :

an N-dimensional array containing a subset of the discrete linear cross-correlation of in1 with in2.

`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** :

first input.

**in2: array** :

second input. Should have the same number of dimensions as in1.

**mode: str {'valid', 'same', 'full'}** :

**a string indicating the size of the output:**

- '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.

- 'full': the output is the full discrete linear cross-correlation of the inputs. (Default)

**Returns**

**out: array** :

an N-dimensional array containing a subset of the discrete linear cross-correlation of in1 with in2.

## Notes

The correlation z of two arrays x and y of rank d is defined as

**z[...,k,...] = sum[..., i_l, ...]**
x[..., i_l,...] * conj(y[..., i_l + k,...])

`scipy.signal.`**`fftconvolve`**(*in1*, *in2*, *mode='full'*)
Convolve two N-dimensional arrays using FFT. See convolve.

`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** : ndarray

Two-dimensional input arrays to be convolved.

**mode: str, optional** :

A string indicating the size of the output:

**`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.

**`full`**
[the output is the full discrete linear cross-correlation] of the inputs. (Default)

**boundary** : str, 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*.

`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** : ndarray

Two-dimensional input arrays to be convolved.

**mode: str, optional** :

A string indicating the size of the output:

**`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.

**`full`**

[the output is the full discrete linear cross-correlation] of the inputs. (Default)

**boundary** : str, 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 cross-correlation of *in1* with *in2*.

`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.

## 4.16.2 B-splines

| | |
|---|---|
| `bspline`(x, n) | B-spline basis function of order n. |
| `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: |
| `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.`**`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.`**`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*.

## 4.16.3 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 {, ...) | Description: |
| `symiirorder2`((input, r, omega {, ...) | Description: |
| `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 steady state of the step response. |
| `filtfilt`(b, a, x[, axis, padtype, padlen]) | A forward-backward filter. |
| `deconvolve`(signal, divisor) | Deconvolves divisor out of signal. |
| `hilbert`(x[, N, axis]) | Compute the analytic signal. |
| `get_window`(window, Nx[, fftbins]) | Return a window of length *Nx* and type *window*. |
| `decimate`(x, q[, n, ftype, axis]) | Downsample the signal x by an integer factor q, using an order n 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

```
>>> import scipy.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]])
>>> sp.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.]])
>>> sp.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

Description:

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.

Inputs:

input – the input signal. c0, z1 – parameters in the transfer function. precision – specifies the precision for calculating initial conditions

of the recursive filter based on mirror-symmetric input.

Output:

output – filtered signal.

`scipy.signal.`**`symiirorder2`**(*input*, *r*, *omega {*, *precision}*) → output

Description:

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

Inputs:

input – the input signal. r, omega – parameters in the transfer function. precision – specifies the precision for calculating initial conditions

of the recursive filter based on mirror-symmetric input.

Output:

output – 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

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* = -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=None or is not given then initial rest is assumed. SEE signal.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 inital conditions on the state vector zi which is used by lfilter to generate the output given the input.

If M=len(b)-1 and N=len(a)-1. Then, the initial conditions are given in the vectors x and y as:

```
x = {x[-1],x[-2],...,x[-M]}
y = {y[-1],y[-2],...,y[-N]}
```

If x is not given, its inital conditions are assumed zero. If either vector is too short, then zeros are added to achieve the proper length.

The output vector zi contains:

```
zi = {z_0[-1], z_1[-1], ..., z_K-1[-1]}  where K=max(M,N).
```

`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 `scipy.signal.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*)

A forward-backward filter.

This function applies a linear filter twice, once forward and once backwards. The combined filter has linear phase.

Before applying the filter, the function can pad 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 end points. On both the forward and backwards passes, the initial condition of the filter is found by using lfilter_zi and scaling it by the end point of the extended data.

**Parameters**

**b** : array_like, 1-D

The numerator coefficient vector of the filter.

**a** : array_like, 1-D

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)).

**Returns**

**y** : ndarray

The filtered output, an array of type numpy.float64 with the same shape as *x*.

**See Also:**

`lfilter_zi`, `lfilter`

## Examples

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.

```
>>> from scipy.signal import butter
>>> b, a = butter(8, 0.125)
>>> y = 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.

`scipy.signal.`**`deconvolve`**(*signal*, *divisor*)

Deconvolves divisor out of signal.

`scipy.signal.`**`hilbert`**(*x*, *N=None*, *axis=-1*)

Compute the analytic signal.

The transformation is done along the last axis by default.

**Parameters**

**x** : array_like

Signal data

**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 *x(t)* is:

```
x_a = F^{-1}(F(x) 2U) = x + i y
```

where `F` is the Fourier transform, `U` the unit step function, and `y` the Hilbert transform of `x`. [R56]

*axis* argument is new in scipy 0.8.0.

### References

[R56]

`scipy.signal.`**`get_window`**`(`*window*, *Nx*, *fftbins=True*`)`

Return a window of length *Nx* and type *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).

### Notes

Window types:

boxcar, triang, blackman, hamming, hanning, bartlett, parzen, bohman, blackmanharris, nuttall, barthann, kaiser (needs beta), gaussian (needs std), general_gaussian (needs power, width), slepian (needs width), chebwin (needs attenuation)

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

```
>>> get_window('triang', 7)
array([ 0.25,  0.5 ,  0.75,  1.  ,  0.75,  0.5 ,  0.25])
>>> get_window(('kaiser', 4.0), 9)
array([ 0.08848053,  0.32578323,  0.63343178,  0.89640418,  1.        ,
        0.89640418,  0.63343178,  0.32578323,  0.08848053])
>>> 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.`**`decimate`**(*x*, *q*, *n=None*, *ftype='iir'*, *axis=-1*)

Downsample the signal x by an integer factor q, using an order n 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** : N-d array

the signal to be downsampled

**q** : int

the downsampling factor

**n** : int or None

the order of the filter (1 less than the length for 'fir')

**ftype** : {'iir' or 'fir'}

the type of the lowpass filter

**axis** : int

the axis along which to decimate

**Returns**

**y** : N-d array

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

```
>>> randgen = np.random.RandomState(9)
>>> npoints = 1e3
>>> noise = randgen.randn(npoints)
>>> x = 3 + 2*np.linspace(0, 1, npoints) + noise
>>> (sp.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.

## 4.16.4 Filter design

| | |
|---|---|
| `bilinear`(b, a[, fs]) | Return a digital filter from an analog one using a bilinear transform. |
| `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. |
| `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. |
| `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: r,p,k |

`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.`**`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

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

Desired window to use. See `scipy.signal.get_window` for a list of windows and required parameters.

**pass_zero** : bool

If True, the gain at the frequency 0 (i.e. the "DC gain") is 1. Otherwise the DC gain is 0.

**scale** : bool

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

Nyquist frequency. Each frequency in *cutoff* must be between 0 and *nyq*.

**Returns**

**h** : 1D 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:

```
>>> firwin(numtaps, f)
```

Use a specific window function:

```
>>> firwin(numtaps, f, window='nuttall')
```

High-pass ('stop' from 0 to f):

```
>>> firwin(numtaps, f, pass_zero=False)
```

Band-pass:

```
>>> firwin(numtaps, [f1, f2], pass_zero=False)
```

Band-stop:

```
>>> firwin(numtaps, [f1, f2])
```

Multi-band (passbands are [0, f1], [f2, f3] and [f4, 1]):

```
>>>firwin(numtaps, [f1, f2, f3, f4])
```

Multi-band (passbands are [f1, f2] and [f3,f4]):

```
>>> 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

Nyquist frequency. Each frequency in *freq* must be between 0 and *nyq* (inclusive).

**antisymmetric** : bool

Flag setting wither resulting impulse responce is symmetric/antisymmetric. See Notes for more details.

**Returns**

**taps** : numpy 1D array of length *numtaps*

The filter coefficients of the FIR filter.

**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

[R54], [R55]

### 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:

```
>>> taps = 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, the compute at that many frequencies. Otherwise, compute the response at frequencies given in worN.

**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 `freqs`.

**Returns**

**w** : ndarray

The 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.

`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}, optional

If None, then compute at 512 frequencies around the unit circle. If a single integer, the compute at that many frequencies. Otherwise, compute the response at frequencies given in worN

**whole** : bool, optional

Normally, frequencies are computed from 0 to pi (upper-half of unit-circle. If whole is True, compute frequencies from 0 to 2*pi.

**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 frequencies at which h was computed.

**h** : ndarray

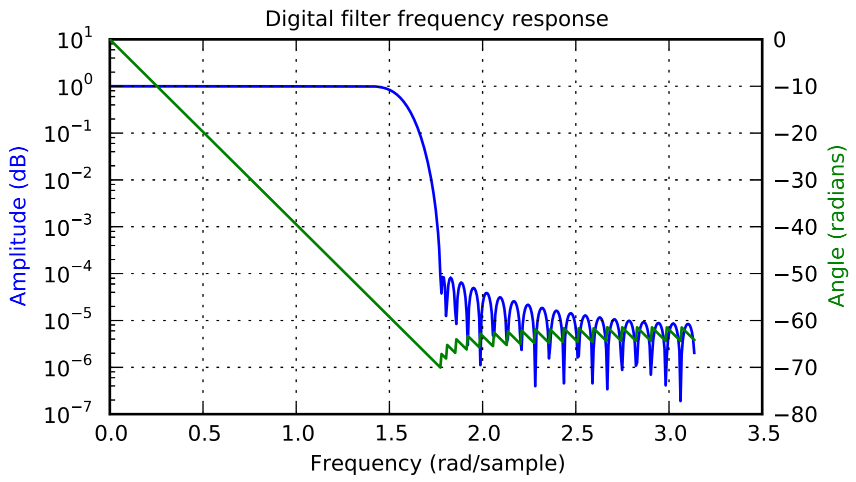
The frequency response.

## 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.

## Examples

```
>>> import scipy.signal
>>> b = sp.signal.firwin(80, 0.5, window=('kaiser', 8))
>>> h, w = sp.signal.freqz(b)

>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.title('Digital filter frequency response')
>>> ax1 = fig.add_subplot(111)

>>> plt.semilogy(h, np.abs(w), 'b')
>>> plt.ylabel('Amplitude (dB)', color='b')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.legend()

>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(w))
>>> plt.plot(h, angles, 'g')
>>> plt.ylabel('Angle (radians)', color='g')
>>> plt.show()
```



`scipy.signal.`**`iirdesign`**(*wp*, *ws*, *gpass*, *gstop*, *analog=0*, *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') or pole-zero ('zpk') form.

**Parameters**

**wp, ws** : float

Passband and stopband edge frequencies, normalized from 0 to 1 (1 corresponds to pi radians / 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]

**gpass** : float

The maximum loss in the passband (dB).

**gstop** : float

The minimum attenuation in the stopband (dB).

**analog** : int, optional

Non-zero to design an analog filter (in this case *wp* and *ws* are in radians / second).

**ftype** : str, optional

The type of IIR filter to design:

- elliptic : 'ellip'
- Butterworth : 'butter',
- Chebyshev I : 'cheby1',
- Chebyshev II: 'cheby2',
- Bessel : 'bessel'

**output** : ['ba', 'zpk'], optional

Type of output: numerator/denominator ('ba') or pole-zero ('zpk'). Default is 'ba'.

**Returns**

**b, a :** :

Numerator and denominator of the IIR filter. Only returned if `output='ba'`.

**z, p, k** : Zeros, poles, and gain of the IIR filter. Only returned if

**''output='zpk'''.** :

`scipy.signal.`**`iirfilter`**(*N*, *Wn*, *rp=None*, *rs=None*, *btype='band'*, *analog=0*, *ftype='butter'*, *output='ba'*)

IIR digital and analog filter design given order and critical points.

Design an Nth order lowpass digital or analog filter and return the filter coefficients in (B,A) (numerator, denominator) or (Z,P,K) form.

**Parameters**

**N** : int

The order of the filter.

**Wn** : array_like

A scalar or length-2 sequence giving the critical frequencies.

**rp** : float, optional

For Chebyshev and elliptic filters provides the maximum ripple in the passband.

**rs** : float, optional

For chebyshev and elliptic filters provides the minimum attenuation in the stop band.

**btype** : str, optional

The type of filter (lowpass, highpass, bandpass, bandstop). Default is bandpass.

**analog** : int, optional

Non-zero to return an analog filter, otherwise a digital filter is returned.

**ftype** : str, optional

The type of IIR filter to design:

- elliptic : 'ellip'
- Butterworth : 'butter',
- Chebyshev I : 'cheby1',
- Chebyshev II: 'cheby2',
- Bessel : 'bessel'

**output** : ['ba', 'zpk'], optional

Type of output: numerator/denominator ('ba') or pole-zero ('zpk'). Default is 'ba'.

**See Also:**

`butterord`, `cheb1ord`, `cheb2ord`, `ellipord`

`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**

**N** : 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 :** :

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.`**`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.

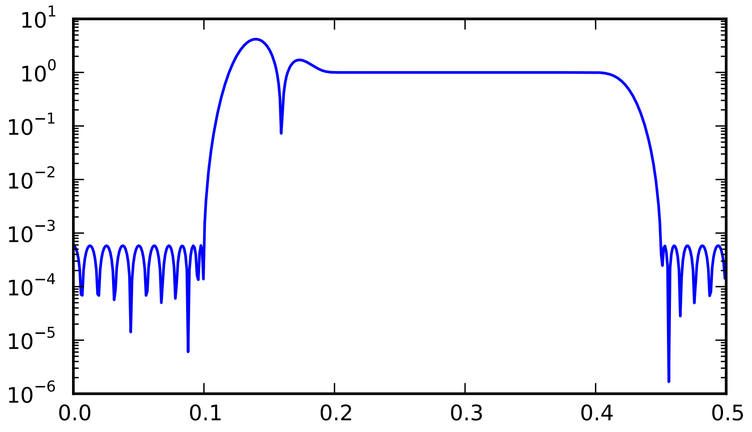
## References

[R57], [R58]

### 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.

```
>>> bpass = sp.signal.remez(72, [0, 0.1, 0.2, 0.4, 0.45, 0.5], [0, 1, 0])
>>> freq, response = sp.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
[<matplotlib.lines.Line2D object at 0xf486790>]
>>> 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

```
>>> vals = [0, 1.3, 1.31, 2.8, 1.25, 2.2, 10.3]
>>> uniq, mult = sp.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, poly, polyval, unique_roots

scipy.signal.**invres**(*r*, *p*, *k*, *tol=0.001*, *rtype='avg'*)

Compute b(s) and a(s) from partial fraction expansion: r,p,k

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

**See Also:**

residue, poly, polyval, unique_roots

### 4.16.5 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 I 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 digital and analog filter design. |

`scipy.signal.`**`butter`**(*N*, *Wn*, *btype='low'*, *analog=0*, *output='ba'*)

Butterworth digital and analog filter design.

Design an Nth order lowpass digital or analog Butterworth filter and return the filter coefficients in (B,A) or (Z,P,K) form.

**See Also:**

`buttord.`

`scipy.signal.`**`buttord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=0*)

Butterworth filter order selection.

Return the order of the lowest order digital 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, normalized from 0 to 1 (1 corresponds to pi radians / 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]

**gpass** : float

The maximum loss in the passband (dB).

**gstop** : float

The minimum attenuation in the stopband (dB).

**analog** : int, optional

Non-zero to design an analog filter (in this case *wp* and *ws* are in radians / second).

**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.

`scipy.signal.`**`cheby1`**(*N*, *rp*, *Wn*, *btype='low'*, *analog=0*, *output='ba'*)

Chebyshev type I digital and analog filter design.

Design an Nth order lowpass digital or analog Chebyshev type I filter and return the filter coefficients in (B,A) or (Z,P,K) form.

**See Also:**

`cheb1ord.`

`scipy.signal.`**`cheb1ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=0*)

Chebyshev type I filter order selection.

Return the order of the lowest order digital 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, normalized from 0 to 1 (1 corresponds to pi radians / 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]

**gpass** : float

The maximum loss in the passband (dB).

**gstop** : float

The minimum attenuation in the stopband (dB).

**analog** : int, optional

Non-zero to design an analog filter (in this case *wp* and *ws* are in radians / second).

**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.

`scipy.signal.`**`cheby2`**(*N*, *rs*, *Wn*, *btype='low'*, *analog=0*, *output='ba'*)

Chebyshev type I digital and analog filter design.

Design an Nth order lowpass digital or analog Chebyshev type I filter and return the filter coefficients in (B,A) or (Z,P,K) form.

**See Also:**

`cheb2ord.`

`scipy.signal.`**`cheb2ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=0*)

Chebyshev type II filter order selection.

Description:

Return the order of the lowest order digital 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, normalized from 0 to 1 (1 corresponds to pi radians / 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]

**gpass** : float

The maximum loss in the passband (dB).

**gstop** : float

The minimum attenuation in the stopband (dB).

**analog** : int, optional

Non-zero to design an analog filter (in this case *wp* and *ws* are in radians / second).

**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.

`scipy.signal.`**`ellip`**(*N*, *rp*, *rs*, *Wn*, *btype='low'*, *analog=0*, *output='ba'*)

Elliptic (Cauer) digital and analog filter design.

Design an Nth order lowpass digital or analog elliptic filter and return the filter coefficients in (B,A) or (Z,P,K) form.

**See Also:**

`ellipord`.

`scipy.signal.`**`ellipord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=0*)

Elliptic (Cauer) filter order selection.

Return the order of the lowest order digital 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, normalized from 0 to 1 (1 corresponds to pi radians / 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]

**gpass** : float

The maximum loss in the passband (dB).

**gstop** : float

The minimum attenuation in the stopband (dB).

**analog** : int, optional

Non-zero to design an analog filter (in this case *wp* and *ws* are in radians / second).

**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.-

`scipy.signal.`**`bessel`**(*N*, *Wn*, *btype='low'*, *analog=0*, *output='ba'*)

Bessel digital and analog filter design.

Design an Nth order lowpass digital or analog Bessel filter and return the filter coefficients in (B,A) or (Z,P,K) form.

## 4.16.6 Continuous-Time Linear Systems

| | |
|---|---|
| `lti`(*args, **kwords) | Linear Time Invariant class which simplifies representation. |
| `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 |
| `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. |

**class** `scipy.signal.`**`lti`**(**args*, ***kwords*)

Linear Time Invariant class which simplifies representation.

### Methods

| |
|---|
| `impulse`([X0, T, N]) |
| `output`(U, T[, X0]) |
| `step`([X0, T, N]) |

`lti.`**`impulse`**(*X0=None*, *T=None*, *N=None*)

`lti.`**`output`**(*U*, *T*, *X0=None*)

`lti.`**`step`**(*X0=None*, *T=None*, *N=None*)

`scipy.signal.`**`lsim`**(*system*, *U*, *T*, *X0=None*, *interp=1*)

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.

**T** : array_like

The time steps at which the input is defined and at which the output is desired.

**X0 :** :

The initial conditions on the state vector (zero by default).

**interp** : {1, 0}

Whether to use linear (1) or zero-order hold (0) interpolation.

**Returns**

**T** : 1D ndarray

Time values for the output.

**yout** : 1D ndarray

System response.

**xout** : ndarray

Time-evolution of the state-vector.

`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** : LTI class or tuple

If specified as a tuple, the system is described as `(num, den)`, `(zero, pole, gain)`, or `(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 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)

**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.

**X0** : 1-D array_like, optional

The initial condition of the state vector. Default: 0 (the zero vector).

**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`

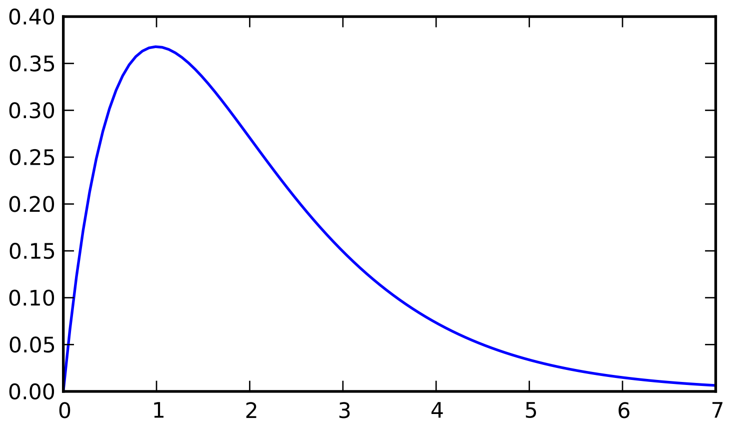
## Notes

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)

```
>>> import scipy.signal
>>> system = ([1.0], [1.0, 2.0, 1.0])
>>> t, y = sp.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 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

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 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

Number of time points to compute if *T* is not given.

****kwargs :** :

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.

## 4.16.7 Discrete-Time Linear Systems

dlsim – simulation of output to a discrete-time linear system. dimpulse – impulse response of a discrete-time LTI system. dstep – step response of a discrete-time LTI system.

## 4.16.8 LTI Representations

| | |
|---|---|
| `tf2zpk`(b, a) | Return zero, pole, gain (z,p,k) representation from a numerator, denominator representation of a linear filter. |
| `zpk2tf`(z, p, k) | Return polynomial transfer function representation from zeros |
| `tf2ss`(num, den) | Transfer function to state-space representation. |
| `ss2tf`(A, B, C, D[, input]) | State-space to transfer function. |
| `zpk2ss`(z, p, k) | Zero-pole-gain representation to state-space representation |
| `ss2zpk`(A, B, C, D[, input]) | State-space representation to zero-pole-gain representation. |
| `cont2discrete`(sys, dt[, method, alpha]) | Transform a continuous to a discrete state-space system. |

`scipy.signal.`**`tf2zpk`**(*b*, *a*)
Return zero, pole, gain (z,p,k) representation from a numerator, denominator representation of a linear filter.

**Parameters**
**b** : ndarray

Numerator polynomial.

**a** : ndarray

Denominator polynomial.

**Returns**
**z** : ndarray

Zeros of the transfer function.

**p** : ndarray

Poles of the transfer function.

**k** : float

System gain.

**If some values of b are too close to 0, they are removed. In that case, a** :

**BadCoefficients warning is emitted.** :

`scipy.signal.`**`zpk2tf`**(*z*, *p*, *k*)
Return polynomial transfer function representation from zeros and poles

**Parameters**
**z** : ndarray

Zeros of the transfer function.

**p** : ndarray

Poles of the transfer function.

**k** : float

System gain.

**Returns**

**b** : ndarray

Numerator polynomial.

**a** : ndarray

Denominator polynomial.

`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.

`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, den** : 1D ndarray

Numerator and denominator polynomials (as sequences) respectively.

`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 matrices.

`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.`**`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"}

**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]

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: http://en.wikipedia.org/wiki/Discretization#Discretization_of_linear_state_space_

Generalize bilinear approximation is based on: http://techteach.no/publications/discretetime_signals_systems/discrete.pdf and

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)

### 4.16.9 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: exp(-a t^2) exp(1j*2*pi*fc*t). |
| `sawtooth`(t[, width]) | Return a periodic sawtooth waveform. |
| `square`(t[, duty]) | Return a periodic square-wave waveform. |
| `sweep_poly`(t, poly[, phi]) | Frequency-swept cosine generator, with a time-dependent frequency specified as a polynomial. |

`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 time unit'; there is no assumption here that the time unit is one second. The important distinction is that the units of rotation are cycles, not radians.

**Parameters**

**t** : ndarray

Times at which to evaluate the waveform.

**f0** : float

Frequency (in Hz) at time t=0.

**t1** : float

Time at which *f1* is specified.

**f1** : float

Frequency (in 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**

**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:**

`scipy.signal.waveforms.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)
```

f1 must be positive, and f0 must be greater than f1.

`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 (Hz). Default is 1000.

**bw** : float, optional

Fractional bandwidth in frequency domain of pulse (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.

`scipy.signal.`**`sawtooth`**`(`*t*, *width=1*`)`

Return a periodic sawtooth waveform.

The sawtooth waveform has a period 2*pi, rises from -1 to 1 on the interval 0 to width*2*pi and drops from 1 to -1 on the interval width*2*pi to 2*pi. *width* must be in the interval [0,1].

**Parameters**

**t** : array_like

Time.

**width** : float, optional

Width of the waveform. Default is 1.

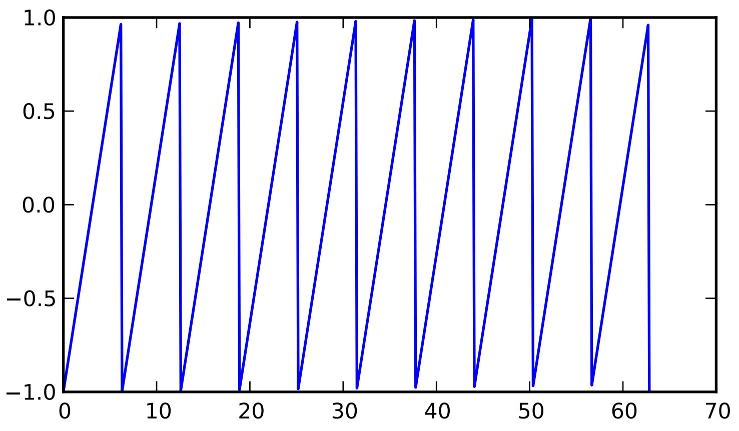
**Returns**

**y** : ndarray

Output array containing the sawtooth waveform.

## Examples

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 20*np.pi, 500)
>>> plt.plot(x, sp.signal.sawtooth(x))
```



`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].

**Parameters**

**t** : array_like

The input time array.

**duty** : float, optional

Duty cycle.

**Returns**

**y** : array_like

The output square wave.

`scipy.signal.sweep_poly(t, poly, phi=0)`

Frequency-swept cosine generator, with a time-dependent frequency specified as a polynomial.

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** : 1D ndarray (or 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 is 0.

**Returns**

**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:**

`scipy.signal.waveforms.chirp`

## Notes

New in version 0.8.0.

### 4.16.10 Window functions

| | |
|---|---|
| get_window(window, Nx[, fftbins]) | Return a window of length *Nx* and type *window*. |
| barthann(M[, sym]) | Return the M-point modified Bartlett-Hann window. |
| bartlett(M[, sym]) | The M-point Bartlett window. |
| blackman(M[, sym]) | The M-point Blackman window. |
| blackmanharris(M[, sym]) | The M-point minimum 4-term Blackman-Harris window. |
| bohman(M[, sym]) | The M-point Bohman window. |
| boxcar(M[, sym]) | The M-point boxcar window. |
| chebwin(M, at[, sym]) | Dolph-Chebyshev window. |
| flattop(M[, sym]) | The M-point Flat top window. |
| gaussian(M, std[, sym]) | Return a Gaussian window of length M with standard-deviation std. |
| general_gaussian(M, p, sig[, sym]) | Return a window with a generalized Gaussian shape. |
| hamming(M[, sym]) | The M-point Hamming window. |
| hann(M[, sym]) | The M-point Hanning window. |
| kaiser(M, beta[, sym]) | Return a Kaiser window of length M with shape parameter beta. |
| nuttall(M[, sym]) | A minimum 4-term Blackman-Harris window according to Nuttall. |
| parzen(M[, sym]) | The M-point Parzen window. |
| slepian(M, width[, sym]) | Return the M-point slepian window. |
| triang(M[, sym]) | The M-point triangular window. |

`scipy.signal.`**`get_window`**`(`*window, Nx, fftbins=True*`)`

Return a window of length *Nx* and type *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).

#### Notes

Window types:

boxcar, triang, blackman, hamming, hanning, bartlett, parzen, bohman, blackmanharris, nuttall, barthann, kaiser (needs beta), gaussian (needs std), general_gaussian (needs power, width), slepian (needs width), chebwin (needs attenuation)

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

```
>>> get_window('triang', 7)
array([ 0.25,  0.5 ,  0.75,  1.  ,  0.75,  0.5 ,  0.25])
```

```
>>> get_window(('kaiser', 4.0), 9)
array([ 0.08848053,  0.32578323,  0.63343178,  0.89640418,  1.        ,
        0.89640418,  0.63343178,  0.32578323,  0.08848053])
>>> 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 the M-point modified Bartlett-Hann window.

`scipy.signal.`**`bartlett`**(*M*, *sym=True*)
The M-point Bartlett window.

`scipy.signal.`**`blackman`**(*M*, *sym=True*)
The M-point Blackman window.

`scipy.signal.`**`blackmanharris`**(*M*, *sym=True*)
The M-point minimum 4-term Blackman-Harris window.

`scipy.signal.`**`bohman`**(*M*, *sym=True*)
The M-point Bohman window.

`scipy.signal.`**`boxcar`**(*M*, *sym=True*)
The M-point boxcar window.

`scipy.signal.`**`chebwin`**(*M*, *at*, *sym=True*)
Dolph-Chebyshev window.

**Parameters**

**M** : int

Window size.

**at** : float

Attenuation (in dB).

**sym** : bool

Generates symmetric window if True.

`scipy.signal.`**`flattop`**(*M*, *sym=True*)
The M-point Flat top window.

`scipy.signal.`**`gaussian`**(*M*, *std*, *sym=True*)
Return a Gaussian window of length M with standard-deviation std.

`scipy.signal.`**`general_gaussian`**(*M*, *p*, *sig*, *sym=True*)
Return a window with a generalized Gaussian shape.

The Gaussian shape is defined as `exp(-0.5*(x/sig)**(2*p))`, the half-power point is at `(2*log(2)))**(1/(2*p)) * sig`.

`scipy.signal.`**`hamming`**(*M*, *sym=True*)
The M-point Hamming window.

`scipy.signal.`**`hann`**(*M*, *sym=True*)
The M-point Hanning window.

`scipy.signal.`**`kaiser`**(*M*, *beta*, *sym=True*)
Return a Kaiser window of length M with shape parameter beta.

`scipy.signal.`**`nuttall`**(*M*, *sym=True*)
A minimum 4-term Blackman-Harris window according to Nuttall.

`scipy.signal.`**`parzen`**(*M*, *sym=True*)
The M-point Parzen window.

`scipy.signal.`**`slepian`**(*M*, *width*, *sym=True*)
Return the M-point slepian window.

`scipy.signal.`**`triang`**(*M*, *sym=True*)
The M-point triangular window.

## 4.16.11 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 |

`scipy.signal.`**`cascade`**(*hk*, *J=7*)
Return (x, phi, psi) at dyadic points K/2**J from filter coefficients.

**Parameters**

**hk :** :

Coefficients of low-pass filter.

**J** : int. optional

Values will be computed at grid points `K/2**J`.

**Returns**

**x :** :

The dyadic points K/2**J for `K=0...N * (2**J)-1` where `len(hk) = len(gk) = N+1`

**phi :** :

The scaling function `phi(x)` at *x*:

N

**phi(x) = sum hk * phi(2x-k)**
k=0

**psi :** :

The wavelet function `psi(x)` at *x*:

N

**phi(x) = sum gk * phi(2x-k)**
k=0

*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.

`scipy.signal.morlet(M, w=5.0, s=1.0, complete=True)`

Complex Morlet wavelet.

**Parameters**

**M** : int

Length of the wavelet.

**w** : float

Omega0

**s** : float

Scaling factor, windowed from -s*2*pi to +s*2*pi.

**complete** : bool

Whether to use the complete or the standard version.

### 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

## 4.17 Sparse matrices (`scipy.sparse`)

SciPy 2-D sparse matrix package.

### 4.17.1 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)])**
with a dense matrix or rank-2 ndarray D

**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]:indices[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 *
>>> from scipy import *
>>> bsr_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)

>>> row  = array([0,0,1,2,2,2])
>>> col  = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> bsr_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])

>>> indptr  = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data    = array([1,2,3,4,5,6]).repeat(4).reshape(6,2,2)
>>> bsr_matrix( (data,indices,indptr), shape=(6,6) ).todense()
matrix([[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

| | |
|---|---|
| dtype | |
| shape | |
| ndim | int(x[, base]) -> integer |
| nnz | |
| blocksize | |
| has_sorted_indices | Determine whether the matrix has sorted indices |

bsr_matrix.**dtype**

bsr_matrix.**shape**

bsr_matrix.**ndim = 2**

bsr_matrix.**nnz**

bsr_matrix.**blocksize**

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

| | |
|---|---|
| data | Data array of the matrix |
| indices | BSR format index array |
| indptr | BSR format index pointer array |

## Methods

| | |
|---|---|
| asformat(format) | Return this matrix in a given sparse format |
| asfptype() | Upcast matrix to a floating point format (if necessary) |
| astype(t) | |
| check_format([full_check]) | check whether the matrix format is valid |
| conj() | |
| conjugate() | |
| copy() | |
| diagonal() | Returns the main diagonal of the matrix |
| dot(other) | |
| eliminate_zeros() | |
| getH() | |
| get_shape() | |
| getcol(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| getdata(ind) | |
| getformat() | |
| getmaxprint() | |
| getnnz() | |
| getrow(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |
| matmat(other) | |
| matvec(other) | |
| mean([axis]) | Average the matrix over the given axis. |
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| prune() | Remove empty space after all non-zero elements. |
| reshape(shape) | |
| set_shape(shape) | |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| sort_indices() | Sort the indices of this matrix *in place* |
| sorted_indices() | Return a copy of this matrix with sorted indices |
| sum([axis]) | Sum the matrix over the given axis. |
| sum_duplicates() | |
| toarray() | |
| tobsr([blocksize, copy]) | |
| tocoo([copy]) | Convert this matrix to COOrdinate format. |
| tocsc() | |
| tocsr() | |
| todense() | |
| todia() | |
| todok() | |
| tolil() | |
| transpose() | |

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.`**`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.`**`diagonal`**`()`
Returns the main diagonal of the matrix

`bsr_matrix.`**`dot`**`(`*other*`)`

`bsr_matrix.`**`eliminate_zeros`**`()`

`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.`**`matmat`**`(`*other*`)`

`bsr_matrix.`**`matvec`**`(`*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.`**`multiply`**`(`*other*`)`
Point-wise multiplication by another matrix

`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.`**`prune`**`()`
Remove empty space after all non-zero elements.

`bsr_matrix.`**`reshape`**`(`*shape*`)`

`bsr_matrix.`**`set_shape`**`(`*shape*`)`

`bsr_matrix.`**`setdiag`**`(`*values*, *k=0*`)`
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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.`**`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.`**`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`**`()`

`bsr_matrix.`**`todia`**`()`

`bsr_matrix.`**`todok`**`()`

`bsr_matrix.`**`tolil`**`()`

`bsr_matrix.`**`transpose`**`()`

**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, ij), [shape=(M, N)])**

**The arguments ‘data’ and ‘ij’ represent three arrays:**

1. data[:] the entries of the matrix, in any order
2. ij[0][:] the row indices of the matrix entries
3. ij[1][:] the column indices of the matrix entries

Where `A[ij[0][k], ij[1][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 *
>>> from scipy import *
>>> coo_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)

>>> row  = array([0,3,1,0])
>>> col  = array([0,3,1,2])
>>> data = array([4,5,7,9])
>>> coo_matrix( (data,(row,col)), shape=(4,4) ).todense()
matrix([[4, 0, 9, 0],
        [0, 7, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 5]])

>>> # example with duplicates
>>> 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])
>>> coo_matrix( (data,(row,col)), shape=(4,4)).todense()
matrix([[3, 0, 1, 0],
        [0, 2, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 1]])
```

### Attributes

| | |
|---|---|
| dtype | |
| shape | |
| ndim | int(x[, base]) -> integer |
| nnz | |

coo_matrix.**dtype**

coo_matrix.**shape**

coo_matrix.**ndim = 2**

coo_matrix.**nnz**

| | |
|---|---|
| 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

| | |
|---|---|
| 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) | |
| getH() | |
| get_shape() | |
| getcol(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| getformat() | |
| getmaxprint() | |
| getnnz() | |
| getrow(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |
| mean([axis]) | Average the matrix over the given axis. |
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| reshape(shape) | |
| set_shape(shape) | |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| sum([axis]) | Sum the matrix over the given axis. |
| 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() | |
| todia() | |
| todok() | |

Continued on next page

Table 4.3 – continued from previous page

| |
|---|
| `tolil`() |
| `transpose`([copy]) |

`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.`**`conj`**()

`coo_matrix.`**`conjugate`**()

`coo_matrix.`**`copy`**()

`coo_matrix.`**`diagonal`**()
Returns the main diagonal of the matrix

`coo_matrix.`**`dot`**(*other*)

`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`**()

`coo_matrix.`**`getrow`**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

`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.`**`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.`**`reshape`**`(`*shape*`)`

`coo_matrix.`**`set_shape`**`(`*shape*`)`

`coo_matrix.`**`setdiag`**`(`*values, k=0*`)`

Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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.`**`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.todense()
matrix([[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.todense()
matrix([[3, 0, 1, 0],
        [0, 2, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 1]])
```

coo_matrix.**todense**()

coo_matrix.**todia**()

coo_matrix.**todok**()

coo_matrix.**tolil**()

coo_matrix.**transpose**(*copy=False*)

**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, ij), [shape=(M, N)])**
where `data` and `ij` satisfy the relationship `a[ij[0, k], ij[1, 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]:indices[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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> csc_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)

>>> row = array([0,2,2,0,1,2])
>>> col = array([0,0,1,2,2,2])
>>> data = array([1,2,3,4,5,6])
>>> csc_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 4],
        [0, 0, 5],
        [2, 3, 6]])

>>> indptr = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csc_matrix( (data,indices,indptr), shape=(3,3) ).todense()
matrix([[1, 0, 4],
        [0, 0, 5],
        [2, 3, 6]])
```

### Attributes

| | |
|---|---|
| dtype | |
| shape | |
| ndim | int(x[, base]) -> integer |
| nnz | |
| has_sorted_indices | Determine whether the matrix has sorted indices |

csc_matrix.**dtype**

csc_matrix.**shape**

csc_matrix.**ndim** = 2

`csc_matrix.`**`nnz`**

`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

| | |
|---|---|
| data | Data array of the matrix |
| indices | CSC format index array |
| indptr | CSC format index pointer array |

## Methods

| | |
|---|---|
| `asformat`(format) | Return this matrix in a given sparse format |
| `asfptype`() | Upcast matrix to a floating point format (if necessary) |
| `astype`(t) | |
| `check_format`([full_check]) | check whether the matrix format is valid |
| `conj`() | |
| `conjugate`() | |
| `copy`() | |
| `diagonal`() | Returns the main diagonal of the matrix |
| `dot`(other) | |
| `eliminate_zeros`() | Remove zero entries from the matrix |
| `getH`() | |
| `get_shape`() | |
| `getcol`(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| `getformat`() | |
| `getmaxprint`() | |
| `getnnz`() | |
| `getrow`(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |
| `mean`([axis]) | Average the matrix over the given axis. |
| `multiply`(other) | Point-wise multiplication by another matrix |
| `nonzero`() | nonzero indices |
| `prune`() | Remove empty space after all non-zero elements. |
| `reshape`(shape) | |
| `set_shape`(shape) | |
| `setdiag`(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| `sort_indices`() | Sort the indices of this matrix *in place* |
| `sorted_indices`() | Return a copy of this matrix with sorted indices |
| `sum`([axis]) | Sum the matrix over the given axis. |
| `sum_duplicates`() | Eliminate duplicate matrix entries by adding them together |
| `toarray`() | |
| `tobsr`([blocksize]) | |
| `tocoo`([copy]) | Return a COOrdinate representation of this matrix |
| `tocsc`([copy]) | |
| `tocsr`() | |
| `todense`() | |
| `todia`() | |

Continued on next page

Table 4.4 – continued from previous page

| |
|---|
| todok() |
| tolil() |
| transpose([copy]) |

`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.`**`check_format`**(*full_check=True*)

check whether the matrix format is valid

**Parameters**

**- full_check** : {bool}

- True - rigorous check, O(N) operations : default
- False - basic check, O(1) operations

`csc_matrix.`**`conj`**()

`csc_matrix.`**`conjugate`**()

`csc_matrix.`**`copy`**()

`csc_matrix.`**`diagonal`**()

Returns the main diagonal of the matrix

`csc_matrix.`**`dot`**(*other*)

`csc_matrix.`**`eliminate_zeros`**()

Remove zero entries from the matrix

The is an *in place* operation

`csc_matrix.`**`getH`**()

`csc_matrix.`**`get_shape`**`()`

`csc_matrix.`**`getcol`**`(`*j*`)`
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

`csc_matrix.`**`getformat`**`()`

`csc_matrix.`**`getmaxprint`**`()`

`csc_matrix.`**`getnnz`**`()`

`csc_matrix.`**`getrow`**`(`*i*`)`
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

`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.`**`multiply`**`(`*other*`)`
Point-wise multiplication by another matrix

`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.`**`prune`**`()`
Remove empty space after all non-zero elements.

`csc_matrix.`**`reshape`**`(`*shape*`)`

`csc_matrix.`**`set_shape`**`(`*shape*`)`

`csc_matrix.`**`setdiag`**`(`*values, k=0*`)`
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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.`**`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.`**`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`**`()`

`csc_matrix.`**`todia`**`()`

`csc_matrix.`**`todok`**`()`

`csc_matrix.`**`tolil`**`()`

`csc_matrix.`**`transpose`**`(`*copy=False*`)`

**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, ij), [shape=(M, N)])**
where `data` and `ij` satisfy the relationship `a[ij[0, k], ij[1, 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]:indices[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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> csr_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)

>>> row = array([0,0,1,2,2,2])
>>> col = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csr_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])

>>> indptr = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csr_matrix( (data,indices,indptr), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])
```

## Attributes

| | |
|---|---|
| `dtype` | |
| `shape` | |
| `ndim` | int(x[, base]) -> integer |
| `nnz` | |
| `has_sorted_indices` | Determine whether the matrix has sorted indices |

`csr_matrix.`**`dtype`**

`csr_matrix.`**`shape`**

`csr_matrix.`**`ndim`** **= 2**

csr_matrix.**nnz**

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

| | |
|---|---|
| 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

| | |
|---|---|
| asformat(format) | Return this matrix in a given sparse format |
| asfptype() | Upcast matrix to a floating point format (if necessary) |
| astype(t) | |
| check_format([full_check]) | check whether the matrix format is valid |
| conj() | |
| conjugate() | |
| copy() | |
| diagonal() | Returns the main diagonal of the matrix |
| dot(other) | |
| eliminate_zeros() | Remove zero entries from the matrix |
| getH() | |
| get_shape() | |
| getcol(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| getformat() | |
| getmaxprint() | |
| getnnz() | |
| getrow(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |
| mean([axis]) | Average the matrix over the given axis. |
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| prune() | Remove empty space after all non-zero elements. |
| reshape(shape) | |
| set_shape(shape) | |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| sort_indices() | Sort the indices of this matrix *in place* |
| sorted_indices() | Return a copy of this matrix with sorted indices |
| sum([axis]) | Sum the matrix over the given axis. |
| sum_duplicates() | Eliminate duplicate matrix entries by adding them together |
| toarray() | |
| tobsr([blocksize, copy]) | |
| tocoo([copy]) | Return a COOrdinate representation of this matrix |
| tocsc() | |
| tocsr([copy]) | |
| todense() | |
| todia() | |

Continued on next page

**Table 4.5 – continued from previous page**

| |
|---|
| todok() |
| tolil() |
| transpose([copy]) |

`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.`**`check_format`**(*full_check=True*)

check whether the matrix format is valid

**Parameters**

**- full_check** : {bool}

- True - rigorous check, O(N) operations : default
- False - basic check, O(1) operations

`csr_matrix.`**`conj`**()

`csr_matrix.`**`conjugate`**()

`csr_matrix.`**`copy`**()

`csr_matrix.`**`diagonal`**()

Returns the main diagonal of the matrix

`csr_matrix.`**`dot`**(*other*)

`csr_matrix.`**`eliminate_zeros`**()

Remove zero entries from the matrix

The is an *in place* operation

`csr_matrix.`**`getH`**()

`csr_matrix.`**`get_shape`**`()`

`csr_matrix.`**`getcol`**`(`*j*`)`
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

`csr_matrix.`**`getformat`**`()`

`csr_matrix.`**`getmaxprint`**`()`

`csr_matrix.`**`getnnz`**`()`

`csr_matrix.`**`getrow`**`(`*i*`)`
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

`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.`**`multiply`**`(`*other*`)`
Point-wise multiplication by another matrix

`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.`**`prune`**`()`
Remove empty space after all non-zero elements.

`csr_matrix.`**`reshape`**`(`*shape*`)`

`csr_matrix.`**`set_shape`**`(`*shape*`)`

`csr_matrix.`**`setdiag`**`(`*values*, *k=0*`)`
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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.`**`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.`**`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`**`()`

`csr_matrix.`**`todia`**`()`

`csr_matrix.`**`todok`**`()`

`csr_matrix.`**`tolil`**`()`

`csr_matrix.`**`transpose`**`(`*copy=False*`)`

**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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> dia_matrix( (3,4), dtype=int8).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)

>>> data = array([[1,2,3,4]]).repeat(3,axis=0)
>>> offsets = array([0,-1,2])
>>> dia_matrix( (data,offsets), shape=(4,4)).todense()
matrix([[1, 0, 3, 0],
        [1, 2, 0, 4],
        [0, 2, 3, 0],
        [0, 0, 3, 4]])
```

### Attributes

| | |
|---|---|
| dtype | |
| shape | |
| ndim | int(x[, base]) -> integer |
| nnz | number of nonzero values |

dia_matrix.**dtype**

dia_matrix.**shape**

dia_matrix.**ndim** = 2

dia_matrix.**nnz**

number of nonzero values

explicit zero values are included in this number

| | |
|---|---|
| data | DIA format data array of the matrix |
| offsets | DIA format offset 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) | |
| getH() | |
| get_shape() | |
| getcol(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| getformat() | |
| getmaxprint() | |
| getnnz() | number of nonzero values |
| getrow(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |

Continued on next page

Table 4.6 – continued from previous page

| | |
|---|---|
| mean([axis]) | Average the matrix over the given axis. |
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| reshape(shape) | |
| set_shape(shape) | |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| sum([axis]) | Sum the matrix over the given axis. |
| toarray() | |
| tobsr([blocksize]) | |
| tocoo() | |
| tocsc() | |
| tocsr() | |
| todense() | |
| todia([copy]) | |
| todok() | |
| tolil() | |
| transpose() | |

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.**conj**()

dia_matrix.**conjugate**()

dia_matrix.**copy**()

dia_matrix.**diagonal**()
Returns the main diagonal of the matrix

dia_matrix.**dot**(*other*)

`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.`**`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.`**`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.`**`reshape`**`(`*shape*`)`

`dia_matrix.`**`set_shape`**`(`*shape*`)`

`dia_matrix.`**`setdiag`**`(`*values*, *k=0*`)`
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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.`**`toarray`**`()`

dia_matrix.**tobsr**(*blocksize=None*)

dia_matrix.**tocoo**()

dia_matrix.**tocsc**()

dia_matrix.**tocsr**()

dia_matrix.**todense**()

dia_matrix.**todia**(*copy=False*)

dia_matrix.**todok**()

dia_matrix.**tolil**()

dia_matrix.**transpose**()

**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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> S = dok_matrix((5,5), dtype=float32)
>>> for i in range(5):
>>>     for j in range(5):
>>>         S[i,j] = i+j # Update element
```

## Attributes

| | |
|---|---|
| shape | |
| ndim | int(x[, base]) -> integer |
| nnz | |

dok_matrix.**shape**

dok_matrix.**ndim** = 2

dok_matrix.**nnz**

| | | |
|---|---|---|
| dtype | dtype | Data type 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) | |
| clear | D.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) | |
| fromkeys(...) | v defaults to None. |
| get(key[, default]) | This overrides the dict.get method, providing type checking |
| getH() | |
| get_shape() | |
| getcol(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| getformat() | |
| getmaxprint() | |
| getnnz() | |
| getrow(i) | Returns a copy of row i of the matrix, as a (1 x n) sparse |
| has_key | D.has_key(k) -> True if D has a key k, else False |
| items | D.items() -> list of D's (key, value) pairs, as 2-tuples |
| iteritems | D.iteritems() -> an iterator over the (key, value) items of D |
| iterkeys | D.iterkeys() -> an iterator over the keys of D |
| itervalues | D.itervalues() -> an iterator over the values of D |
| keys | D.keys() -> list of D's keys |
| mean([axis]) | Average the matrix over the given axis. |
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| pop | D.pop(k[,d]) -> v, remove specified key and return the corresponding value. |
| popitem | D.popitem() -> (k, v), remove and return some (key, value) pair as a |
| reshape(shape) | |
| resize(shape) | Resize the matrix in-place to dimensions given by 'shape'. |
| set_shape(shape) | |
| setdefault | D.setdefault(k[,d]) -> D.get(k,d), also set D[k]=d if k not in D |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |

Continued on next page

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| | |
|---|---|
| split(cols_or_rows[, columns]) | |
| sum([axis]) | Sum the matrix over the given axis. |
| take(cols_or_rows[, columns]) | |
| toarray() | |
| 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() | |
| todia() | |
| todok([copy]) | |
| tolil() | |
| transpose() | Return the transpose |
| update | D.update(E, **F) -> None. Update D from dict/iterable E and F. |
| values | D.values() -> list of D's values |
| viewitems | D.viewitems() -> a set-like object providing a view on D's items |
| viewkeys | D.viewkeys() -> a set-like object providing a view on D's keys |
| viewvalues | D.viewvalues() -> an object providing a view on D's values |

`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`**

D.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*`)`

**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 an (m x 1) sparse matrix (column vector).

`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) sparse matrix (row vector).

`dok_matrix.`**`has_key`**
D.has_key(k) -> True if D has a key k, else False

`dok_matrix.`**`items`**
D.items() -> list of D's (key, value) pairs, as 2-tuples

`dok_matrix.`**`iteritems`**
D.iteritems() -> an iterator over the (key, value) items of D

`dok_matrix.`**`iterkeys`**
D.iterkeys() -> an iterator over the keys of D

`dok_matrix.`**`itervalues`**
D.itervalues() -> an iterator over the values of D

`dok_matrix.`**`keys`**
D.keys() -> list of D's keys

`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.`**`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`**

D.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`**

D.popitem() -> (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty.

`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`**

D.setdefault(k[,d]) -> D.get(k,d), also set D[k]=d if k not in D

`dok_matrix.`**`setdiag`**`(`*values, k=0*`)`

Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`dok_matrix.`**`split`**`(`*cols_or_rows, columns=1*`)`

`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.`**`take`**`(`*cols_or_rows, columns=1*`)`

`dok_matrix.`**`toarray`**`()`

`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`**`()`

`dok_matrix.`**`todia`**`()`

`dok_matrix.`**`todok`**`(`*copy=False*`)`

`dok_matrix.`**`tolil`**`()`

`dok_matrix.`**`transpose`**`()`
Return the transpose

`dok_matrix.`**`update`**
D.update(E, **F) -> None. Update D from dict/iterable E and F. If E has a .keys() method, does: for k in E: D[k] = E[k] If E 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`**
D.values() -> list of D's values

`dok_matrix.`**`viewitems`**
D.viewitems() -> a set-like object providing a view on D's items

`dok_matrix.`**`viewkeys`**
D.viewkeys() -> a set-like object providing a view on D's keys

`dok_matrix.`**`viewvalues`**
D.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 an efficient structure for constructing sparse matrices incrementally.

**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.tocsc())

**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

| | |
|---|---|
| `shape` | |
| `ndim` | int(x[, base]) -> integer |
| `nnz` | |

`lil_matrix.`**`shape`**

`lil_matrix.`**`ndim`** **= 2**

`lil_matrix.`**`nnz`**

| | | |
|---|---|---|
| dtype | dtype | Data type of the matrix |
| 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) | |
| `getH`() | |
| `get_shape`() | |
| `getcol`(j) | Returns a copy of column j of the matrix, as an (m x 1) sparse |
| `getformat`() | |
| `getmaxprint`() | |
| `getnnz`() | |
| `getrow`(i) | Returns a copy of the 'i'th row. |
| `getrowview`(i) | Returns a view of the 'i'th row (without copying). |
| `mean`([axis]) | Average the matrix over the given axis. |

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Table 4.8 – continued from previous page

| | |
|---|---|
| multiply(other) | Point-wise multiplication by another matrix |
| nonzero() | nonzero indices |
| reshape(shape) | |
| set_shape(shape) | |
| setdiag(values[, k]) | Fills the diagonal elements {a_ii} with the values from the given sequence. |
| sum([axis]) | Sum the matrix over the given axis. |
| 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() | |
| todia() | |
| todok() | |
| 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*`)`

`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`**`()`

`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.`**`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.`**`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.`**`reshape`**`(`*shape*`)`

`lil_matrix.`**`set_shape`**`(`*shape*`)`

`lil_matrix.`**`setdiag`**`(`*values*, *k=0*`)`
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

`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`**`()`

`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**()

lil_matrix.**todia**()

lil_matrix.**todok**()

lil_matrix.**tolil**(*copy=False*)

lil_matrix.**transpose**()

### Functions

Building sparse matrices:

| | |
|---|---|
| eye(m, n[, k, dtype, format]) | eye(m, n) returns a sparse (m x n) matrix where the k-th diagonal |
| identity(n[, dtype, format]) | Identity matrix in sparse format |
| kron(A, B[, format]) | kronecker product of sparse matrices A and B |
| kronsum(A, B[, format]) | kronecker sum of sparse matrices A and B |
| spdiags(data, diags, m, n[, format]) | Return a sparse matrix from diagonals. |
| 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 uniformely distributed values. |

scipy.sparse.**eye**(*m, n, k=0, dtype='d', format=None*)
eye(m, n) returns a sparse (m x n) matrix where the k-th diagonal is all ones and everything else is zeros.

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** : integer

Shape of the identity matrix.

**dtype :** :

Data type of the matrix

**format** : string

Sparse format of the result, e.g. format="csr", etc.

## Examples

```
>>> identity(3).todense()
matrix([[ 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** : string

format of the result (e.g. "csr")

**Returns**

**kronecker product in a sparse matrix format** :

## Examples

```
>>> A = csr_matrix(array([[0,2],[5,0]]))
>>> B = csr_matrix(array([[1,2],[3,4]]))
>>> kron(A,B).todense()
matrix([[ 0,  0,  2,  4],
        [ 0,  0,  6,  8],
        [ 5, 10,  0,  0],
        [15, 20,  0,  0]])

>>> kron(A,[[1,2],[3,4]]).todense()
matrix([[ 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** : string

format of the result (e.g. "csr")

**Returns**

**kronecker sum in a sparse matrix format** :

`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** : format of the result (e.g. "csr")

By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

**See Also:**

**`dia_matrix`**
the sparse DIAgonal format.

## Examples

```
>>> data = array([[1,2,3,4],[1,2,3,4],[1,2,3,4]])
>>> diags = array([0,-1,2])
>>> spdiags(data, diags, 4, 4).todense()
matrix([[1, 0, 3, 0],
        [1, 2, 0, 4],
        [0, 2, 3, 0],
        [0, 0, 3, 4]])
```

`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.todense()
matrix([[1, 2, 0, 0, 3],
        [4, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> tril(A).todense()
matrix([[1, 0, 0, 0, 0],
        [4, 5, 0, 0, 0],
        [0, 0, 8, 0, 0]])
>>> tril(A).nnz
4
>>> tril(A, k=1).todense()
matrix([[1, 2, 0, 0, 0],
        [4, 5, 0, 0, 0],
        [0, 0, 8, 9, 0]])
>>> tril(A, k=-1).todense()
matrix([[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.todense()
matrix([[1, 2, 0, 0, 3],
        [4, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> triu(A).todense()
matrix([[1, 2, 0, 0, 3],
        [0, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> triu(A).nnz
8
>>> triu(A, k=1).todense()
matrix([[0, 2, 0, 0, 3],
        [0, 0, 0, 6, 7],
        [0, 0, 0, 9, 0]])
>>> triu(A, k=-1).todense()
matrix([[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** :

grid of sparse matrices with compatible shapes an entry of None implies an all-zero matrix

**format** : sparse format of the result (e.g. "csr")

by default an appropriate sparse matrix format is returned. This choice is subject to change.

## 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]] ).todense()
matrix([[1, 2, 5],
        [3, 4, 6],
        [0, 0, 7]])

>>> bmat( [[A,None],[None,C]] ).todense()
matrix([[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** : string

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

**See Also:**

**vstack**
stack sparse matrices vertically (row wise)

## Examples

```
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix([[1,2],[3,4]])
>>> B = coo_matrix([[5],[6]])
>>> hstack( [A,B] ).todense()
matrix([[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** : string

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

**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] ).todense()
matrix([[1, 2],
        [3, 4],
        [5, 6]])
```

`scipy.sparse.`**`rand`**(*m*, *n*, *density=0.01*, *format='coo'*, *dtype=None*)

Generate a sparse matrix of the given shape and density with uniformely distributed values.

**Parameters**

**m, n: int** :

shape of the matrix

**density: real** :

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** :

sparse matrix format.

**dtype: dtype** :

type of the returned matrix values.

## Notes

Only float types are supported for now.

Identifying sparse matrices:

| |
|---|
| `issparse`(x) |
| `isspmatrix`(x) |
| `isspmatrix_csc`(x) |
| `isspmatrix_csr`(x) |
| `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*)

Graph algorithms:

| | |
|---|---|
| cs_graph_components(x) | Determine connected components of a graph stored as a compressed sparse row or column matrix. |

scipy.sparse.**cs_graph_components**(*x*)

Determine connected components of a graph stored as a compressed sparse row or column matrix.

For speed reasons, the symmetry of the matrix x is not checked. A nonzero at index *(i, j)* means that node *i* is connected to node *j* by an edge. The number of rows/columns of the matrix thus corresponds to the number of nodes in the graph.

**Parameters**

**x: ndarray-like, 2 dimensions, or sparse matrix** :

The adjacency matrix of the graph. Only the upper triangular part is used.

**Returns**

**n_comp: int** :

The number of connected components.

**label: ndarray (ints, 1 dimension):** :

The label array of each connected component (-2 is used to indicate empty rows in the matrix: 0 everywhere, including diagonal). This array has the length of the number of nodes, i.e. one label for each node of the graph. Nodes having the same label belong to the same connected component.

### Notes

The matrix is assumed to be symmetric and the upper triangular part of the matrix is used. The matrix is converted to a CSR matrix unless it is already a CSR.

### Examples

```
>>> from scipy.sparse import cs_graph_components
>>> import numpy as np
>>> D = np.eye(4)
>>> D[0,1] = D[1,0] = 1
>>> cs_graph_components(D)
(3, array([0, 0, 1, 2]))
>>> from scipy.sparse import dok_matrix
>>> cs_graph_components(dok_matrix(D))
(3, array([0, 0, 1, 2]))
```

## Exceptions

| |
|---|
| SparseEfficiencyWarning |
| SparseWarning |

**exception** scipy.sparse.**SparseEfficiencyWarning**

**exception** `scipy.sparse.SparseWarning`

### 4.17.2 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 lil_matrix (recommended) or dok_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.

#### 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.todense(), 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).

## 4.18 Sparse linear algebra (`scipy.sparse.linalg`)

### 4.18.1 Abstract linear operators

| | |
|---|---|
| `LinearOperator`(shape, matvec[, rmatvec, ...]) | Common interface for performing matrix vector products |
| `aslinearoperator`(A) | Return A as a LinearOperator. |

**class** `scipy.sparse.linalg.`**`LinearOperator`**(*shape*, *matvec*, *rmatvec=None*, *matmat=None*, *dtype=None*)

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.

**Parameters**

**shape** : tuple

Matrix dimensions (M,N)

**matvec** : callable f(v)

Returns returns A * v.

**Other Parameters**

**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.

## Examples

```
>>> from scipy.sparse.linalg import LinearOperator
>>> from scipy import *
>>> def mv(v):
...     return array([ 2*v[0], 3*v[1]])
...
>>> A = LinearOperator( (2,2), matvec=mv )
>>> A
<2x2 LinearOperator with unspecified dtype>
>>> A.matvec( ones(2) )
array([ 2.,  3.])
>>> A * ones(2)
array([ 2.,  3.])
```

## Methods

| | |
|---|---|
| matmat(X) | Matrix-matrix multiplication |
| matvec(x) | Matrix-vector multiplication |

`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 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 rank-1 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 to ensure that y has the correct shape and type.

`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 additonal information.

### Examples

```
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```

## 4.18.2 Solving linear problems

Direct methods for linear equation systems:

| | |
|---|---|
| spsolve(A, b[, permc_spec, use_umfpack]) | Solve the sparse linear system Ax=b |
| 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

`scipy.sparse.linalg.`**`factorized`**`(`*A*`)`

Return a fuction for solving a sparse linear system, with A pre-factorized.

**Example:**

solve = factorized( A ) # Makes LU decomposition. x1 = solve( rhs1 ) # Uses the LU factors. x2 = solve( rhs2 ) # Uses again the LU factors.

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 superceeded 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 superceeded 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 superceeded 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 superceeded 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. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

**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.

**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 [BJM] [BPh] 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

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.

**Returns**

**x** : array or 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

### Notes

The LGMRES algorithm [BJM] [BPh] 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

[BJM], [BPh]

`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 superceeded 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 superceeded 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. |

`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, LinearOperatorLinear}

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

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

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

Explicit limitation on number of iterations (for safety).

**show** : bool

Display an iteration log.

**calc_var** : bool

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

[R63], [R64], [R65]

## 4.18.3 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 |
| lobpcg(A, X[, B, M, Y, tol, maxiter, ...]) | Solve symmetric partial eigenproblems with optional preconditioning |

`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** : An N x N matrix, array, sparse matrix, or LinearOperator representing

the operation A * x, where A is a real or complex square matrix.

**k** : integer

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 of *k* eigenvectors. `v[:, i]` is the eigenvector corresponding to the eigenvalue w[i].

**Other Parameters**

**M** : An N x N matrix, 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. For best results, M should be of the same type as A. Additionally:

- If sigma==None, M is positive definite
- If sigma is specified, M is positive semi-definite

If sigma==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

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** : array

Starting vector for iteration.

**ncv** : integer

The number of Lanczos vectors generated *ncv* must be greater than *k*; it is recommended that `ncv > 2*k`.

**which** : string [’LM’ | ‘SM’ | ‘LR’ | ‘SR’ | ‘LI’ | ‘SI’]

**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** : integer

Maximum number of Arnoldi update iterations allowed

**tol** : float

Relative accuracy for eigenvalues (stopping criterion) The default value of 0 implies machine precision.

**return_eigenvectors** : boolean

Return eigenvectors (True) in addition to eigenvalues

**Minv** : N x N matrix, array, sparse matrix, or linear operator

See notes in M, above.

**OPinv** : N x N matrix, array, sparse matrix, or linear operator

See notes in sigma, above.

**OPpart** : ‘r’ or ‘i’.

See notes in sigma, above

**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 [R59] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [R60].

### References

[R59], [R60]

### Examples

Find 6 eigenvectors of the identity matrix:

```
>>> id = np.identity(13)
>>> vals, vecs = sp.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** : integer

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 of k eigenvectors The v[i] is the eigenvector corresponding to the eigenvector 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. For best results, M should be of the same type as A. Additionally:

- If sigma == 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 == 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** : array

Starting vector for iteration.

**ncv** : integer

The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that ncv > 2*k

**which** : string ['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** : integer

Maximum number of Arnoldi update iterations allowed

**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** : boolean

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 [R61] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [R62].

### References

[R61], [R62]

### Examples

```
>>> id = np.identity(13)
>>> vals, vecs = sp.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*)

Solve symmetric partial eigenproblems with optional preconditioning

This function implements the Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG).

**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** : boolean, 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)

Singular values problems:

| | |
|---|---|
| `svds`(A[, k, ncv, tol]) | Compute k singular values/vectors for a sparse matrix using ARPACK. |

`scipy.sparse.linalg.`**`svds`**(*A*, *k=6*, *ncv=None*, *tol=0*)

Compute k singular values/vectors for a sparse matrix using ARPACK.

**Parameters**

**A** : sparse matrix

Array to compute the SVD on

**k** : int, optional

Number of singular values and vectors to compute.

**ncv** : integer

The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2*k

**tol** : float, optional

Tolerance for singular values. Zero (default) means machine precision.

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 A. |

`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 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 [SLU]

**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 [SLU]

**panel_size** : int, optional

Expert option for customizing the panel size. See SuperLU user's guide for details [SLU]

**options** : dict, optional

Dictionary containing additional expert options to SuperLU. See SuperLU user guide [SLU] (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.dsolve._superlu.SciPyLUType

Object, which has a `solve` method.

**See Also:**

**`spilu`**
incomplete LU decomposition

## Notes

This function uses the SuperLU library.

## References

[SLU]

`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 A.

The resulting object is an approximation to the inverse of A.

**Parameters**

**A** :

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.

**milu** : str, optional

Which version of modified ILU to use. (Choices: `silu`, `smilu_1`, `smilu_2` (default), `smilu_3`.)

**Remaining other options** :

Same as for `splu`

**Returns**

**invA_approx** : scipy.sparse.linalg.dsolve._superlu.SciPyLUType

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.

### References

[SLU]

## 4.18.4 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 incompatable.", -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 incompatable."}, '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 incompatable.", -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 incompatable."}, '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

## 4.19 Spatial algorithms and data structures (`scipy.spatial`)

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.

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` | |
| `leafnode` | |
| `node` | |
| `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 whose distance is at most r |
| `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

**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** : integer or one-dimensional array of integers

The number of pairs. Note that this is internally stored in a numpy int, and so may overflow if very large (two billion).

`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** : integer

The number of nearest neighbors to return.

**eps** : nonnegative float

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

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.

**Returns**

**d** : 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 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** : array of integers

The locations of the neighbors in self.data. i is the same shape as d.

## Examples

```
>>> from scipy.spatial import KDTree
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = KDTree(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]))
```

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

The tree containing points to search against

**r** : positive float

The maximum distance

**p** : float 1<=p<=infinity

Which Minkowski norm to use

**eps** : nonnegative float

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 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 whose distance is at most r

**Parameters**

**r** : positive float

The maximum distance

**p** : float 1<=p<=infinity

Which Minkowski norm to use

**eps** : nonnegative float

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** : set

set of pairs (i,j), i<j, for which the corresponing 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

**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 mto 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.

**leafsize** : positive integer

The number of points at which the algorithm switches over to brute-force.

## Methods

| | |
|---|---|
| `query`(self, x[, k, eps, p, distance_upper_bound]) | Query the kd-tree for nearest neighbors. |

`cKDTree.`**`query`**(*self*, *x*, *k=1*, *eps=0*, *p=2*, *distance_upper_bound=np.inf*)

Query the kd-tree for nearest neighbors.

**Parameters**

**x** : array_like, last dimension self.m

An array of points to query.

**k** : int

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** : non-negative 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.

**Returns**

**d** : ndarray 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.

## 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]) | Computes the pairwise distances between m original observations in n-dimensional space. |
| `cdist`(XA, XB[, metric, p, V, VI, w]) | Computes distance between each pair of observation vectors in the |
| `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*)

Computes the pairwise distances between m original observations in n-dimensional space. 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 the :math:'ij'th entry.

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.

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,

   $$1 - \frac{uv^T}{|u|_2 |v|_2}$$

   where |*|_2 is the 2 norm of its argument *.

7. `Y = pdist(X, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u})(v - \bar{v})^T}{|(u - \bar{u})||(v - \bar{v})|^T}$$

   where $\bar{v}$ is the mean of the elements of vector v.

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

    $$d(u, v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

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)*(u-v).T).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** : string or function

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

The weight vector (for weighted Minkowski).

**p** : double

The p-norm to apply (for Minkowski, weighted and unweighted)

**V** : ndarray

The variance vector (for standardized Euclidean).

**VI** : ndarray

The inverse of the covariance matrix (for Mahalanobis).

**Returns**

**Y** : ndarray

A condensed distance matrix.

**See Also:**

`squareform`
converts between condensed distance matrices and square distance matrices.

`scipy.spatial.distance.`**`cdist`**(*XA*, *XB*, *metric='euclidean'*, *p=2*, *V=None*, *VI=None*, *w=None*)

Computes distance between each pair of observation vectors in the Cartesian product of two collections of vectors. `XA` is a $m_A$ by $n$ array while `XB` is a $m_B$ by $n$ array. A $m_A$ by $m_B$ array is returned. An exception is thrown if `XA` and `XB` do not have the same number of columns.

A rectangular distance matrix `Y` 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.

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,

   $$\frac{1 - uv^T}{|u|_2 |v|_2}$$

   where $|*|_2$ is the 2-norm of its argument *.

7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$\frac{1 - (u - n|u|_1)(v - n|v|_1)^T}{|(u - n|u|_1)|_2 |(v - n|v|_1)|^T}$$

   where $|*|_1$ is the Manhattan (or 1-norm) of its argument, and $n$ is the common dimensionality of the vectors.

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

$$d(u,v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

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 sokalsneath 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)*(u-v).T).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.

**XB** : ndarray

An $m_B$ by $n$ array of $m_B$ original observations in an $n$-dimensional space.

**metric** : string or function

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', 'wminkowski', 'yule'.

**w** : ndarray

The weight vector (for weighted Minkowski).

**p** : double

The p-norm to apply (for Minkowski, weighted and unweighted)

**V** : ndarray

The variance vector (for standardized Euclidean).

**VI** : ndarray

The inverse of the covariance matrix (for Mahalanobis).

**Returns**

**Y** : ndarray

A $m_A$ by $m_B$ distance matrix.

`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.

**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.

**force**

[string] 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] 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.

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 the variable D passed is a valid distance matrix. |
| `is_valid_y`(y[, warning, throw, name]) | Returns `True` if the variable `y` passed is a valid condensed |
| `num_obs_dm`(d) | Returns the number of original observations that correspond to a |
| `num_obs_y`(Y) | Returns the number of original observations that correspond to a |

`scipy.spatial.distance.`**`is_valid_dm`**`(`*D*, *tol=0.0*, *throw=False*, *name='D'*, *warning=False*`)`

Returns True if the variable D passed 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** : double

The distance matrix should be symmetric. tol is the maximum difference between the :math:'ij'th entry and the :math:'ji'th entry for the distance metric to be considered symmetric.

**throw** : bool

An exception is thrown if the distance matrix passed is not valid.

**name** : string

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

Instead of throwing an exception, a warning message is raised.

**Returns**

**Returns ‘‘True‘‘ if the variable ‘‘D‘‘ passed is a valid** :

**distance matrix. 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 variable `y` passed 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.

**throws** : throw, 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 `D`.

**Parameters**

**d** : ndarray

The target distance matrix.

**Returns**

**numobs** : 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 `Y`.

**Parameters**

**Y** : ndarray

The number of original observations in the condensed observation `Y`.

**Returns**

**n** : int

The number of observations in the condensed distance matrix passed.

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 n-vectors `u` and |
| `canberra`(u, v) | Computes the Canberra distance between two n-vectors u and v, |
| `chebyshev`(u, v) | Computes the Chebyshev distance between two n-vectors u and v, |
| `cityblock`(u, v) | Computes the Manhattan distance between two n-vectors u and v, |
| `correlation`(u, v) | Computes the correlation distance between two n-vectors `u` and `v`, which is defined as .. |
| `cosine`(u, v) | Computes the Cosine distance between two n-vectors u and v, which |
| `dice`(u, v) | Computes the Dice dissimilarity between two boolean n-vectors |
| `euclidean`(u, v) | Computes the Euclidean distance between two n-vectors `u` and `v`, |
| `hamming`(u, v) | Computes the Hamming distance between two n-vectors `u` and |
| `jaccard`(u, v) | Computes the Jaccard-Needham dissimilarity between two boolean |
| `kulsinski`(u, v) | Computes the Kulsinski dissimilarity between two boolean n-vectors |
| `mahalanobis`(u, v, VI) | Computes the Mahalanobis distance between two n-vectors `u` and `v`, |
| `matching`(u, v) | Computes the Matching dissimilarity between two boolean n-vectors |
| `minkowski`(u, v, p) | Computes the Minkowski distance between two vectors `u` and `v`, |
| `rogerstanimoto`(u, v) | Computes the Rogers-Tanimoto dissimilarity between two boolean |
| `russellrao`(u, v) | Computes the Russell-Rao dissimilarity between two boolean n-vectors |
| `seuclidean`(u, v, V) | Returns the standardized Euclidean distance between two n-vectors |
| `sokalmichener`(u, v) | Computes the Sokal-Michener dissimilarity between two boolean vectors |
| `sokalsneath`(u, v) | Computes the Sokal-Sneath dissimilarity between two boolean vectors |
| `sqeuclidean`(u, v) | Computes the squared Euclidean distance between two n-vectors u and v, |
| `yule`(u, v) | Computes the Yule dissimilarity between two boolean n-vectors u and v, |

`scipy.spatial.distance.`**`braycurtis`**(*u*, *v*)

Computes the Bray-Curtis distance between two n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Bray-Curtis distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`canberra`**(*u*, *v*)

Computes the Canberra distance between two n-vectors u and v, which is defined as

$$\sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Canberra distance between vectors `u` and `v`.

## Notes

Whe 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 between two n-vectors u and v, which is defined as

$$\max_i |u_i - v_i|.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Chebyshev distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`cityblock`**`(`*u*, *v*`)`

Computes the Manhattan distance between two n-vectors u and v, which is defined as

$$\sum_i |u_i - v_i|.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The City Block distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`correlation`**`(`*u*, *v*`)`

Computes the correlation distance between two n-vectors `u` and `v`, which is defined as

$$1 - frac(u - \bar{u})(v - \bar{v})^T ||(u - \bar{u})||_2 ||(v - \bar{v})||_2^T$$

where $\bar{u}$ is the mean of a vectors elements and `n` is the common dimensionality of `u` and `v`.

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The correlation distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`cosine`**`(`*u*, *v*`)`

Computes the Cosine distance between two n-vectors u and v, which is defined as

$$1 - \frac{uv^T}{||u||_2||v||_2}.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Cosine distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`dice`**`(`*u*, *v*`)`

Computes the Dice dissimilarity between two boolean n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Dice dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`euclidean`**`(`*u*, *v*`)`

Computes the Euclidean distance between two n-vectors `u` and `v`, which is defined as

$$||u - v||_2$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`hamming`**`(`*u*, *v*`)`

Computes the Hamming distance between two n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Hamming distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`jaccard`**`(`*u*, *v*`)`

**Computes the Jaccard-Needham dissimilarity between two boolean**

n-vectors u and v, which is

**rac{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** : ndarray

An $n$-dimensional vector.

**v**

[ndarray] An $n$-dimensional vector.

**Returns**

**d** : double

The Jaccard distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`kulsinski`**`(`*u*, *v*`)`

**Computes the Kulsinski dissimilarity between two boolean n-vectors**

u and v, which is defined as

**rac{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** : ndarray

An $n$-dimensional vector.

**v**

[ndarray] An $n$-dimensional vector.

**Returns**

**d** : double

The Kulsinski distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`mahalanobis`**`(`*u*, *v*, *VI*`)`

Computes the Mahalanobis distance between two n-vectors `u` and `v`, which is defiend as

$$(u - v)V^{-1}(u - v)^T$$

where `VI` is the inverse covariance matrix $V^{-1}$.

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Mahalanobis distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`matching`**`(`*u*, *v*`)`

Computes the Matching dissimilarity between two boolean n-vectors u and v, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Matching dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`minkowski`**(*u*, *v*, *p*)

Computes the Minkowski distance between two vectors `u` and `v`, defined as

$$||u-v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$

**Parameters**

**u** : ndarray

An n-dimensional vector.

**v** : ndarray

An n-dimensional vector.

**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 n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Rogers-Tanimoto dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`russellrao`**(*u*, *v*)

Computes the Russell-Rao dissimilarity between two boolean n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Russell-Rao dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`seuclidean`**`(`*u*, *v*, *V*`)`

Returns the standardized Euclidean distance between two n-vectors `u` and `v`. `V` is an n-dimensional vector of component variances. It is usually computed among a larger collection vectors.

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**V** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The standardized Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`sokalmichener`**`(`*u*, *v*`)`

Computes the Sokal-Michener dissimilarity between two boolean vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Sokal-Michener dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`sokalsneath`**`(`*u*, *v*`)`

Computes the Sokal-Sneath dissimilarity between two boolean vectors `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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Sokal-Sneath dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`sqeuclidean`**(*u*, *v*)

Computes the squared Euclidean distance between two n-vectors u and v, which is defined as

$$||u - v||_2^2.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The squared Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`yule`**(*u*, *v*)

Computes the Yule dissimilarity between two boolean n-vectors u and v, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Yule dissimilarity between vectors `u` and `v`.

## References

## Copyright Notice

## Functions

| | |
|---|---|
| `braycurtis`(u, v) | Computes the Bray-Curtis distance between two n-vectors `u` and |
| `canberra`(u, v) | Computes the Canberra distance between two n-vectors u and v, |
| `cdist`(XA, XB[, metric, p, V, VI, w]) | Computes distance between each pair of observation vectors in the |
| `chebyshev`(u, v) | Computes the Chebyshev distance between two n-vectors u and v, |
| `cityblock`(u, v) | Computes the Manhattan distance between two n-vectors u and v, |
| `correlation`(u, v) | Computes the correlation distance between two n-vectors `u` and `v`, which is defined as .. |
| `cosine`(u, v) | Computes the Cosine distance between two n-vectors u and v, which |
| `dice`(u, v) | Computes the Dice dissimilarity between two boolean n-vectors |
| `euclidean`(u, v) | Computes the Euclidean distance between two n-vectors `u` and `v`, |
| `hamming`(u, v) | Computes the Hamming distance between two n-vectors `u` and |
| `is_valid_dm`(D[, tol, throw, name, warning]) | Returns True if the variable D passed is a valid distance matrix. |
| `is_valid_y`(y[, warning, throw, name]) | Returns `True` if the variable `y` passed is a valid condensed |
| `jaccard`(u, v) | Computes the Jaccard-Needham dissimilarity between two boolean |
| `kulsinski`(u, v) | Computes the Kulsinski dissimilarity between two boolean n-vectors |
| `mahalanobis`(u, v, VI) | Computes the Mahalanobis distance between two n-vectors `u` and `v`, |
| `matching`(u, v) | Computes the Matching dissimilarity between two boolean n-vectors |
| `minkowski`(u, v, p) | Computes the Minkowski distance between two vectors `u` and `v`, |
| `norm`(x[, ord]) | Matrix or vector norm. |
| `num_obs_dm`(d) | Returns the number of original observations that correspond to a |
| `num_obs_y`(Y) | Returns the number of original observations that correspond to a |
| `pdist`(X[, metric, p, w, V, VI]) | Computes the pairwise distances between m original observations in n-dimensional space. |
| `rogerstanimoto`(u, v) | Computes the Rogers-Tanimoto dissimilarity between two boolean |
| `russellrao`(u, v) | Computes the Russell-Rao dissimilarity between two boolean n-vectors |
| `seuclidean`(u, v, V) | Returns the standardized Euclidean distance between two n-vectors |
| `sokalmichener`(u, v) | Computes the Sokal-Michener dissimilarity between two boolean vectors |
| `sokalsneath`(u, v) | Computes the Sokal-Sneath dissimilarity between two boolean vectors |
| `sqeuclidean`(u, v) | Computes the squared Euclidean distance between two n-vectors u and v, |
| `squareform`(X[, force, checks]) | Converts a vector-form distance vector to a square-form distance matrix, and vice-versa. |
| `wminkowski`(u, v, p, w) | Computes the weighted Minkowski distance between two vectors `u` |
| `yule`(u, v) | Computes the Yule dissimilarity between two boolean n-vectors u and v, |

Delaunay triangulation:

| | |
|---|---|
| `Delaunay`(points) | Delaunay tesselation in N dimensions |
| `tsearch`(tri, xi) | Find simplices containing the given points. |

**class** `scipy.spatial.`**`Delaunay`**(*points*)

Delaunay tesselation in N dimensions New in version 0.9.

**Parameters**

**points** : ndarray of floats, shape (npoints, ndim)

Coordinates of points to triangulate

### Notes

The tesselation is computed using the Qhull libary [Qhull].

### References

[Qhull]

### 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. |

`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.

| | | |
|---|---|---|
| points | ndarray of double, shape (npoints, ndim) | Points in the triangulation |
| vertices | ndarray of ints, shape (nsimplex, ndim+1) | Indices of vertices forming simplices in the triangulation |
| 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.) |

### Methods

| | |
|---|---|
| `find_simplex`(xi[, bruteforce]) | Find the simplices containing the given points. |
| `lift_points`(tri, x) | Lift points to the Qhull paraboloid. |
| `plane_distance`(xi) | Compute hyperplane distances to the point *xi* from all simplices. |

`Delaunay.`**`find_simplex`**(*xi*, *bruteforce=False*)

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

**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`**(*tri*, *x*)

Lift points to the Qhull paraboloid.

`Delaunay.`**`plane_distance`**(*xi*)

Compute hyperplane distances to the point *xi* from all simplices.

`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`

## 4.20 Distance computations (`scipy.spatial.distance`)

### 4.20.1 Function Reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

| | |
|---|---|
| `pdist`(X[, metric, p, w, V, VI]) | Computes the pairwise distances between m original observations in n-dimensional space. |
| `cdist`(XA, XB[, metric, p, V, VI, w]) | Computes distance between each pair of observation vectors in the |
| `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*)

Computes the pairwise distances between m original observations in n-dimensional space. 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 the :math:'ij'th entry.

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.

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,

   $$1 - \frac{uv^T}{|u|_2 |v|_2}$$

   where |*|_2 is the 2 norm of its argument *.

7. `Y = pdist(X, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u})(v - \bar{v})^T}{|(u - \bar{u})||(v - \bar{v})|^T}$$

   where $\bar{v}$ is the mean of the elements of vector v.

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

    $$d(u,v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

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)*(u-v).T).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** : string or function

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

The weight vector (for weighted Minkowski).

**p** : double

The p-norm to apply (for Minkowski, weighted and unweighted)

**V** : ndarray

The variance vector (for standardized Euclidean).

**VI** : ndarray

The inverse of the covariance matrix (for Mahalanobis).

**Returns**

**Y** : ndarray

A condensed distance matrix.

**See Also:**

**squareform**
converts between condensed distance matrices and square distance matrices.

`scipy.spatial.distance.`**`cdist`**(*XA*, *XB*, *metric='euclidean'*, *p=2*, *V=None*, *VI=None*, *w=None*)

Computes distance between each pair of observation vectors in the Cartesian product of two collections of vectors. `XA` is a $m_A$ by $n$ array while `XB` is a $m_B$ by $n$ array. A $m_A$ by $m_B$ array is returned. An exception is thrown if `XA` and `XB` do not have the same number of columns.

A rectangular distance matrix `Y` 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.

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,

$$\frac{1 - uv^T}{|u|_2 |v|_2}$$

   where $|*|_2$ is the 2-norm of its argument *.

7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

$$\frac{1 - (u - n|u|_1)(v - n|v|_1)^T}{|(u - n|u|_1)|_2 |(v - n|v|_1)|^T}$$

   where $|*|_1$ is the Manhattan (or 1-norm) of its argument, and $n$ is the common dimensionality of the vectors.

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

$$d(u, v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

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 sokalsneath 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)*(u-v).T).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.

**XB** : ndarray

An $m_B$ by $n$ array of $m_B$ original observations in an $n$-dimensional space.

**metric** : string or function

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', 'wminkowski', 'yule'.

**w** : ndarray

The weight vector (for weighted Minkowski).

**p** : double

The p-norm to apply (for Minkowski, weighted and unweighted)

**V** : ndarray

The variance vector (for standardized Euclidean).

**VI** : ndarray

The inverse of the covariance matrix (for Mahalanobis).

**Returns**

**Y** : ndarray

A $m_A$ by $m_B$ distance matrix.

`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.

**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.

**force**

[string] 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] 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.

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 the variable D passed is a valid distance matrix. |
| `is_valid_y`(y[, warning, throw, name]) | Returns `True` if the variable `y` passed is a valid condensed |
| `num_obs_dm`(d) | Returns the number of original observations that correspond to a |
| `num_obs_y`(Y) | Returns the number of original observations that correspond to a |

`scipy.spatial.distance.`**`is_valid_dm`**(*D*, *tol=0.0*, *throw=False*, *name='D'*, *warning=False*)

Returns True if the variable D passed 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** : double

The distance matrix should be symmetric. tol is the maximum difference between the :math:'ij'th entry and the :math:'ji'th entry for the distance metric to be considered symmetric.

**throw** : bool

An exception is thrown if the distance matrix passed is not valid.

**name** : string

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

Instead of throwing an exception, a warning message is raised.

**Returns**

**Returns ''True'' if the variable ''D'' passed is a valid** :

**distance matrix. 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 variable `y` passed 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.

**throws** : throw, 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 `D`.

**Parameters**

**d** : ndarray

The target distance matrix.

**Returns**

**numobs** : 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 `Y`.

**Parameters**

**Y** : ndarray

The number of original observations in the condensed observation `Y`.

**Returns**

**n** : int

The number of observations in the condensed distance matrix passed.

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 n-vectors `u` and |
| `canberra`(u, v) | Computes the Canberra distance between two n-vectors u and v, |
| `chebyshev`(u, v) | Computes the Chebyshev distance between two n-vectors u and v, |
| `cityblock`(u, v) | Computes the Manhattan distance between two n-vectors u and v, |
| `correlation`(u, v) | Computes the correlation distance between two n-vectors `u` and `v`, which is defined as .. |
| `cosine`(u, v) | Computes the Cosine distance between two n-vectors u and v, which |
| `dice`(u, v) | Computes the Dice dissimilarity between two boolean n-vectors |
| `euclidean`(u, v) | Computes the Euclidean distance between two n-vectors `u` and `v`, |
| `hamming`(u, v) | Computes the Hamming distance between two n-vectors `u` and |
| `jaccard`(u, v) | Computes the Jaccard-Needham dissimilarity between two boolean |
| `kulsinski`(u, v) | Computes the Kulsinski dissimilarity between two boolean n-vectors |
| `mahalanobis`(u, v, VI) | Computes the Mahalanobis distance between two n-vectors `u` and `v`, |
| `matching`(u, v) | Computes the Matching dissimilarity between two boolean n-vectors |
| `minkowski`(u, v, p) | Computes the Minkowski distance between two vectors `u` and `v`, |
| `rogerstanimoto`(u, v) | Computes the Rogers-Tanimoto dissimilarity between two boolean |
| `russellrao`(u, v) | Computes the Russell-Rao dissimilarity between two boolean n-vectors |
| `seuclidean`(u, v, V) | Returns the standardized Euclidean distance between two n-vectors |
| `sokalmichener`(u, v) | Computes the Sokal-Michener dissimilarity between two boolean vectors |
| `sokalsneath`(u, v) | Computes the Sokal-Sneath dissimilarity between two boolean vectors |
| `sqeuclidean`(u, v) | Computes the squared Euclidean distance between two n-vectors u and v, |
| `yule`(u, v) | Computes the Yule dissimilarity between two boolean n-vectors u and v, |

`scipy.spatial.distance.`**`braycurtis`**(*u*, *v*)

Computes the Bray-Curtis distance between two n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Bray-Curtis distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`canberra`**(*u*, *v*)

Computes the Canberra distance between two n-vectors u and v, which is defined as

$$\sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Canberra distance between vectors `u` and `v`.

### Notes

Whe 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 between two n-vectors u and v, which is defined as

$$\max_i |u_i - v_i|.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Chebyshev distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`cityblock`**(*u*, *v*)

Computes the Manhattan distance between two n-vectors u and v, which is defined as

$$\sum_i |u_i - v_i|.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The City Block distance between vectors `u` and `v`.

scipy.spatial.distance.**correlation**(*u*, *v*)

Computes the correlation distance between two n-vectors u and v, which is defined as

$$1 - frac(u - \bar{u})(v - \bar{v})^T ||(u - \bar{u})||_2 ||(v - \bar{v})||_2^T$$

where $\bar{u}$ is the mean of a vectors elements and n is the common dimensionality of u and v.

**Parameters**
**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The correlation distance between vectors u and v.

scipy.spatial.distance.**cosine**(*u*, *v*)

Computes the Cosine distance between two n-vectors u and v, which is defined as

$$1 - \frac{uv^T}{||u||_2 ||v||_2}.$$

**Parameters**
**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The Cosine distance between vectors u and v.

scipy.spatial.distance.**dice**(*u*, *v*)

Computes the Dice dissimilarity between two boolean n-vectors u and v, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The Dice dissimilarity between vectors u and v.

scipy.spatial.distance.**euclidean**(*u*, *v*)

Computes the Euclidean distance between two n-vectors u and v, which is defined as

$$||u - v||_2$$

**Parameters**
**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`hamming`**`(`*u*, *v*`)`

Computes the Hamming distance between two n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The Hamming distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`jaccard`**`(`*u*, *v*`)`

**Computes the Jaccard-Needham dissimilarity between two boolean**
n-vectors u and v, which is

**rac{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** : ndarray

An $n$-dimensional vector.

**v**

[ndarray] An $n$-dimensional vector.

**Returns**
**d** : double

The Jaccard distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`kulsinski`**`(`*u*, *v*`)`

**Computes the Kulsinski dissimilarity between two boolean n-vectors**
u and v, which is defined as

**rac{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** : ndarray

An $n$-dimensional vector.

**v**
[ndarray] An $n$-dimensional vector.

**Returns**
**d** : double

The Kulsinski distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`mahalanobis`**`(`*u*, *v*, *VI*`)`
Computes the Mahalanobis distance between two n-vectors `u` and `v`, which is defiend as

$$(u - v)V^{-1}(u - v)^T$$

where `VI` is the inverse covariance matrix $V^{-1}$.

**Parameters**
**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**
**d** : double

The Mahalanobis distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`matching`**`(`*u*, *v*`)`
Computes the Matching dissimilarity between two boolean n-vectors u and v, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Matching dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`minkowski`**(*u*, *v*, *p*)

Computes the Minkowski distance between two vectors `u` and `v`, defined as

$$||u - v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$

**Parameters**

**u** : ndarray

An n-dimensional vector.

**v** : ndarray

An n-dimensional vector.

**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 n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Rogers-Tanimoto dissimilarity between vectors *u* and *v*.

`scipy.spatial.distance.`**`russellrao`**(*u*, *v*)

Computes the Russell-Rao dissimilarity between two boolean n-vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Russell-Rao dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`seuclidean`**`(`*u*, *v*, *V*`)`

Returns the standardized Euclidean distance between two n-vectors `u` and `v`. `V` is an n-dimensional vector of component variances. It is usually computed among a larger collection vectors.

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**V** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The standardized Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`sokalmichener`**`(`*u*, *v*`)`

Computes the Sokal-Michener dissimilarity between two boolean vectors `u` and `v`, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Sokal-Michener dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`sokalsneath`**`(`*u*, *v*`)`

Computes the Sokal-Sneath dissimilarity between two boolean vectors `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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Sokal-Sneath dissimilarity between vectors `u` and `v`.

`scipy.spatial.distance.`**`sqeuclidean`**`(u, v)`

Computes the squared Euclidean distance between two n-vectors u and v, which is defined as

$$||u - v||_2^2.$$

**Parameters**

**u** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The squared Euclidean distance between vectors `u` and `v`.

`scipy.spatial.distance.`**`yule`**`(u, v)`

Computes the Yule dissimilarity between two boolean n-vectors u and v, which 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** : ndarray

An $n$-dimensional vector.

**v** : ndarray

An $n$-dimensional vector.

**Returns**

**d** : double

The Yule dissimilarity between vectors `u` and `v`.

### 4.20.2 References

### 4.20.3 Copyright Notice

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## 4.21 Special functions (`scipy.special`)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules. Exceptions are noted.

### 4.21.1 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` | errprint({flag}) sets the error printing flag for special functions |

`scipy.special.`**`errprint`**`()`

errprint({flag}) sets the error printing flag for special functions (from the cephesmodule). The output is the previous state. With errprint(0) no error messages are shown; the default is errprint(1). If no argument is given the current state of the flag is returned and no change occurs.

### 4.21.2 Available functions

#### Airy functions

| | |
|---|---|
| `airy`(x[, out1, out2, out3, out4]) | (Ai,Aip,Bi,Bip)=airy(z) calculates the Airy functions and their derivatives |
| `airye`(x[, out1, out2, out3, out4]) | (Aie,Aipe,Bie,Bipe)=airye(z) calculates the exponentially scaled Airy functions and |
| `ai_zeros`(nt) | Compute the zeros of Airy Functions Ai(x) and Ai'(x), a and a' |
| `bi_zeros`(nt) | Compute the zeros of Airy Functions Bi(x) and Bi'(x), b and b' |

`scipy.special.`**`airy`**`(`*x*[, *out1*, *out2*, *out3*, *out4*] **= <ufunc 'airy'>**`)`

(Ai,Aip,Bi,Bip)=airy(z) calculates the Airy functions and their derivatives evaluated at real or complex number z. The Airy functions Ai and Bi are two independent solutions of y''(x)=xy. Aip and Bip are the first derivatives evaluated at x of Ai and Bi respectively.

`scipy.special.`**`airye`**`(`*x*[, *out1*, *out2*, *out3*, *out4*] **= <ufunc 'airye'>**`)`

(Aie,Aipe,Bie,Bipe)=airye(z) calculates the exponentially scaled Airy functions and their derivatives evaluated at real or complex number z. airye(z)[0:1] = airy(z)[0:1] * exp(2.0/3.0*z*sqrt(z)) airye(z)[2:3] = airy(z)[2:3] * exp(-abs((2.0/3.0*z*sqrt(z)).real))

`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])** :

### Elliptic Functions and Integrals

| | |
|---|---|
| ellipj(x1, x2[, out1, out2, out3, out4]) | (sn,cn,dn,ph)=ellipj(u,m) calculates the Jacobian elliptic functions of |
| ellipk(...) | This function is rather imprecise around m==1. |
| ellipkm1(x[, out]) | y=ellipkm1(1 - m) returns the complete integral of the first kind: |
| ellipkinc(x1, x2[, out]) | y=ellipkinc(phi,m) returns the incomplete elliptic integral of the first |
| ellipe(x[, out]) | y=ellipe(m) returns the complete integral of the second kind: |
| ellipeinc(x1, x2[, out]) | y=ellipeinc(phi,m) returns the incomplete elliptic integral of the |

scipy.special.**ellipj**(*x1*, *x2*[, *out1*, *out2*, *out3*, *out4*] = **<ufunc 'ellipj'>**)

(sn,cn,dn,ph)=ellipj(u,m) calculates the Jacobian elliptic functions of parameter m between 0 and 1, and real u. The returned functions are often written sn(u|m), cn(u|m), and dn(u|m). The value of 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) returns the complete integral of the first kind: integral(1/sqrt(1-m*sin(t)**2), t=0..pi/2*)

This function is rather imprecise around m==1. For more precision around this point, use ellipkm1.

scipy.special.**ellipkm1**(*x*[, *out*] = **<ufunc 'ellipkm1'>**)

y=ellipkm1(1 - m) returns the complete integral of the first kind: integral(1/sqrt(1-m*sin(t)**2),t=0..pi/2)

scipy.special.**ellipkinc**(*x1*, *x2*[, *out*] = **<ufunc 'ellipkinc'>**)

y=ellipkinc(phi,m) returns the incomplete elliptic integral of the first kind: integral(1/sqrt(1-m*sin(t)**2),t=0..phi)

scipy.special.**ellipe**(*x*[, *out*] = **<ufunc 'ellipe'>**)

y=ellipe(m) returns the complete integral of the second kind: integral(sqrt(1-m*sin(t)**2),t=0..pi/2)

scipy.special.**ellipeinc**(*x1*, *x2*[, *out*] = **<ufunc 'ellipeinc'>**)

y=ellipeinc(phi,m) returns the incomplete elliptic integral of the second kind: integral(sqrt(1-m*sin(t)**2),t=0..phi)

### Bessel Functions

| | |
|---|---|
| `jn`(x1, x2[, out]) | y=jv(v,z) returns the Bessel function of real order v at complex z. |
| `jv`(x1, x2[, out]) | y=jv(v,z) returns the Bessel function of real order v at complex z. |
| `jve`(x1, x2[, out]) | y=jve(v,z) returns the exponentially scaled Bessel function of real order |
| `yn`(x1, x2[, out]) | y=yn(n,x) returns the Bessel function of the second kind of integer |
| `yv`(x1, x2[, out]) | y=yv(v,z) returns the Bessel function of the second kind of real |
| `yve`(x1, x2[, out]) | y=yve(v,z) returns the exponentially scaled Bessel function of the second |
| `kn`(x1, x2[, out]) | y=kn(n,x) returns the modified Bessel function of the second kind (sometimes called the third kind) for |
| `kv`(x1, x2[, out]) | y=kv(v,z) returns the modified Bessel function of the second kind (sometimes called the third kind) for |
| `kve`(x1, x2[, out]) | y=kve(v,z) returns the exponentially scaled, modified Bessel function |
| `iv`(x1, x2[, out]) | y=iv(v,z) returns the modified Bessel function of real order v of |
| `ive`(x1, x2[, out]) | y=ive(v,z) returns the exponentially scaled modified Bessel function of |
| `hankel1`(x1, x2[, out]) | y=hankel1(v,z) returns the Hankel function of the first kind for real order v and complex argument z. |
| `hankel1e`(x1, x2[, out]) | y=hankel1e(v,z) returns the exponentially scaled Hankel function of the first |
| `hankel2`(x1, x2[, out]) | y=hankel2(v,z) returns the Hankel function of the second kind for real order v and complex argument z. |
| `hankel2e`(x1, x2[, out]) | y=hankel2e(v,z) returns the exponentially scaled Hankel function of the second |

`scipy.special.`**`jn`**(*x1*, *x2*[, *out*] = **<ufunc 'jv'>**)
y=jv(v,z) returns the Bessel function of real order v at complex z.

`scipy.special.`**`jv`**(*x1*, *x2*[, *out*] = **<ufunc 'jv'>**)
y=jv(v,z) returns the Bessel function of real order v at complex z.

`scipy.special.`**`jve`**(*x1*, *x2*[, *out*] = **<ufunc 'jve'>**)
y=jve(v,z) returns the exponentially scaled Bessel function of real order v at complex z: jve(v,z) = jv(v,z) * exp(-abs(z.imag))

`scipy.special.`**`yn`**(*x1*, *x2*[, *out*] = **<ufunc 'yn'>**)
y=yn(n,x) returns the Bessel function of the second kind of integer order n at x.

`scipy.special.`**`yv`**(*x1*, *x2*[, *out*] = **<ufunc 'yv'>**)
y=yv(v,z) returns the Bessel function of the second kind of real order v at complex z.

`scipy.special.`**`yve`**(*x1*, *x2*[, *out*] = **<ufunc 'yve'>**)
y=yve(v,z) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'kn'>**)
y=kn(n,x) returns the modified Bessel function of the second kind (sometimes called the third kind) for integer order n at x.

`scipy.special.`**`kv`**(*x1*, *x2*[, *out*] = **<ufunc 'kv'>**)
y=kv(v,z) returns the modified Bessel function of the second kind (sometimes called the third kind) for real order v at complex z.

`scipy.special.`**`kve`**(*x1*, *x2*[, *out*] = **<ufunc 'kve'>**)
y=kve(v,z) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'iv'>**)
y=iv(v,z) returns the modified Bessel function of real order v of z. If z is of real type and negative, v must be

integer valued.

`scipy.special.`**`ive`**(*x1*, *x2*[, *out*] = **<ufunc 'ive'>**)
y=ive(v,z) returns the exponentially scaled modified Bessel function of real order v and complex z: ive(v,z) = iv(v,z) * exp(-abs(z.real))

`scipy.special.`**`hankel1`**(*x1*, *x2*[, *out*] = **<ufunc 'hankel1'>**)
y=hankel1(v,z) returns the Hankel function of the first kind for real order v and complex argument z.

`scipy.special.`**`hankel1e`**(*x1*, *x2*[, *out*] = **<ufunc 'hankel1e'>**)
y=hankel1e(v,z) returns the exponentially scaled Hankel function of the first kind for real order v and complex argument z: hankel1e(v,z) = hankel1(v,z) * exp(-1j * z)

`scipy.special.`**`hankel2`**(*x1*, *x2*[, *out*] = **<ufunc 'hankel2'>**)
y=hankel2(v,z) returns the Hankel function of the second kind for real order v and complex argument z.

`scipy.special.`**`hankel2e`**(*x1*, *x2*[, *out*] = **<ufunc 'hankel2e'>**)
y=hankel2e(v,z) returns the exponentially scaled Hankel function of the second kind for real order v and complex argument z: hankel1e(v,z) = hankel1(v,z) * exp(1j * z)

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' |
| `jnyn_zeros`(n, nt) | Compute nt zeros of the Bessel functions Jn(x), Jn'(x), Yn(x), and |
| `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 |
| `y1_zeros`(nt[, complex]) | Returns nt (complex or real) zeros of Y1(z), z1, and the value |
| `y1p_zeros`(nt[, complex]) | Returns nt (complex or real) zeros of Y1'(z), z1', and the value |

`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 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[, out]) | y=j0(x) returns the Bessel function of order 0 at x. |
| j1(x[, out]) | y=j1(x) returns the Bessel function of order 1 at x. |
| y0(x[, out]) | y=y0(x) returns the Bessel function of the second kind of order 0 at x. |
| y1(x[, out]) | y=y1(x) returns the Bessel function of the second kind of order 1 at x. |
| i0(x[, out]) | y=i0(x) returns the modified Bessel function of order 0 at x. |
| i0e(x[, out]) | y=i0e(x) returns the exponentially scaled modified Bessel function |
| i1(x[, out]) | y=i1(x) returns the modified Bessel function of order 1 at x. |
| i1e(x[, out]) | y=i1e(x) returns the exponentially scaled modified Bessel function |
| k0(x[, out]) | y=k0(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of |
| k0e(x[, out]) | y=k0e(x) returns the exponentially scaled modified Bessel function |
| k1(x[, out]) | y=i1(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of |
| k1e(x[, out]) | y=k1e(x) returns the exponentially scaled modified Bessel function |

scipy.special.**j0**(*x*[, *out*] = **<ufunc 'j0'>**)
y=j0(x) returns the Bessel function of order 0 at x.

scipy.special.**j1**(*x*[, *out*] = **<ufunc 'j1'>**)
y=j1(x) returns the Bessel function of order 1 at x.

scipy.special.**y0**(*x*[, *out*] = **<ufunc 'y0'>**)
y=y0(x) returns the Bessel function of the second kind of order 0 at x.

scipy.special.**y1**(*x*[, *out*] = **<ufunc 'y1'>**)
y=y1(x) returns the Bessel function of the second kind of order 1 at x.

scipy.special.**i0**(*x*[, *out*] = **<ufunc 'i0'>**)
y=i0(x) returns the modified Bessel function of order 0 at x.

`scipy.special.`**`i0e`**(*x*[, *out* ] = **<ufunc 'i0e'>**)
y=i0e(x) returns the exponentially scaled modified Bessel function of order 0 at x. i0e(x) = exp(-|x|) * i0(x).

`scipy.special.`**`i1`**(*x*[, *out* ] = **<ufunc 'i1'>**)
y=i1(x) returns the modified Bessel function of order 1 at x.

`scipy.special.`**`i1e`**(*x*[, *out* ] = **<ufunc 'i1e'>**)
y=i1e(x) returns the exponentially scaled modified Bessel function of order 0 at x. i1e(x) = exp(-|x|) * i1(x).

`scipy.special.`**`k0`**(*x*[, *out* ] = **<ufunc 'k0'>**)
y=k0(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of order 0 at x.

`scipy.special.`**`k0e`**(*x*[, *out* ] = **<ufunc 'k0e'>**)
y=k0e(x) returns the exponentially scaled modified Bessel function of the second kind (sometimes called the third kind) of order 0 at x. k0e(x) = exp(x) * k0(x).

`scipy.special.`**`k1`**(*x*[, *out* ] = **<ufunc 'k1'>**)
y=i1(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of order 1 at x.

`scipy.special.`**`k1e`**(*x*[, *out* ] = **<ufunc 'k1e'>**)
y=k1e(x) returns the exponentially scaled modified Bessel function of the second kind (sometimes called the third kind) of order 1 at x. k1e(x) = exp(x) * k1(x)

## Integrals of Bessel Functions

| | |
|---|---|
| `itj0y0`(x[, out1, out2]) | (ij0,iy0)=itj0y0(x) returns simple integrals from 0 to x of the zeroth order |
| `it2j0y0`(x[, out1, out2]) | (ij0,iy0)=it2j0y0(x) returns the integrals int((1-j0(t))/t,t=0..x) and |
| `iti0k0`(x[, out1, out2]) | (ii0,ik0)=iti0k0(x) returns simple integrals from 0 to x of the zeroth order |
| `it2i0k0`(x[, out1, out2]) | (ii0,ik0)=it2i0k0(x) returns the integrals int((i0(t)-1)/t,t=0..x) and |
| `besselpoly`(x1, x2, x3[, out]) | y=besselpoly(a,lam,nu) returns the value of the integral: |

`scipy.special.`**`itj0y0`**(*x*[, *out1*, *out2* ] = **<ufunc 'itj0y0'>**)
(ij0,iy0)=itj0y0(x) returns simple integrals from 0 to x of the zeroth order bessel functions j0 and y0.

`scipy.special.`**`it2j0y0`**(*x*[, *out1*, *out2* ] = **<ufunc 'it2j0y0'>**)
(ij0,iy0)=it2j0y0(x) returns the integrals int((1-j0(t))/t,t=0..x) and int(y0(t)/t,t=x..infinitity).

`scipy.special.`**`iti0k0`**(*x*[, *out1*, *out2* ] = **<ufunc 'iti0k0'>**)
(ii0,ik0)=iti0k0(x) returns simple integrals from 0 to x of the zeroth order modified bessel functions i0 and k0.

`scipy.special.`**`it2i0k0`**(*x*[, *out1*, *out2* ] = **<ufunc 'it2i0k0'>**)
(ii0,ik0)=it2i0k0(x) returns the integrals int((i0(t)-1)/t,t=0..x) and int(k0(t)/t,t=x..infinitity).

`scipy.special.`**`besselpoly`**(*x1*, *x2*, *x3*[, *out* ] = **<ufunc 'besselpoly'>**)
y=besselpoly(a,lam,nu) returns the value of the integral: integral(x**lam * jv(nu,2*a*x),x=0..1).

## 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 |
| `sph_yn`(n, z) | Compute the spherical Bessel function yn(z) and its derivative for |
| `sph_jnyn`(n, z) | Compute the spherical Bessel functions, jn(z) and yn(z) and their |
| `sph_in`(n, z) | Compute the spherical Bessel function in(z) and its derivative for |
| `sph_kn`(n, z) | Compute the spherical Bessel function kn(z) and its derivative for |
| `sph_inkn`(n, z) | Compute the spherical Bessel functions, in(z) and kn(z) and their |

`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 |
| `riccati_yn`(n, x) | Compute the Ricatti-Bessel function of the second kind and its |

`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`(x1, x2[, out]) | y=struve(v,x) returns the Struve function Hv(x) of order v at x, x |
| `modstruve`(x1, x2[, out]) | y=modstruve(v,x) returns the modified Struve function Lv(x) of order |
| `itstruve0`(x[, out]) | y=itstruve0(x) returns the integral of the Struve function of order 0 |
| `it2struve0`(x[, out]) | y=it2struve0(x) returns the integral of the Struve function of order 0 |
| `itmodstruve0`(x[, out]) | y=itmodstruve0(x) returns the integral of the modified Struve function |

`scipy.special.`**`struve`**(*x1*, *x2*[, *out*] = **<ufunc 'struve'>**)
y=struve(v,x) returns the Struve function Hv(x) of order v at x, x must be positive unless v is an integer.

`scipy.special.`**`modstruve`**(*x1*, *x2*[, *out*] = **<ufunc 'modstruve'>**)
y=modstruve(v,x) returns the modified Struve function Lv(x) of order v at x, x must be positive unless v is an integer and it is recommended that |v|<=20.

`scipy.special.`**`itstruve0`**(*x*[, *out*] = **<ufunc 'itstruve0'>**)
y=itstruve0(x) returns the integral of the Struve function of order 0 from 0 to x: integral(H0(t), t=0..x).

`scipy.special.`**`it2struve0`**(*x*[, *out*] = **<ufunc 'it2struve0'>**)
y=it2struve0(x) returns the integral of the Struve function of order 0 divided by t from x to infinity: integral(H0(t)/t, t=x..inf).

`scipy.special.`**`itmodstruve0`**(*x*[, *out*] = **<ufunc 'itmodstruve0'>**)
y=itmodstruve0(x) returns the integral of the modified Struve function of order 0 from 0 to x: integral(L0(t), t=0..x).

### Raw Statistical Functions

**See Also:**

`scipy.stats`: Friendly versions of these functions.

| | |
|---|---|
| `bdtr`(x1, x2, x3[, out]) | y=bdtr(k,n,p) returns the sum of the terms 0 through k of the |
| `bdtrc`(x1, x2, x3[, out]) | y=bdtrc(k,n,p) returns the sum of the terms k+1 through n of the |
| `bdtri`(x1, x2, x3[, out]) | p=bdtri(k,n,y) finds the probability p such that the sum of the |
| `btdtr`(x1, x2, x3[, out]) | y=btdtr(a,b,x) returns the area from zero to x under the beta |
| `btdtri`(x1, x2, x3[, out]) | x=btdtri(a,b,p) returns the pth quantile of the beta distribution. It is |
| `fdtr`(x1, x2, x3[, out]) | y=fdtr(dfn,dfd,x) returns the area from zero to x under the F density |
| `fdtrc`(x1, x2, x3[, out]) | y=fdtrc(dfn,dfd,x) returns the complemented F distribution function. |
| `fdtri`(x1, x2, x3[, out]) | x=fdtri(dfn,dfd,p) finds the F density argument x such that |
| `gdtr`(x1, x2, x3[, out]) | y=gdtr(a,b,x) returns the integral from zero to x of the gamma |
| `gdtrc`(x1, x2, x3[, out]) | y=gdtrc(a,b,x) returns the integral from x to infinity of the gamma |
| `gdtria`(x1, x2, x3[, out]) | |
| `gdtrib`(x1, x2, x3[, out]) | |
| `gdtrix`(x1, x2, x3[, out]) | |
| `nbdtr`(x1, x2, x3[, out]) | y=nbdtr(k,n,p) returns the sum of the terms 0 through k of the |
| `nbdtrc`(x1, x2, x3[, out]) | y=nbdtrc(k,n,p) returns the sum of the terms k+1 to infinity of the |
| `nbdtri`(x1, x2, x3[, out]) | p=nbdtri(k,n,y) finds the argument p such that nbdtr(k,n,p)=y. |
| `pdtr`(x1, x2[, out]) | y=pdtr(k,m) returns the sum of the first k terms of the Poisson |
| `pdtrc`(x1, x2[, out]) | y=pdtrc(k,m) returns the sum of the terms from k+1 to infinity of the |
| `pdtri`(x1, x2[, out]) | m=pdtri(k,y) returns the Poisson variable m such that the sum |
| `stdtr`(x1, x2[, out]) | p=stdtr(df,t) returns the integral from minus infinity to t of the Student t |
| `stdtridf`(x1, x2[, out]) | t=stdtridf(p,t) returns the argument df such that stdtr(df,t) is equal to p. |
| `stdtrit`(x1, x2[, out]) | t=stdtrit(df,p) returns the argument t such that stdtr(df,t) is equal to p. |

Continued on next page

**Table 4.9 – continued from previous page**

| | |
|---|---|
| chdtr(x1, x2[, out]) | p=chdtr(v,x) Returns the area under the left hand tail (from 0 to x) of the Chi |
| chdtrc(x1, x2[, out]) | p=chdtrc(v,x) returns the area under the right hand tail (from x to |
| chdtri(x1, x2[, out]) | x=chdtri(v,p) returns the argument x such that chdtrc(v,x) is equal |
| ndtr(x[, out]) | y=ndtr(x) returns the area under the standard Gaussian probability |
| ndtri(x[, out]) | x=ndtri(y) returns the argument x for which the area udnder the |
| smirnov(x1, x2[, out]) | y=smirnov(n,e) returns the exact Kolmogorov-Smirnov complementary |
| smirnovi(x1, x2[, out]) | e=smirnovi(n,y) returns e such that smirnov(n,e) = y. |
| kolmogorov(x[, out]) | p=kolmogorov(y) returns the complementary cumulative distribution |
| kolmogi(x[, out]) | y=kolmogi(p) returns y such that kolmogorov(y) = p |
| tklmbda(x1, x2[, out]) | |
| logit(x[, out]) | NULL |
| expit(x[, out]) | NULL |

scipy.special.**bdtr**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'bdtr'>**)
y=bdtr(k,n,p) returns the sum of the terms 0 through k of the Binomial probability density: sum(nCj p**j (1-p)**(n-j),j=0..k)

scipy.special.**bdtrc**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'bdtrc'>**)
y=bdtrc(k,n,p) returns the sum of the terms k+1 through n of the Binomial probability density: sum(nCj p**j (1-p)**(n-j), j=k+1..n)

scipy.special.**bdtri**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'bdtri'>**)
p=bdtri(k,n,y) finds the probability p such that the sum of the terms 0 through k of the Binomial probability density is equal to the given cumulative probability y.

scipy.special.**btdtr**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'btdtr'>**)
y=btdtr(a,b,x) 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**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'btdtri'>**)
x=btdtri(a,b,p) returns the pth quantile of the beta distribution. It is effectively the inverse of btdtr returning the value of x for which btdtr(a,b,x) = p. SEE ALSO betaincinv

scipy.special.**fdtr**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'fdtr'>**)
y=fdtr(dfn,dfd,x) 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**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'fdtrc'>**)
y=fdtrc(dfn,dfd,x) returns the complemented F distribution function.

scipy.special.**fdtri**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'fdtri'>**)
x=fdtri(dfn,dfd,p) finds the F density argument x such that fdtr(dfn,dfd,x)=p.

scipy.special.**gdtr**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'gdtr'>**)
y=gdtr(a,b,x) 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**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'gdtrc'>**)
y=gdtrc(a,b,x) returns the integral from x to infinity of the gamma probability density function. SEE gdtr, gdtri

scipy.special.**gdtria**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'gdtria'>**)

scipy.special.**gdtrib**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'gdtrib'>**)

`scipy.special.`**`gdtrix`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'gdtrix'>**)

`scipy.special.`**`nbdtr`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'nbdtr'>**)
y=nbdtr(k,n,p) 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`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'nbdtrc'>**)
y=nbdtrc(k,n,p) returns the sum of the terms k+1 to infinity of the negative binomial distribution.

`scipy.special.`**`nbdtri`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'nbdtri'>**)
p=nbdtri(k,n,y) finds the argument p such that nbdtr(k,n,p)=y.

`scipy.special.`**`pdtr`**(*x1*, *x2*[, *out*] = **<ufunc 'pdtr'>**)
y=pdtr(k,m) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'pdtrc'>**)
y=pdtrc(k,m) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'pdtri'>**)
m=pdtri(k,y) 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.`**`stdtr`**(*x1*, *x2*[, *out*] = **<ufunc 'stdtr'>**)
p=stdtr(df,t) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'stdtridf'>**)
t=stdtridf(p,t) returns the argument df such that stdtr(df,t) is equal to p.

`scipy.special.`**`stdtrit`**(*x1*, *x2*[, *out*] = **<ufunc 'stdtrit'>**)
t=stdtrit(df,p) returns the argument t such that stdtr(df,t) is equal to p.

`scipy.special.`**`chdtr`**(*x1*, *x2*[, *out*] = **<ufunc 'chdtr'>**)
p=chdtr(v,x) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'chdtrc'>**)
p=chdtrc(v,x) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'chdtri'>**)
x=chdtri(v,p) returns the argument x such that chdtrc(v,x) is equal to p.

`scipy.special.`**`ndtr`**(*x*[, *out*] = **<ufunc 'ndtr'>**)
y=ndtr(x) 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.`**`ndtri`**(*x*[, *out*] = **<ufunc 'ndtri'>**)
x=ndtri(y) returns the argument x for which the area udnder the Gaussian probability density function (integrated from minus infinity to x) is equal to y.

`scipy.special.`**`smirnov`**(*x1*, *x2*[, *out*] = **<ufunc 'smirnov'>**)
y=smirnov(n,e) 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`**(*x1*, *x2*[, *out*] = **<ufunc 'smirnovi'>**)
e=smirnovi(n,y) returns e such that smirnov(n,e) = y.

`scipy.special.`**`kolmogorov`**(*x*[, *out*] = **<ufunc 'kolmogorov'>**)
p=kolmogorov(y) 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`**(*x*[, *out*] = **<ufunc 'kolmogi'>**)
y=kolmogi(p) returns y such that kolmogorov(y) = p

`scipy.special.`**`tklmbda`**(*x1*, *x2*[, *out*] = **<ufunc 'tklmbda'>**)

`scipy.special.`**`logit`**(*x*[, *out*] = **<ufunc 'logit'>**)
NULL

`scipy.special.`**`expit`**(*x*[, *out*] = **<ufunc 'expit'>**)
NULL

## Gamma and Related Functions

| | |
|---|---|
| `gamma`(x[, out]) | y=gamma(z) returns the gamma function of the argument. The gamma |
| `gammaln`(x[, out]) | y=gammaln(z) returns the base e logarithm of the absolute value of the |
| `gammainc`(x1, x2[, out]) | y=gammainc(a,x) returns the incomplete gamma integral defined as |
| `gammaincinv`(x1, x2[, out]) | gammaincinv(a, y) returns x such that gammainc(a, x) = y. |
| `gammaincc`(x1, x2[, out]) | y=gammaincc(a,x) returns the complemented incomplete gamma integral |
| `gammainccinv`(x1, x2[, out]) | x=gammainccinv(a,y) returns x such that gammaincc(a,x) = y. |
| `beta`(x1, x2[, out]) | y=beta(a,b) returns gamma(a) * gamma(b) / gamma(a+b) |
| `betaln`(x1, x2[, out]) | y=betaln(a,b) returns the natural logarithm of the absolute value of |
| `betainc`(x1, x2, x3[, out]) | y=betainc(a,b,x) returns the incomplete beta integral of the |
| `betaincinv`(x1, x2, x3[, out]) | x=betaincinv(a,b,y) returns x such that betainc(a,b,x) = y. |
| `psi`(x[, out]) | y=psi(z) is the derivative of the logarithm of the gamma function |
| `rgamma`(x[, out]) | y=rgamma(z) returns one divided by the gamma function of x. |
| `polygamma`(n, x) | Polygamma function which is the nth derivative of the digamma (psi) |
| `multigammaln`(a, d) | returns the log of multivariate gamma, also sometimes called the |

`scipy.special.`**`gamma`**(*x*[, *out*] = **<ufunc 'gamma'>**)
y=gamma(z) returns the gamma function of the argument. 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`**(*x*[, *out*] = **<ufunc 'gammaln'>**)
y=gammaln(z) returns the base e logarithm of the absolute value of the gamma function of z: ln(**|gamma(z)|**)

`scipy.special.`**`gammainc`**(*x1*, *x2*[, *out*] = **<ufunc 'gammainc'>**)
y=gammainc(a,x) returns the incomplete gamma integral 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`**(*x1*, *x2*[, *out*] = **<ufunc 'gammaincinv'>**)
gammaincinv(a, y) returns x such that gammainc(a, x) = y.

`scipy.special.`**`gammaincc`**(*x1*, *x2*[, *out*] = **<ufunc 'gammaincc'>**)
y=gammaincc(a,x) returns the 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`**(*x1*, *x2*[, *out*] = **<ufunc 'gammainccinv'>**)
x=gammainccinv(a,y) returns x such that gammaincc(a,x) = y.

scipy.special.**beta**(*x1*, *x2*[, *out*] = **<ufunc 'beta'>**)
y=beta(a,b) returns gamma(a) * gamma(b) / gamma(a+b)

scipy.special.**betaln**(*x1*, *x2*[, *out*] = **<ufunc 'betaln'>**)
y=betaln(a,b) returns the natural logarithm of the absolute value of beta: ln(|beta(x)|).

scipy.special.**betainc**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'betainc'>**)
y=betainc(a,b,x) returns 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).

scipy.special.**betaincinv**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'betaincinv'>**)
x=betaincinv(a,b,y) returns x such that betainc(a,b,x) = y.

scipy.special.**psi**(*x*[, *out*] = **<ufunc 'psi'>**)
y=psi(z) is the derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

scipy.special.**rgamma**(*x*[, *out*] = **<ufunc 'rgamma'>**)
y=rgamma(z) returns one divided by the gamma function of x.

scipy.special.**polygamma**(*n*, *x*)
Polygamma function which is the nth derivative of the digamma (psi) function.

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

Reference:

R. J. Muirhead, Aspects of multivariate statistical theory (Wiley Series in probability and mathematical statistics).

## Error Function and Fresnel Integrals

| | |
|---|---|
| erf(x[, out]) | y=erf(z) returns the error function of complex argument defined as |
| erfc(x[, out]) | y=erfc(x) returns 1 - erf(x). |
| erfinv(y) | |
| erfcinv(y) | |
| fresnel(x[, out1, out2]) | (ssa,cca)=fresnel(z) returns the fresnel sin and cos integrals: integral(sin(pi/2 |
| fresnel_zeros(nt) | Compute nt complex zeros of the sine and cosine fresnel integrals |
| modfresnelp(x[, out1, out2]) | (fp,kp)=modfresnelp(x) returns the modified fresnel integrals F_+(x) and K_+(x) |
| modfresnelm(x[, out1, out2]) | (fm,km)=modfresnelp(x) returns the modified fresnel integrals F_-(x) amd K_-(x) |

scipy.special.**erf**(*x*[, *out*] = **<ufunc 'erf'>**)
y=erf(z) returns the error function of complex argument defined as as 2/sqrt(pi)*integral(exp(-t**2),t=0..z)

`scipy.special.`**`erfc`**(*x*[, *out*] = **<ufunc 'erfc'>**)
y=erfc(x) returns 1 - erf(x).

`scipy.special.`**`erfinv`**(*y*)

`scipy.special.`**`erfcinv`**(*y*)

`scipy.special.`**`fresnel`**(*x*[, *out1*, *out2*] = **<ufunc 'fresnel'>**)
(ssa,cca)=fresnel(z) returns the fresnel sin and cos integrals: integral(sin(pi/2 * t**2),t=0..z) and integral(cos(pi/2 * t**2),t=0..z) for real or complex z.

`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*[, *out1*, *out2*] = **<ufunc 'modfresnelp'>**)
(fp,kp)=modfresnelp(x) returns the modified fresnel integrals F_+(x) and K_+(x) as fp=integral(exp(1j*t*t),t=x..inf) and kp=1/sqrt(pi)*exp(-1j*(x*x+pi/4))*fp

`scipy.special.`**`modfresnelm`**(*x*[, *out1*, *out2*] = **<ufunc 'modfresnelm'>**)
(fm,km)=modfresnelp(x) returns the modified fresnel integrals F_-(x) amd K_-(x) as fp=integral(exp(-1j*t*t),t=x..inf) and kp=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`(x1, x2, x3[, out]) | y=lpmv(m,v,x) returns the associated legendre function of integer order |
| `sph_harm` | Compute spherical harmonics. |

`scipy.special.`**`lpmv`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'lpmv'>**)
y=lpmv(m,v,x) returns the associated legendre function of integer order m and real degree v (s.t. v>-m-1 or v<m): |x|<=1.

`scipy.special.`**`sph_harm`** = **<numpy.lib.function_base.vectorize object at 0x38bea10>**
Compute spherical harmonics.

This is a ufunc and may take scalar or array arguments like any other ufunc. The inputs will be broadcasted against each other.

**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.

These are not universal functions:

| | |
|---|---|
| `lpn`(n, z) | Compute sequence of Legendre functions of the first kind (polynomials), |
| `lqn`(n, z) | Compute sequence of Legendre functions of the second kind, |
| `lpmn`(m, n, z) | Associated Legendre functions of the first kind, Pmn(z) and its |
| `lqmn`(m, n, z) | Associated Legendre functions of the second kind, Qmn(z) and its |

`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 functions of the first kind, Pmn(z) and its derivative, Pmn'(z) of order m and degree n. 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.

z can be complex.

**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

**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

`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.

### Orthogonal polynomials

The following functions evaluate values of orthogonal polynomials:

| | |
|---|---|
| `eval_legendre` | Evaluate Legendre polynomial at a point. |
| `eval_chebyt` | Evaluate Chebyshev T polynomial at a point. |
| `eval_chebyu` | Evaluate Chebyshev U polynomial at a point. |
| `eval_chebyc` | Evaluate Chebyshev C polynomial at a point. |
| `eval_chebys` | Evaluate Chebyshev S polynomial at a point. |
| `eval_jacobi` | Evaluate Jacobi polynomial at a point. |
| `eval_laguerre` | Evaluate Laguerre polynomial at a point. |
| `eval_genlaguerre` | Evaluate generalized Laguerre polynomial at a point. |
| `eval_hermite` | Evaluate Hermite polynomial at a point. |
| `eval_hermitenorm` | Evaluate normalized Hermite polynomial at a point. |
| `eval_gegenbauer` | Evaluate Gegenbauer polynomial at a point. |
| `eval_sh_legendre` | Evaluate shifted Legendre polynomial at a point. |
| `eval_sh_chebyt` | Evaluate shifted Chebyshev T polynomial at a point. |
| `eval_sh_chebyu` | Evaluate shifted Chebyshev U polynomial at a point. |
| `eval_sh_jacobi` | Evaluate shifted Jacobi polynomial at a point. |

`scipy.special.`**`eval_legendre`**`()`

Evaluate Legendre polynomial at a point.

`scipy.special.`**`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`**`()`

Evaluate Chebyshev U polynomial at a point.

`scipy.special.`**`eval_chebyc`**`()`

Evaluate Chebyshev C polynomial at a point.

`scipy.special.`**`eval_chebys`**`()`

Evaluate Chebyshev S polynomial at a point.

`scipy.special.`**`eval_jacobi`**`()`

Evaluate Jacobi polynomial at a point.

`scipy.special.`**`eval_laguerre`**`()`

Evaluate Laguerre polynomial at a point.

`scipy.special.`**`eval_genlaguerre`**`()`

Evaluate generalized Laguerre polynomial at a point.

`scipy.special.`**`eval_hermite`**`()`

Evaluate Hermite polynomial at a point.

`scipy.special.`**`eval_hermitenorm`**`()`

Evaluate normalized Hermite polynomial at a point.

`scipy.special.`**`eval_gegenbauer`**`()`
Evaluate Gegenbauer polynomial at a point.

`scipy.special.`**`eval_sh_legendre`**`()`
Evaluate shifted Legendre polynomial at a point.

`scipy.special.`**`eval_sh_chebyt`**`()`
Evaluate shifted Chebyshev T polynomial at a point.

`scipy.special.`**`eval_sh_chebyu`**`()`
Evaluate shifted Chebyshev U polynomial at a point.

`scipy.special.`**`eval_sh_jacobi`**`()`
Evaluate shifted Jacobi polynomial at a point.

The functions below, in turn, return *orthopoly1d* objects, which functions 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.

| | |
|---|---|
| `legendre`(n[, monic]) | Returns the nth order Legendre polynomial, P_n(x), orthogonal over |
| `chebyt`(n[, monic]) | Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal |
| `chebyu`(n[, monic]) | Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal |
| `chebyc`(n[, monic]) | Return nth order Chebyshev polynomial of first kind, Cn(x). Orthogonal |
| `chebys`(n[, monic]) | Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal |
| `jacobi`(n, alpha, beta[, monic]) | Returns the nth order Jacobi polynomial, P^(alpha,beta)_n(x) |
| `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 |
| `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) |

`scipy.special.`**`legendre`**`(`*n*, *monic=0*`)`
Returns the nth order Legendre polynomial, P_n(x), orthogonal over [-1,1] with weight function 1.

`scipy.special.`**`chebyt`**`(`*n*, *monic=0*`)`
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=0*`)`
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=0*`)`
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=0*`)`
Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal over [-2,2] with weight function (1-(x/)**2)**(1/2).

`scipy.special.`**`jacobi`**`(`*n*, *alpha*, *beta*, *monic=0*`)`
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=0*)
Return the nth order Laguerre polynoimal, L_n(x), orthogonal over [0,inf) with weighting function exp(-x)

`scipy.special.`**`genlaguerre`**(*n*, *alpha*, *monic=0*)
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=0*)
Return the nth order Hermite polynomial, H_n(x), orthogonal over (-inf,inf) with weighting function exp(-x**2)

`scipy.special.`**`hermitenorm`**(*n*, *monic=0*)
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=0*)
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=0*)
Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weighting function 1.

`scipy.special.`**`sh_chebyt`**(*n*, *monic=0*)
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=0*)
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=0*)
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:** Large-order polynomials obtained from these functions are numerically unstable.
`orthopoly1d` objects are converted to `poly1d`, when doing arithmetic. `numpy.poly1d` works in power basis and cannot represent high-order polynomials accurately, which can cause significant inaccuracy.

## Hypergeometric Functions

| | |
|---|---|
| `hyp2f1`(x1, x2, x3, x4[, out]) | y=hyp2f1(a,b,c,z) returns the gauss hypergeometric function |
| `hyp1f1`(x1, x2, x3[, out]) | y=hyp1f1(a,b,x) returns the confluent hypergeometeric function |
| `hyperu`(x1, x2, x3[, out]) | y=hyperu(a,b,x) returns the confluent hypergeometric function of the |
| `hyp0f1`(v, z) | Confluent hypergeometric limit function 0F1. |
| `hyp2f0`(x1, x2, x3, x4[, out1, out2]) | (y,err)=hyp2f0(a,b,x,type) returns (y,err) with the hypergeometric function 2F0 in y and an error estimate in err. The input type determines a convergence factor and |
| `hyp1f2`(x1, x2, x3, x4[, out1, out2]) | (y,err)=hyp1f2(a,b,c,x) returns (y,err) with the hypergeometric function 1F2 in y and an error estimate in err. |
| `hyp3f0`(x1, x2, x3, x4[, out1, out2]) | (y,err)=hyp3f0(a,b,c,x) returns (y,err) with the hypergeometric function 3F0 in y and an error estimate in err. |

`scipy.special.`**`hyp2f1`**(*x1*, *x2*, *x3*, *x4*[, *out*] = **<ufunc 'hyp2f1'>**)
y=hyp2f1(a,b,c,z) returns the gauss hypergeometric function ( 2F1(a,b;c;z) ).

scipy.special.**hyp1f1**(*x1*, *x2*, *x3*[, *out* ] = **<ufunc 'hyp1f1'>**)
y=hyp1f1(a,b,x) returns the confluent hypergeometeric function ( 1F1(a,b;x) ) evaluated at the values a, b, and x.

scipy.special.**hyperu**(*x1*, *x2*, *x3*[, *out* ] = **<ufunc 'hyperu'>**)
y=hyperu(a,b,x) returns the confluent hypergeometric function of the second kind U(a,b,x).

scipy.special.**hyp0f1**(*v*, *z*)
Confluent hypergeometric limit function 0F1. Limit as q->infinity of 1F1(q;a;z/q)

scipy.special.**hyp2f0**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2* ] = **<ufunc 'hyp2f0'>**)
(y,err)=hyp2f0(a,b,x,type) returns (y,err) with the hypergeometric function 2F0 in y and an error estimate in err. The input type determines a convergence factor and can be either 1 or 2.

scipy.special.**hyp1f2**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2* ] = **<ufunc 'hyp1f2'>**)
(y,err)=hyp1f2(a,b,c,x) returns (y,err) with the hypergeometric function 1F2 in y and an error estimate in err.

scipy.special.**hyp3f0**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2* ] = **<ufunc 'hyp3f0'>**)
(y,err)=hyp3f0(a,b,c,x) returns (y,err) with the hypergeometric function 3F0 in y and an error estimate in err.

### Parabolic Cylinder Functions

| | |
|---|---|
| pbdv(x1, x2[, out1, out2]) | (d,dp)=pbdv(v,x) returns (d,dp) with the parabolic cylinder function Dv(x) in |
| pbvv(x1, x2[, out1, out2]) | (v,vp)=pbvv(v,x) returns (v,vp) with the parabolic cylinder function Vv(x) in |
| pbwa(x1, x2[, out1, out2]) | (w,wp)=pbwa(a,x) returns (w,wp) with the parabolic cylinder function W(a,x) in |

scipy.special.**pbdv**(*x1*, *x2*[, *out1*, *out2* ] = **<ufunc 'pbdv'>**)
(d,dp)=pbdv(v,x) returns (d,dp) with the parabolic cylinder function Dv(x) in d and the derivative, Dv'(x) in dp.

scipy.special.**pbvv**(*x1*, *x2*[, *out1*, *out2* ] = **<ufunc 'pbvv'>**)
(v,vp)=pbvv(v,x) returns (v,vp) with the parabolic cylinder function Vv(x) in v and the derivative, Vv'(x) in vp.

scipy.special.**pbwa**(*x1*, *x2*[, *out1*, *out2* ] = **<ufunc 'pbwa'>**)
(w,wp)=pbwa(a,x) returns (w,wp) with the parabolic cylinder function W(a,x) in w and the derivative, W'(a,x) in wp. May not be accurate for large (>5) arguments in a and/or x.

These are not universal functions:

| | |
|---|---|
| pbdv_seq(v, x) | Compute sequence of parabolic cylinder functions Dv(x) and |
| pbvv_seq(v, x) | Compute sequence of parabolic cylinder functions Dv(x) and |
| pbdn_seq(n, z) | Compute sequence of parabolic cylinder functions Dn(z) and |

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(x1, x2[, out]) | lmbda=mathieu_a(m,q) returns the characteristic value for the even solution, |
| mathieu_b(x1, x2[, out]) | lmbda=mathieu_b(m,q) returns the characteristic value for the odd solution, |

`scipy.special.`**`mathieu_a`**(*x1*, *x2*[, *out*] = **<ufunc 'mathieu_a'>**)
lmbda=mathieu_a(m,q) returns the characteristic value for the even solution, ce_m(z,q), of Mathieu's equation

`scipy.special.`**`mathieu_b`**(*x1*, *x2*[, *out*] = **<ufunc 'mathieu_b'>**)
lmbda=mathieu_b(m,q) 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 |
| `mathieu_odd_coef`(m, q) | Compute expansion coefficients for even mathieu functions and |

`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`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_cem(m,q,x) returns the even Mathieu function, ce_m(x,q), |
| `mathieu_sem`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_sem(m,q,x) returns the odd Mathieu function, se_m(x,q), |
| `mathieu_modcem1`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_modcem1(m,q,x) evaluates the even modified Matheiu function |
| `mathieu_modcem2`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_modcem2(m,q,x) evaluates the even modified Matheiu function |
| `mathieu_modsem1`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_modsem1(m,q,x) evaluates the odd modified Matheiu function |
| `mathieu_modsem2`(x1, x2, x3[, out1, out2]) | (y,yp)=mathieu_modsem2(m,q,x) evaluates the odd modified Matheiu function |

`scipy.special.`**`mathieu_cem`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_cem'>**)
(y,yp)=mathieu_cem(m,q,x) 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)

`scipy.special.`**`mathieu_sem`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_sem'>**)
(y,yp)=mathieu_sem(m,q,x) 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).

`scipy.special.`**`mathieu_modcem1`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_modcem1'>**)
(y,yp)=mathieu_modcem1(m,q,x) evaluates the even modified Matheiu function of the first kind, Mc1m(x,q), and its derivative at x for order m and parameter q.

`scipy.special.`**`mathieu_modcem2`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_modcem2'>**)
(y,yp)=mathieu_modcem2(m,q,x) evaluates the even modified Matheiu function of the second kind, Mc2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

`scipy.special.`**`mathieu_modsem1`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_modsem1'>**)
(y,yp)=mathieu_modsem1(m,q,x) evaluates the odd modified Matheiu function of the first kind, Ms1m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

`scipy.special.`**`mathieu_modsem2`**(*x1*, *x2*, *x3*[, *out1*, *out2*] = **<ufunc 'mathieu_modsem2'>**)
(y,yp)=mathieu_modsem2(m,q,x) evaluates the odd modified Matheiu function of the second kind, Ms2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

### Spheroidal Wave Functions

| | |
|---|---|
| pro_ang1(x1, x2, x3, x4[, out1, out2]) | (s,sp)=pro_ang1(m,n,c,x) computes the prolate sheroidal angular function |
| pro_rad1(x1, x2, x3, x4[, out1, out2]) | (s,sp)=pro_rad1(m,n,c,x) computes the prolate sheroidal radial function |
| pro_rad2(x1, x2, x3, x4[, out1, out2]) | (s,sp)=pro_rad2(m,n,c,x) computes the prolate sheroidal radial function |
| obl_ang1(x1, x2, x3, x4[, out1, out2]) | (s,sp)=obl_ang1(m,n,c,x) computes the oblate sheroidal angular function |
| obl_rad1(x1, x2, x3, x4[, out1, out2]) | (s,sp)=obl_rad1(m,n,c,x) computes the oblate sheroidal radial function |
| obl_rad2(x1, x2, x3, x4[, out1, out2]) | (s,sp)=obl_rad2(m,n,c,x) computes the oblate sheroidal radial function |
| pro_cv(x1, x2, x3[, out]) | cv=pro_cv(m,n,c) computes the characteristic value of prolate spheroidal |
| obl_cv(x1, x2, x3[, out]) | cv=obl_cv(m,n,c) computes the characteristic value of oblate spheroidal |
| pro_cv_seq(m, n, c) | Compute a sequence of characteristic values for the prolate |
| obl_cv_seq(m, n, c) | Compute a sequence of characteristic values for the oblate |

scipy.special.**pro_ang1**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'pro_ang1'>**)
: (s,sp)=pro_ang1(m,n,c,x) computes the prolate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**pro_rad1**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'pro_rad1'>**)
: (s,sp)=pro_rad1(m,n,c,x) computes the prolate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**pro_rad2**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'pro_rad2'>**)
: (s,sp)=pro_rad2(m,n,c,x) computes the prolate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**obl_ang1**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'obl_ang1'>**)
: (s,sp)=obl_ang1(m,n,c,x) computes the oblate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**obl_rad1**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'obl_rad1'>**)
: (s,sp)=obl_rad1(m,n,c,x) computes the oblate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**obl_rad2**(*x1*, *x2*, *x3*, *x4*[, *out1*, *out2*] = **<ufunc 'obl_rad2'>**)
: (s,sp)=obl_rad2(m,n,c,x) computes the oblate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

scipy.special.**pro_cv**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'pro_cv'>**)
: cv=pro_cv(m,n,c) computes the characteristic value of prolate spheroidal wave functions of order m,n (n>=m) and spheroidal parameter c.

scipy.special.**obl_cv**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'obl_cv'>**)
: cv=obl_cv(m,n,c) 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(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=pro_ang1_cv(m,n,c,cv,x) computes the prolate sheroidal angular function |
| pro_rad1_cv(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=pro_rad1_cv(m,n,c,cv,x) computes the prolate sheroidal radial function |
| pro_rad2_cv(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=pro_rad2_cv(m,n,c,cv,x) computes the prolate sheroidal radial function |
| obl_ang1_cv(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=obl_ang1_cv(m,n,c,cv,x) computes the oblate sheroidal angular function |
| obl_rad1_cv(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=obl_rad1_cv(m,n,c,cv,x) computes the oblate sheroidal radial function |
| obl_rad2_cv(x1, x2, x3, x4, x5[, out1, out2]) | (s,sp)=obl_rad2_cv(m,n,c,cv,x) computes the oblate sheroidal radial function |

scipy.special.**pro_ang1_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'pro_ang1_cv'>**)

(s,sp)=pro_ang1_cv(m,n,c,cv,x) computes the prolate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

scipy.special.**pro_rad1_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'pro_rad1_cv'>**)

(s,sp)=pro_rad1_cv(m,n,c,cv,x) computes the prolate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

scipy.special.**pro_rad2_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'pro_rad2_cv'>**)

(s,sp)=pro_rad2_cv(m,n,c,cv,x) computes the prolate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

scipy.special.**obl_ang1_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'obl_ang1_cv'>**)

(s,sp)=obl_ang1_cv(m,n,c,cv,x) computes the oblate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

scipy.special.**obl_rad1_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'obl_rad1_cv'>**)

(s,sp)=obl_rad1_cv(m,n,c,cv,x) computes the oblate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

scipy.special.**obl_rad2_cv**(*x1*, *x2*, *x3*, *x4*, *x5*[, *out1*, *out2*] = **<ufunc 'obl_rad2_cv'>**)

(s,sp)=obl_rad2_cv(m,n,c,cv,x) computes the oblate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

### Kelvin Functions

| | |
|---|---|
| kelvin(x[, out1, out2, out3, out4]) | (Be, Ke, Bep, Kep)=kelvin(x) returns the tuple (Be, Ke, Bep, Kep) which containes |
| kelvin_zeros(nt) | Compute nt zeros of all the kelvin functions returned in a length 8 tuple of arrays of length nt. |
| ber(x[, out]) | y=ber(x) returns the Kelvin function ber x |
| bei(x[, out]) | y=bei(x) returns the Kelvin function bei x |
| berp(x[, out]) | y=berp(x) returns the derivative of the Kelvin function ber x |
| beip(x[, out]) | y=beip(x) returns the derivative of the Kelvin function bei x |
| ker(x[, out]) | y=ker(x) returns the Kelvin function ker x |
| kei(x[, out]) | y=kei(x) returns the Kelvin function ker x |
| kerp(x[, out]) | y=kerp(x) returns the derivative of the Kelvin function ker x |
| keip(x[, out]) | y=keip(x) returns the derivative of the Kelvin function kei x |

`scipy.special.`**`kelvin`**(*x*[, *out1*, *out2*, *out3*, *out4*] = **<ufunc 'kelvin'>**)
(Be, Ke, Bep, Kep)=kelvin(x) returns the tuple (Be, Ke, Bep, Kep) which containes 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*[, *out*] = **<ufunc 'ber'>**)
y=ber(x) returns the Kelvin function ber x

`scipy.special.`**`bei`**(*x*[, *out*] = **<ufunc 'bei'>**)
y=bei(x) returns the Kelvin function bei x

`scipy.special.`**`berp`**(*x*[, *out*] = **<ufunc 'berp'>**)
y=berp(x) returns the derivative of the Kelvin function ber x

`scipy.special.`**`beip`**(*x*[, *out*] = **<ufunc 'beip'>**)
y=beip(x) returns the derivative of the Kelvin function bei x

`scipy.special.`**`ker`**(*x*[, *out*] = **<ufunc 'ker'>**)
y=ker(x) returns the Kelvin function ker x

`scipy.special.`**`kei`**(*x*[, *out*] = **<ufunc 'kei'>**)
y=kei(x) returns the Kelvin function ker x

`scipy.special.`**`kerp`**(*x*[, *out*] = **<ufunc 'kerp'>**)
y=kerp(x) returns the derivative of the Kelvin function ker x

`scipy.special.`**`keip`**(*x*[, *out*] = **<ufunc 'keip'>**)
y=keip(x) returns the derivative of the Kelvin function kei x

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

## Other Special Functions

| | |
|---|---|
| expn(x1, x2[, out]) | y=expn(n,x) returns the exponential integral for integer n and |
| exp1(x[, out]) | y=exp1(z) returns the exponential integral (n=1) of complex argument |
| expi(x[, out]) | y=expi(x) returns an exponential integral of argument x defined as |
| wofz(x[, out]) | y=wofz(z) returns the value of the fadeeva function for complex argument |
| dawsn(x[, out]) | y=dawsn(x) returns dawson's integral: exp(-x**2) * |
| shichi(x[, out1, out2]) | (shi,chi)=shichi(x) returns the hyperbolic sine and cosine integrals: |
| sici(x[, out1, out2]) | (si,ci)=sici(x) returns in si the integral of the sinc function from 0 to x: |
| spence(x[, out]) | y=spence(x) returns the dilogarithm integral: -integral(log t / |
| lambertw(z[, k, tol]) | Lambert W function. |
| zeta(x1, x2[, out]) | y=zeta(x,q) returns the Riemann zeta function of two arguments: |
| zetac(x[, out]) | y=zetac(x) returns 1.0 - the Riemann zeta function: sum(k**(-x), k=2..inf) |

scipy.special.**expn**(*x1*, *x2*[, *out*] = **<ufunc 'expn'>**)
y=expn(n,x) 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**(*x*[, *out*] = **<ufunc 'exp1'>**)
y=exp1(z) returns the exponential integral (n=1) of complex argument z: integral(exp(-z*t)/t,t=1..inf).

scipy.special.**expi**(*x*[, *out*] = **<ufunc 'expi'>**)
y=expi(x) returns an exponential integral of argument x defined as integral(exp(t)/t,t=-inf..x). See expn for a different exponential integral.

scipy.special.**wofz**(*x*[, *out*] = **<ufunc 'wofz'>**)
y=wofz(z) returns the value of the fadeeva function for complex argument z: exp(-z**2)*erfc(-i*z)

scipy.special.**dawsn**(*x*[, *out*] = **<ufunc 'dawsn'>**)
y=dawsn(x) returns dawson's integral: exp(-x**2) * integral(exp(t**2),t=0..x).

scipy.special.**shichi**(*x*[, *out1*, *out2*] = **<ufunc 'shichi'>**)
(shi,chi)=shichi(x) returns the hyperbolic sine and cosine integrals: integral(sinh(t)/t,t=0..x) and eul + ln x + integral((cosh(t)-1)/t,t=0..x) where eul is Euler's Constant.

`scipy.special.sici(x[, out1, out2] = <ufunc 'sici'>)`
(si,ci)=sici(x) returns in si the integral of the sinc function from 0 to x: integral(sin(t)/t,t=0..x). It returns in ci the cosine integral: eul + ln x + integral((cos(t) - 1)/t,t=0..x).

`scipy.special.spence(x[, out] = <ufunc 'spence'>)`
y=spence(x) returns the dilogarithm integral: -integral(log t / (t-1),t=1..x)

`scipy.special.lambertw(z, k=0, tol=1e-8)`
Lambert W function.

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 $w \exp(w)$. Here, the branches are indexed by the integer *k*.

**Parameters**

**z** : array_like

Input argument

**k** : integer, optional

Branch index

**tol** : float

Evaluation tolerance

## 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 Corless et al, "On the Lambert W function", Adv. Comp. Math. 5 (1996) 329-359, available online here: http://www.apmaths.uwo.ca/~djeffrey/Offprints/W-adv-cm.pdf

TODO: use a series expansion when extremely close to the branch point at *-1/e* and make sure that the proper branch is chosen there

## Examples

The Lambert W function is the inverse of *w exp(w)*:

```
>>> from scipy.special import lambertw
>>> w = lambertw(1)
>>> w
```

0.567143290409783872999968662210355550 >>> w*exp(w) 1.0

Any branch gives a valid inverse:

```
>>> w = lambertw(1, k=3)
>>> w
```

(-2.8535817554090378072068187234910812 + 17.113535539412145912607826671159289j) >>> w*exp(w) (1.0 + 3.5075477124212226194278700785075126e-36j)

### 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^{ldots}}}*:

```
>>> def tower(z, n):
```

... if n == 0: ... return z ... return z ** tower(z, n-1) ... >>> tower(0.5, 100) 0.641185744504986 >>> -lambertw(-log(0.5))/log(0.5) 0.6411857445049859844862004821148236665628209571911

### Properties

The Lambert W function grows roughly like the natural logarithm for large arguments:

```
>>> lambertw(1000)
```

5.2496028524016 >>> log(1000) 6.90775527898214 >>> lambertw(10**100) 224.843106445119 >>> log(10**100) 230.258509299405

The principal branch of the Lambert W function has a rational Taylor series expansion around *z = 0*:

```
>>> nprint(taylor(lambertw, 0, 6), 10)
```

[0.0, 1.0, -1.0, 1.5, -2.666666667, 5.208333333, -10.8]

Some special values and limits are:

```
>>> lambertw(0)
```

0.0 >>> lambertw(1) 0.567143290409784 >>> lambertw(e) 1.0 >>> lambertw(inf) +inf >>> lambertw(0, k=-1) -inf >>> lambertw(0, k=3) -inf >>> lambertw(inf, k=3) (+inf + 18.8495559215388j)

The *k = 0* and *k = -1* branches join at *z = -1/e* where *W(z) = -1* for both branches. Since *-1/e* can only be represented approximately with mpmath numbers, evaluating the Lambert W function at this point only gives *-1* approximately:

```
>>> lambertw(-1/e, 0)
```

-0.99999999999999837133022867 >>> lambertw(-1/e, -1) -1.00000000000000162866977180

If *-1/e* happens to round in the negative direction, there might be a small imaginary part:

```
>>> lambertw(-1/e)
```

(-1.0 + 8.22007971511612e-9j)

`scipy.special.`**`zeta`**(*x1*, *x2*[, *out*] = **<ufunc 'zeta'>**)
y=zeta(x,q) returns the Riemann zeta function of two arguments: sum((k+q)**(-x),k=0..inf)

`scipy.special.`**`zetac`**(*x*[, *out*] = **<ufunc 'zetac'>**)
y=zetac(x) returns 1.0 - the Riemann zeta function: sum(k**(-x), k=2..inf)

### Convenience Functions

| | |
|---|---|
| cbrt(x[, out]) | y=cbrt(x) returns the real cube root of x. |
| exp10(x[, out]) | y=exp10(x) returns 10 raised to the x power. |
| exp2(x[, out]) | y=exp2(x) returns 2 raised to the x power. |
| radian(x1, x2, x3[, out]) | y=radian(d,m,s) returns the angle given in (d)egrees, (m)inutes, and |
| cosdg(x[, out]) | y=cosdg(x) calculates the cosine of the angle x given in degrees. |
| sindg(x[, out]) | y=sindg(x) calculates the sine of the angle x given in degrees. |
| tandg(x[, out]) | y=tandg(x) calculates the tangent of the angle x given in degrees. |
| cotdg(x[, out]) | y=cotdg(x) calculates the cotangent of the angle x given in degrees. |
| log1p(x[, out]) | y=log1p(x) calculates log(1+x) for use when x is near zero. |
| expm1(x[, out]) | y=expm1(x) calculates exp(x) - 1 for use when x is near zero. |
| cosm1(x[, out]) | y=calculates cos(x) - 1 for use when x is near zero. |
| round(x[, out]) | y=Returns the nearest integer to x as a double precision |

`scipy.special.`**`cbrt`**(*x*[, *out*] = **<ufunc 'cbrt'>**)
y=cbrt(x) returns the real cube root of x.

`scipy.special.`**`exp10`**(*x*[, *out*] = **<ufunc 'exp10'>**)
y=exp10(x) returns 10 raised to the x power.

`scipy.special.`**`exp2`**(*x*[, *out*] = **<ufunc 'exp2'>**)
y=exp2(x) returns 2 raised to the x power.

`scipy.special.`**`radian`**(*x1*, *x2*, *x3*[, *out*] = **<ufunc 'radian'>**)
y=radian(d,m,s) returns the angle given in (d)egrees, (m)inutes, and (s)econds in radians.

`scipy.special.`**`cosdg`**(*x*[, *out*] = **<ufunc 'cosdg'>**)
y=cosdg(x) calculates the cosine of the angle x given in degrees.

`scipy.special.`**`sindg`**(*x*[, *out*] = **<ufunc 'sindg'>**)
y=sindg(x) calculates the sine of the angle x given in degrees.

`scipy.special.`**`tandg`**(*x*[, *out*] = **<ufunc 'tandg'>**)
y=tandg(x) calculates the tangent of the angle x given in degrees.

`scipy.special.`**`cotdg`**(*x*[, *out*] = **<ufunc 'cotdg'>**)
y=cotdg(x) calculates the cotangent of the angle x given in degrees.

`scipy.special.`**`log1p`**(*x*[, *out*] = **<ufunc 'log1p'>**)
y=log1p(x) calculates log(1+x) for use when x is near zero.

`scipy.special.`**`expm1`**(*x*[, *out*] = **<ufunc 'expm1'>**)
y=expm1(x) calculates exp(x) - 1 for use when x is near zero.

`scipy.special.`**`cosm1`**(*x*[, *out*] = **<ufunc 'cosm1'>**)
y=calculates cos(x) - 1 for use when x is near zero.

`scipy.special.`**`round`**(*x*[, *out*] = **<ufunc 'round'>**)
y=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.

## 4.22 Statistical functions (`scipy.stats`)

This module contains a large number of probability distributions as well as a growing library of statistical functions.

Each included distribution is an instance of the class rv_continous: For each given name the following methods are available:

| | |
|---|---|
| rv_continuous([momtype, a, b, xa, xb, xtol, ...]) | A generic continuous random variable class meant for subclassing. |
| rv_continuous.rvs(*args, **kwds) | Random variates of given type. |
| rv_continuous.pdf(x, *args, **kwds) | Probability density function at x of the given RV. |
| rv_continuous.logpdf(x, *args, **kwds) | Log of the probability density function at x of the given RV. |
| rv_continuous.cdf(x, *args, **kwds) | Cumulative distribution function at x of the given RV. |
| rv_continuous.logcdf(x, *args, **kwds) | Log of the cumulative distribution function at x of the given RV. |
| rv_continuous.sf(x, *args, **kwds) | Survival function (1-cdf) at x of the given RV. |
| rv_continuous.logsf(x, *args, **kwds) | Log of the survival function of the given RV. |
| rv_continuous.ppf(q, *args, **kwds) | Percent point function (inverse of cdf) at q of the given RV. |
| rv_continuous.isf(q, *args, **kwds) | Inverse survival function at q of the given RV. |
| rv_continuous.moment(n, *args, **kwds) | n'th order non-central moment of distribution |
| rv_continuous.stats(*args, **kwds) | Some statistics of the given RV |
| rv_continuous.entropy(*args, **kwds) | Differential entropy of the RV. |
| rv_continuous.fit(data, *args, **kwds) | Return MLEs for shape, location, and scale parameters from data. |
| rv_continuous.expect([func, args, loc, ...]) | calculate expected value of a function with respect to the distribution |
| rv_continuous.median(*args, **kwds) | Median of the distribution. |
| rv_continuous.mean(*args, **kwds) | Mean of the distribution |
| rv_continuous.var(*args, **kwds) | Variance of the distribution |
| rv_continuous.std(*args, **kwds) | Standard deviation of the distribution. |
| rv_continuous.interval(alpha, *args, **kwds) | Confidence interval with equal areas around the median |

**class** scipy.stats.**rv_continuous**(*momtype=1*, *a=None*, *b=None*, *xa=-10.0*, *xb=10.0*, *xtol=1e-14*, *badvalue=None*, *name=None*, *longname=None*, *shapes=None*, *extradoc=None*)

A generic continuous random variable class meant for subclassing.

rv_continuous is a base class to construct specific distribution classes and instances from 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.

**xa** : float, optional

Lower bound for fixed point calculation for generic ppf.

**xb** : float, optional

Upper bound for fixed point calculation for generic ppf.

**xtol** : float, optional

The tolerance for fixed point calculation for generic ppf.

**badvalue** : object, 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.

**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.

## Notes

**Frozen 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

**Subclassing**

New random variables can be defined by subclassing rv_continuous class and re-defining at least the

_pdf or the _cdf method (normalized to location 0 and scale 1) which will be given clean arguments (in between a and b) and passing the argument check method

If postive argument checking is not correct for your RV then you will also need to re-define

```
_argcheck
```

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, and _logsf but you could.

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=<str> where <str> 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

OR

You can override

**_munp**
takes n and shape parameters and returns the nth non-central moment of the distribution.

### Examples

To create a new Gaussian distribution, we would do the following:

```
class gaussian_gen(rv_continuous):
    "Gaussian distribution"
    def _pdf:
        ...
    ...
```

### Methods

| | | |
|---|---|---|
| rvs(<shape(s)>, loc=0, scale=1, size=1) | | random variates |
| pdf(x, <shape(s)>, loc=0, scale=1) | | probability density function |
| logpdf(x, <shape(s)>, loc=0, scale=1) | | log of the probability density function |
| cdf(x, <shape(s)>, loc=0, scale=1) | | cumulative density function |
| logcdf(x, <shape(s)>, loc=0, scale=1) | | log of the cumulative density function |
| sf(x, <shape(s)>, loc=0, scale=1) | | survival function (1-cdf — sometimes more accurate) |
| logsf(x, <shape(s)>, loc=0, scale=1) | | log of the survival function |
| ppf(q, <shape(s)>, loc=0, scale=1) | | percent point function (inverse of cdf — quantiles) |
| isf(q, <shape(s)>, loc=0, scale=1) | | inverse survival function (inverse of sf) |
| moment(n, <shape(s)>, loc=0, scale=1) | | non-central n-th moment of the distribution. May not work for array arguments. |
| stats(<shape(s)>, loc=0, scale=1, moments='mv') | | mean('m'), variance('v'), skew('s'), and/or kurtosis('k') |
| entropy(<shape(s)>, loc=0, scale=1) | | (differential) entropy of the RV. |
| fit(data, <shape(s)>, loc=0, scale=1) | | Parameter estimates for generic data |
| expect(func=None, args=(), loc=0, scale=1, lb=None, ub=None, | | conditional=False, **kwds) Expected value of a function with respect to the distribution. Additional kwd arguments passed to integrate.quad |
| median(<shape(s)>, loc=0, scale=1) | | Median of the distribution. |
| mean(<shape(s)>, loc=0, scale=1) | | Mean of the distribution. |

Continued on next page

**Table 4.10 – continued from previous page**

| | | |
|---|---|---|
| std(<shape(s)>, loc=0, scale=1) | | Standard deviation of the distribution. |
| var(<shape(s)>, loc=0, scale=1) | | Variance of the distribution. |
| interval(alpha, <shape(s)>, loc=0, scale=1) | | Interval that with `alpha` percent probability contains a random realization of this distribution. |
| __call__(<shape(s)>, loc=0, scale=1) | | Calling a distribution instance creates a frozen RV object with the same methods but holding the given shape, location, and scale fixed. See Notes section. |
| **Parameters for Methods** | | |
| x | array_like | quantiles |
| q | array_like | lower or upper tail probability |
| <shape(s)> | array_like | shape parameters |
| loc | array_like, optional | location parameter (default=0) |
| scale | array_like, optional | scale parameter (default=1) |
| size | int or tuple of ints, optional | shape of random variates (default computed from input arguments ) |
| moments | string, optional | composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv') |
| n | int | order of moment to calculate in method moments |
| **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. | | |

`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=1)

**Returns**

**rvs** : array_like

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 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**

**cdf** : array_like

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 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** : array_like

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).

**kwds** : keyword arguments, optional

These can include "loc" and "scale", as well as other keyword arguments relevant for a given distribution.

`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

scale parameter (default=1)

**moments** : string, optional

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default='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

scale parameter (default=1)

`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.

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.

`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

location and scale only tested on a few examples

**Parameters**

**all parameters are keyword parameters** :

**func** : function (default: identity mapping)

Function for which integral is calculated. Takes only one argument.

**args** : tuple

argument (parameters) of the distribution

**lb, ub** : numbers

lower and upper bound for integration, default is set to the support of the distribution

**conditional** : boolean (False)

If true then 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.

**Additional keyword arguments are passed to the integration routine.** :

**Returns**

**expected value** : float

## Notes

This function has not been checked for it's behavior when the integral is not finite. The integration behavior 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=0)

**scale** : array_like, optional

scale parameter (default=1)

**Returns**

**median** : float

the median of the distribution.

**See Also:**

`self.ppf`

`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.`**`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.`**`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.`**`interval`**`(`*alpha*, **args*, ***kwds*`)`

Confidence interval with equal areas around the median

**Parameters**

**alpha** : array_like float in [0,1]

Probability that an rv will be drawn from the returned range

**arg1, arg2, ...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

**loc: array_like, optioal** :

location parameter (deafult = 0)

**scale** : array_like, optional

scale paramter (default = 1)

**Returns**

**a, b: array_like (float)** :

end-points of range that contain alpha % of the rvs

Calling the instance as a function returns a frozen pdf whose shape, location, and scale parameters are fixed.

Similarly, each discrete distribution is an instance of the class rv_discrete:

| | |
|---|---|
| `rv_discrete`([a, b, name, badvalue, ...]) | A generic discrete random variable class meant for subclassing. |
| `rv_discrete.rvs`(*args, **kwargs) | Random variates of given type. |
| `rv_discrete.pmf`(k, *args, **kwds) | Probability mass function at k of the given RV. |
| `rv_discrete.logpmf`(k, *args, **kwds) | Log of the probability mass function at k of the given RV. |
| `rv_discrete.cdf`(k, *args, **kwds) | Cumulative distribution function at k of the given RV |
| `rv_discrete.logcdf`(k, *args, **kwds) | Log of the cumulative distribution function at k of the given RV |
| `rv_discrete.sf`(k, *args, **kwds) | Survival function (1-cdf) at k of the given RV |
| `rv_discrete.logsf`(k, *args, **kwds) | Log of the survival function (1-cdf) at k of the given RV |
| `rv_discrete.ppf`(q, *args, **kwds) | Percent point function (inverse of cdf) at q of the given RV |
| `rv_discrete.isf`(q, *args, **kwds) | Inverse survival function (1-sf) at q of the given RV |
| `rv_discrete.stats`(*args, **kwds) | Some statistics of the given discrete RV |
| `rv_discrete.moment`(n, *args, **kwds) | n'th non-central moment of the distribution |
| `rv_discrete.entropy`(*args, **kwds) | |
| `rv_discrete.expect`([func, args, loc, lb, ...]) | calculate expected value of a function with respect to the distribution |
| `rv_discrete.median`(*args, **kwds) | Median of the distribution. |
| `rv_discrete.mean`(*args, **kwds) | Mean of the distribution |
| `rv_discrete.var`(*args, **kwds) | Variance of the distribution |
| `rv_discrete.std`(*args, **kwds) | Standard deviation of the distribution. |
| `rv_discrete.interval`(alpha, *args, **kwds) | Confidence interval with equal areas around the median |

**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*)

A generic discrete random variable class meant for subclassing.

`rv_discrete` is a base class to construct specific distribution classes and instances from for discrete random variables. rv_discrete can be used to construct an arbitrary distribution with defined by a list of support points and the 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

(xk, pk) where xk are points (integers) with positive probability pk with sum(pk) = 1

**inc** : integer

increment for the support of the distribution, default: 1 other values have not been tested

**badvalue** : object, optional

The value in (masked) arrays that indicates a value that should be ignored.

**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 first two arguments for all its methods.

**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.

## Notes

Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object:

**myrv = generic(<shape(s)>, loc=0)**

- frozen RV object with the same methods but holding the given shape and location fixed.

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).

To create a new discrete distribution, we would do the following:

```
class poisson_gen(rv_continuous):
    #"Poisson distribution"
    def _pmf(self, k, mu):
        ...
```

and create an instance

poisson = poisson_gen(name="poisson", shapes="mu", longname='A Poisson')

The docstring can be created from a template.

## Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = generic.numargs
>>> [ <shape(s)> ] = ['Replace with resonable value', ]*numargs
```

Display frozen pmf:

```
>>> rv = generic(<shape(s)>)
>>> x = np.arange(0, np.min(rv.dist.b, 3)+1)
>>> h = plt.plot(x, rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = generic.cdf(x, <shape(s)>)
>>> h = plt.semilogy(np.abs(x-generic.ppf(prb, <shape(s)>))+1e-20)
```

Random number generation:

```
>>> R = generic.rvs(<shape(s)>, size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7), (0.1, 0.2, 0.3, 0.1, 0.1, 0.1, 0.1)]
>>> custm = rv_discrete(name='custm', values=vals)
>>> h = plt.plot(vals[0], custm.pmf(vals[0]))
```

## Methods

| | |
|---|---|
| generic.rvs(<shape(s)>, loc=0, size=1) | random variates |
| generic.pmf(x, <shape(s)>, loc=0) | probability mass function |
| logpmf(x, <shape(s)>, loc=0) | log of the probability density function |
| generic.cdf(x, <shape(s)>, loc=0) | cumulative density function |
| generic.logcdf(x, <shape(s)>, loc=0) | log of the cumulative density function |
| generic.sf(x, <shape(s)>, loc=0) | survival function (1-cdf — sometimes more accurate) |
| generic.logsf(x, <shape(s)>, loc=0, scale=1) | log of the survival function |
| generic.ppf(q, <shape(s)>, loc=0) | percent point function (inverse of cdf — percentiles) |
| generic.isf(q, <shape(s)>, loc=0) | inverse survival function (inverse of sf) |
| generic.moment(n, <shape(s)>, loc=0) | non-central n-th moment of the distribution. May not work for array arguments. |
| generic.stats(<shape(s)>, loc=0, moments='mv') | mean('m', axis=0), variance('v'), skew('s'), and/or kurtosis('k') |
| generic.entropy(<shape(s)>, loc=0) | entropy of the RV |
| generic.fit(data, <shape(s)>, loc=0) | Parameter estimates for generic data |
| generic.expect(func=None, args=(), loc=0, lb=None, ub=None, conditional=False) | Expected value of a function with respect to the distribution. Additional kwd arguments passed to integrate.quad |
| generic.median(<shape(s)>, loc=0) | Median of the distribution. |
| generic.mean(<shape(s)>, loc=0) | Mean of the distribution. |
| generic.std(<shape(s)>, loc=0) | Standard deviation of the distribution. |
| generic.var(<shape(s)>, loc=0) | Variance of the distribution. |
| generic.interval(alpha, <shape(s)>, loc=0) | Interval that with `alpha` percent probability contains a random realization of this distribution. |
| generic(<shape(s)>, loc=0) | calling a distribution instance returns a frozen distribution |

`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=1)

**Returns**

**rvs** : array_like

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 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**

**cdf** : array_like

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 (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.`**`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**

**k** : array_like

quantile corresponding to the lower tail probability, q.

`rv_discrete.`**`isf`**`(`*q*, **args*, ***kwds*`)`

Inverse survival function (1-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** : array_like

quantile corresponding to the upper tail probability, q.

`rv_discrete.`**`stats`**`(`**args*, ***kwds*`)`

Some statistics of the given discrete 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)

**moments** : string, optional

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default='mv')

**Returns**

**stats** : sequence

of requested moments.

`rv_discrete.`**`moment`**(*n*, **args*, ***kwds*)

n'th non-central moment of the 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** : float, optional

location parameter (default=0)

**scale** : float, optional

scale parameter (default=1)

`rv_discrete.`**`entropy`**(**args*, ***kwds*)

`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**

**fn** : function (default: identity mapping)

Function for which sum is calculated. Takes only one argument.

**args** : tuple

argument (parameters) of the distribution

**optional keyword parameters** :

**lb, ub** : numbers

lower and upper bound for integration, default is set to the support of the distribution, lb and ub are inclusive (ul<=k<=ub)

**conditional** : boolean (False)

If true then the expectation 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 (k such that ul<=k<=ub).

**Returns**

**expected value** : float

## 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=0)

**scale** : array_like, optional

scale parameter (default=1)

**Returns**
**median** : float

the median of the distribution.

**See Also:**

`self.ppf`

`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.`**`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.`**`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.`**`interval`**`(`*alpha*, **args*, ***kwds*`)`

Confidence interval with equal areas around the median

**Parameters**

**alpha** : array_like float in [0,1]

Probability that an rv will be drawn from the returned range

**arg1, arg2, ...** : array_like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

**loc: array_like, optioal** :

location parameter (deafult = 0)

**scale** : array_like, optional

scale paramter (default = 1)

**Returns**

**a, b: array_like (float)** :

end-points of range that contain alpha % of the rvs

## 4.22.1 Continuous distributions

| | |
|---|---|
| `norm` | A normal continuous random variable. |
| `alpha` | An alpha continuous random variable. |

Continued on next page

**Table 4.11 – continued from previous page**

| | |
|---|---|
| anglit | An anglit continuous random variable. |
| arcsine | An arcsine continuous random variable. |
| beta | A beta continuous random variable. |
| betaprime | A beta prima 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. |
| 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-Sanders) 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. |
| 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. |
| halfcauchy | A Half-Cauchy continuous random variable. |
| halflogistic | A half-logistic continuous random variable. |
| halfnorm | A half-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 continuous random variable. |
| loggamma | A log gamma continuous random variable. |
| loglaplace | A log-Laplace continuous random variable. |

Continued on next page

Table 4.11 – continued from previous page

| | |
|---|---|
| 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. |
| pareto | A Pareto 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.`**norm = <scipy.stats.distributions.norm_gen object at 0x3b10250>**

A normal continuous random variable.

The location (loc) keyword specifies the mean. The scale (scale) keyword specifies the standard deviation.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = norm(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `norm` is:

```
norm.pdf(x) = exp(-x**2/2)/sqrt(2*pi)
```

## Examples

```
>>> from scipy.stats import norm
>>> numargs = norm.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = norm()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = norm.cdf(x, )
>>> h = plt.semilogy(np.abs(x - norm.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = norm.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.`**`alpha`** **= <scipy.stats.distributions.alpha_gen object at 0x3b104d0>**

An alpha continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = alpha(a, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import alpha
>>> numargs = alpha.numargs
>>> [ a ] = [0.9,] * numargs
>>> rv = alpha(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = alpha.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - alpha.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = alpha.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, scale=1, size=1) | 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.distributions.anglit_gen object at 0x3b10610>**

An anglit continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = anglit(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import anglit
>>> numargs = anglit.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = anglit()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = anglit.cdf(x, )
>>> h = plt.semilogy(np.abs(x - anglit.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = anglit.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.arcsine_gen object at 0x3b10690>**

An arcsine continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = arcsine(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for arcsine is:

```
arcsine.pdf(x) = 1/(pi*sqrt(x*(1-x)))
for 0 < x < 1.
```

## Examples

```
>>> from scipy.stats import arcsine
>>> numargs = arcsine.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = arcsine()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = arcsine.cdf(x, )
>>> h = plt.semilogy(np.abs(x - arcsine.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = arcsine.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.beta_gen object at 0x3b10950>**

A beta continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = beta(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `beta` is:

```
beta.pdf(x, a, b) = gamma(a+b)/(gamma(a)*gamma(b)) * x**(a-1) *
(1-x)**(b-1),
```

for $0 < x < 1, a > 0, b > 0$.

## Examples

```
>>> from scipy.stats import beta
>>> numargs = beta.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = beta(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = beta.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - beta.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = beta.rvs(a, b, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.betaprime_gen object at 0x3b10a90>**

A beta prima continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = betaprime(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `betaprime` is:

```
betaprime.pdf(x, a, b) =
    gamma(a+b) / (gamma(a)*gamma(b)) * x**(a-1) * (1-x)**(-a-b)
```

for `x > 0`, `a > 0`, `b > 0`.

## Examples

```
>>> from scipy.stats import betaprime
>>> numargs = betaprime.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = betaprime(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = betaprime.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - betaprime.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = betaprime.rvs(a, b, size=100)
```

## Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.bradford_gen object at 0x3b10b10>**

A Bradford continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = bradford(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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)`.

## Examples

```
>>> from scipy.stats import bradford
>>> numargs = bradford.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = bradford(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = bradford.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - bradford.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = bradford.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.burr_gen object at 0x3b10e50>**

A Burr continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c, d** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = burr(c, d, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import burr
>>> numargs = burr.numargs
>>> [ c, d ] = [0.9,] * numargs
>>> rv = burr(c, d)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = burr.cdf(x, c, d)
>>> h = plt.semilogy(np.abs(x - burr.ppf(prb, c, d)) + 1e-20)
```

Random number generation

```
>>> R = burr.rvs(c, d, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, d, loc=0, scale=1, size=1) | 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.distributions.cauchy_gen object at 0x3b85050>**

A Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = cauchy(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `cauchy` is:

```
cauchy.pdf(x) = 1 / (pi * (1 + x**2))
```

## Examples

```
>>> from scipy.stats import cauchy
>>> numargs = cauchy.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = cauchy()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = cauchy.cdf(x, )
>>> h = plt.semilogy(np.abs(x - cauchy.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = cauchy.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.chi_gen object at 0x3b85210>**

A chi continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**df** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = chi(df, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### 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`.

### Examples

```
>>> from scipy.stats import chi
>>> numargs = chi.numargs
>>> [ df ] = [0.9,] * numargs
>>> rv = chi(df)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = chi.cdf(x, df)
>>> h = plt.semilogy(np.abs(x - chi.ppf(prb, df)) + 1e-20)
```

Random number generation

```
>>> R = chi.rvs(df, size=100)
```

### Methods

| | |
|---|---|
| rvs(df, loc=0, scale=1, size=1) | 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.distributions.chi2_gen object at 0x3b854d0>**

A chi-squared continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**df** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = chi2(df, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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)
```

## Examples

```
>>> from scipy.stats import chi2
>>> numargs = chi2.numargs
>>> [ df ] = [0.9,] * numargs
>>> rv = chi2(df)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = chi2.cdf(x, df)
>>> h = plt.semilogy(np.abs(x - chi2.ppf(prb, df)) + 1e-20)
```

Random number generation

```
>>> R = chi2.rvs(df, size=100)
```

## Methods

| | |
|---|---|
| rvs(df, loc=0, scale=1, size=1) | 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.distributions.cosine_gen object at 0x3b85510>**

A cosine continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape, :**

**location, and scale parameters returning a "frozen" continuous RV object: :**

**rv = cosine(loc=0, scale=1) :**

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import cosine
>>> numargs = cosine.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = cosine()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = cosine.cdf(x, )
>>> h = plt.semilogy(np.abs(x - cosine.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = cosine.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.dgamma_gen object at 0x3b85610>**

A double gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = dgamma(a, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import dgamma
>>> numargs = dgamma.numargs
>>> [ a ] = [0.9,] * numargs
>>> rv = dgamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = dgamma.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - dgamma.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = dgamma.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, scale=1, size=1) | 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.distributions.dweibull_gen object at 0x3b85950>**

A double Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = dweibull(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `dweibull` is:

```
dweibull.pdf(x, c) = c / 2 * abs(x)**(c-1) * exp(-abs(x)**c)
```

## Examples

```
>>> from scipy.stats import dweibull
>>> numargs = dweibull.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = dweibull(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = dweibull.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - dweibull.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = dweibull.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.erlang_gen object at 0x3b85990>**

An Erlang continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**n** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = erlang(n, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The Erlang distribution is a special case of the Gamma distribution, with the shape parameter an integer.

## Examples

```
>>> from scipy.stats import erlang
>>> numargs = erlang.numargs
>>> [ n ] = [0.9,] * numargs
>>> rv = erlang(n)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = erlang.cdf(x, n)
>>> h = plt.semilogy(np.abs(x - erlang.ppf(prb, n)) + 1e-20)
```

Random number generation

```
>>> R = erlang.rvs(n, size=100)
```

### Methods

| | |
|---|---|
| rvs(n, loc=0, scale=1, size=1) | 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 |

`scipy.stats.`**expon = <scipy.stats.distributions.expon_gen object at 0x3b85b10>**

An exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape, :**

**location, and scale parameters returning a "frozen" continuous RV object: :**

**rv = expon(loc=0, scale=1) :**

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `expon` is:

```
expon.pdf(x) = exp(-x)
```

for `x >= 0`.

The scale parameter is equal to `scale = 1.0 / lambda`.

## Examples

```
>>> from scipy.stats import expon
>>> numargs = expon.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = expon()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = expon.cdf(x, )
>>> h = plt.semilogy(np.abs(x - expon.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = expon.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.`**`exponweib`** **= <scipy.stats.distributions.exponweib_gen object at 0x3b85c50>**

An exponentiated Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = exponweib(a, c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import exponweib
>>> numargs = exponweib.numargs
>>> [ a, c ] = [0.9,] * numargs
>>> rv = exponweib(a, c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = exponweib.cdf(x, a, c)
>>> h = plt.semilogy(np.abs(x - exponweib.ppf(prb, a, c)) + 1e-20)
```

Random number generation

```
>>> R = exponweib.rvs(a, c, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, c, loc=0, scale=1, size=1) | 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.distributions.exponpow_gen object at 0x3b85e50>**

An exponential power continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = exponpow(b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import exponpow
>>> numargs = exponpow.numargs
>>> [ b ] = [0.9,] * numargs
>>> rv = exponpow(b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = exponpow.cdf(x, b)
>>> h = plt.semilogy(np.abs(x - exponpow.ppf(prb, b)) + 1e-20)
```

Random number generation

```
>>> R = exponpow.rvs(b, size=100)
```

### Methods

| | |
|---|---|
| rvs(b, loc=0, scale=1, size=1) | 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.distributions.f_gen object at 0x3b89390>**

An F continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**dfn, dfd** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = f(dfn, dfd, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import f
>>> numargs = f.numargs
>>> [ dfn, dfd ] = [0.9,] * numargs
>>> rv = f(dfn, dfd)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = f.cdf(x, dfn, dfd)
>>> h = plt.semilogy(np.abs(x - f.ppf(prb, dfn, dfd)) + 1e-20)
```

Random number generation

```
>>> R = f.rvs(dfn, dfd, size=100)
```

### Methods

| | |
|---|---|
| rvs(dfn, dfd, loc=0, scale=1, size=1) | 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.distributions.fatiguelife_gen object at 0x3b85ed0>**

A fatigue-life (Birnbaum-Sanders) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = fatiguelife(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import fatiguelife
>>> numargs = fatiguelife.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = fatiguelife(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = fatiguelife.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - fatiguelife.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = fatiguelife.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.fisk_gen object at 0x3b10d10>**

A Fisk continuous random variable.

The Fisk distribution is also known as the log-logistic distribution, and equals the Burr distribution with `d=1`.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = fisk(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**See Also:**

burr

## Examples

```
>>> from scipy.stats import fisk
>>> numargs = fisk.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = fisk(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = fisk.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - fisk.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = fisk.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.foldcauchy_gen object at 0x3b89210>**

A folded Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = foldcauchy(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import foldcauchy
>>> numargs = foldcauchy.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = foldcauchy(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = foldcauchy.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - foldcauchy.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = foldcauchy.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.foldnorm_gen object at 0x3b89410>**

A folded normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = foldnorm(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import foldnorm
>>> numargs = foldnorm.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = foldnorm(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = foldnorm.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - foldnorm.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = foldnorm.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.frechet_r_gen object at 0x3b89590>**

A Frechet right (or Weibull minimum) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = frechet_r(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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`.

## Examples

```
>>> from scipy.stats import frechet_r
>>> numargs = frechet_r.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = frechet_r(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = frechet_r.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - frechet_r.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = frechet_r.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.frechet_l_gen object at 0x3b89090>**

A Frechet left (or Weibull maximum) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = frechet_l(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import frechet_l
>>> numargs = frechet_l.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = frechet_l(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = frechet_l.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - frechet_l.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = frechet_l.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.genlogistic_gen object at 0x3b89650>**

A generalized logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = genlogistic(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import genlogistic
>>> numargs = genlogistic.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = genlogistic(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genlogistic.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - genlogistic.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = genlogistic.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.`**`genpareto`** **= <scipy.stats.distributions.genpareto_gen object at 0x3b89b10>**

A generalized Pareto continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = genpareto(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `genpareto` is:

```
genpareto.pdf(x, c) = (1 + c * x)**(-1 - 1/c)
```

for `c != 0`, and for `x >= 0` for all c, and `x < 1/abs(c)` for `c < 0`.

## Examples

```
>>> from scipy.stats import genpareto
>>> numargs = genpareto.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = genpareto(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genpareto.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - genpareto.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = genpareto.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.genexpon_gen object at 0x3b89ad0>**

A generalized exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b, c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = genexpon(a, b, c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## References

"An Extension of Marshall and Olkin's Bivariate Exponential Distribution", H.K. Ryu, Journal of the American Statistical Association, 1993.

"The Exponential Distribution: Theory, Methods and Applications", N. Balakrishnan, Asit P. Basu.

## Examples

```
>>> from scipy.stats import genexpon
>>> numargs = genexpon.numargs
>>> [ a, b, c ] = [0.9,] * numargs
>>> rv = genexpon(a, b, c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genexpon.cdf(x, a, b, c)
>>> h = plt.semilogy(np.abs(x - genexpon.ppf(prb, a, b, c)) + 1e-20)
```

Random number generation

```
>>> R = genexpon.rvs(a, b, c, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, c, loc=0, scale=1, size=1) | 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.distributions.genextreme_gen object at 0x3b89fd0>**

A generalized extreme value continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = genextreme(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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
```

## Examples

```
>>> from scipy.stats import genextreme
>>> numargs = genextreme.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = genextreme(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genextreme.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - genextreme.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = genextreme.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.gausshyper_gen object at 0x3b920d0>**

A Gauss hypergeometric continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b, c, z** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gausshyper(a, b, c, z, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### 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))`

### Examples

```
>>> from scipy.stats import gausshyper
>>> numargs = gausshyper.numargs
>>> [ a, b, c, z ] = [0.9,] * numargs
>>> rv = gausshyper(a, b, c, z)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gausshyper.cdf(x, a, b, c, z)
>>> h = plt.semilogy(np.abs(x - gausshyper.ppf(prb, a, b, c, z)) + 1e-20)
```

Random number generation

```
>>> R = gausshyper.rvs(a, b, c, z, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, c, z, loc=0, scale=1, size=1) | 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.distributions.gamma_gen object at 0x3b901d0>**

A gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gamma(a, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**See Also:**

`erlang`, `expon`

## Notes

When `a` is an integer, this is the Erlang distribution, and for `a=1` it is the exponential distribution.

The probability density function for `gamma` is:

```
gamma.pdf(x, a) = x**(a-1) * exp(-x) / gamma(a)
```

for `x >= 0`, `a > 0`.

## Examples

```
>>> from scipy.stats import gamma
>>> numargs = gamma.numargs
>>> [ a ] = [0.9,] * numargs
>>> rv = gamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gamma.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - gamma.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = gamma.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, scale=1, size=1) | 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.distributions.gengamma_gen object at 0x3b902d0>**

A generalized gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gengamma(a, c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import gengamma
>>> numargs = gengamma.numargs
>>> [ a, c ] = [0.9,] * numargs
>>> rv = gengamma(a, c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gengamma.cdf(x, a, c)
>>> h = plt.semilogy(np.abs(x - gengamma.ppf(prb, a, c)) + 1e-20)
```

Random number generation

```
>>> R = gengamma.rvs(a, c, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, c, loc=0, scale=1, size=1) | 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.distributions.genhalflogistic_gen object at 0x3b90450>**

A generalized half-logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = genhalflogistic(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import genhalflogistic
>>> numargs = genhalflogistic.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = genhalflogistic(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genhalflogistic.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - genhalflogistic.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = genhalflogistic.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.gilbrat_gen object at 0x3b985d0>**

A Gilbrat continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gilbrat(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `gilbrat` is:

```
gilbrat.pdf(x) = 1/(x*sqrt(2*pi)) * exp(-1/2*(log(x))**2)
```

## Examples

```
>>> from scipy.stats import gilbrat
>>> numargs = gilbrat.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = gilbrat()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gilbrat.cdf(x, )
>>> h = plt.semilogy(np.abs(x - gilbrat.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = gilbrat.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.gompertz_gen object at 0x3b905d0>**

A Gompertz (or truncated Gumbel) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gompertz(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### 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`.

### Examples

```
>>> from scipy.stats import gompertz
>>> numargs = gompertz.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = gompertz(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gompertz.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - gompertz.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = gompertz.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.gumbel_r_gen object at 0x3b90750>**

A right-skewed Gumbel continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape, :**

**location, and scale parameters returning a "frozen" continuous RV object: :**

**rv = gumbel_r(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import gumbel_r
>>> numargs = gumbel_r.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = gumbel_r()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gumbel_r.cdf(x, )
>>> h = plt.semilogy(np.abs(x - gumbel_r.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = gumbel_r.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.gumbel_l_gen object at 0x3b908d0>**

A left-skewed Gumbel continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = gumbel_l(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import gumbel_l
>>> numargs = gumbel_l.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = gumbel_l()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gumbel_l.cdf(x, )
>>> h = plt.semilogy(np.abs(x - gumbel_l.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = gumbel_l.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.halfcauchy_gen object at 0x3b90bd0>**

A Half-Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = halfcauchy(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `halfcauchy` is:

```
halfcauchy.pdf(x) = 2 / (pi * (1 + x**2))
```

for `x >= 0`.

## Examples

```
>>> from scipy.stats import halfcauchy
>>> numargs = halfcauchy.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = halfcauchy()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halfcauchy.cdf(x, )
>>> h = plt.semilogy(np.abs(x - halfcauchy.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = halfcauchy.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.halflogistic_gen object at 0x3b90d10>**

A half-logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object: :**

**rv = halflogistic(loc=0, scale=1) :**

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import halflogistic
>>> numargs = halflogistic.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = halflogistic()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halflogistic.cdf(x, )
>>> h = plt.semilogy(np.abs(x - halflogistic.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = halflogistic.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.halfnorm_gen object at 0x3b90e90>**

A half-normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a “frozen” continuous RV object:** :

**rv = halfnorm(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### Notes

The probability density function for `halfnorm` is:

```
halfnorm.pdf(x) = sqrt(2/pi) * exp(-x**2/2)
```

for `x > 0`.

### Examples

```
>>> from scipy.stats import halfnorm
>>> numargs = halfnorm.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = halfnorm()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halfnorm.cdf(x, )
>>> h = plt.semilogy(np.abs(x - halfnorm.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = halfnorm.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.`**`hypsecant`** **= <scipy.stats.distributions.hypsecant_gen object at 0x3b90e10>**

A hyperbolic secant continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = hypsecant(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `hypsecant` is:

```
hypsecant.pdf(x) = 1/pi * sech(x)
```

## Examples

```
>>> from scipy.stats import hypsecant
>>> numargs = hypsecant.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = hypsecant()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = hypsecant.cdf(x, )
>>> h = plt.semilogy(np.abs(x - hypsecant.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = hypsecant.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.invgamma_gen object at 0x3b92390>**

An inverted gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = invgamma(a, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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.

## Examples

```
>>> from scipy.stats import invgamma
>>> numargs = invgamma.numargs
>>> [ a ] = [0.9,] * numargs
>>> rv = invgamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invgamma.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - invgamma.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = invgamma.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, scale=1, size=1) | 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.distributions.invgauss_gen object at 0x3b923d0>**

An inverse Gaussian continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**mu** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = invgauss(mu, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

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
>>> numargs = invgauss.numargs
>>> [ mu ] = [0.9,] * numargs
>>> rv = invgauss(mu)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invgauss.cdf(x, mu)
>>> h = plt.semilogy(np.abs(x - invgauss.ppf(prb, mu)) + 1e-20)
```

Random number generation

```
>>> R = invgauss.rvs(mu, size=100)
```

## Methods

| | |
|---|---|
| rvs(mu, loc=0, scale=1, size=1) | 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.distributions.invweibull_gen object at 0x3b924d0>**

An inverted Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = invweibull(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### Notes

The probability density function for `invweibull` is:

```
invweibull.pdf(x, c) = c * x**(-c-1) * exp(-x**(-c))
```

for `x > 0`, `c > 0`.

### Examples

```
>>> from scipy.stats import invweibull
>>> numargs = invweibull.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = invweibull(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invweibull.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - invweibull.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = invweibull.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.johnsonsb_gen object at 0x3b92650>**

A Johnson SB continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = johnsonb(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import johnsonb
>>> numargs = johnsonb.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = johnsonb(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = johnsonb.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - johnsonb.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = johnsonb.rvs(a, b, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.johnsonsu_gen object at 0x3b92810>**

A Johnson SU continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = johnsonsu(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import johnsonsu
>>> numargs = johnsonsu.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = johnsonsu(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = johnsonsu.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - johnsonsu.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = johnsonsu.rvs(a, b, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.ksone_gen object at 0x3b02e50>**

General Kolmogorov-Smirnov one-sided test.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**n** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = ksone(n, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**Examples** :

**——** :

**>>> from scipy.stats import ksone** :

**>>> numargs = ksone.numargs** :

**>>> [ n ] = [0.9,] * numargs** :

**>>> rv = ksone(n)** :

**Display frozen pdf** :

**>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))** :

**>>> h = plt.plot(x, rv.pdf(x))** :

**Check accuracy of cdf and ppf** :

**>>> prb = ksone.cdf(x, n)** :

**>>> h = plt.semilogy(np.abs(x - ksone.ppf(prb, n)) + 1e-20)** :

**Random number generation** :

**>>> R = ksone.rvs(n, size=100)** :

### Methods

| | |
|---|---|
| rvs(n, loc=0, scale=1, size=1) | 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 |

`scipy.stats.`**`kstwobign`** **= <scipy.stats.distributions.kstwobign_gen object at 0x3b10090>**

Kolmogorov-Smirnov two-sided test for large N.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = kstwobign(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**Examples** :

**——** :

**>>> from scipy.stats import kstwobign** :

**>>> numargs = kstwobign.numargs** :

**>>> [ ] = [0.9,] * numargs** :

**>>> rv = kstwobign()** :

**Display frozen pdf** :

**>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))** :

**>>> h = plt.plot(x, rv.pdf(x))** :

**Check accuracy of cdf and ppf** :

**>>> prb = kstwobign.cdf(x, )** :

**>>> h = plt.semilogy(np.abs(x - kstwobign.ppf(prb, )) + 1e-20)** :

**Random number generation** :

**>>> R = kstwobign.rvs(size=100)** :

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.`**`laplace`** **= <scipy.stats.distributions.laplace_gen object at 0x3b92990>**

A Laplace continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = laplace(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `laplace` is:

```
laplace.pdf(x) = 1/2 * exp(-abs(x))
```

## Examples

```
>>> from scipy.stats import laplace
>>> numargs = laplace.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = laplace()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = laplace.cdf(x, )
>>> h = plt.semilogy(np.abs(x - laplace.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = laplace.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.logistic_gen object at 0x3b92750>**

A logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = logistic(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `logistic` is:

```
logistic.pdf(x) = exp(-x) / (1+exp(-x))**2
```

## Examples

```
>>> from scipy.stats import logistic
>>> numargs = logistic.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = logistic()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = logistic.cdf(x, )
>>> h = plt.semilogy(np.abs(x - logistic.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = logistic.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.loggamma_gen object at 0x3b981d0>**

A log gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = loggamma(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### Notes

The probability density function for `loggamma` is:

```
loggamma.pdf(x, c) = exp(c*x-exp(x)) / gamma(c)
```

for all `x, c > 0`.

### Examples

```
>>> from scipy.stats import loggamma
>>> numargs = loggamma.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = loggamma(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = loggamma.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - loggamma.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = loggamma.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.loglaplace_gen object at 0x3b98450>**

A log-Laplace continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = loglaplace(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import loglaplace
>>> numargs = loglaplace.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = loglaplace(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = loglaplace.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - loglaplace.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = loglaplace.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.lognorm_gen object at 0x3b98490>**

A lognormal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**s** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = lognorm(s, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

If log x is normally distributed with mean mu and variance sigma**2, then x is log-normally distributed with shape paramter sigma and scale parameter exp(mu).

## Examples

```
>>> from scipy.stats import lognorm
>>> numargs = lognorm.numargs
>>> [ s ] = [0.9,] * numargs
>>> rv = lognorm(s)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = lognorm.cdf(x, s)
>>> h = plt.semilogy(np.abs(x - lognorm.ppf(prb, s)) + 1e-20)
```

Random number generation

```
>>> R = lognorm.rvs(s, size=100)
```

### Methods

| | |
|---|---|
| rvs(s, loc=0, scale=1, size=1) | 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.distributions.lomax_gen object at 0x3b9b5d0>**

A Lomax (Pareto of the second kind) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = lomax(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import lomax
>>> numargs = lomax.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = lomax(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = lomax.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - lomax.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = lomax.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.maxwell_gen object at 0x3b98750>**

A Maxwell continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = maxwell(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

A special case of a `chi` distribution, with `df = 3`, `loc = 0.0`, and given `scale = 1.0 / sqrt(a)`, where a is the parameter used in the Mathworld description [R88].

The probability density function for `maxwell` is:

```
maxwell.pdf(x, a) = sqrt(2/pi)x**2 * exp(-x**2/2)
```

for `x > 0`.

## References

[R88]

## Examples

```
>>> from scipy.stats import maxwell
>>> numargs = maxwell.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = maxwell()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = maxwell.cdf(x, )
>>> h = plt.semilogy(np.abs(x - maxwell.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = maxwell.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.mielke_gen object at 0x3b98a50>**

A Mielke's Beta-Kappa continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**k, s** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = mielke(k, s, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import mielke
>>> numargs = mielke.numargs
>>> [ k, s ] = [0.9,] * numargs
>>> rv = mielke(k, s)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = mielke.cdf(x, k, s)
>>> h = plt.semilogy(np.abs(x - mielke.ppf(prb, k, s)) + 1e-20)
```

Random number generation

```
>>> R = mielke.rvs(k, s, size=100)
```

## Methods

| | |
|---|---|
| rvs(k, s, loc=0, scale=1, size=1) | 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.distributions.nakagami_gen object at 0x3b98b90>**

A Nakagami continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**nu** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = nakagami(nu, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import nakagami
>>> numargs = nakagami.numargs
>>> [ nu ] = [0.9,] * numargs
>>> rv = nakagami(nu)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = nakagami.cdf(x, nu)
>>> h = plt.semilogy(np.abs(x - nakagami.ppf(prb, nu)) + 1e-20)
```

Random number generation

```
>>> R = nakagami.rvs(nu, size=100)
```

### Methods

| | |
|---|---|
| rvs(nu, loc=0, scale=1, size=1) | 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.distributions.ncx2_gen object at 0x3b98c10>**

A non-central chi-squared continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**df, nc** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = ncx2(df, nc, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `ncx2` is:

```
ncx2.pdf(x, df, nc) = exp(-(nc+df)/2) * 1/2 * (x/nc)**((df-2)/4)
                      * I[(df-2)/2](sqrt(nc*x))
```

for `x > 0`.

## Examples

```
>>> from scipy.stats import ncx2
>>> numargs = ncx2.numargs
>>> [ df, nc ] = [0.9,] * numargs
>>> rv = ncx2(df, nc)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = ncx2.cdf(x, df, nc)
>>> h = plt.semilogy(np.abs(x - ncx2.ppf(prb, df, nc)) + 1e-20)
```

Random number generation

```
>>> R = ncx2.rvs(df, nc, size=100)
```

### Methods

| | |
|---|---|
| rvs(df, nc, loc=0, scale=1, size=1) | 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.distributions.ncf_gen object at 0x3b98d10>**

A non-central F distribution continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**dfn, dfd, nc** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = ncf(dfn, dfd, nc, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import ncf
>>> numargs = ncf.numargs
>>> [ dfn, dfd, nc ] = [0.9,] * numargs
>>> rv = ncf(dfn, dfd, nc)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = ncf.cdf(x, dfn, dfd, nc)
>>> h = plt.semilogy(np.abs(x - ncf.ppf(prb, dfn, dfd, nc)) + 1e-20)
```

Random number generation

```
>>> R = ncf.rvs(dfn, dfd, nc, size=100)
```

### Methods

| | |
|---|---|
| rvs(dfn, dfd, nc, loc=0, scale=1, size=1) | 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.distributions.nct_gen object at 0x3b9b0d0>**

A non-central Student's T continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**df, nc** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = nct(df, nc, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`, `nc > 0`.

## Examples

```
>>> from scipy.stats import nct
>>> numargs = nct.numargs
>>> [ df, nc ] = [0.9,] * numargs
>>> rv = nct(df, nc)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = nct.cdf(x, df, nc)
>>> h = plt.semilogy(np.abs(x - nct.ppf(prb, df, nc)) + 1e-20)
```

Random number generation

```
>>> R = nct.rvs(df, nc, size=100)
```

### Methods

| | |
|---|---|
| rvs(df, nc, loc=0, scale=1, size=1) | 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.`**`pareto`** **= <scipy.stats.distributions.pareto_gen object at 0x3b9b410>**

A Pareto continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = pareto(b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### Notes

The probability density function for `pareto` is:

```
pareto.pdf(x, b) = b / x**(b+1)
```

for `x >= 1`, `b > 0`.

### Examples

```
>>> from scipy.stats import pareto
>>> numargs = pareto.numargs
>>> [ b ] = [0.9,] * numargs
>>> rv = pareto(b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = pareto.cdf(x, b)
>>> h = plt.semilogy(np.abs(x - pareto.ppf(prb, b)) + 1e-20)
```

Random number generation

```
>>> R = pareto.rvs(b, size=100)
```

### Methods

| | |
|---|---|
| rvs(b, loc=0, scale=1, size=1) | 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.`**`powerlaw`** **= <scipy.stats.distributions.powerlaw_gen object at 0x3b9b490>**

A power-function continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = powerlaw(a, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### Notes

The probability density function for `powerlaw` is:

```
powerlaw.pdf(x, a) = a * x**(a-1)
```

for `0 <= x <= 1`, `a > 0`.

### Examples

```
>>> from scipy.stats import powerlaw
>>> numargs = powerlaw.numargs
>>> [ a ] = [0.9,] * numargs
>>> rv = powerlaw(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powerlaw.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - powerlaw.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = powerlaw.rvs(a, size=100)
```

## Methods

| | |
|---|---|
| rvs(a, loc=0, scale=1, size=1) | 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.distributions.powerlognorm_gen object at 0x3b9b710>**

A power log-normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c, s** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = powerlognorm(c, s, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import powerlognorm
>>> numargs = powerlognorm.numargs
>>> [ c, s ] = [0.9,] * numargs
>>> rv = powerlognorm(c, s)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powerlognorm.cdf(x, c, s)
>>> h = plt.semilogy(np.abs(x - powerlognorm.ppf(prb, c, s)) + 1e-20)
```

Random number generation

```
>>> R = powerlognorm.rvs(c, s, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, s, loc=0, scale=1, size=1) | 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.distributions.powernorm_gen object at 0x3b9b890>**

A power normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = powernorm(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import powernorm
>>> numargs = powernorm.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = powernorm(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powernorm.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - powernorm.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = powernorm.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.rdist_gen object at 0x3b9ba10>**

An R-distributed continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = rdist(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import rdist
>>> numargs = rdist.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = rdist(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rdist.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - rdist.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = rdist.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.reciprocal_gen object at 0x3b9bd10>**

A reciprocal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = reciprocal(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import reciprocal
>>> numargs = reciprocal.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = reciprocal(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = reciprocal.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - reciprocal.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = reciprocal.rvs(a, b, size=100)
```

## Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.rayleigh_gen object at 0x3b9bb90>**

A Rayleigh continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape, :**

**location, and scale parameters returning a "frozen" continuous RV object: :**

**rv = rayleigh(loc=0, scale=1) :**

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `rayleigh` is:

```
rayleigh.pdf(r) = r * exp(-r**2/2)
```

for `x >= 0`.

## Examples

```
>>> from scipy.stats import rayleigh
>>> numargs = rayleigh.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = rayleigh()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rayleigh.cdf(x, )
>>> h = plt.semilogy(np.abs(x - rayleigh.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = rayleigh.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.rice_gen object at 0x3b9bc50>**

A Rice continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = rice(b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import rice
>>> numargs = rice.numargs
>>> [ b ] = [0.9,] * numargs
>>> rv = rice(b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rice.cdf(x, b)
>>> h = plt.semilogy(np.abs(x - rice.ppf(prb, b)) + 1e-20)
```

Random number generation

```
>>> R = rice.rvs(b, size=100)
```

### Methods

| | |
|---|---|
| rvs(b, loc=0, scale=1, size=1) | 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.distributions.recipinvgauss_gen object at 0x3b9f090>**

A reciprocal inverse Gaussian continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**mu** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = recipinvgauss(mu, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import recipinvgauss
>>> numargs = recipinvgauss.numargs
>>> [ mu ] = [0.9,] * numargs
>>> rv = recipinvgauss(mu)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = recipinvgauss.cdf(x, mu)
>>> h = plt.semilogy(np.abs(x - recipinvgauss.ppf(prb, mu)) + 1e-20)
```

Random number generation

```
>>> R = recipinvgauss.rvs(mu, size=100)
```

## Methods

| | |
|---|---|
| rvs(mu, loc=0, scale=1, size=1) | 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.distributions.semicircular_gen object at 0x3b9f250>**

A semicircular continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = semicircular(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `semicircular` is:

```
semicircular.pdf(x) = 2/pi * sqrt(1-x**2)
```

for `-1 <= x <= 1`.

## Examples

```
>>> from scipy.stats import semicircular
>>> numargs = semicircular.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = semicircular()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = semicircular.cdf(x, )
>>> h = plt.semilogy(np.abs(x - semicircular.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = semicircular.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.t_gen object at 0x3b98890>**

A Student's T continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**df** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = t(df, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import t
>>> numargs = t.numargs
>>> [ df ] = [0.9,] * numargs
>>> rv = t(df)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = t.cdf(x, df)
>>> h = plt.semilogy(np.abs(x - t.ppf(prb, df)) + 1e-20)
```

Random number generation

```
>>> R = t.rvs(df, size=100)
```

### Methods

| | |
|---|---|
| rvs(df, loc=0, scale=1, size=1) | 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.distributions.triang_gen object at 0x3b9f350>**

A triangular continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = triang(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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)`.

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
>>> numargs = triang.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = triang(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = triang.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - triang.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = triang.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.truncexpon_gen object at 0x3b9f650>**

A truncated exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = truncexpon(b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `truncexpon` is:

```
truncexpon.pdf(x, b) = exp(-x) / (1-exp(-b))
```

for `0 < x < b`.

## Examples

```
>>> from scipy.stats import truncexpon
>>> numargs = truncexpon.numargs
>>> [ b ] = [0.9,] * numargs
>>> rv = truncexpon(b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = truncexpon.cdf(x, b)
>>> h = plt.semilogy(np.abs(x - truncexpon.ppf(prb, b)) + 1e-20)
```

Random number generation

```
>>> R = truncexpon.rvs(b, size=100)
```

### Methods

| | |
|---|---|
| rvs(b, loc=0, scale=1, size=1) | 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.distributions.truncnorm_gen object at 0x3b9f690>**

A truncated normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a, b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = truncnorm(a, b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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
```

## Examples

```
>>> from scipy.stats import truncnorm
>>> numargs = truncnorm.numargs
>>> [ a, b ] = [0.9,] * numargs
>>> rv = truncnorm(a, b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = truncnorm.cdf(x, a, b)
>>> h = plt.semilogy(np.abs(x - truncnorm.ppf(prb, a, b)) + 1e-20)
```

Random number generation

```
>>> R = truncnorm.rvs(a, b, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, b, loc=0, scale=1, size=1) | 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.distributions.tukeylambda_gen object at 0x3b9f750>**

A Tukey-Lamdba continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**lam** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = tukeylambda(lam, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

### 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)

### Examples

```
>>> from scipy.stats import tukeylambda
>>> numargs = tukeylambda.numargs
>>> [ lam ] = [0.9,] * numargs
>>> rv = tukeylambda(lam)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = tukeylambda.cdf(x, lam)
>>> h = plt.semilogy(np.abs(x - tukeylambda.ppf(prb, lam)) + 1e-20)
```

Random number generation

```
>>> R = tukeylambda.rvs(lam, size=100)
```

## Methods

| | |
|---|---|
| rvs(lam, loc=0, scale=1, size=1) | 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.distributions.uniform_gen object at 0x3b9f910>**

A uniform continuous random variable.

This distribution is constant between *loc* and `loc = scale`.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = uniform(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Examples

```
>>> from scipy.stats import uniform
>>> numargs = uniform.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = uniform()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = uniform.cdf(x, )
>>> h = plt.semilogy(np.abs(x - uniform.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = uniform.rvs(size=100)
```

## Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.vonmises_gen object at 0x3b9fa90>**

A Von Mises continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**b** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = vonmises(b, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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, b) = exp(b*cos(x)) / (2*pi*I[0](b))
```

for `-pi <= x <= pi`, `b > 0`.

## Examples

```
>>> from scipy.stats import vonmises
>>> numargs = vonmises.numargs
>>> [ b ] = [0.9,] * numargs
>>> rv = vonmises(b)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = vonmises.cdf(x, b)
>>> h = plt.semilogy(np.abs(x - vonmises.ppf(prb, b)) + 1e-20)
```

Random number generation

```
>>> R = vonmises.rvs(b, size=100)
```

### Methods

| | |
|---|---|
| rvs(b, loc=0, scale=1, size=1) | 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.`**`wald`** **= <scipy.stats.distributions.wald_gen object at 0x3b9fdd0>**

A Wald continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = wald(loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## Notes

The probability density function for `wald` is:

```
wald.pdf(x, a) = 1/sqrt(2*pi*x**3) * exp(-(x-1)**2/(2*x))
```

for `x > 0`.

## Examples

```
>>> from scipy.stats import wald
>>> numargs = wald.numargs
>>> [  ] = [0.9,] * numargs
>>> rv = wald()
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = wald.cdf(x, )
>>> h = plt.semilogy(np.abs(x - wald.ppf(prb, )) + 1e-20)
```

Random number generation

```
>>> R = wald.rvs(size=100)
```

### Methods

| | |
|---|---|
| rvs(loc=0, scale=1, size=1) | 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.distributions.frechet_r_gen object at 0x3b89710>**

A Frechet right (or Weibull minimum) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = weibull_min(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import weibull_min
>>> numargs = weibull_min.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = weibull_min(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = weibull_min.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - weibull_min.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = weibull_min.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.frechet_l_gen object at 0x3b894d0>**

A Frechet left (or Weibull maximum) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = weibull_max(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

**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.

## Examples

```
>>> from scipy.stats import weibull_max
>>> numargs = weibull_max.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = weibull_max(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = weibull_max.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - weibull_max.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = weibull_max.rvs(c, size=100)
```

## Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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.distributions.wrapcauchy_gen object at 0x3b9fe90>**

A wrapped Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**c** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape,** :

**location, and scale parameters returning a "frozen" continuous RV object:** :

**rv = wrapcauchy(c, loc=0, scale=1)** :

- Frozen RV object with the same methods but holding the given shape, location, and scale fixed.

## 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`.

## Examples

```
>>> from scipy.stats import wrapcauchy
>>> numargs = wrapcauchy.numargs
>>> [ c ] = [0.9,] * numargs
>>> rv = wrapcauchy(c)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = wrapcauchy.cdf(x, c)
>>> h = plt.semilogy(np.abs(x - wrapcauchy.ppf(prb, c)) + 1e-20)
```

Random number generation

```
>>> R = wrapcauchy.rvs(c, size=100)
```

### Methods

| | |
|---|---|
| rvs(c, loc=0, scale=1, size=1) | 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 |

## 4.22.2 Discrete distributions

| | |
|---|---|
| `binom` | A binom discrete random variable. |
| `bernoulli` | A bernoulli discrete random variable. |
| `nbinom` | A negative binomial discrete random variable. |
| `geom` | A geometric discrete random variable. |
| `hypergeom` | A hypergeometric discrete random variable. |
| `logser` | A logarithmic discrete random variable. |
| `poisson` | A Poisson discrete random variable. |
| `planck` | A discrete exponential discrete random variable. |
| `boltzmann` | A truncated discrete exponential discrete random variable. |
| `randint` | A discrete uniform (random integer) discrete random variable. |
| `zipf` | A Zipf discrete random variable. |
| `dlaplace` | A discrete Laplacian discrete random variable. |

`scipy.stats.`**`binom`** **= <scipy.stats.distributions.binom_gen object at 0x3b9f6d0>**

A binom discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**n, pr** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = binom(n, pr, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Binomial distribution

Counts the number of successes in *n* independent trials when the probability of success each time is *pr*.

binom.pmf(k,n,p) = choose(n,k)*p**k*(1-p)**(n-k) for k in {0,1,...,n}

## Examples

```
>>> from scipy.stats import binom
>>> numargs = binom.numargs
>>> [ n, pr ] = Replace with reasonable value * numargs
>>> rv = binom(n, pr)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = binom.cdf(x, n, pr)
>>> h = plt.semilogy(np.abs(x - binom.ppf(prb, n, pr)) + 1e-20)
```

Random number generation

```
>>> R = binom.rvs(n, pr, size=100)
```

## Methods

| | |
|---|---|
| rvs(n, pr, loc=0, size=1) | Random variates. |
| pmf(x, n, pr, loc=0) | Probability mass function. |
| logpmf(x, n, pr, loc=0) | Log of the probability mass function. |
| cdf(x, n, pr, loc=0) | Cumulative density function. |
| logcdf(x, n, pr, loc=0) | Log of the cumulative density function. |
| sf(x, n, pr, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, n, pr, loc=0) | Log of the survival function. |
| ppf(q, n, pr, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, n, pr, loc=0) | Inverse survival function (inverse of sf). |
| stats(n, pr, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(n, pr, loc=0) | (Differential) entropy of the RV. |
| fit(data, n, pr, loc=0) | Parameter estimates for generic data. |
| expect(func, n, pr, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(n, pr, loc=0) | Median of the distribution. |
| mean(n, pr, loc=0) | Mean of the distribution. |
| var(n, pr, loc=0) | Variance of the distribution. |
| std(n, pr, loc=0) | Standard deviation of the distribution. |
| interval(alpha, n, pr, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`bernoulli`** **= <scipy.stats.distributions.bernoulli_gen object at 0x3ba51d0>**

A bernoulli discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**pr** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = bernoulli(pr, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Bernoulli distribution

1 if binary experiment succeeds, 0 otherwise. Experiment succeeds with probabilty *pr*.

**bernoulli.pmf(k,p) = 1-p if k = 0**
= p if k = 1

for k = 0,1

## Examples

```
>>> from scipy.stats import bernoulli
>>> numargs = bernoulli.numargs
>>> [ pr ] = Replace with reasonable value * numargs
>>> rv = bernoulli(pr)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = bernoulli.cdf(x, pr)
>>> h = plt.semilogy(np.abs(x - bernoulli.ppf(prb, pr)) + 1e-20)
```

Random number generation

```
>>> R = bernoulli.rvs(pr, size=100)
```

## Methods

| | |
|---|---|
| rvs(pr, loc=0, size=1) | Random variates. |
| pmf(x, pr, loc=0) | Probability mass function. |
| logpmf(x, pr, loc=0) | Log of the probability mass function. |
| cdf(x, pr, loc=0) | Cumulative density function. |
| logcdf(x, pr, loc=0) | Log of the cumulative density function. |
| sf(x, pr, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, pr, loc=0) | Log of the survival function. |
| ppf(q, pr, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, pr, loc=0) | Inverse survival function (inverse of sf). |
| stats(pr, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(pr, loc=0) | (Differential) entropy of the RV. |
| fit(data, pr, loc=0) | Parameter estimates for generic data. |
| expect(func, pr, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(pr, loc=0) | Median of the distribution. |
| mean(pr, loc=0) | Mean of the distribution. |
| var(pr, loc=0) | Variance of the distribution. |
| std(pr, loc=0) | Standard deviation of the distribution. |
| interval(alpha, pr, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`nbinom`** **= <scipy.stats.distributions.nbinom_gen object at 0x3ba5250>**

A negative binomial discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**n, pr** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = nbinom(n, pr, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Probability mass function, given by `np.choose(k+n-1, n-1) * p**n * (1-p)**k` for `k >= 0`.

## Examples

```
>>> from scipy.stats import nbinom
>>> numargs = nbinom.numargs
>>> [ n, pr ] = Replace with reasonable value * numargs
>>> rv = nbinom(n, pr)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = nbinom.cdf(x, n, pr)
>>> h = plt.semilogy(np.abs(x - nbinom.ppf(prb, n, pr)) + 1e-20)
```

Random number generation

```
>>> R = nbinom.rvs(n, pr, size=100)
```

## Methods

| | |
|---|---|
| rvs(n, pr, loc=0, size=1) | Random variates. |
| pmf(x, n, pr, loc=0) | Probability mass function. |
| logpmf(x, n, pr, loc=0) | Log of the probability mass function. |
| cdf(x, n, pr, loc=0) | Cumulative density function. |
| logcdf(x, n, pr, loc=0) | Log of the cumulative density function. |
| sf(x, n, pr, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, n, pr, loc=0) | Log of the survival function. |
| ppf(q, n, pr, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, n, pr, loc=0) | Inverse survival function (inverse of sf). |
| stats(n, pr, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(n, pr, loc=0) | (Differential) entropy of the RV. |
| fit(data, n, pr, loc=0) | Parameter estimates for generic data. |
| expect(func, n, pr, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(n, pr, loc=0) | Median of the distribution. |
| mean(n, pr, loc=0) | Mean of the distribution. |
| var(n, pr, loc=0) | Variance of the distribution. |
| std(n, pr, loc=0) | Standard deviation of the distribution. |
| interval(alpha, n, pr, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`geom`** **= <scipy.stats.distributions.geom_gen object at 0x3ba5350>**

A geometric discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**pr** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = geom(pr, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Geometric distribution

geom.pmf(k,p) = (1-p)**(k-1)*p for k >= 1

## Examples

```
>>> from scipy.stats import geom
>>> numargs = geom.numargs
>>> [ pr ] = Replace with reasonable value * numargs
>>> rv = geom(pr)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = geom.cdf(x, pr)
>>> h = plt.semilogy(np.abs(x - geom.ppf(prb, pr)) + 1e-20)
```

Random number generation

```
>>> R = geom.rvs(pr, size=100)
```

## Methods

| | |
|---|---|
| rvs(pr, loc=0, size=1) | Random variates. |
| pmf(x, pr, loc=0) | Probability mass function. |
| logpmf(x, pr, loc=0) | Log of the probability mass function. |
| cdf(x, pr, loc=0) | Cumulative density function. |
| logcdf(x, pr, loc=0) | Log of the cumulative density function. |
| sf(x, pr, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, pr, loc=0) | Log of the survival function. |
| ppf(q, pr, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, pr, loc=0) | Inverse survival function (inverse of sf). |
| stats(pr, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(pr, loc=0) | (Differential) entropy of the RV. |
| fit(data, pr, loc=0) | Parameter estimates for generic data. |
| expect(func, pr, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(pr, loc=0) | Median of the distribution. |
| mean(pr, loc=0) | Mean of the distribution. |
| var(pr, loc=0) | Variance of the distribution. |
| std(pr, loc=0) | Standard deviation of the distribution. |
| interval(alpha, pr, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`hypergeom`** **= <scipy.stats.distributions.hypergeom_gen object at 0x3ba5ad0>**

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.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**M, n, N** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = hypergeom(M, n, N, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## 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 N - (M-n) <= k <= min(m,N)
```

## Examples

```
>>> from scipy.stats import hypergeom
>>> numargs = hypergeom.numargs
>>> [ M, n, N ] = Replace with reasonable value * numargs
>>> rv = hypergeom(M, n, N)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = hypergeom.cdf(x, M, n, N)
>>> h = plt.semilogy(np.abs(x - hypergeom.ppf(prb, M, n, N)) + 1e-20)
```

Random number generation

```
>>> R = hypergeom.rvs(M, n, N, size=100)
```

## Methods

| | |
|---|---|
| rvs(M, n, N, loc=0, size=1) | 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. |
| fit(data, M, n, N, loc=0) | Parameter estimates for generic data. |
| 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.distributions.logser_gen object at 0x3ba5a10>**

A logarithmic discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**pr** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = logser(pr, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Logarithmic (Log-Series, Series) distribution

logser.pmf(k,p) = - p**k / (k*log(1-p)) for k >= 1

## Examples

```
>>> from scipy.stats import logser
>>> numargs = logser.numargs
>>> [ pr ] = Replace with reasonable value * numargs
>>> rv = logser(pr)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = logser.cdf(x, pr)
>>> h = plt.semilogy(np.abs(x - logser.ppf(prb, pr)) + 1e-20)
```

Random number generation

```
>>> R = logser.rvs(pr, size=100)
```

## Methods

| | |
|---|---|
| rvs(pr, loc=0, size=1) | Random variates. |
| pmf(x, pr, loc=0) | Probability mass function. |
| logpmf(x, pr, loc=0) | Log of the probability mass function. |
| cdf(x, pr, loc=0) | Cumulative density function. |
| logcdf(x, pr, loc=0) | Log of the cumulative density function. |
| sf(x, pr, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, pr, loc=0) | Log of the survival function. |
| ppf(q, pr, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, pr, loc=0) | Inverse survival function (inverse of sf). |
| stats(pr, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(pr, loc=0) | (Differential) entropy of the RV. |
| fit(data, pr, loc=0) | Parameter estimates for generic data. |
| expect(func, pr, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(pr, loc=0) | Median of the distribution. |
| mean(pr, loc=0) | Mean of the distribution. |
| var(pr, loc=0) | Variance of the distribution. |
| std(pr, loc=0) | Standard deviation of the distribution. |
| interval(alpha, pr, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`poisson`** **= <scipy.stats.distributions.poisson_gen object at 0x3ba5dd0>**

A Poisson discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**mu** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = poisson(mu, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Poisson distribution

poisson.pmf(k, mu) = exp(-mu) * mu**k / k! for k >= 0

## Examples

```
>>> from scipy.stats import poisson
>>> numargs = poisson.numargs
>>> [ mu ] = Replace with reasonable value * numargs
>>> rv = poisson(mu)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = poisson.cdf(x, mu)
>>> h = plt.semilogy(np.abs(x - poisson.ppf(prb, mu)) + 1e-20)
```

Random number generation

```
>>> R = poisson.rvs(mu, size=100)
```

### Methods

| | |
|---|---|
| rvs(mu, loc=0, size=1) | 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. |
| fit(data, mu, loc=0) | Parameter estimates for generic data. |
| 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.`**`planck`** **= <scipy.stats.distributions.planck_gen object at 0x3ba5d10>**

A discrete exponential discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**lamda** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = planck(lamda, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Planck (Discrete Exponential)

planck.pmf(k,b) = (1-exp(-b))*exp(-b*k) for k*b >= 0

## Examples

```
>>> from scipy.stats import planck
>>> numargs = planck.numargs
>>> [ lamda ] = Replace with reasonable value * numargs
>>> rv = planck(lamda)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = planck.cdf(x, lamda)
>>> h = plt.semilogy(np.abs(x - planck.ppf(prb, lamda)) + 1e-20)
```

Random number generation

```
>>> R = planck.rvs(lamda, size=100)
```

### Methods

| | |
|---|---|
| rvs(lamda, loc=0, size=1) | Random variates. |
| pmf(x, lamda, loc=0) | Probability mass function. |
| logpmf(x, lamda, loc=0) | Log of the probability mass function. |
| cdf(x, lamda, loc=0) | Cumulative density function. |
| logcdf(x, lamda, loc=0) | Log of the cumulative density function. |
| sf(x, lamda, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, lamda, loc=0) | Log of the survival function. |
| ppf(q, lamda, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, lamda, loc=0) | Inverse survival function (inverse of sf). |
| stats(lamda, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(lamda, loc=0) | (Differential) entropy of the RV. |
| fit(data, lamda, loc=0) | Parameter estimates for generic data. |
| expect(func, lamda, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(lamda, loc=0) | Median of the distribution. |
| mean(lamda, loc=0) | Mean of the distribution. |
| var(lamda, loc=0) | Variance of the distribution. |
| std(lamda, loc=0) | Standard deviation of the distribution. |
| interval(alpha, lamda, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`boltzmann`** **= <scipy.stats.distributions.boltzmann_gen object at 0x3ba5910>**

A truncated discrete exponential discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**lamda, N** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = boltzmann(lamda, N, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

### Notes

Boltzmann (Truncated Discrete Exponential)

boltzmann.pmf(k,b,N) = (1-exp(-b))*exp(-b*k)/(1-exp(-b*N)) for k=0,..,N-1

### Examples

```
>>> from scipy.stats import boltzmann
>>> numargs = boltzmann.numargs
>>> [ lamda, N ] = Replace with reasonable value * numargs
>>> rv = boltzmann(lamda, N)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = boltzmann.cdf(x, lamda, N)
>>> h = plt.semilogy(np.abs(x - boltzmann.ppf(prb, lamda, N)) + 1e-20)
```

Random number generation

```
>>> R = boltzmann.rvs(lamda, N, size=100)
```

### Methods

| | |
|---|---|
| rvs(lamda, N, loc=0, size=1) | Random variates. |
| pmf(x, lamda, N, loc=0) | Probability mass function. |
| logpmf(x, lamda, N, loc=0) | Log of the probability mass function. |
| cdf(x, lamda, N, loc=0) | Cumulative density function. |
| logcdf(x, lamda, N, loc=0) | Log of the cumulative density function. |
| sf(x, lamda, N, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, lamda, N, loc=0) | Log of the survival function. |
| ppf(q, lamda, N, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, lamda, N, loc=0) | Inverse survival function (inverse of sf). |
| stats(lamda, N, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(lamda, N, loc=0) | (Differential) entropy of the RV. |
| fit(data, lamda, N, loc=0) | Parameter estimates for generic data. |
| expect(func, lamda, N, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(lamda, N, loc=0) | Median of the distribution. |
| mean(lamda, N, loc=0) | Mean of the distribution. |
| var(lamda, N, loc=0) | Variance of the distribution. |
| std(lamda, N, loc=0) | Standard deviation of the distribution. |
| interval(alpha, lamda, N, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

scipy.stats.**randint = <scipy.stats.distributions.randint_gen object at 0x3ba58d0>**

A discrete uniform (random integer) discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**min, max** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = randint(min, max, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Discrete Uniform

Random integers >=min and <max.

randint.pmf(k,min, max) = 1/(max-min) for min <= k < max.

## Examples

```
>>> from scipy.stats import randint
>>> numargs = randint.numargs
>>> [ min, max ] = Replace with reasonable value * numargs
>>> rv = randint(min, max)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = randint.cdf(x, min, max)
>>> h = plt.semilogy(np.abs(x - randint.ppf(prb, min, max)) + 1e-20)
```

Random number generation

```
>>> R = randint.rvs(min, max, size=100)
```

### Methods

| | |
|---|---|
| rvs(min, max, loc=0, size=1) | Random variates. |
| pmf(x, min, max, loc=0) | Probability mass function. |
| logpmf(x, min, max, loc=0) | Log of the probability mass function. |
| cdf(x, min, max, loc=0) | Cumulative density function. |
| logcdf(x, min, max, loc=0) | Log of the cumulative density function. |
| sf(x, min, max, loc=0) | Survival function (1-cdf — sometimes more accurate). |
| logsf(x, min, max, loc=0) | Log of the survival function. |
| ppf(q, min, max, loc=0) | Percent point function (inverse of cdf — percentiles). |
| isf(q, min, max, loc=0) | Inverse survival function (inverse of sf). |
| stats(min, max, loc=0, moments='mv') | Mean('m'), variance('v'), skew('s'), and/or kurtosis('k'). |
| entropy(min, max, loc=0) | (Differential) entropy of the RV. |
| fit(data, min, max, loc=0) | Parameter estimates for generic data. |
| expect(func, min, max, loc=0, lb=None, ub=None, conditional=False) | Expected value of a function (of one argument) with respect to the distribution. |
| median(min, max, loc=0) | Median of the distribution. |
| mean(min, max, loc=0) | Mean of the distribution. |
| var(min, max, loc=0) | Variance of the distribution. |
| std(min, max, loc=0) | Standard deviation of the distribution. |
| interval(alpha, min, max, loc=0) | Endpoints of the range that contains alpha percent of the distribution |

`scipy.stats.`**`zipf`** **= <scipy.stats.distributions.zipf_gen object at 0x3ba5e50>**

A Zipf discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = zipf(a, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

## Notes

Zipf distribution

zipf.pmf(k,a) = 1/(zeta(a)*k**a) for k >= 1

## Examples

```
>>> from scipy.stats import zipf
>>> numargs = zipf.numargs
>>> [ a ] = Replace with reasonable value * numargs
>>> rv = zipf(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = zipf.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - zipf.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = zipf.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, size=1) | 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. |
| fit(data, a, loc=0) | Parameter estimates for generic data. |
| 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.`**`dlaplace`** **= <scipy.stats.distributions.dlaplace_gen object at 0x3ba9150>**

A discrete Laplacian discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

**Parameters**

**x** : array_like

quantiles

**q** : array_like

lower or upper tail probability

**a** : array_like

shape parameters

**loc** : array_like, optional

location parameter (default=0)

**scale** : array_like, optional

scale parameter (default=1)

**size** : int or tuple of ints, optional

shape of random variates (default computed from input arguments )

**moments** : str, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

**Alternatively, the object may be called (as a function) to fix the shape and** :

**location parameters returning a "frozen" discrete RV object:** :

**rv = dlaplace(a, loc=0)** :

- Frozen RV object with the same methods but holding the given shape and location fixed.

### Notes

Discrete Laplacian distribution.

dlaplace.pmf(k,a) = tanh(a/2) * exp(-a*abs(k)) for a > 0.

### Examples

```
>>> from scipy.stats import dlaplace
>>> numargs = dlaplace.numargs
>>> [ a ] = Replace with reasonable value * numargs
>>> rv = dlaplace(a)
```

Display frozen pdf

```
>>> x = np.linspace(0, np.minimum(rv.dist.b, 3))
>>> h = plt.plot(x, rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = dlaplace.cdf(x, a)
>>> h = plt.semilogy(np.abs(x - dlaplace.ppf(prb, a)) + 1e-20)
```

Random number generation

```
>>> R = dlaplace.rvs(a, size=100)
```

### Methods

| | |
|---|---|
| rvs(a, loc=0, size=1) | 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. |
| fit(data, a, loc=0) | Parameter estimates for generic data. |
| 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 |

### 4.22.3 Statistical functions

Several of these functions have a similar version in scipy.stats.mstats which work for masked arrays.

| | |
|---|---|
| `gmean`(a[, axis, dtype]) | Compute the geometric mean along the specified axis. |
| `hmean`(a[, axis, dtype]) | Calculates the harmonic mean along the specified axis. |
| `mean` | |
| `cmedian`(a[, numbins]) | Returns the computed median value of an array. |
| `median` | |
| `mode`(a[, axis]) | Returns an array of the modal (most common) value in the passed array. |
| `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 |
| `moment`(a[, moment, axis]) | Calculates the nth moment about the mean for a sample. |
| `variation`(a[, axis]) | Computes the coefficient of variation, the ratio of the biased standard deviation to the mean. |
| `skew`(a[, axis, bias]) | Computes the skewness of a data set. |
| `kurtosis`(a[, axis, fisher, bias]) | Computes the kurtosis (Fisher or Pearson) of a dataset. |
| `describe`(a[, axis]) | Computes several descriptive statistics of the passed array. |
| `skewtest`(a[, axis]) | Tests whether the skew is different from the normal distribution. |
| `kurtosistest`(a[, axis]) | Tests whether a dataset has normal kurtosis |
| `normaltest`(a[, axis]) | Tests whether a sample differs from a normal distribution. |

`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, optional, default axis=0

Axis along which the geometric mean is computed.

**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, optional, default axis=0

Axis along which the harmonic mean is computed.

**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.`**`cmedian`**(*a*, *numbins=1000*)
Returns the computed median value of an array.

All of the values in the input array are used. The input array is first histogrammed using *numbins* bins. The bin containing the median is selected by searching for the halfway point in the cumulative histogram. The median value is then computed by linearly interpolating across that bin.

**Parameters**

**a** : array_like

Input array.

**numbins** : int

The number of bins used to histogram the data. More bins give greater accuracy to the approximation of the median.

**Returns**

**cmedian** : float

An approximation of the median.

## References

[CRCProbStat2000] Section 2.2.6

[CRCProbStat2000]

`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, optional

Axis along which to operate. Default is 0, i.e. the first axis.

**Returns**

**vals** : ndarray

Array of modal values.

**counts** : 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.`**`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, 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**

**tmean** : float

`scipy.stats.`**`tvar`**(*a*, *limits=None*, *inclusive=(1*, *1)*)

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

`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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero

**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*, *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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero.

**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=(1, 1)*)

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

`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

`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

order of central moment that is returned

**axis** : int or None

Axis along which the central moment is computed. If None, then the data array is raveled. The default axis is zero.

**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.`**`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

Axis along which to calculate the coefficient of variation.

### References

[CRCProbStat2000] Section 2.2.20

[CRCProbStat2000]

`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

axis along which skewness is calculated

**bias** : bool

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

[CRCProbStat2000] Section 2.2.24.1

[CRCProbStat2000]

`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

Axis along which the kurtosis is calculated

**fisher** : bool

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

**bias** : bool

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

[CRCProbStat2000] Section 2.2.25

[CRCProbStat2000]

`scipy.stats.`**`describe`**(*a*, *axis=0*)

Computes several descriptive statistics of the passed array.

**Parameters**

**a** : array_like

data

**axis** : int or None

axis along which statistics are calculated. If axis is None, then data array is raveled. The default axis is zero.

**Returns**

**size of the data** : int

length of data along axis

**(min, max): tuple of ndarrays or floats** :

minimum and maximum value of data array

**arithmetic mean** : ndarray or float

mean of data along axis

**unbiased variance** : ndarray or float

variance of the data along axis, denominator is number of observations minus one.

**biased skewness** : ndarray or float

skewness, based on moment calculations with denominator equal to the number of observations, i.e. no degrees of freedom correction

**biased kurtosis** : ndarray or float

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.`**`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

**axis** : int or None

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : float

a 2-sided p-value for the hypothesis test

### Notes

The sample size must be at least 8.

`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

the axis to operate along, or None to work on the whole array. The default is the first axis.

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : 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.`**`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 [R93], [R94] 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

If None, the array is treated as a single data set, regardless of its shape. Otherwise, each 1-d array along axis *axis* is tested.

**Returns**

**k2** : 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`.

**p-value** : float or array

A 2-sided chi squared probability for the hypothesis test.

### References

[R93], [R94]

| | |
|---|---|
| itemfreq(a) | Returns a 2D array of item frequencies. |
| scoreatpercentile(a, per[, limit]) | Calculate the score at the given *per* percentile of the sequence *a*. |
| percentileofscore(a, score[, kind]) | The percentile rank of a score relative to a list of scores. |
| histogram2(a, bins) | Compute histogram using divisions in bins. |
| histogram(a[, numbins, defaultlimits, ...]) | Separates the range into several bins and returns the number of instances of a in each bin. |
| cumfreq(a[, numbins, defaultreallimits, weights]) | Returns a cumulative frequency histogram, using the histogram function. |
| relfreq(a[, numbins, defaultreallimits, weights]) | Returns a relative frequency histogram, using the histogram function. |

scipy.stats.**itemfreq**(*a*)

Returns a 2D array of item frequencies.

**Parameters**

**a** : array_like of rank 1

Input array.

**Returns**

**itemfreq** : ndarray of rank 2

A 2D frequency table (col [0:n-1]=scores, col n=frequencies). Column 1 contains item values, column 2 contains their respective counts.

### Notes

This uses a loop that is only reasonably fast if the number of unique elements is not large. For integers, numpy.bincount is much faster. This function currently does not support strings or multi-dimensional scores.

### Examples

```
>>> 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.**scoreatpercentile**(*a*, *per*, *limit=()*)

Calculate the score at the given *per* percentile of the sequence *a*.

For example, the score at per=50 is the median. If the desired quantile lies between two data points, we interpolate between them. If the parameter *limit* is provided, it should be a tuple (lower, upper) of two values. Values of *a* outside this (closed) interval will be ignored.

**Parameters**

**a** : ndarray

Values from which to extract score.

**per** : int or float

Percentile at which to extract score.

**limit** : tuple, optional

Tuple of two scalars, the lower and upper limits within which to compute the percentile.

**Returns**

**score** : float

Score at percentile.

**See Also:**

`percentileofscore`

## Examples

```
>>> from scipy import stats
>>> a = np.arange(100)
>>> stats.scoreatpercentile(a, 50)
49.5
```

`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*.

### Examples

Three-quarters of the given values lie below a given score:

```
>>> 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:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3)
70.0
```

Only 2/5 values are strictly less than 3:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0
```

But 4/5 values are less than or equal to 3:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0
```

The average between the weak and the strict scores is

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0
```

`scipy.stats.`**`histogram2`**(*a*, *bins*)

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 of a in each bin. This histogram is based on numpy's histogram but has a larger range by default if default limits is not set.

**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 then 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, the number of extra points is printed to standard output. Default is False.

**Returns**

**histogram: ndarray** :

Number of points (or sum of weights) in each bin.

**low_range: 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`

`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.

**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 then 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**

**cumfreq** : ndarray

Binned values of cumulative frequency.

**lowerreallimit** : float

Lower real limit

**binsize** : float

Width of each bin.

**extrapoints** : int

Extra points.

### Examples

```
>>> x = [1, 4, 2, 1, 3, 1]
>>> cumfreqs, lowlim, binsize, extrapoints = sp.stats.cumfreq(x, numbins=4)
>>> cumfreqs
array([ 3.,  4.,  5.,  6.])
>>> cumfreqs, lowlim, binsize, extrapoints =     ...     sp.stats.cumfreq(x, numbins=4, defaultr
>>> cumfreqs
array([ 1.,  2.,  3.,  3.])
>>> extrapoints
3
```

`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 then 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**

**relfreq** : ndarray

Binned values of relative frequency.

**lowerreallimit** : float

Lower real limit

**binsize** : float

Width of each bin.

**extrapoints** : int

Extra points.

## Examples

```
>>> a = np.array([1, 4, 2, 1, 3, 1])
>>> relfreqs, lowlim, binsize, extrapoints = sp.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
```

| | |
|---|---|
| `obrientransform`(*args) | Computes a transform on input data (any number of columns). |
| `signaltonoise`(a[, axis, ddof]) | The signal-to-noise ratio of the input data. |
| `bayes_mvs`(data[, alpha]) | Bayesian confidence intervals for the mean, var, and std. |
| `sem`(a[, axis, ddof]) | Calculates the standard error of the mean (or standard error of measurement) of the values in 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 mean and standard deviation. |

`scipy.stats.`**`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.`**`signaltonoise`**(*a*, *axis=0*, *ddof=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** :

If axis is equal to None, the array is first ravel'd. If axis is an integer, this is the axis over which to operate. Default is 0.

**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**

**Returns a 3 output arguments for each of mean, variance, and standard deviation.** :

**Each of the outputs is a pair:**
(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.

**mctr, (ma, mb) :** :

Estimates for mean

**vctr, (va, vb) :** :

Estimates for variance

**sctr, (sa, sb) :** :

Estimates for standard deviation

## Notes

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.`**`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.

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* 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.

**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).

`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

If *axis* is equal to None, the array is first raveled. If *axis* is an integer, this is the axis over which to operate. Default is 0.

**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([[-1.1649, -1.4319, -0.8554, -1.0189],
       [-0.8661, -1.5035, -0.9737, -0.6154],
       [-0.888 , -1.3817, -0.5461, -1.1156],
       [-2.3043, -2.2014, -1.9921, -2.5241],
       [-2.0773, -1.9212, -2.0506, -2.0328]])
```

| | |
|---|---|
| `threshold`(a[, threshmin, threshmax, newval]) | Clip array to a given value. |
| `trimboth`(a, proportiontocut) | 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 |

`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*)

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 or int

Proportion of total data set to trim of each end.

**Returns**

**out** : ndarray

Trimmed version of array *a*.

### 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** : string, {'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 |
| `spearmanr`(a[, b, axis]) | Calculates a Spearman rank-order correlation coefficient and the p-value |
| `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 |

`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**

**F-value** : float

The computed F-value of the test.

**p-value** : 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 (**'stats.kruskal'_**) although with some loss of power.

The algorithm is from Heiman[2], pp.394-7.

## References

[R79], [R80]

`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** : 1D array

**y** : 1D array the same length as x

**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**

**rho: 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.

**p-value** : 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

[CRCProbStat2000] Section 14.7

[CRCProbStat2000]

## Examples

```
>>> 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)
>>> spearmanr(x2n)
(0.059969996999699973, 0.55338590803773591)
>>> spearmanr(x2n[:,0], x2n[:,1])
(0.059969996999699973, 0.55338590803773591)
>>> rho, pval = 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 = 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.        ]])
>>> spearmanr(x2n, y2n, axis=None)
(0.10816770419260482, 0.1273562188027364)
>>> spearmanr(x2n.ravel(), y2n.ravel())
(0.10816770419260482, 0.1273562188027364)

>>> xint = np.random.randint(10,size=(100,2))
>>> 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**

**r** : float

R value

**p-value** : float

2-tailed p-value

## References

http://www.childrens-mercy.org/stats/definitions/biserial.htm

### 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**

**Kendall's tau** : float

The tau statistic.

**p-value** : 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

```
>>> x1 = [12, 2, 1, 12, 2]
>>> x2 = [1, 4, 7, 1, 0]
>>> tau, p_value = sp.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

**r-value** : float

correlation coefficient

**p-value** : 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
>>> import numpy as np
>>> 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
```

| | |
|---|---|
| ttest_1samp(a, popmean[, axis]) | Calculates the T-test for the mean of ONE group of scores *a*. |
| ttest_ind(a, b[, axis]) | Calculates the T-test for the means of TWO INDEPENDENT samples of scores. |
| 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]) | Calculates a one-way chi square test. |
| ks_2samp(data1, data2) | Computes the Kolmogorov-Smirnof statistic on 2 samples. |
| mannwhitneyu(x, y[, use_continuity]) | Computes the Mann-Whitney rank test on samples x and y. |
| tiecorrect(rankvals) | Tie-corrector for ties in Mann Whitney U and Kruskal Wallis H tests. |
| ranksums(x, y) | Compute the Wilcoxon rank-sum statistic for two samples. |
| wilcoxon(x[, y]) | 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 |

scipy.stats.**ttest_1samp**(*a*, *popmean*, *axis=0*)

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

two-tailed p-value

## Examples

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

>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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*)

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.

**Parameters**

**a, b** : sequence of ndarrays

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

**axis** : int, optional

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

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.

## Examples

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

```
>>> #fix seed to get the same result
>>> 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, 0.78849443369564765)
```

test with sample with different means

```
>>> rvs3 = stats.norm.rvs(loc=8,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs3)
(-5.0434013458585092, 5.4302979468623391e-007)
```

`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** : sequence of ndarrays

The arrays must have the same shape.

**axis** : int, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : 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.

## 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'*, ***kwds*)

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** : string or array or callable

string: name of a distribution in scipy.stats

array: 1-D observations of random variables

callable: function to generate random variables, requires keyword argument *size*

**cdf** : string or callable

string: name of a distribution in scipy.stats, if rvs is a string then cdf can evaluate to *False* or be the same as rvs callable: function to evaluate cdf

**args** : tuple, sequence

distribution parameters, used if rvs or cdf are strings

**N** : int

sample size if rvs is string or callable

**alternative** : 'two_sided' (default), 'less' or 'greater'

defines the alternative hypothesis (see explanation)

**mode** : 'approx' (default) or 'asymp'

defines the distribution used for calculating p-value

'approx' : use approximation to exact distribution of test statistic

'asymp' : use asymptotic distribution of test statistic

**Returns**

**D** : float

KS test statistic, either D, D+ or D-

**p-value** : 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
>>> import numpy as np
>>> from scipy.stats import kstest

>>> x = np.linspace(-15,15,9)
>>> kstest(x,'norm')
(0.44435602715924361, 0.038850142705171065)

>>> np.random.seed(987654321) # set random seed to get the same result
>>> kstest('norm','',N=100)
(0.058352892479417884, 0.88531190944151261)
```

is equivalent to this

```
>>> np.random.seed(987654321)
>>> kstest(stats.norm.rvs(size=100),'norm')
(0.058352892479417884, 0.88531190944151261)
```

Test against one-sided alternative hypothesis:

```
>>> np.random.seed(987654321)
```

Shift distribution to larger values, so that cdf_dgp(x)< norm.cdf(x):

```
>>> x = stats.norm.rvs(loc=0.2, size=100)
>>> kstest(x,'norm', alternative = 'less')
(0.12464329735846891, 0.040989164077641749)
```

Reject equal distribution against alternative hypothesis: less

```
>>> kstest(x,'norm', alternative = 'greater')
(0.0072115233216311081, 0.98531158590396395)
```

Don't reject equal distribution against alternative hypothesis: greater

```
>>> 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 kstest 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 a alpha=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*)

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

observed frequencies in each category

**f_exp** : array, optional

expected frequencies in each category. By default the categories are assumed to be equally likely.

**ddof** : int, optional

adjustment to the degrees of freedom for the p-value

**Returns**

**chisquare statistic** : float

The chisquare test statistic

**p** : float

The p-value of the test.

## 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 then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distributions is not a chisquare, in which case this test is not appropriate.

## References

[R78]

`scipy.stats.`**`ks_2samp`**`(`*data1*, *data2*`)`

Computes the Kolmogorov-Smirnof 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**

**a, b** : sequence of 1-D ndarrays

two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different

**Returns**

**D** : float

KS statistic

**p-value** : 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
>>> import numpy as np
>>> from scipy.stats import ks_2samp

>>> #fix random seed to get the same result
>>> np.random.seed(12345678);

>>> n1 = 200  # size of first sample
>>> n2 = 300  # size of second sample
```

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)
>>> ks_2samp(rvs1,rvs2)
(0.20833333333333337, 4.6674975515806989e-005)
```

slightly different distribution we cannot reject the null hypothesis at a 10% or lower alpha since the pvalue at 0.144 is higher than 10%

```
>>> rvs3 = stats.norm.rvs(size=n2,loc=0.01,scale=1.0)
>>> ks_2samp(rvs1,rvs3)
(0.10333333333333333, 0.14498781825751686)
```

identical distribution we cannot reject the null hypothesis since the pvalue is high, 41%

```
>>> rvs4 = stats.norm.rvs(size=n2,loc=0.0,scale=1.0)
>>> 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**

**u** : float

The Mann-Whitney statistics.

**prob** : 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-corrector for ties in Mann Whitney U and Kruskal Wallis H tests. See Siegel, S. (1956) Nonparametric Statistics for the Behavioral Sciences. New York: McGraw-Hill. Code adapted from |Stat rankind.c code.

**Returns**

**T correction factor for U or H** :

`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 **'stats.mannwhitneyu'_**

**Parameters**

**x,y** : array_like

The data from the two samples

**Returns**

**z-statistic** : float

The test statistic under the large-sample approximation that the rank sum statistic is normally distributed

**p-value** : float

The two-sided p-value of the test

### References

[R95]

`scipy.stats.`**`wilcoxon`**`(`*x*, *y=None*`)`

Calculate the Wilcoxon signed-rank test.

The Wilcoxon signed-rank test tests the null hypothesis that two related samples come from the same distribution. It is a 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.

**Returns**

**z-statistic** : float

The test statistic under the large-sample approximation that the signed-rank statistic is normally distributed.

**p-value** : 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

[R97]

`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**

**H-statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

**p-value** : 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

[R84]

`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**

**friedman chi-square statistic** : float

the test statistic, correcting for ties

**p-value** : 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

[R83]

| | |
|---|---|
| `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. |
| `anderson`(x[, dist]) | Anderson-Darling test for data coming from a particular distribution |
| `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. |
| `mood`(x, y) | Perform Mood's test for equal scale parameters. |
| `oneway`(*args, **kwds) | Test for equal means in two or more samples from the normal distribution. |

`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**

**p-value** : 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

[R73]

`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**

**T** : float

The test statistic.

**p-value** : float

The p-value of the test.

## References

[R74], [R75]

`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**

**W** : float

The test statistic.

**p-value** : 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

[R85], [R86], [R87]

`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

[R96]

`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**

**A2** : float

The Anderson-Darling test statistic

**critical** : list

The critical values for this distribution

**sig** : 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

[R67], [R68], [R69], [R70], [R71], [R72]

`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

[R76]

`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

[R81], [R82]

`scipy.stats.`**`mood`**`(`*x*, *y*`)`

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.

**Returns**

**p-value** : float

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.

`scipy.stats.`**`oneway`**(**args*, ***kwds*)

Test for equal means in two or more samples from the normal distribution.

If the keyword parameter <equal_var> is true then the variances are assumed to be equal, otherwise they are not assumed to be equal (default).

Return test statistic and the p-value giving the probability of error if the null hypothesis (equal means) is rejected at this value.

## 4.22.4 Contingency table functions

| | |
|---|---|
| `fisher_exact`(table[, alternative]) | Performs a Fisher exact test on a 2x2 contingency table. |
| `chi2_contingency`(observed[, correction]) | 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*. |

`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. In R language, this 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:

```
>>> 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.

`scipy.stats.`**`chi2_contingency`**(*observed*, *correction=True*)
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 [R77] *observed*. The expected frequencies are computed based on the marginal sums under the assumption of independence; see scipy.stats.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.

**Returns**

**chi2** : float

The chi-square test statistic. Without the Yates' correction, this is the sum of the squares of the observed values minus the expected values, divided by the expected values. With Yates' correction, 0.5 is subtracted from the squared differences before dividing by the expected values.

**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`

## 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)
```

## References

[R77]

## Examples

A two-way example (2 x 3):

```
>>> obs = np.array([[10, 10, 20], [20, 20, 20]])
>>> chi2_contingency(obs)
(2.7777777777777777,
 0.24935220877729619,
 2,
 array([[ 12.,  12.,  16.],
        [ 18.,  18.,  24.]]))
```

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 type numpy.float64, same shape as *observed*.

The expected frequencies, based on the marginal sums of the table.

## Examples

```
>>> observed = np.array([[10, 10, 20],[20, 20, 20]])
>>> 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.

## 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]]])
```

### 4.22.5 General linear model

| | |
|---|---|
| glm(data, para) | Calculates a linear model fit ... |

scipy.stats.**glm**(*data*, *para*)

Calculates a linear model fit ... anova/ancova/lin-regress/t-test/etc. Taken from:

Peterson et al. Statistical limitations in functional neuroimaging I. Non-inferential methods and statistical models. Phil Trans Royal Soc Lond B 354: 1239-1260.

**Returns**

**statistic, p-value ???** :

### 4.22.6 Plot-tests

| | |
|---|---|
| probplot(x[, sparams, dist, fit, plot]) | Calculate quantiles for a probability plot of sample data against a specified theoretical distribution. |
| ppcc_max(x[, brack, dist]) | Returns the shape parameter that maximizes the probability plot correlation coefficient for the given data to a one-parameter family of distributions. |
| ppcc_plot(x, a, b[, dist, plot, N]) | Returns (shape, ppcc), and optionally plots shape vs. |

scipy.stats.**probplot**(*x*, *sparams=()*, *dist='norm'*, *fit=True*, *plot=None*)

Calculate quantiles for a probability plot of sample data against a specified theoretical distribution.

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 (location(s) and scale(s)).

**dist** : str, optional

Distribution function name. The default is 'norm' for a normal probability plot.

**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 with methods "plot", "title", "xlabel", "ylabel" and "text". The matplotlib.pyplot module or a Matplotlib axes object can be used, or a custom object with the same methods. By default, no plot is created.

**Returns**

**(osm, osr)** : tuple of ndarrays

Tuple of theoretical quantiles (osm, or order statistic medians) and ordered responses (osr).

**(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`; `plot.show()` or `plot.savefig('figname.png')` should be used after calling `probplot`.

## Examples

```
>>> import scipy.stats as stats
>>> 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 2 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)
```

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*)

Returns (shape, ppcc), and optionally plots shape vs. ppcc (probability plot correlation coefficient) as a function of shape parameter for a one-parameter family of distributions from shape value a to b.

See also ppcc_max

## 4.22.7 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 |
| `betai`(a, b, x) | Returns the incomplete |
| `chisquare`(f_obs[, f_exp]) | Calculates a one-way |
| `count_tied_groups`(x[, use_missing]) | Counts the number of tied values in |
| `describe`(a[, axis]) | Computes several descriptive |
| `f_oneway`(*args) | Performs a 1-way ANOVA, |
| `f_value_wilks_lambda`(ER, EF, dfnum, dfden, a, b) | Calculation of Wilks lambda |
| `find_repeats`(arr) | Find repeats in arr and |
| `friedmanchisquare`(*args) | Friedman Chi-Square is a |
| `gmean`(a[, axis]) | Compute the geometric mean |
| `hmean`(a[, axis]) | Calculates the harmonic mea |
| `kendalltau`(x, y[, use_ties, use_missing]) | Computes Kendall's rank correlation |
| `kendalltau_seasonal`(x) | Computes a multivariate extensi |
| `kruskalwallis`(*args) | Compute the Kruskal-Wallis |
| `kruskalwallis`(*args) | Compute the Kruskal-Wallis |
| `ks_twosamp`(data1, data2[, alternative]) | Computes the Kolmogorov-Smirnov |
| `ks_twosamp`(data1, data2[, alternative]) | Computes the Kolmogorov-Smirnov |
| `kurtosis`(a[, axis, fisher, bias]) | Computes the kurtosis (Fisher |
| `kurtosistest`(a[, axis]) | Tests whether a |
| `linregress`(*args) | Calculate a |
| `mannwhitneyu`(x, y[, use_continuity]) | Computes the Mann-Whitney |
| `plotting_positions`(data[, alpha, beta]) | Returns plotting positions (or |
| `mode`(a[, axis]) | Returns an array of the modal |
| `moment`(a[, moment, axis]) | Calculates the nth moment |
| `mquantiles`(a[, prob, alphap, betap, axis, limit]) | Computes empirical quantiles |
| `msign`(x) | Returns the sign of x, |
| `normaltest`(a[, axis]) | Tests whether a sample |
| `obrientransform`(*args) | Computes a transform on i |
| `pearsonr`(x, y) | Calculates a Pearson correlation |
| `plotting_positions`(data[, alpha, beta]) | Returns plotting positions (or |
| `pointbiserialr`(x, y) | Calculates a point biserial corre |
| `rankdata`(data[, axis, use_missing]) | Returns the rank (also known as ord |
| | |

Table 4.12 – continued fron

| | |
|---|---|
| scoreatpercentile(data, per[, limit, ...]) | Calculate the score at the |
| sem(a[, axis]) | Calculates the standard error of the mean ( |
| signaltonoise(data[, axis]) | Calculates the signal-to-noise ratio, as the |
| skew(a[, axis, bias]) | Computes the skewness |
| skewtest(a[, axis]) | Tests whether the skew is |
| spearmanr(x, y[, use_ties]) | Calculates a Spearman rank-or |
| theilslopes(y[, x, alpha]) | Computes the Theil slope over |
| threshold(a[, threshmin, threshmax, newval]) | Clip array to |
| tmax(a, upperlimit[, axis, inclusive]) | Compute the |
| tmean(a[, limits, inclusive]) | Compute the |
| tmin(a[, lowerlimit, axis, inclusive]) | Compute the |
| trim(a[, limits, inclusive, relative, axis]) | Trims an array by masking |
| trima(a[, limits, inclusive]) | Trims an array by masking |
| trimboth(data[, proportiontocut, inclusive, ...]) | Trims the data by masking the int(proportiontocut*n) smallest and int( |
| trimmed_stde(a[, limits, inclusive, axis]) | Returns the standard error of the |
| trimr(a[, limits, inclusive, axis]) | Trims an array by masking so |
| trimtail(data[, proportiontocut, tail, ...]) | Trims the data by masking |
| tsem(a[, limits, inclusive]) | Compute the trimmed |
| ttest_onesamp(a, popmean) | Calculates the T-test for the |
| ttest_ind(a, b[, axis]) | Calculates the T-test for the m |
| ttest_onesamp(a, popmean) | Calculates the T-test for the |
| ttest_rel(a, b[, axis]) | Calculates the T-test on TWO |
| tvar(a[, limits, inclusive]) | Compute the |
| variation(a[, axis]) | Computes the coefficient of variation, th |
| winsorize(a[, limits, inclusive, inplace, axis]) | Returns a Winsorized versi |
| zmap(scores, compare[, axis, ddof]) | Calculates the re |
| zscore(a[, axis, ddof]) | Calculates the z score of each value in |

`scipy.stats.mstats.`**`argstoarray`**`(*args)`

Constructs a 2D array from a sequence of sequences. Sequences are filled with missing values to match the length of the longest sequence.

**Returns**

**output** : MaskedArray

a (mxn) masked array, where m is the number of arguments and n the length of the longest argument.

`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*)

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

observed frequencies in each category

**f_exp** : array, optional

expected frequencies in each category. By default the categories are assumed to be equally likely.

**ddof** : int, optional

adjustment to the degrees of freedom for the p-value

**Returns**

**chisquare statistic** : float

The chisquare test statistic

**p** : float

The p-value of the test.

### 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 then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distributions is not a chisquare, in which case this test is not appropriate.

### References

[R89]

`scipy.stats.mstats.`**`count_tied_groups`**(*x*, *use_missing=False*)

**Counts the number of tied values in x, and returns a dictionary**

(nb of ties: nb of groups).

**Parameters**

**x** : sequence

Sequence of data on which to counts the ties

**use_missing** : boolean

Whether to consider missing values as tied.

### Examples

```
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> count_tied_groups(z)
>>> {2:1, 3:2}
>>> # The ties were 0 (3x), 2 (3x) and 3 (2x)
>>> z = ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> count_tied_groups(z)
>>> {2:2, 3:1}
>>> # The ties were 0 (2x), 2 (3x) and 3 (2x)
>>> z[[1,-1]] = masked
>>> count_tied_groups(z, use_missing=True)
>>> {2:2, 3:1}
>>> # The ties were 2 (3x), 3 (2x) and masked (2x)
```

`scipy.stats.mstats.`**`describe`**`(`*a*, *axis=0*`)`

Computes several descriptive statistics of the passed array.

**Parameters**

**a** : array

**axis** : int or None

**Returns**

**n** : int

(size of the data (discarding missing values)

**mm** : (int, int)

min, max

**arithmetic mean** : float

**unbiased variance** : float

**biased skewness** : float

**biased kurtosis** : float

### 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: f-value, probability

`scipy.stats.mstats.`**`f_value_wilks_lambda`**(*ER*, *EF*, *dfnum*, *dfden*, *a*, *b*)

Calculation of Wilks lambda F-statistic for multivarite 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: chi-square statistic, associated p-value

`scipy.stats.mstats.`**`gmean`**(*a*, *axis=0*)

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, optional, default axis=0

Axis along which the geometric mean is computed.

**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.mstats.`**`hmean`**`(`*a*, *axis=0*`)`
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, optional, default axis=0

Axis along which the harmonic mean is computed.

**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.mstats.`**`kendalltau`**`(`*x*, *y*, *use_ties=True*, *use_missing=False*`)`
Computes Kendall's rank correlation tau on two variables *x* and *y*.

**Parameters**
**xdata: sequence** :

First data list (for example, time).

**ydata: 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**

**tau** : float

Kendall tau

**prob**

[float] Approximate 2-side p-value.

`scipy.stats.mstats.`**`kendalltau_seasonal`**`(`*x*`)`

Computes a multivariate extension Kendall's rank correlation tau, designed for seasonal data.

**Parameters**

**x: 2D array** :

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**

**H-statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

**p-value** : 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

[R90]

`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**

**H-statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

**p-value** : 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

[R90]

`scipy.stats.mstats.`**`ks_twosamp`**`(`*data1*, *data2*, *alternative='two_sided'*`)`

Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**

**data1** : sequence

First data set

**data2**

[sequence] Second data set

**alternative**

[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

**Returns**

**d** : float

Value of the Kolmogorov Smirnov test

**p**

[float] Corresponding p-value.

`scipy.stats.mstats.`**`ks_twosamp`**`(`*data1*, *data2*, *alternative='two_sided'*`)`

Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**

**data1** : sequence

First data set

**data2**
[sequence] Second data set

**alternative**
[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

**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

Axis along which the kurtosis is calculated

**fisher** : bool

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

**bias** : bool

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

[CRCProbStat2000] Section 2.2.25

[CRCProbStat2000]

`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

the axis to operate along, or None to work on the whole array. The default is the first axis.

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : 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

**r-value**

[float] correlation coefficient

**p-value**

[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
>>> import numpy as np
>>> 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 on samples x and y. Missing values in x and/or y are discarded.

**Parameters**

**x** : sequence

y : sequence use_continuity : {True, False} optional

Whether a continuity correction (1/2.) should be taken into account.

**Returns**

**u** : float

The Mann-Whitney statistics

**prob**

[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, optional

Axis along which to operate. Default is 0, i.e. the first axis.

**Returns**
: **vals** : ndarray

Array of modal values.

**counts** : 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

order of central moment that is returned

**axis** : int or None

Axis along which the central moment is computed. If None, then the data array is raveled. The default axis is zero.

**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-g).x[i] +g.x[i+1]`, where `x[j]` is the j-th order statistic, `i = (floor(n*p+m))`, `m=alpha+p*(1-alpha-beta)` and `g = n*p + m - i`.

**Typical values of (alpha,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)* : (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

**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.

**alpha** : float, optional

Plotting positions parameter, default is 0.4.

**beta** : 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

Tuple of (lower, upper) values. Values of *a* outside this closed interval are ignored.

**Returns**

**mquantiles** : MaskedArray

An array containing the calculated quantiles.

## 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 [R91], [R92] 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

If None, the array is treated as a single data set, regardless of its shape. Otherwise, each 1-d array along axis *axis* is tested.

**Returns**

**k2** : 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`.

**p-value** : float or array

A 2-sided chi squared probability for the hypothesis test.

### References

[R91], [R92]

`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** : 1D array

**y** : 1D array the same length as x

**Returns**

**(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**

**r** : float

R value

**p-value**
[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.

### 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**
[{boolean} 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*)
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.

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* 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.mstats.`**`signaltonoise`**(*data*, *axis=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

axis along which skewness is calculated

**bias** : bool

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

[CRCProbStat2000] Section 2.2.24.1

[CRCProbStat2000]

`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

**axis** : int or None

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : 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** : 1D array

**y**

[1D array the same length as x] The lengths of both arrays must be > 2.

**use_ties**

[{True, False} optional] Whether the correction for ties should be computed.

**Returns**

**(Spearman correlation coefficient,** :

2-tailed p-value)

`scipy.stats.mstats.`**`theilslopes`**`(`*y*, *x=None*, *alpha=0.05*`)`

Computes the Theil slope over the dataset (x,y), as the median of all slopes between paired values.

**Parameters**

**y** : sequence

Dependent variable.

**x**

[{None, sequence} optional] Independent variable. If None, use arange(len(y)) instead.

**alpha**

[float] Confidence degree.

**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

`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**

**a, with values less (greater) than threshmin (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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero.

**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, 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**

**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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero

**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 == 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 == 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** : {(True, True) tuple} optional

If relative==False, tuple indicating whether values exactly equal to the absolute limits are allowed. If relative==True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**relative** : {False, True} optional

Whether to consider the limits as absolute values (False) or proportions to cut (True).

**axis** : {None, integer}, 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** : sequence

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** : {(True,True) 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 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**

[{0.2, 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.

**inclusive**

[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**

[{None, integer}, 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 of the data 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. 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**

[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**

[{None, integer}, optional] Axis along which to trim.

`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 int(trim*n) values from ONE tail of the data along the given axis, where n is the number of unmasked values.

**Parameters**

**data** : {ndarray}

Data to trim.

**proportiontocut**

[{0.2, 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.

**tail**

[{'left','right'} optional] If left (right), the `proportiontocut` lowest (greatest) values will be masked.

**inclusive**

[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**

[{None, integer}, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

`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

`scipy.stats.mstats.`**`ttest_onesamp`**(*a*, *popmean*)

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

two-tailed p-value

## Examples

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

>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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.

**Parameters**

**a, b** : sequence of ndarrays

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

**axis** : int, optional

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

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.

## Examples

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

>>> #fix seed to get the same result
>>> 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, 0.78849443369564765)
```

test with sample with different means

```
>>> rvs3 = stats.norm.rvs(loc=8,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs3)
(-5.0434013458585092, 5.4302979468623391e-007)
```

`scipy.stats.mstats.`**`ttest_onesamp`**`(`*a*, *popmean*`)`

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

two-tailed p-value

## Examples

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

>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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=None*)

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** : sequence of ndarrays

The arrays must have the same shape.

**axis** : int, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : 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.

## 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

`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

Axis along which to calculate the coefficient of variation.

### References

[CRCProbStat2000] Section 2.2.20

[CRCProbStat2000]

`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 (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.

`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.

**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).

`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

If *axis* is equal to None, the array is first raveled. If *axis* is an integer, this is the axis over which to operate. Default is 0.

**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([[-1.1649, -1.4319, -0.8554, -1.0189],
       [-0.8661, -1.5035, -0.9737, -0.6154],
       [-0.888 , -1.3817, -0.5461, -1.1156],
       [-2.3043, -2.2014, -1.9921, -2.5241],
       [-2.0773, -1.9212, -2.0506, -2.0328]])
```

### 4.22.8 Univariate and multivariate kernel density estimation (`scipy.stats.kde`)

| | |
|---|---|
| `gaussian_kde`(dataset) | Representation of a kernel-density estimate using Gaussian kernels. |

**class** `scipy.stats.`**`gaussian_kde`**(*dataset*)

Representation of a kernel-density estimate using Gaussian kernels.

**Parameters**

**dataset** : (# of dims, # of data)-array

datapoints to estimate from

#### Attributes

| | | |
|---|---|---|
| d | int | number of dimensions |
| n | int | number of datapoints |

#### Methods

| | | |
|---|---|---|
| kde.evaluate(points) | array | evaluate the estimated pdf on a provided set of points |
| kde(points) | array | same as kde.evaluate(points) |
| kde.integrate_gaussian(mean, cov) | float | multiply pdf with a specified Gaussian and integrate over the whole domain |
| kde.integrate_box_1d(low, high) | float | integrate pdf (1D only) between two bounds |
| kde.integrate_box(low_bounds, high_bounds) | float | integrate pdf over a rectangular space between low_bounds and high_bounds |
| kde.integrate_kde(other_kde) | float | integrate two kernel density estimates multiplied together |
| kde.resample(size=None) | array | randomly sample a dataset from the estimated pdf. |
| kde.covariance_factor() | float | computes the coefficient that multiplies the data covariance matrix to obtain the kernel covariance matrix. Set this method to kde.scotts_factor or kde.silverman_factor (or subclass to provide your own). The default is scotts_factor. |

For many more stat related functions install the software R and the interface package rpy.

## 4.23 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 |
| `betai`(a, b, x) | Returns the incomplete |
| `chisquare`(f_obs[, f_exp]) | Calculates a one-way |
| `count_tied_groups`(x[, use_missing]) | Counts the number of tied values in |
| `describe`(a[, axis]) | Computes several descriptive |
| `f_oneway`(*args) | Performs a 1-way ANOVA, |
| `f_value_wilks_lambda`(ER, EF, dfnum, dfden, a, b) | Calculation of Wilks lambda |
| `find_repeats`(arr) | Find repeats in arr and |
| | |

Table 4.13 – continued fron

| | |
|---|---|
| friedmanchisquare(*args) | Friedman Chi-Square is a |
| gmean(a[, axis]) | Compute the geometric mear |
| hmean(a[, axis]) | Calculates the harmonic mea |
| kendalltau(x, y[, use_ties, use_missing]) | Computes Kendall's rank correlation |
| kendalltau_seasonal(x) | Computes a multivariate extensi |
| kruskalwallis(*args) | Compute the Kruskal-Wallis |
| kruskalwallis(*args) | Compute the Kruskal-Wallis |
| ks_twosamp(data1, data2[, alternative]) | Computes the Kolmogorov-Smirnov |
| ks_twosamp(data1, data2[, alternative]) | Computes the Kolmogorov-Smirnov |
| kurtosis(a[, axis, fisher, bias]) | Computes the kurtosis (Fisher |
| kurtosistest(a[, axis]) | Tests whether a |
| linregress(*args) | Calculate a |
| mannwhitneyu(x, y[, use_continuity]) | Computes the Mann-Whitney |
| plotting_positions(data[, alpha, beta]) | Returns plotting positions (or |
| mode(a[, axis]) | Returns an array of the modal |
| moment(a[, moment, axis]) | Calculates the nth moment |
| mquantiles(a[, prob, alphap, betap, axis, limit]) | Computes empirical quantiles |
| msign(x) | Returns the sign of x, |
| normaltest(a[, axis]) | Tests whether a sample |
| obrientransform(*args) | Computes a transform on i |
| pearsonr(x, y) | Calculates a Pearson correlation |
| plotting_positions(data[, alpha, beta]) | Returns plotting positions (or |
| pointbiserialr(x, y) | Calculates a point biserial corre |
| rankdata(data[, axis, use_missing]) | Returns the rank (also known as orc |
| scoreatpercentile(data, per[, limit, ...]) | Calculate the score at the |
| sem(a[, axis]) | Calculates the standard error of the mean ( |
| signaltonoise(data[, axis]) | Calculates the signal-to-noise ratio, as the |
| skew(a[, axis, bias]) | Computes the skewness |
| skewtest(a[, axis]) | Tests whether the skew is |
| spearmanr(x, y[, use_ties]) | Calculates a Spearman rank-or |
| theilslopes(y[, x, alpha]) | Computes the Theil slope over |
| threshold(a[, threshmin, threshmax, newval]) | Clip array to |
| tmax(a, upperlimit[, axis, inclusive]) | Compute the |
| tmean(a[, limits, inclusive]) | Compute the |
| tmin(a[, lowerlimit, axis, inclusive]) | Compute the |
| trim(a[, limits, inclusive, relative, axis]) | Trims an array by masking |
| trima(a[, limits, inclusive]) | Trims an array by masking |
| trimboth(data[, proportiontocut, inclusive, ...]) | Trims the data by masking the int(proportiontocut*n) smallest and int( |
| trimmed_stde(a[, limits, inclusive, axis]) | Returns the standard error of the |
| trimr(a[, limits, inclusive, axis]) | Trims an array by masking so |
| trimtail(data[, proportiontocut, tail, ...]) | Trims the data by masking |
| tsem(a[, limits, inclusive]) | Compute the trimmed |
| ttest_onesamp(a, popmean) | Calculates the T-test for the |
| ttest_ind(a, b[, axis]) | Calculates the T-test for the m |
| ttest_onesamp(a, popmean) | Calculates the T-test for the |
| ttest_rel(a, b[, axis]) | Calculates the T-test on TWO |
| tvar(a[, limits, inclusive]) | Compute the |
| variation(a[, axis]) | Computes the coefficient of variation, th |
| winsorize(a[, limits, inclusive, inplace, axis]) | Returns a Winsorized versi |
| zmap(scores, compare[, axis, ddof]) | Calculates the re |

**Table 4.13 – continued fron**

| | |
|---|---|
| zscore(a[, axis, ddof]) | Calculates the z score of each value in |

`scipy.stats.mstats.`**`argstoarray`**(**args*)

Constructs a 2D array from a sequence of sequences. Sequences are filled with missing values to match the length of the longest sequence.

**Returns**

**output** : MaskedArray

a (mxn) masked array, where m is the number of arguments and n the length of the longest argument.

`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*)

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

observed frequencies in each category

**f_exp** : array, optional

expected frequencies in each category. By default the categories are assumed to be equally likely.

**ddof** : int, optional

adjustment to the degrees of freedom for the p-value

**Returns**

**chisquare statistic** : float

The chisquare test statistic

**p** : float

The p-value of the test.

### 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 then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distributions is not a chisquare, in which case this test is not appropriate.

### References

[R89]

`scipy.stats.mstats.`**`count_tied_groups`**(*x*, *use_missing=False*)

**Counts the number of tied values in x, and returns a dictionary**
(nb of ties: nb of groups).

**Parameters**
**x** : sequence

Sequence of data on which to counts the ties

**use_missing** : boolean

Whether to consider missing values as tied.

### Examples

```
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> count_tied_groups(z)
>>> {2:1, 3:2}
>>> # The ties were 0 (3x), 2 (3x) and 3 (2x)
>>> z = ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> count_tied_groups(z)
>>> {2:2, 3:1}
>>> # The ties were 0 (2x), 2 (3x) and 3 (2x)
>>> z[[1,-1]] = masked
>>> count_tied_groups(z, use_missing=True)
>>> {2:2, 3:1}
>>> # The ties were 2 (3x), 3 (2x) and masked (2x)
```

`scipy.stats.mstats.`**`describe`**(*a*, *axis=0*)
Computes several descriptive statistics of the passed array.

**Parameters**
**a** : array

**axis** : int or None

**Returns**
**n** : int

(size of the data (discarding missing values)

**mm** : (int, int)

min, max

**arithmetic mean** : float

**unbiased variance** : float

**biased skewness** : float

**biased kurtosis** : float

### 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: f-value, probability

`scipy.stats.mstats.`**`f_value_wilks_lambda`**(*ER*, *EF*, *dfnum*, *dfden*, *a*, *b*)

Calculation of Wilks lambda F-statistic for multivarite 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: chi-square statistic, associated p-value

`scipy.stats.mstats.`**`gmean`**(*a*, *axis=0*)

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, optional, default axis=0

Axis along which the geometric mean is computed.

**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.mstats.`**`hmean`**(*a*, *axis=0*)

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, optional, default axis=0

Axis along which the harmonic mean is computed.

**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.mstats.`**`kendalltau`**(*x*, *y*, *use_ties=True*, *use_missing=False*)
Computes Kendall's rank correlation tau on two variables *x* and *y*.

**Parameters**

**xdata: sequence** :

First data list (for example, time).

**ydata: 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**

**tau** : float

Kendall tau

**prob**
[float] Approximate 2-side p-value.

`scipy.stats.mstats.`**`kendalltau_seasonal`**(*x*)
Computes a multivariate extension Kendall's rank correlation tau, designed for seasonal data.

**Parameters**

**x: 2D array** :

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**

**H-statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

**p-value** : 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

[R90]

`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**

**H-statistic** : float

The Kruskal-Wallis H statistic, corrected for ties

**p-value** : 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

[R90]

`scipy.stats.mstats.`**`ks_twosamp`**`(`*data1*, *data2*, *alternative='two_sided'*`)`

Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**

**data1** : sequence

First data set

**data2**
[sequence] Second data set

**alternative**
[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

**Returns**
**d** : float

Value of the Kolmogorov Smirnov test

**p**
[float] Corresponding p-value.

`scipy.stats.mstats.`**`ks_twosamp`**(*data1*, *data2*, *alternative='two_sided'*)
Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**
**data1** : sequence

First data set

**data2**
[sequence] Second data set

**alternative**
[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

**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

Axis along which the kurtosis is calculated

**fisher** : bool

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

**bias** : bool

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

[CRCProbStat2000] Section 2.2.25

[CRCProbStat2000]

`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

the axis to operate along, or None to work on the whole array. The default is the first axis.

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : 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

**r-value**
[float] correlation coefficient

**p-value**
[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
>>> import numpy as np
>>> 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 on samples x and y. Missing values in x and/or y are discarded.

**Parameters**
**x** : sequence

y : sequence use_continuity : {True, False} optional

Whether a continuity correction (1/2.) should be taken into account.

**Returns**
**u** : float

The Mann-Whitney statistics

**prob**
[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, optional

Axis along which to operate. Default is 0, i.e. the first axis.

**Returns**
**vals** : ndarray

Array of modal values.

**counts** : 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

order of central moment that is returned

**axis** : int or None

Axis along which the central moment is computed. If None, then the data array is raveled. The default axis is zero.

**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-g).x[i] +g.x[i+1]`, where `x[j]` is the j-th order statistic, `i = (floor(n*p+m))`, `m=alpha+p*(1-alpha-beta)` and `g = n*p + m - i`.

**Typical values of (alpha,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)* : (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

**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.

**alpha** : float, optional

Plotting positions parameter, default is 0.4.

**beta** : 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

Tuple of (lower, upper) values. Values of *a* outside this closed interval are ignored.

**Returns**

**mquantiles** : MaskedArray

An array containing the calculated quantiles.

## 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 [R91], [R92] 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

If None, the array is treated as a single data set, regardless of its shape. Otherwise, each 1-d array along axis *axis* is tested.

**Returns**

**k2** : 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`.

**p-value** : float or array

A 2-sided chi squared probability for the hypothesis test.

## References

[R91], [R92]

`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** : 1D array

**y** : 1D array the same length as x

**Returns**

**(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**

**r** : float

R value

**p-value**

[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.

## 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**
[{boolean} 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*)
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.

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* 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.mstats.`**`signaltonoise`**(*data*, *axis=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

axis along which skewness is calculated

**bias** : bool

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

[CRCProbStat2000] Section 2.2.24.1

[CRCProbStat2000]

`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

**axis** : int or None

**Returns**

**z-score** : float

The computed z-score for this test.

**p-value** : 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** : 1D array

**y**

[1D array the same length as x] The lengths of both arrays must be > 2.

**use_ties**

[{True, False} optional] Whether the correction for ties should be computed.

**Returns**

**(Spearman correlation coefficient,** :

2-tailed p-value)

`scipy.stats.mstats.`**`theilslopes`**(*y*, *x=None*, *alpha=0.05*)

Computes the Theil slope over the dataset (x,y), as the median of all slopes between paired values.

**Parameters**

**y** : sequence

Dependent variable.

**x**

[{None, sequence} optional] Independent variable. If None, use arange(len(y)) instead.

**alpha**

[float] Confidence degree.

**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

`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**

**a, with values less (greater) than threshmin (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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero.

**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, 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**

**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** : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero

**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 == 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 == 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** : {(True, True) tuple} optional

If relative==False, tuple indicating whether values exactly equal to the absolute limits are allowed. If relative==True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**relative** : {False, True} optional

Whether to consider the limits as absolute values (False) or proportions to cut (True).

**axis** : {None, integer}, 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** : sequence

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** : {(True,True) 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 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**

[{0.2, 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.

**inclusive**

[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**

[{None, integer}, 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 of the data 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. 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**
[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**
[{None, integer}, optional] Axis along which to trim.

`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 int(trim*n) values from ONE tail of the data along the given axis, where n is the number of unmasked values.

**Parameters**
**data** : {ndarray}

Data to trim.

**proportiontocut**
[{0.2, 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.

**tail**
[{'left','right'} optional] If left (right), the `proportiontocut` lowest (greatest) values will be masked.

**inclusive**
[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

**axis**
[{None, integer}, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

`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

`scipy.stats.mstats.`**`ttest_onesamp`**(*a*, *popmean*)
Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

**Returns**
**t** : float or array

t-statistic

**prob** : float or array

two-tailed p-value

### Examples

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

>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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.

**Parameters**

**a, b** : sequence of ndarrays

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

**axis** : int, optional

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

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.

### Examples

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

>>> #fix seed to get the same result
>>> 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, 0.78849443369564765)
```

test with sample with different means

```
>>> rvs3 = stats.norm.rvs(loc=8,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs3)
(-5.0434013458585092, 5.4302979468623391e-007)
```

`scipy.stats.mstats.`**`ttest_onesamp`**`(`*a*, *popmean*`)`

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

**Returns**

**t** : float or array

t-statistic

**prob** : float or array

two-tailed p-value

### Examples

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

>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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=None*)

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** : sequence of ndarrays

The arrays must have the same shape.

**axis** : int, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

**Returns**

**t** : float or array

t-statistic

**prob** : 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.

## 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

`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

Axis along which to calculate the coefficient of variation.

## References

[CRCProbStat2000] Section 2.2.20

[CRCProbStat2000]

`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 (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.

`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.

**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).

`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

If *axis* is equal to None, the array is first raveled. If *axis* is an integer, this is the axis over which to operate. Default is 0.

**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([[-1.1649, -1.4319, -0.8554, -1.0189],
       [-0.8661, -1.5035, -0.9737, -0.6154],
       [-0.888 , -1.3817, -0.5461, -1.1156],
       [-2.3043, -2.2014, -1.9921, -2.5241],
       [-2.0773, -1.9212, -2.0506, -2.0328]])
```

## 4.24 C/C++ integration (`scipy.weave`)

**Warning:** This documentation is work-in-progress and unorganized.

### 4.24.1 C/C++ integration

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

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 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 affect 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 there 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 (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.

**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[, ...]) |
| ext_function_from_specs(name, code_block, ...) |
| ext_module(name[, compiler]) |

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