Fast Reconstruction of Accelerated Dynamic MRI Using Manifold Kernel Regression

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Abstract. We present a novel method for fast reconstruction of dynamic MRI from undersampled k-space data, thus enabling highly accelerated acquisition. The method is based on kernel regression along the manifold structure of the sequence derived directly from k-space data. Unlike compressed sensing techniques which require solving a complex optimisation problem, our reconstruction is fast, taking under 5 seconds for a 30 frame sequence on conventional hardware. We demonstrate our method on 10 retrospectively undersampled cardiac cine MR sequences, showing improved performance over state-of-the-art compressed sensing.

1 Introduction

Dynamic Magnetic Resonance imaging (MRI), for example, cardiac imaging, functional MRI, angiography or contrast agent uptake studies, is constrained by motion or intensity changes that occur over the duration of the image acquisition. Due to physical limits on the speed of acquisition in MRI, a compromise between the proportion of k-space and the frequency of time points acquired needs to be determined, resulting in a trade-off between spatial and temporal resolution. Accelerating the acquisition of each frame of a dynamic sequence is therefore a popular approach used to improve spatial or temporal resolution, or to enhance patient comfort by reducing scanning time [1]. One method of acceleration is through the undersampling of k-space, for example, by acquiring only a subset of phase-encode lines. The resultant missing lines of k-space, can then be completed through interpolation [8][11] or compressed sensing [7][5][9] techniques, which are active areas of current research.

While MRI acquisition of dynamic sequences is difficult to obtain at high-resolution ordinarily, the additional temporal structure of the images can be utilised to aid reconstruction. Compressed sensing methods such as [9][5][10][14] have been developed which incorporate temporal information, allowing for high rates of k-space undersampling. These methods require the reconstructed images to adhere to a specified model (such as sparsity in some domain), typically resulting in complex optimisation problems that can be slow to solve.

N. Navab et al. (Eds.): MICCAI 2015, Part III, LNCS 9351, pp. 510–518, 2015.
DOI: 10.1007/978-3-319-24574-4_61

Interpolation techniques have also previously been used in the reconstruction of undersampled k-space [8][11]. These generally require regular sampling in the k-t domain, and interpolate from neighbouring sampled locations in space and time. However, while these methods are fast, they typically have not been able to obtain the same levels of acquisition acceleration with comparable image quality as compressed sensing methods.

In this paper, we propose an alternative method of completing the missing lines of k-space, based on learning the underlying temporal manifold structure of k-space directly from the acquired data. Recent work [4][12] has shown that the inter-frame changes involved in dynamic MRI sequences, such as free-breathing cardiac or lung motion MRI, can be well-parameterised by non-linear dimensionality reduction techniques such as manifold learning. Motivated by developments in compressive manifold learning [2], we propose to exploit this to build a temporal manifold directly from undersampled k-space data. We then reconstruct the unknown lines of k-space through kernel regression in manifold space.

We demonstrate the performance of our proposed algorithm on ten retrospectively undersampled cardiac cine sequences, comparing to state-of-the-art compressed sensing techniques [9][5]. As our algorithm requires computation solely in k-space, our method is significantly faster than compressed sensing algorithms, while achieving comparable rates of acceleration and improved accuracy. Furthermore, the algorithm does not require strict conditions on the sampling pattern used.

2 Methods

Dynamic MRI involves acquisition of raw data in k-t space, that is, acquiring a time series of k-space frames (often 2D) at varying time points t. Cartesian undersampling in MRI is a common method used to accelerate acquisition of a frame by sampling a subset of k-space locations in the phase-encode direction (and fully in the frequency-encode direction). In this paper, we aim to use manifold learning to extract the temporal structure of a sequence directly from the common locations of k-space that are sampled in all frames.

2.1 Manifold Learning

Manifold learning has been applied to dynamic MR images in a number of recent applications [4][12]. While most medical imaging applications have so far involved manifold learning in image space, recent work [12], in which the learnt structure of a temporal sequence was used for respiratory gating, has shown that manifold learning can also be performed directly on k-space data.

In this paper, we use Laplacian Eigenmaps, which has been successfully applied in dynamic MRI applications [13][4][12]. The aim is to find an embedding which preserves the structure of the dataset by ensuring that data points (k-space samples of each frame of the sequence) which are “close” in the high-dimensional space remain "close" in the low-dimensional embedding. This is done by minimising the following cost function:

$$C(\mathbf{x}) = \sum_{ij} (\mathbf{x}_i - \mathbf{x}_j)^T (\mathbf{x}_i - \mathbf{x}_j) W_{ij} \tag{1}$$

which minimises the weighted Euclidean distance between the embedding coordinates $\mathbf{x}_i$ and $\mathbf{x}_j$ of data points i and j, respectively, in the low-dimensional embedding. The measure of closeness between points i and j is defined by the weight, W_{ij}, which indicates their similarity. The solution to (1) is obtained using properties of the graph of the data. We define a diagonal matrix as the column (or row) sum of the weights for each vertex $D_{ii} = \sum_j W_{ij}$, and the graph Laplacian as an operator on the graph vertices $\mathbf{L} = \mathbf{D} - \mathbf{W}$. Using these, we can rewrite the cost function as [3]:

$$C(\mathbf{x}) = \sum_{ij} (\mathbf{x}_i - \mathbf{x}_j)^T (\mathbf{x}_i - \mathbf{x}_j) W_{ij} = 2\mathbf{x}^T \mathbf{L} \mathbf{x} \tag{2}$$

After adding the constraint $\mathbf{x}^T \mathbf{D} \mathbf{x} = 1$ to eliminate arbitrary scale factors in the solution, the m-dimensional solution to (2) is given by the eigenvectors $\mathbf{x}$ of the generalised eigenvalue problem:

$$\mathbf{L}\mathbf{x} = \lambda \mathbf{D} \mathbf{x} \tag{3}$$

corresponding to the m smallest non-zero eigenvalues (λ).

In order to maintain the local structure of the data, the graph edge weights $\mathbf{W}$ are set to correspond to the neighbourhood (defined using k-nearest neighbours in the space of the original data) similarities between data points. One commonly-used metric is based on the ℓ_2 (Euclidean) norm distance $d_{st} = \|\mathbf{y}_s - \mathbf{y}_t\|_2^2$ between the sampled k-space lines at times s and t. Here $\mathbf{y}_.$ represents all the k-space values at a given time point which have been commonly sampled in all time frames. The final weights are then obtained using a Gaussian kernel function:

$$W_{st} = \begin{cases} e^{-\frac{\|\mathbf{y}_s - \mathbf{y}_t\|^2}{2\sigma^2}} & \text{if } s,\, t \text{ are neighbours in distance;} \\ 0 & \text{otherwise.} \end{cases}$$

where σ indicates the variance of the Gaussian.

2.2 Manifold Learning of Under-Sampled k-space

We require a time-varying sampling mask with a number of lines of k-space which are sampled in all frames of the sequence in order to construct the manifold. Recent work [2][12] has introduced the theory of *compressive manifold learning*, showing that for data that lies on a low-dimensional manifold, only a random subsample of the data is needed to retrieve that manifold. However, the data distribution of k-space is such that the majority of energy lies in the centre of k-space; we therefore require the central line of k-space to be fully-sampled in all frames. We show in Section 3.1 how the manifold created varies with number of lines of k-space used and that good approximations can be obtained even when using a single line. The left panel of Fig. 3b shows an example of a temporal mask with a sixth of the k-space phase-encoding lines sampled.

2.3 k-space Interpolation Using Manifold Kernel Regression

We assume, for the purposes of interpolation, that the manifold co-ordinates obtained as above would be common to all lines of k-space. Empirically, we have found this to give a good approximation when interpolating k-space. Each missing phase-encoding line of k-space is interpolated individually using manifold kernel regression along the manifold. This has previously been used to estimate the appearance of brain images of particular populations at unsampled locations [6]. For each frame, each unknown line in k-space is interpolated from the filled frames of the same line using weights based on the manifold co-ordinates as found in the previous section. The values $\mathbf{y}_f$ of each line of k-space in frame f are calculated using:

$$\mathbf{y}_f = \frac{\sum_i \kappa(\mathbf{x}_f, \mathbf{x}_i)\mathbf{y}_i}{\sum_j \kappa(\mathbf{x}_f, \mathbf{x}_j)} \tag{4}$$

Here $\mathbf{y}_i$ are the values of the sampled k-space line in frame i and $\kappa(\mathbf{x}_f, \cdot)$ is a kernel determining the distance between the manifold co-ordinates $\mathbf{x}_f$ of frame f and all other filled frames. As with the construction of the manifold, we use a Gaussian kernel given by:

$$\kappa(\mathbf{x}_f, \mathbf{x}_i) = \frac{1}{\sqrt{2\pi}\phi} e^{-\frac{\|\mathbf{x}_f - \mathbf{x}_i\|_2}{2\phi^2}} \tag{5}$$

where ϕ is chosen to be half the standard deviation of the manifold embedding co-ordinates. This means that data which are very far away in manifold co-ordinates are given less weight than those close together.

2.4 Algorithm Summary

Given time-varying sampling mask with at least the central line of k-space sampled in all frames, the missing lines of k-space are interpolated as follows:

1. Calculate manifold co-ordinates from the common line(s) of k-space sampled in all frames using Equation 3.
2. Interpolate each remaining line of k-space from the sampled frames of the same line using Equation 4.

3 Experiments and Results

Fully-sampled, short-axis cardiac cine scans were acquired from 10 subjects on a Siemens 1.5T scanner using retrospective gating. All datasets contain 30 temporal frames of size 256 × 256 with a 320 × 320 mm field of view and 10 mm slice thickness. These were generated using a combination of 32-channel data. Coil sensitivity maps were normalised to a body coil image to produce a single complex-valued image set that could either be back-transformed to regenerate complex k-space samples or further processed to form magnitude images. These images were then retrospectively undersampled for analysis.

3.1 Manifold Creation

We first show that even a subsample of the k-space lines can approximate the low-dimensional manifold of a full acquisition if the central line of k-space is included. Fig. 3.1 shows the 1-dimensional manifold created from the commonly-sampled lines of k-space of an example subject, using varying numbers of k-space lines. It can be seen that this manifold approximates the changes occurring during the cardiac cycle, even when only a single central line is used.

3.2 Comparison to State-of-the-Art Compressed Sensing Algorithms

We compare the results of our proposed reconstruction with those from two state-of-the-art dynamic MRI acceleration schemes: Dictionary Learning Temporal Gradient (DLTG) compressed sensing [5] and a Low Rank plus Sparse (LRS) reconstruction [9]. In both cases, we use the implementations and sampling masks provided by the toolboxes of the authors to ensure no bias in performance is caused by sub-optimal sampling for their method. All reconstructions were implemented in MATLAB and run on a 3.4GHz Intel Core i7-2600 CPU.

Fig. 3.2 shows the mask and example frames using the proposed method compared to DLTG. The mask in this case uses an 8 times undersampling scheme with the central nine lines of k-space used to build a 1-D manifold. The DLTG framework uses a patch size of 4×4×4 and 600 dictionary atoms for all subjects.

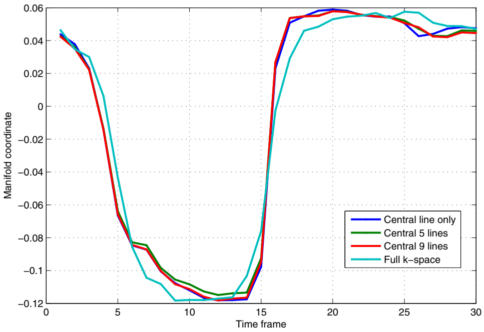
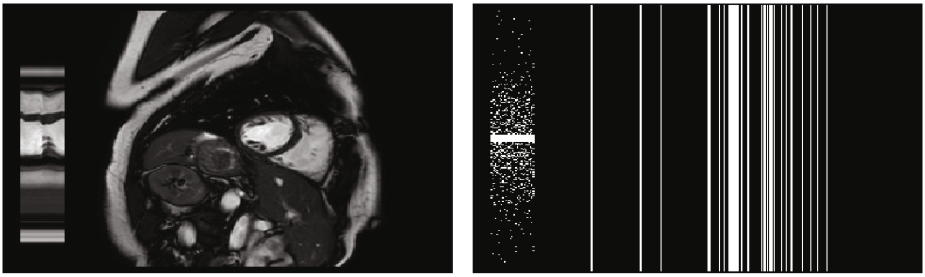
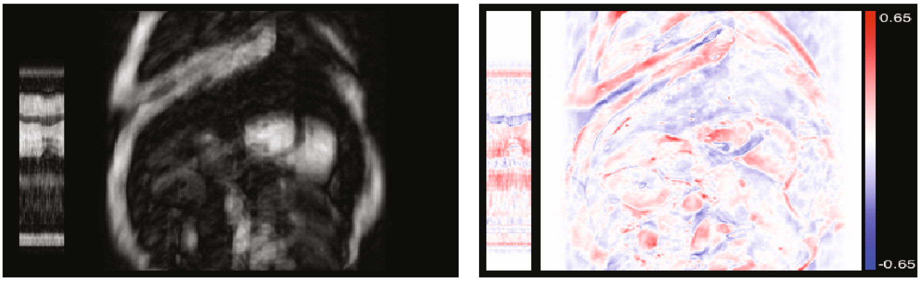
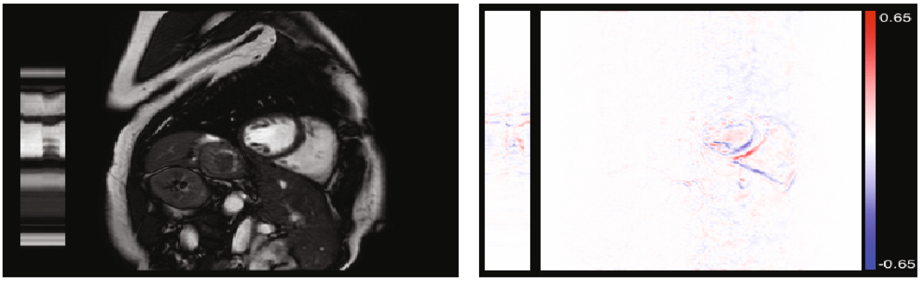


Fig. 1. 1-D Manifold created from cardiac cine sequence of example subject using varying number of lines of k-space.

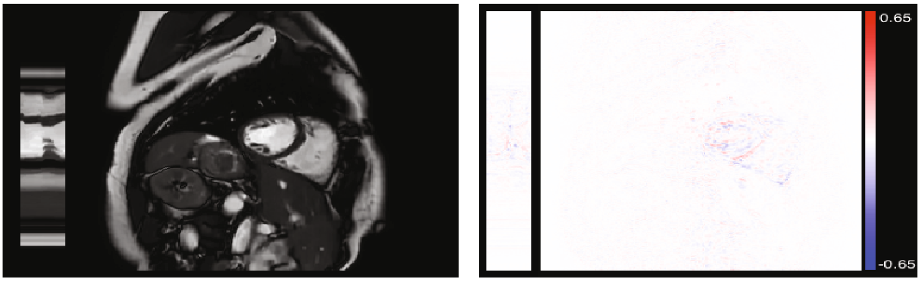

(a) Original (b) Mask



(c) Zero-filled (d) Error in (c)

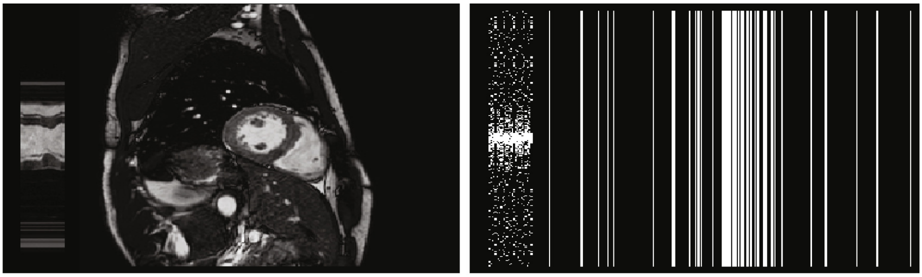


(e) Proposed (f) Error in (e)

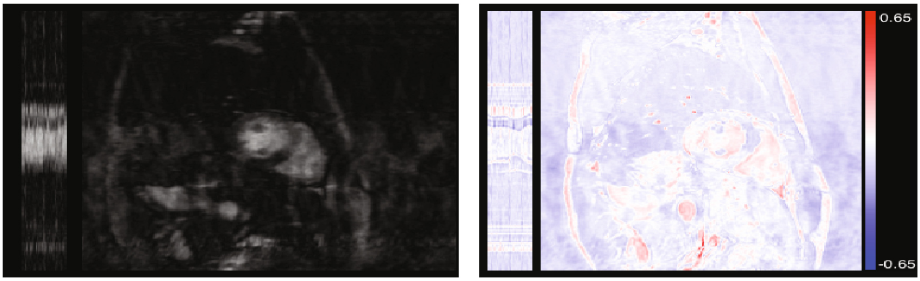


(g) DLTG (h) Error in (g)

Fig. 2. Example reconstruction of retrospectively undersampled (x8) cardiac cine images comparing proposed reconstructions with DLTG [5]. The temporal profile of the sequence and errors are shown on the left of each sub-figure.

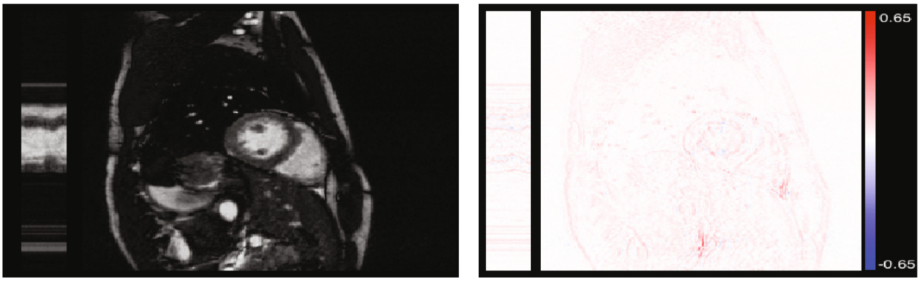


(a) Original (b) Mask



(c) Zero-filled (d) Error in (c)

(e) Proposed (f) Error in (e)



(g) LRS (h) Error in (g)

Fig. 3. Example reconstruction of retrospectively undersampled (x6) cardiac cine images comparing proposed reconstruction and LRS [9]. The temporal profile of the sequence and errors are shown on the left of each sub-figure.

The initial mean PSNR, taken over the all frames of all sequences, of the zero-filled reconstruction is 21.7dB. The mean PSNR of the DLTG reconstruction was 32.8±2.2dB while that of our proposed method was 31.6±1.7dB. However the gain in reconstruction time is significant - our method taking under 5 seconds for every sequence while the mean reconstruction time for DLTG being 53 hours.

We also compare our method to LRS using the mask provided by the authors for cardiac cine sequences, providing a 6 times undersampling. Default LRS parameters are used for all sequences. Example sequence, mask and reconstructions are shown in Fig. 3.2. The 1-D manifold here is constructed from the central line of k-space only. The mean PSNR over all sequences of the zero-filled reconstructions is 21.2dB. Our proposed method improves the PSNR to 33.1±1.4dB compared to 30.7±1.9dB for LRS, while taking 3 seconds for each subject compared to the 46 seconds of LRS on average.

4 Discussion

We have presented a method for fast reconstruction of undersampled k-space for accelerated dynamic MRI acquisition. Compared to state-of-the-art compressed sensing, our method achieves good reconstruction quality at significantly faster speeds. In this paper, we have not optimised sampling for our method, instead showing how it can be used with existing strategies for comparison. Optimising the sampling mask is the subject of ongoing work.

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