

Fast reconstruction of highly-undersampled dynamic MRI using random sampling and manifold interpolation

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INTRODUCTION

Acquisition acceleration techniques are particularly valuable for dynamic MRI where the speed of motion involved inhibits high-resolution imaging. Acceleration by undersampling k-space [1][2][3] can lead to improved spatial or temporal resolution or decreased scan time and improved patient comfort. Existing techniques for the reconstruction of undersampled k-space are computationally expensive, reducing their utility in a clinical setting. We present an algorithm for fast dynamic MRI reconstruction based on random sampling and manifold-based interpolation. We demonstrate results on both cardiac real-time and cardiac cine MRI, showing how the proposed algorithm performs at varying undersampling rates. The algorithm is fast, reconstructing 200 frames of real-time MRI in under 60 seconds, and can also be used as an initialisation to speed up convergence of more complex compressed sensing strategies.

METHODS

Acquisition and subjects: Real-time, free-breathing MR using a balanced steady state free procession sequence was used to acquire data from a healthy volunteer with spatial resolution of 2x2x10mm and temporal resolution of 117ms per frame (FA/TE/TR = 20/1.2/2.4ms). The short-axis view was acquired for 200 dynamics with a matrix of size 128x128. Additionally, fully-sampled short-axis cardiac cine scans from 10 subjects were acquired using retrospective gating. Datasets consisted of 30 temporal frames of size 256x256 with a 320x320mm field of view and 10mm slice thickness. These were generated using an optimal combination of 32-channel data, reconstructed using SENSE. We demonstrate our results on Cartesian sampling, by retrospectively applying a sampling mask where one-dimensional k-space lines are drawn randomly from a Gaussian distribution, ensuring the central seven lines of k-space fully-sampled in every frame.

Manifold representation: Reconstruction takes place by manifold-based interpolation of undersampled k-space. Manifold learning of dynamic MRI aims to find a low-dimensional non-linear representation of the data sequence. By considering each k-space frame of the sequence as an individual data point, the underlying structure (given by the manifold coordinates m) of the sequence can be found by:

$$\min \sum_i \sum_j (m_i - m_j)^2 W_{ij} \text{ where } W_{ij} \text{ represents the weights between frames } i \text{ and } j \text{ and are given by the differences between the k-space}$$

values u of each frame: $W_{ij} = \exp(-\|u_i - u_j\|/2\sigma^2)$ if i and j are within the k nearest neighbour frames, and zero otherwise. We calculate these weights using the fully-sampled central lines of k-space. It has been shown in [2][4] that good approximations to a data manifold can be obtained even when using only a subset of the data. For free-breathing MRI, we choose to project the data manifold on to two manifold dimensions, which corresponds well to the cardiac and respiratory motions [2][5].

k-Space Interpolation: Having determined a weight for each frame based on the manifold coordinates obtained as above, each unknown line of k-space is interpolated from the sampled locations. The values of an unknown k-space line Y_f are calculated using: $Y_f = \sum_i \kappa(m_f, m_i) Y_i / \sum_i \kappa(m_f, m_i)$ where Y_i are the values of the sampled k-space line in frame i and $\kappa(m_f)$ is a kernel determining the distance between the manifold coordinates of frame f and each of the other filled frames: $\kappa(m_f, m_i) = (2\sigma\pi^2)^{-1/2} \exp(-(2\sigma^2)^{-1}\|m_f - m_i\|_2^2)$. σ is chosen to be half the standard deviation of the manifold embedding coordinates m .

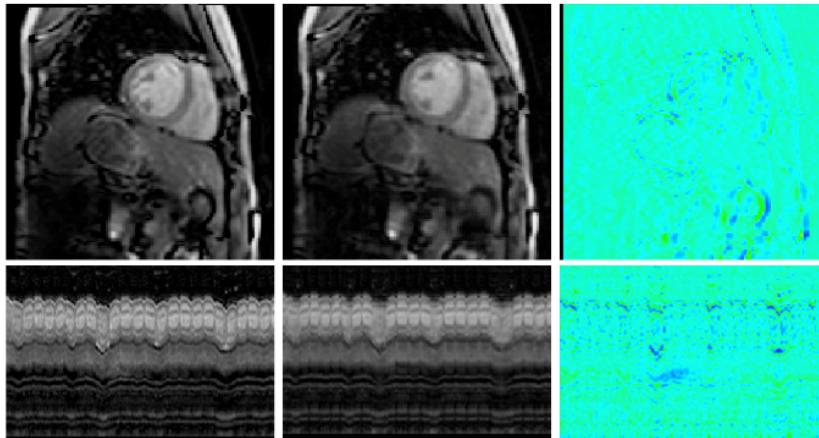


Figure 1: (L-R): original fully-sampled sequence with example frame, reconstructed frame with 8-fold acceleration, difference images between original and reconstruction.

REFERENCES: [1] Caballero et al. IEEE TMI 33(4), 2014 [2] Poddar et al. [3] Otazo et al. MRM, April 2014 [4] Wakin et al. arXiv:1002-260 [5] Bhatia et al. IEEE TMI 33(2), 2014.

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RESULTS: Figure 1 demonstrates the algorithm on the real-time free-breathing dataset, undersampled by a factor of 8. The mean PSNR over all frames at acceleration rates of 2, 4 and 8, respectively were found to be: 30.8, 25 and 21.2 for zero-filling, and 38.7, 33.3 and 30.0 using manifold interpolation. In all cases, the manifold reconstruction of the sequence took less than 60 seconds in total, using MATLAB on an Intel i7 3.4GHz machine.

For the 10 cardiac cine datasets were reconstructed in 5 seconds for an acceleration factor of 8 resulting in a mean RMS error of 1.5%. For comparison a published Low Rank + Sparse (LRS) method [3] required 49sec to achieve RMS error of 2.5%. Using manifold interpolation to initialise the LRS method allowed reconstruction in 19+5sec with RMS error of 1.2%.

CONCLUSION: The proposed manifold interpolation approach provides a method for fast reconstruction of dynamic MRI and that can achieve good performance compared to state-of-the-art. The method can be used on its own or as an initialiser to more complex compressed sensing algorithms.