Real Time Dynamic MRI with Dynamic Total Variation

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Abstract. In this study, we propose a novel scheme for real time dynamic magnetic resonance imaging (dMRI) reconstruction. Different from previous methods, the reconstructions of the second frame to the last frame are independent in our scheme, which only require the first frame as the reference. Therefore, this scheme can be naturally implemented in parallel. After the first frame is reconstructed, all the later frames can be processed as soon as the k-space data is acquired. As an extension of the convention total variation, a new online model called dynamic total variation is used to exploit the sparsity on both spatial and temporal domains. In addition, we design an accelerated reweighted least squares algorithm to solve the challenging reconstruction problem. This algorithm is motivated by the special structure of partial Fourier transform in sparse MRI. The proposed method is compared with 4 state-of-the-art online and offline methods on in-vivo cardiac dMRI datasets. The results show that our method significantly outperforms previous online methods, and is comparable to the offline methods in terms of reconstruction accuracy.

1 Introduction

Dynamic magnetic resonance imaging (dMRI) is an important medical imaging technique that widely used in hospitals for medical diagnosis and medical research. In general, there is a trade-off between the spatial resolution and temporal resolution, due to the acquisition speed of MR scanner. The undersampling often results in aliasing artifacts if the inverse Fourier transform is directly applied. Fortunately, the MR image sequence often provides redundant information in both spatial and temporal domains, which makes the use of compressive sensing (CS) theory repeatedly successful in MRI [1–4].

Based on the reconstruction schemes, the dMRI reconstruction methods can be online or offline. Most of existing methods are offline as they require the data of all frames to be collected before reconstruction. These methods applies sophisticated techniques that exploit the redundancies of the whole dataset, such as motion correction [5–7], dictionary learning [8], group clustering [9] and low rank approximation [10]. By these offline methods, the MR images can be reconstructed accurately but the drawbacks are their relatively slow speeds.

Online reconstruction means that the reconstruction of one frame only relies on the previous frames but not the later frames. Therefore, it is possible to reconstruct each frame once the corresponding k-space data is acquired. Of course, online reconstruction is much more difficult due to the lack of entire information as well as the concerns of reconstruction speed. Previous online methods usually assume that the difference between two adjacent frames are very small, either in the image or wavelet domain [11–13]. The difference can be reconstructed by sparsity regularization and the images are then updated by these changes. However, due to the lack of entire information, these methods have been shown to be less accurate than the state-of-the-art offline methods. And they all suffer from error accumulation, which makes them not feasible for relatively long sequences. Moreover, it is difficult for these methods to achieve real time reconstruction (i.e. the ideal case of online reconstruction), as they have to wait for the reconstruction of previous frame.
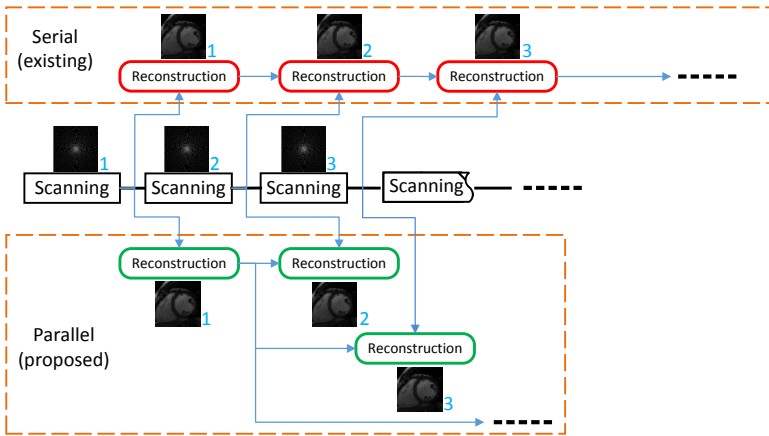

Fig. 1. Comparison between the proposed scheme and the existing online scheme

The data acquisition speed can be very fast with some recent developed techniques [14], e.g. 20ms, while real time MRI is still limited by the speed of iterative reconstruction methods. To bridge this gap, we propose a new online reconstruction scheme in this study, where the first frame is used to guide all the later reconstructions to exploit the temporal redundancy. A comparison with previous online methods is shown in Fig. 1. In contrast to previous serial system, our scheme is parallel and can naturally avoid error accumulation. After the first frame is reconstructed, all the later frames can be processed as soon as the data is acquired. In this new scheme, the sparsity assumptions in previous online methods may not hold any more. To address this issue, we extend the conventional spatial total variation (TV) to dynamic total variation (dTV), to exploit the sparsity in both spatial and temporal domains. An accelerated reweighted least squares algorithm is proposed to solve the dTV reconstruction

by observing the diagonally dominant prior in CS-MRI. Finally, the proposed method is validated on in-vivo cardiac MR sequences with comparisons to the state-of-the-art online and offline methods. Our contributions are from the novel scheme, the robust modeling to the efficient algorithm, which make real time dMRI much more feasible than before.

2   Modeling with Dynamic Total Variation

Dynamic MR images are significantly similar in the temporal domain, that the same organ(s) is contained through the whole image sequence. After the first frame is obtained, intuition tells that the later frames should be very close to it. This motivates us to design a new online reconstruction scheme, which has been presented in Fig. 1. With the prior information in the first frame, it is possible to guide the later reconstructions with fewer k-space measurements. As we always use the first frame but not the previous frame as reference, the reconstruction problem becomes more challenging. The assumptions in previous online method may not hold any more, e.g. the difference image is sparse [12].

To address this problem, we propose a new sparsity inducing norm called dynamic total variation (dTV) to utilize both spatial and temporal correlations in online reconstruction. For an image x with N pixels, its dTV is defined as:

$$dTV(x,r) = \sum_{i=1}^{N} \sqrt{(\nabla_x(x-r)_i)^2 + (\nabla_y(x-r)_i)^2} \qquad (1)$$

where r denotes a reference image (the first frame in this work) that has similar boundaries as x, ∇_x and ∇_y denote the gradients along the x and y directions. It means that the sparsity in gradient domain is not fixed but dynamic to a reference image. When there is no reference image, i.e. r is a zero image, it is identical to the conventional spatial TV. A similar idea of residual coding has been successfully applied in image registration [15].

We denote x_t as the frame at time t and $X = [x_1, x_2, ..., x_T]$ denotes the whole T images to be reconstructed. The dMRI reconstruction is therefore to solve x_t from an inverse problem $b_t = R_t F x_t$, where b_t is the measurement vector that may contain noise; R_t is a submatrix of the identity matrix that indicates undersampling, F denotes the Fourier transform. With the proposed dTV, the dMRI reconstruction is formulated as:

$$\min_{x_t} dTV(x_t, x_1), \text{ s.t. } ||R_t F x_t - b_t||_2 \le \epsilon \text{ for } t = 2, ..., T \qquad (2)$$

Same as that in existing online methods [11–13], the first frame should be reconstructed accurately with more k-space sampling. From this formulation, our scheme can be clearly observed. The reconstruction of each frame (except the first frame) only depends on the first one, but not the previous one. Therefore, it can be implemented in parallel to avoid waiting in the serial scheme.

Here, we only have a mild assumption, that the motions of organs are bounded. This assumption is quite natural because the cardiac motion is near periodic in

breath-hold imaging. If we divide the cardiac motion into several phases, the frame with the closest phase to the first frame should have minimum reconstruction error, and vice versa. One of the advantages of the proposed dTV is that it can always sparsify the images even in the worst case.

3   Preconditioning in Fast MRI Reconstruction

The reconstruction speed of offline methods is often not of big concern. However, fast reconstruction is essential to online methods. In this section, we proposed a new algorithm to efficiently minimize (2). Let $z = x_t - x_1$, and the problem (2) can be written as the Lagrange relaxed form of TV minimization:

$$\min_z \{\frac{1}{2}||Az - y||_2^2 + \lambda||z||_{TV}\} \qquad (3)$$

where $A = R_t F$, $y = b_t - R_t F x_1$ and λ is a parameter. There are many methods to solve (3) in the literature of convex optimization. Some of them have very fast convergence rate (e.g. [16]), but the computational cost in each iteration is very high. Some other methods are less computationally expensive in each iteration, such as that in [17], while they converge relatively slower. We expect to design an algorithm with both fast convergence and low computational cost.

Our algorithm is based on the reweighted least squares framework [16, 18], which can converge exponentially fast. Let D_1, D_2 be two N-by-N two first-order finite difference matrices in vertical and horizontal directions. The TV can be re-formulated as $||z||_{TV} = ||[D_1 z, D_2 z]||_{2,1}$, where the $\ell_{2,1}$ norm is the summation of the ℓ_2 norm of each row, $[x, y]$ denotes concatenating two vectors x, y horizontally. With this notations, the problem (3) can be solved by iteratively updating the weight matrix W and the solution z [16, 18]. W is a diagonal matrix with the i-th diagonal entry:

$$W_i^k = 1/\sqrt{(\nabla_x z_i^k)^2 + (\nabla_y z_i^k)^2}, \text{ for } i = 1, 2, ..., N, \qquad (4)$$

where k is the iteration counter. z^{k+1} is updated by solving the following linear equation:

$$(A^*A + \lambda D_1^* W^k D_1 + \lambda D_2^* W^k D_2)z = A^*y. \qquad (5)$$

where * denotes the conjugate transpose. This step dominates the computational cost of the whole algorithm. There is close form solution $z^k = S^{-1}A^*y$ for (5), where $S = A^*A + \lambda D_1^* W^k D_1 + \lambda D_2^* W^k D_2$ denotes the system matrix. However, the exact inversion is often not computationally feasible. In [16], this subproblem is solved by the conventional conjugate gradient method. Besides, a faster version called preconditioned conjugate gradient (PCG) method [18] can be used here. It requires a preconditioner P that is close to S and the inverse can be obtained efficiently. The design of good preconditioner P is problem-dependent and not easy due to the tradeoff between accuracy and computational cost.

We observe that the matrix $R_t^* R_t$ is diagonal, and more importantly, $A^* A = F^* R_t^* R_t F$ is therefore diagonally dominant. Thus, an accurate approximation could be made by removing the non-diagonal elements. Due to the properties of the Fourier transform, all the diagonal elements of $A^* A$ is equal to the mean of diagonal elements of $R^* R$, i.e. the sampling ratio s. Motivated by this, we define a new preconditioner $P = sI + \lambda D_1^* W^k D_1 + \lambda D_2^* W^k D_2$ to accelerate the whole algorithm, where I is the identity matrix.

The proposed preconditioner P is a symmetric penta-diagonal matrix, which has no closed form inverse. Fortunately, P is diagonally dominant as the regularization parameter λ is often very small in CS-MRI. It is not hard to find the incomplete LU decomposition of such penta-diagonal matrix $P \approx LU$, where L and U are a lower triangle matrix and an upper triangle matrix, respectively. The time complexity for the decomposition and inversion is $\mathcal{O}(N)$. To our best knowledge, this is the first study to accelerate MRI reconstruction with such preconditioner. We summarize the whole algorithm to solve (3) in Algorithm 1. All N-by-N matrices can be efficiently stored using sparse matrices in MATLAB.

Algorithm 1. dTV Reconstruction

Input: $A = R_t F$, x_1, $y = b_t - R_t F x_1$, z^1, λ, $k = 1$
Output: z, $x_t = z + x_1$.
while not meet the stopping criterion **do**
  Update W^k by (4)
  Update $S = A^* A + \lambda D_1^* W^k D_1 + \lambda D_2^* W^k D_2$
  Update $P = sI + \lambda D_1^* W^k D_1 + \lambda D_2^* W^k D_2 = LU$, $P^{-1} \approx U^{-1} L^{-1}$
  while not meet the PCG stopping criterion **do**
    Update z^{k+1} by PCG for $Sz = A^* y$ with preconditioner $P \approx LU$
  end while
  Update $k = k + 1$
end while

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4   Experiments

We compare our method with two online method modified CS (MCS) [13], the approach based on difference image (DI) [12] and two state-of-the-art offline methods k-t SLR [10] and the dictionary learning based method DLTG [8]. The codes are downloaded from each author's website and we use their default parameter settings for all experiments. For our method, we set $\lambda = 0.001$ for all experiments. In-vivo breath-hold cardiac perfusion and cine datasets are used here, which contains image sequences of $192 \times 192 \times 40$ and $256 \times 256 \times 24$, respectively. The proposed reconstruction method can be combined with the fast acquisition hardware radial FLASH [14] for real time imaging. Therefore, the radial sampling mask is used to simulate undersampling. The root-mean-square error (RMSE) is used as the metric for result evaluation. The ground-truth image is obtained by inverse FFT with full sampling.
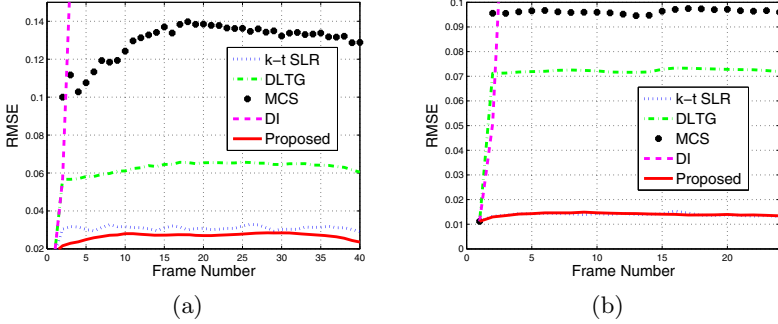
Fig. 2. Reconstruction accuracy comparisons of different methods. (a) On the perfusion dataset. (b) On the cine dataset. Our method and k-t SLR almost overlap on the second dataset.

The first frame is often required to be reconstructed very accurately for all online methods [13, 12]. Therefore, we use 1/2 sampling for the first frame and 1/6 sampling for the rest frames. The reconstruction RMSEs are shown in Fig. 2. From these results, it is obvious that the previous online methods [13, 12] have larger reconstruction errors than the offline methods [8, 10], while the proposed real time method is comparable or even better than the k-t SLR [10] on both datasets. The DLTG is currently designed for real-valued images [8], and it seems less effective on the complex-valued data here. DI does not perform as good as that presented in the paper [12]. From the 4th and 5th frame, it starts to fail. However, in [12], the curve of DI is often between those of k-t SLR and MCS. We found that it used the full sampling for the first frame, while the reconstruction error occurs at the first frame here with 1/2 sampling. With the same setting in [12], we conduct additional experiments for DI. It shows that DI starts to fail after 20-30 frames. These results demonstrate that DI is very sensitive to error accumulation.

A frame of the reconstructed perfusion sequence is shown in Fig. 3. Visible artifacts can be obviously observed on the images reconstructed by MCS and DI. The image reconstructed by DLTG tends to be blurry. In contrast, the reconstruction results of k-t SLR and the proposed method are similar to the ground-truth image, and less noisy.

We vary the sampling ratios of the second frame to the end frame and compare the average reconstruction errors of all frames. Those results are presented in Fig. 4, which demonstrates the comparable performance of our method to the state-of-the-art offline methods. At a low sampling ratio that we are interested, the proposed method seems to be even better. As the previous online methods [13, 12] are much less accurate, they are not compared in these experiments. For the $192 \times 192 \times 40$ perfusion sequence, the average reconstruction speed of our method is 0.71 seconds for each frame on a desktop with Intel i7-3770 CPU.
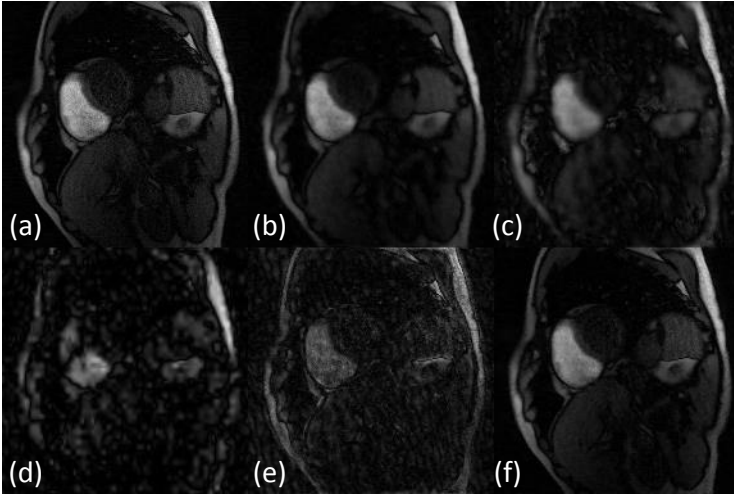
Fig. 3. Results of the third frame of the perfusion sequence at sampling ratio 1/6. (a) The ground-truth image with full sampling. The rest images are reconstructed by (b) k-t SLR; (c) DLTG; (d) MCS; (e) DI; (f) the proposed method.
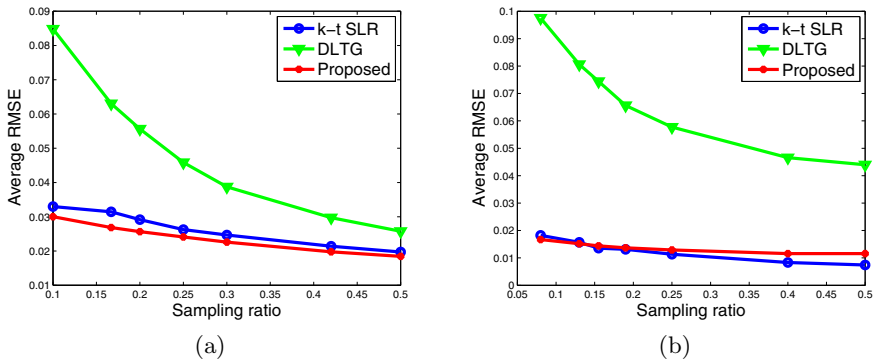

Fig. 4. Comparisons with the offline methods k-t SLR and DLTG at different sampling ratios. (a) On the perfusion dataset. (b) On the cine dataset.

5   Conclusion

In this paper, we have proposed a novel scheme for parallel reconstruction, a robust model to exploit both spatial and temporal redundancies, and an accelerated reweighted least squares algorithm to solve the reconstruction problem. Experiments on in-vivo cardiac perfusion and cine datasets have validated the efficiency and effectiveness of our method over the state-of-the-arts. These contributions make real time dMRI much more feasible than before. We will combine our method in parallel imaging as future work [19].

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