

Fast Preconditioning for Accelerated Multi-contrast MRI Reconstruction^{*}

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Abstract. Real-time reconstruction in multi-contrast magnetic resonance imaging (MC-MRI) is very challenging due to the slow scanning and reconstruction process. In this study, we propose a novel algorithm to accelerate the MC-MRI reconstruction in the framework of compressed sensing. The problem is formulated as the minimization of the least square data fitting with joint total variation (JTV) regularization term. We first utilized the iterative reweighted least square (IRLS) framework to reformulate the problem. A joint preconditioner is dexterously designed to efficiently compute the inverse of large transform matrix at each iteration. We compared our algorithm with eight cutting-edge compressive sensing MRI algorithms on real MC-MRI dataset. Extensive experiments demonstrate that the proposed algorithm can achieve far better reconstruction performance than all other eight cutting-edge methods.

1 Introduction

The multi-contrast magnetic resonance imaging (MC-MRI) is an important enhancement to MRI technology. The MC-MRI better serves the clinic diagnosis [15], because it generates multiple MR images with different contrast setting for visualizing the same anatomical cross section. However, the primary technical difficulty of real-time MC-MRI is the dramatically increased scanning and processing time for obtaining the examinational results.

The study of compressive sensing (CS) theory [3,7] has shown that, if the transformed data is sparse, an accurate original could be reconstructed from

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highly under-sampled k -space data, which significantly reduce the amount of required samples and consequently reduce the time cost. Motivated by the aforementioned CS theory, Lustig et al. proposed their pioneering work for compressed sensing MRI [10]. However, the SparseMRI is too slow for real-time MRI. Afterwards, the Operator-splitting [11] and the variable splitting [14] methods were separately proposed to accelerate the MRI reconstruction. Recently, a composite splitting algorithm [9] has been also proposed. However, these single-contrast MRI methods have not addressed the joint reconstruction of MC-MRI. An efficient extension for multiple contrast problem is non-trivial, because of the underlying correlations existing between those contrasts.

There has been some attempts to recover all the contrasts jointly. Among current algorithms, the FCSA-MT [8] delivers best reconstruction accuracy. Given the cross-contrast structural sparsity as prior knowledge, the reconstructed images by FCSA-MT enjoys better accuracy than the individual algorithms and other joint algorithms, e.g. Bayesian CS [2] and SPGL1 [12]. However, the efficiency of FCSA-MT is still impeded by the suboptimal convergence rate of FISTA framework [1]. The IRLS-MIL method [13] solves the regularized least square problem using the matrix inverse lemma. FIRLS [4,5,6] relaxes the sparsity regularization under the IRLS framework and boost the conjugate gradient descent method (CG) by a special preconditioning. However, it is unclear how these IRLS based algorithms can be used to efficiently solve the joint MC-MRI reconstruction with the JTV regularization.

In this paper we propose a novel algorithm for joint reconstruction of MC-MRI. Our method inherits its exponentially convergence property of IRLS framework. Moreover, we dexterously design a joint “pseudo-diagonal” preconditioner \mathcal{P} for efficiently solving the inverse problem in IRLS at each iteration. The proposed algorithm is able to efficiently deliver better fidelity due to the utilization of structural sparsity across contrasts and the more accurate approximation given by \mathcal{P} . Extensive experiments have been conducted to compare the proposed algorithm with eight cutting-edge methods for MC-MRI. The experimental results demonstrate that the proposed algorithm can achieve far better performance than all other methods.

2 Algorithm

2.1 Problem Formulation

Joint total variation (JTV) regularization well characterizes the correlated light intensity change in all contrasts. Assuming Gaussian noise, the objective function for joint MC-MRI reconstruction could be formulated as below:

$$\min_{\mathbf{X}} \sum_{s=1}^T \|A_s(\mathbf{X}(:, s)) - b_s\|_2^2 + \lambda \|\mathbf{X}\|_{JTV}, \quad (1)$$

where A_s is partial Fourier Transform matrix, \mathbf{X} is the $\mathbb{R}^{N \times T}$ concatenating matrix of all contrasts and b_s is the noisy observation. We have T contrasts,

each of which has $N = m \times n$ pixels. The JTV regularizer is $\|[D_1\mathbf{X}, D_2\mathbf{X}]\|_{2,1}$, where D_1 and D_2 are $\mathbb{R}^{N \times N}$ first-order finite difference matrix. Here, the $l_{2,1}$ norm is the summation of the l_2 norm of each row of the matrix concatenated by $[\cdot, \cdot]$. To avoid repetition, here we only derive the isotropic form of JTV term.

The problem (1) was solved by a FISTA framework [1]. It is not fast enough because at each iteration the solution of problem after the primal-dual relaxation of JTV still takes $1/\mathcal{O}(k^2)$ time to converge, where k is the iteration mark [1]. To further accelerate it, we consider to first approximate the JTV term by IRLS. Applying the Young’s inequality and the Majorization Minimization method [4]:

$$Q(\mathbf{X}, W^k) = \sum_{s=1}^T \|A_s(\mathbf{X}(:, s)) - b_s\|_2^2 + \frac{\lambda}{2} \left[\sum_{s=1}^T \mathbf{X}(:, s)^T D_1^T W^k D_1 \mathbf{X}(:, s) + \sum_{s=1}^T \mathbf{X}(:, s)^T D_2^T W^k D_2 \mathbf{X}(:, s) + Tr((W^k)^{-1}) \right], \tag{2}$$

where $Tr(\star)$ denotes the trace operator. W^k is the weight matrix at the k -th iteration, and its diagonal elements are:

$$W^k(i) = 1/\sqrt{\sum_{s=1}^T G_1^k(i, s)^2 + G_2^k(i, s)^2 + \theta}, \quad i = 1, \dots, N, \tag{3}$$

where $G_1^k(i, s) = D_1(i, :)X^k(:, s)$ and $G_2^k(i, s) = D_2(i, :)X^k(:, s)$ are the 2-D gradient matrix which are updated along with solution X^k . Small positive constant θ is for avoiding infinite weight. The original non-smooth problem has been approximated by the below smooth problem:

$$\hat{\mathbf{X}}^{k+1} = \underset{\mathbf{X}}{arg \min} Q(\mathbf{X}, W^k), \tag{4}$$

the solution of which could converge to the minimizer in exponential rate [4].

Algorithm 1. FCMRI

Input $A_s, b_s, \mathbf{X}^1, W^1, D_1, D_2, Err^1 \leftarrow \inf, \epsilon, \lambda \leftarrow 1e^{-3}, k \leftarrow 1$.
while $Err^k \geq \epsilon$ **do**
 Update W^k by Eq(3);
 Update $\tilde{\mathbf{A}}$ by $\tilde{A}_s = A_s^T A_s + \lambda D_1^T W^k D_1 + \lambda D_2^T W^k D_2, s = 1, \dots, T$;
 Update \mathcal{P} Eq(7);
 while NOT reach the stopping criterion of CG **do**
 Update \mathbf{X}^k through solving Eq(6) by CG;
 end while
 Update $Err^{k+1} = \sum_{s=1}^T \|A_s \mathbf{X}^k(:, s) - b_s\|_2^2, k \leftarrow k + 1$;
end while
Output \mathbf{X}^k .

2.2 Accelerating IRLS Framework

At each iteration, we need to solve problem (4). After eliminating constant terms and setting the first-order derivative zero, we easily find that the solution could be obtained by solving following linear system:

$$\tilde{\mathbf{A}}\mathbf{X} = \begin{bmatrix} \ddots & & \\ & \tilde{A}_s & \\ & & \ddots \end{bmatrix} \begin{pmatrix} \vdots \\ \mathbf{X}(:, s) \\ \vdots \end{pmatrix} = \tilde{\mathbf{b}}, \quad s = 1, \dots, T. \tag{5}$$

$\tilde{\mathbf{A}}$ is a block-wise diagonal matrix where $\tilde{A}_s = A_s^T A_s + \lambda D_1^T W^k D_1 + \lambda D_2^T W^k D_2$ and $\tilde{\mathbf{b}}$ consists of $\tilde{b}_s = A_s^T b_s$. While IRLS based algorithms can converge exponentially fast, the final speed is also determined by the time complexity of each iteration. For our scenario where N is large, it is impractical to directly inverse \tilde{A} , because the exact inverse of \tilde{A} takes $\mathcal{O}(N^3 T)$ time complexity.

An alternative is the conjugate gradient (CG) descent method. However, the actual convergence rate of CG is largely determined by the condition number of \tilde{A}_s , i.e. $k(\tilde{A}_s) = \lambda_{max}/\lambda_{min}$, where λ here is the set of eigenvalues of \tilde{A}_s . Unfortunately, in our case, \tilde{A}_s is usually not well-conditioned leading to slow actual convergence. One way to accelerate CG is to precondition on \tilde{A}_s and use CG to solve the below problem for instead:

$$\mathcal{P}^{-1} \tilde{\mathbf{A}}\mathbf{X} = \mathcal{P}^{-1} \tilde{\mathbf{b}}. \tag{6}$$

If $\mathcal{P} = I$, the \mathcal{P}^{-1} is trivial, but the CG is not accelerated. For ideal $\mathcal{P} = \tilde{\mathbf{A}}$, the \mathcal{P}^{-1} will be difficult, but solving (6) becomes fast because every eigenvalue of $\tilde{\mathbf{A}}^{-1} \tilde{\mathbf{A}}$ is one. A good preconditioner should balance the tradeoff. For solving all contrasts jointly, we suggest to use the block-wise diagonal preconditioner:

$$\mathcal{P} = \begin{bmatrix} \ddots & & \\ & P_s & \\ & & \ddots \end{bmatrix}, \quad s = 1, \dots, T. \tag{7}$$

Penta-diagonal matrix $P_s = \alpha_s I + \lambda D_1^T W^k D_1 + \lambda D_2^T W^k D_2$, where α_s is the mean of diagonal elements of $A_s^T A_s$, and I is an identity matrix of N . This is motivated by the fact that $A_s^T A_s$ is diagonal dominant and the $D_{(1,2)}$ is sparse. The complexity of \mathcal{P}^{-1} could be alleviated by incomplete LU decomposition, $\mathcal{P}_s^{-1} = L^{-1} U^{-1}$. It only takes $\mathcal{O}(NT)$ time to obtain \mathcal{P}^{-1} . $\mathcal{P}_s^{-1} \tilde{A}_s$ with its eigenvalues more closely clustered makes the convergence of CG faster and accelerates the reconstruction of all contrasts. The preconditioner (7) can also deliver better reconstructed accuracy than other preconditioners, e.g. Jacobi preconditioner, because P_s preserves more non-diagonal information making a more precise approximation of \tilde{A}_s .

3 Experiments

3.1 Experimental Setup

Our experiments are conducted on the complex value in-vivo Turbo Spin Echo (TSE) slices images [2]. These 256×256 MR images can cover 24 cm field of view. Besides, we also conducted experiments on SRI24 dataset. White Gaussian noise n_s of standard deviation $\sigma = 0.01$ was added to the measurements b_s , where $b_s = A_s \mathbf{X}(:, s) + n_s$. The regularization weight λ is 1e-3. We computed the SNR and RMSE as the metrics of fidelity and the CPU time for speed comparison. Radial and slice shape sample masks were employed separately. To eliminate the randomness, all experiments were repeated for 100 times before recording. All experiments were executed on PC equipped with Intel i7-4770 CPU.

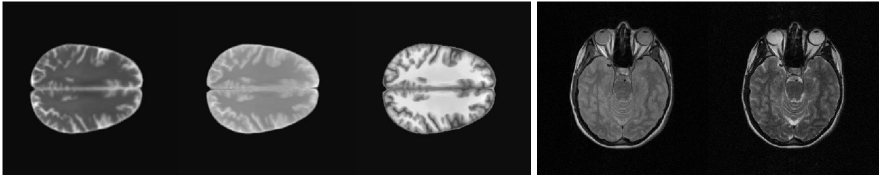


Fig. 1. Original images for experiments. Left: SRI24 three contrast MRI; Right: complex valued in-vivo Turbo Spin Echo (TSE) two contrast MRI.

3.2 Numerical Results

We first conducted experiments to compare the proposed algorithm with the individual algorithms [9,10,11,14], which recover MC-MRI individually. Figure 2(a) shows the comparison results. It is clear to see that our algorithm converged in few seconds, which was resulted from the exponential convergence rate of IRLS framework and the linear time complexity brought by the proposed joint preconditioning.

Moreover, we observe from Figure 2(b) that the slow convergence speed of FCSA-MT [8] was obviously alleviated by the removal of group wavelet sparsity term (FISAT-JTV). This is caused by the massy calculation of wavelet sparsity regularized subproblem in FCSA-MT. Besides, the splitting structure of FCSA-MT algorithm also constrains the speed of the faster subproblem because it can only be updated until the other iterative solution has converged, which takes another $1/\mathcal{O}(k^2)$ time complexity [1]. Fortunately, in this image reconstruction task, the removal of group wavelet sparsity term does not influence too much on the reconstructed accuracy. This evidence, in return, well supports the formulation of our algorithm Eq(1) with only JTV regularization term.

The benefit of our algorithm in accelerating convergence is more clearly presented in Table 1 and Figure 3. We compared the proposed algorithm with the FISTA-JTV, which has the exactly identical formulation as Eq(1). As shown in Figure 3, FISTA-JTV took at least double time to converge under 35% sample ratio, and even more under 25%. Different from the nested primal-dual iterative

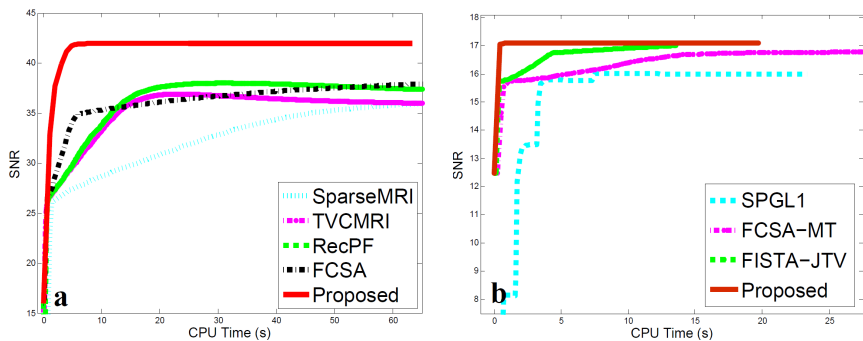


Fig. 2. Performance comparison between the proposed and all existing MC-MRI methods. a: SNR vs Time between the proposed and individual CS-MRI algorithms on SRI24 data; b: SNR vs Time between the proposed and joint CS-MRI algorithms on TSE data. Radial mask with 35% sample ratio was employed.

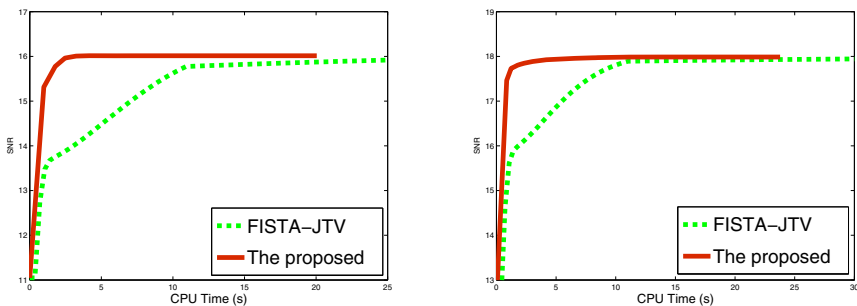


Fig. 3. Convergence time comparison between the proposed and FISTA-JTV under ratio radial mask of 25% (left) and 35% (right) sample ratio on TSE data.

solution, our algorithm inherits both exponentially fast convergence rate from IRLS and the linear time complexity of a well-designed PCG. We also observe in Figure 3 that the speed advantage the proposed method became even more significant when fewer sample data are available. To further verify its potential in reducing the amount of required samples, more comparisons were presented in Table 1. The proposed algorithm has a more robust convergence speed under low sample ratio scenario, e.g. 20%, meanwhile the good SNR is still maintained. For example, the SNR difference between the proposed and SPGL1 increased by 74% when the sample ratio decreased from 30% to 20%.

In Figure 4, we can visually indicate that our algorithm delivered the smallest reconstructed errors. This is because our formulation Eq(1) with JTV better characterized the group gradient sparsity across multiple contrasts. Besides, the exponential convergence rate granted by IRLS guaranteed a more complete convergence to the minimizer after certain number of iterations.

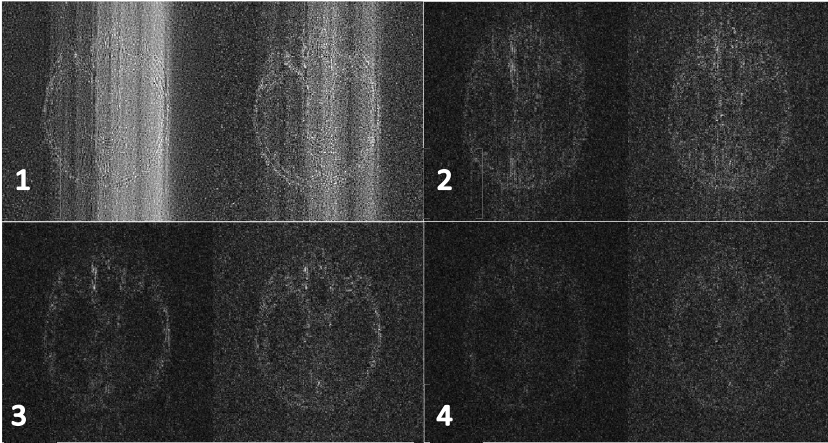


Fig. 4. Reconstructed absolute error comparison for the joint MC-MRI methods. 1) Bayesian CS [2]; 2) SPGL1 [12]; 3) FCSA-MT [8]; 4) the proposed. Best view in $\times 2$ PDF.

Table 1. Additional reconstruction results on TSE data with different type of sample mask under 20% or 30% sample rate. The CPU Time and SNR comparison between Bayesian CS [2], SPGL1 [12], FCSA-MT [8], FISTA-JTV and the proposed algorithm.

Mask	Sample Ratio	Metrics	Bayesian CS	SPGL1	FCSA-MT	FISTA-JTV	The Proposed
Radial	30%	RMSE	0.3068	0.1648	0.1267	0.1255	0.1248
		SNR (dB)	11.2806	15.0429	17.0382	17.0770	17.0962
		Time (s)	1348.59	56.91	44.73	20.18	6.62
	20%	RMSE	0.3712	0.2118	0.1534	0.1541	0.1521
		SNR (dB)	9.1084	12.9261	15.5363	15.5223	15.5427
		Time (s)	3096.49	89.16	90.09	25.67	6.72
Slice	30%	RMSE	0.2913	0.2256	0.2042	0.2052	0.2030
		SNR (dB)	10.3723	12.1847	13.0681	13.0414	13.1571
		Time (s)	598.51	41.73	58.20	29.01	5.52
	20%	RMSE	0.3045	0.2899	0.2283	0.2343	0.2191
		SNR (dB)	9.8634	10.3546	12.0297	11.8192	12.0380
		Time (s)	2177.41	35.79	51.89	27.52	9.25

4 Conclusion

This paper proposes a novel algorithm to accelerate multi-contrast MRI. Our proposed algorithm inherits the exponentially fast convergence from the IRLS and the linear time complexity at each iteration due to the joint pseudo-diagonal preconditioning on CG. These properties make our algorithm more feasible to implement real-time MC-MRI due to the fast reconstruction speed and the reduced sample requirement.

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