

EFFICIENT ACCELERATED DYNAMIC MRI RECONSTRUCTION BASED ON ROBUST SEPARATION AND COMPRESSION OF LOW RANK AND SPARSE COMPONENTS

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Abstract

The Low rank and Sparse (L+S) matrix decomposition model has been proposed in literature to reconstruct the accelerated dynamic MRI data. The limitations of L+S model include delicate separation and compression of the low-rank and sparse components from the acquired dynamic MRI data; also, the algorithm is computationally expensive. In this paper, Compressed Singular Value Decomposition (cSVD) is employed in L+S model for robust separation and P-Thresholding based compression of low rank and sparse components. The results show that the proposed method provides efficient reconstruction of accelerated dynamic MRI data in terms of quantifying parameters. Moreover, the proposed method possess highly parallel nature and demonstrate reduced in computation time using Graphic-Processing-Unit (GPU).

INTRODUCTION

Dynamic Magnetic Resonance Imaging (dMRI) is beneficial for the analysis of anatomical and physiological processes of human internal body e.g., heart. Long scan time is a major limitation of MRI which increases the cost and patient discomfort. Parallel MRI (pMRI) is a robust method to accelerate MRI scan time by acquiring fewer number of k-space lines using multiple receiver coils [1]. The drawback of undersampling is that it leads to artefacts in the MR images.

An alternative method for reconstructing MR images from the acquired randomly undersampled data is Compressed Sensing (CS) [2]. CS is based upon the principle that an image is recovered from randomly undersampled k-space data using a nonlinear reconstruction with a sparser representation in a known transform domain. However, CS is computationally expensive due to its iterative nature,

and the Acceleration Factor (AF) is limited by the number of sparse coefficients.

A significant increase in the AF has been achieved in literature by combining CS and pMRI based on distributed compressed sensing theory [3]. This approach has been proposed for highly accelerated dMRI data e.g., cardiac-perfusion-MRI and cardiac-cine MRI data. However, the AF is still limited by the number of receiver coils.

The Low-rank plus Sparse (L+S) matrix decomposition model [4] has been proposed in recent literature to separate the background i.e., static information associated with the Low-rank (L) components and the foreground i.e., dynamic information associated with Sparse (S) components in the dMRI data. In dMRI, the L+S model enables the suppression of background information which tends

to increase the AF. The L+S model is described by the following expression:

$$\min(L, S) \frac{1}{2} \|E(L + S) - d\|_2^2 + \lambda_L \|L\|_* + \lambda_S \|TS\|_1$$

For an accurate reconstruction of dMRI data requires a robust separation and compression of the L and S components. The standard L+S model uses conventional SVD [4] to approximate the low-rank information. The low rank and sparse components are compressed by applying Iterative Soft Thresholding (IST) on the singular values of L components (background) and truncating the low values coefficients of the S components in the transform domain respectively. This leads to a small contamination from the S components into the L components in the reconstructed dMRI data. Further, it is also computationally expensive due to the iterative nature and big data matrices involved in the reconstruction algorithm.

Compressed Singular Value Decomposition (cSVD) [5] is a contemporary approach which can be used as part of L+S decomposition model instead of conventional SVD for the robust approximation of low rank components and P-Thresholding [6] for the compression of low rank and sparse components. These modifications in the standard L+S model are expected to achieve good quality of reconstructed dMRI data with considerably reduces the computation time using GPU.

Method

In this paper we propose to use cSVD and P-Thresholding as part of L+S model to reconstruct the accelerated dMRI data as shown in Fig. 1.

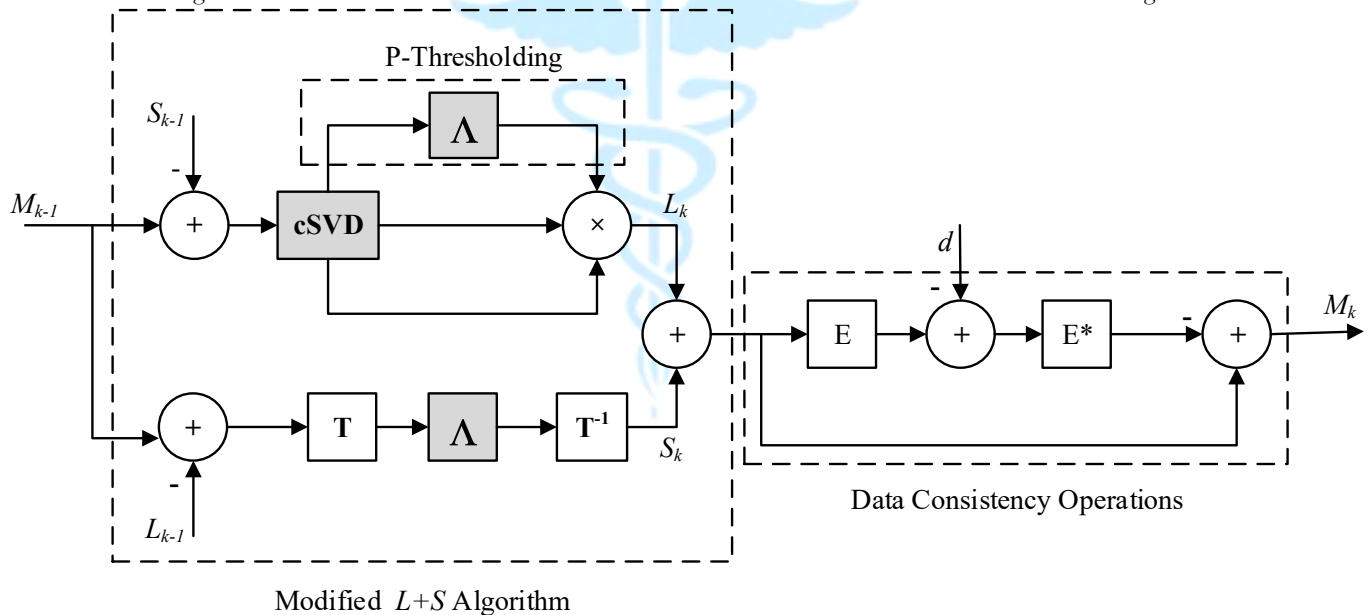


Fig. 1. Block diagram of the proposed method which incorporates cSVD in L+S algorithm and P-Thresholding (Λ) where E stands for encoding operator, T stands for temporal FFT and d stands for multicoil undersampled data.

Compressed Singular Value Decomposition (cSVD)

In the proposed method, to obtain the low rank SVD approximation of data matrix $M \in \mathbb{R}^{m \times n}$ with a target rank k with $m \geq n$, a random test matrix (R) is generated by $\text{rand}(n, l)$, where $l = k + \text{constant}$. The random test matrix is used to sketch the low rank matrix (L) and the resulting matrix is compressed into an extremely small matrix (named as 'Compressed

matrix' in Fig. 2). The restricted isometry property is applied to ensure symmetry between the data points in the compressed matrix. Eigen decomposition is applied to the compressed matrix to first approximate and then update the right and left singular values according to the target rank k . The whole process of cSVD is shown in Fig. 2.

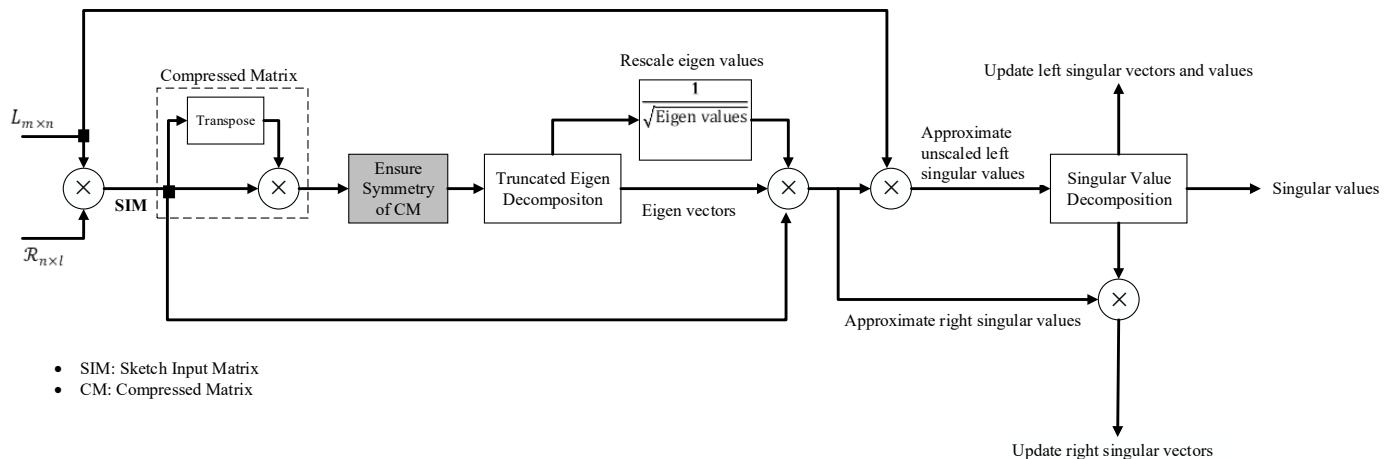


Fig. 2. Block Diagram of cSVD

P-Thresholding

The P-Thresholding based iterative algorithm is a modification of IST and minimizes non-convex optimization functions. It has been shown that the proposed P-Thresholding iterative algorithm can be used effectively to recover fully sampled image from the acquired under-sampled data in MRI. This paper introduces an improved iterative algorithm based on

$$(\mathbf{G}_{\lambda, \mathbf{P}}(\mathbf{x}))_{\mathbf{k}} = \text{sgn}(\mathbf{x}_{\mathbf{k}}) \max\{|\mathbf{x}_{\mathbf{k}}| - \lambda_{\mathbf{p}} |\mathbf{x}_{\mathbf{k}}|^{\mathbf{P}-1}\} \quad (2)$$

In Eq. (2), $\mathbf{G}$ is thresholding function, λ is the thresholding value, $\mathbf{P}$ is the value which add weight to the elements of coefficient β and sgn is the signum

P-Thresholding technique for accelerated dMRI reconstruction. The use of P-thresholding function additionally promotes sparsity in the S components which are already sparse in the transform domain which is a key feature for CS used in pMRI based image reconstruction e.g., L+S model. The P-Thresholding technique obeys the following equation.

function. Table.1 shows the pseudocode for P-Thresholding used in the reconstruction process of S components in the transform domain.

Table 1: Pseudo code for P-Thresholding operation applied on S components in the transform domain

Inputs:

λ = Thresholding parameter

$\mathbf{x} = \Psi \mathbf{m}$

where,

$\mathbf{m}$ = under sampled MRI image

Ψ = Sparsifying transform

P-Thresholding Operation:

$\mathbf{p} = -0.5$

$\mathbf{r} = \max\{|\mathbf{x}_{\mathbf{k}}| - \lambda_{\mathbf{p}} |\mathbf{x}_{\mathbf{k}}|^{\mathbf{P}-1}\}$

$(\mathbf{G}_{\lambda, \mathbf{P}}(\mathbf{x}))_{\mathbf{k}} = \text{sgn}(\mathbf{x}_{\mathbf{k}}) \cdot \mathbf{r}$

Output:

$\mathbf{Y} = \Psi'(\mathbf{G}_{\lambda, \mathbf{P}}(\mathbf{x}))_{\mathbf{k}}$

Results and Discussion

The experiments are performed on two data sets, one is cardiac cine MRI data acquired with 3T Scanner at Case Western Reserve University USA [7] and the other is cardiac perfusion MRI data available publically [4]. Both of these data sets were retrospectively undersampled at Acceleration Factors of (AF) 6 & 8.

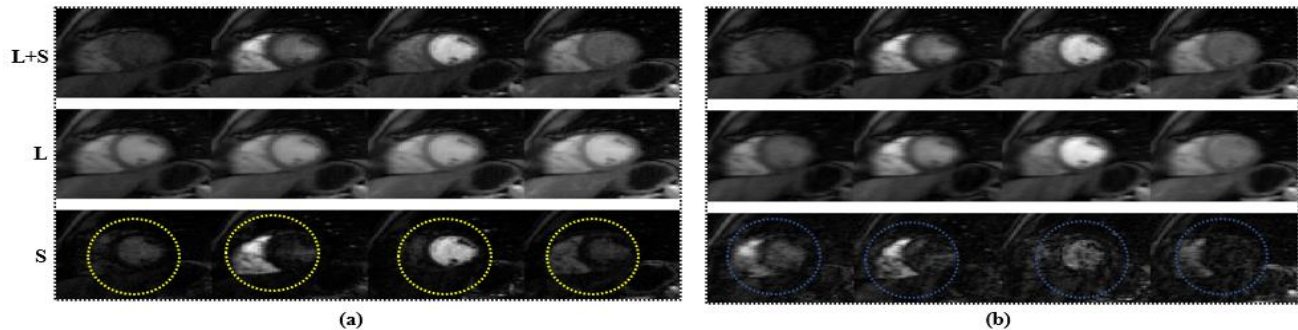


Fig. 3. Reconstruction results of 3T cardiac perfusion MRI data: which depicts robust separation of the low rank and sparse components in the proposed method as shown in yellow circles in (a) as compared to the standard method (shown in blue circles in (b)). Here S is the Sparse image, L is the low rank image while L+S shows the full reconstructed image.

Table 2 provides a comparison of the proposed method and standard method in terms of quantifying parameters. Artifact power (AP) [8] is the square of the difference error between the reference and

The results are compared with Otazo's method, as a gold standard [4]. For a fair comparison between the proposed method and standard method [4], simulations are performed by setting the same values of all the parameters on the same machine i.e., Intel(R) Core (TM) i7-4790, having 3.60GHz processor with 16GB RAM. Fig. 3 shows the reconstruction results of four different frames (out of 11) of cardiac perfusion data set at AF=8.

reconstructed images, Root-Mean-Square-Error (RMSE) [9] is the measure of difference between reference and reconstructed images and Peak-Signal-to-Noise-Ratio (PSNR) [8,10] is another frequently used parameter in assessing quality of the reconstructed images. PSNR is the ratio between the maximum possible value of a signal and the value of distorting noise that affects the quality of its representation. Our proposed method represents superior quality of the reconstructed dMRI data as compared to the standard method in terms of quantifying parameters.

Table 2. Qualitative analysis of the proposed method and standard method

Quantifying parameter	The proposed method	Standard method [4]
AP	0.015	0.029
RMSE	0.013	0.018
PSNR	87.640	85.930

Further, to assess the parallel nature of the proposed method, simulations on GPU are performed using MATLAB's parallel computing toolbox on NVIDIA GeForce GTX 780M, with 11230 MB memory and 2304 cores with graphic clock of 862 MHz. Table 3 provides a comparison of the reconstruction times for the CPU and GPU implementation of the proposed and standard method.

Table 3: Computation time analysis using CPU and GPU for the proposed method and standard method

The proposed method		Standard method [4]	
CPU time(s)	GPU time (s)	CPU time (s)	GPU time(s)

149.38	43.38	138.31	51.34
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The reduced computation time in the proposed method using GPU depicts that the proposed method is highly parallelizable as compared to standard method. Central-Line-Profile (CLP) [11] represent the intensity variation along the center of images. Fig. 4

represent the CLP of the reconstructed images of the proposed method using CPU and GPU. The corresponding CLP depicts there is no significant difference in the reconstructed images.

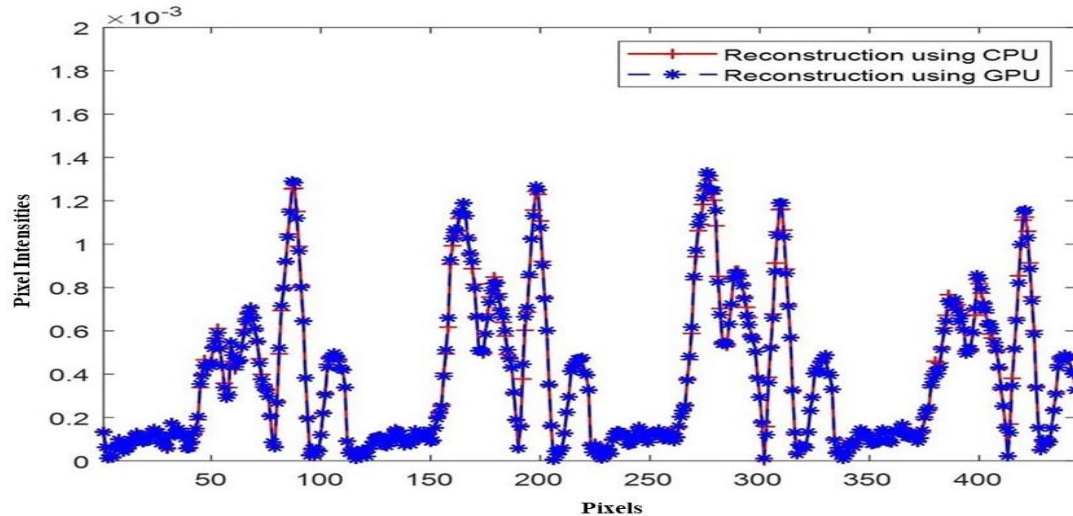


Fig. 4. Comparison of the central line profiles of the proposed method using CPU and GPU

The results show an improved reconstructed quality of the dMRI data using the proposed method and is highly parallelizable as compared to the standard method.

Conclusion

The proposed method demonstrates a robust separation and compression of the dMRI data into low-rank and sparse components. The proposed method represent superior quality of the reconstructed dMRI data as compared to standard method. The cSVD and other parts of the proposed method are highly parallelizable and can achieve further speed-up on GPU using memory optimization. Our future intention is to analyze advance compressed sensing techniques to further efficiently reconstruct the accelerated dMRI data.

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