Motion and Contrast Enhancement Separation Model Reconstruction from Partial Measurements in Dynamic MRI

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Abstract. We propose a motion and contrast enhancement separation model in dynamic magnetic resonance imaging (MRI). Furthermore, the reconstruction is done from partial measurements to achieve faster dynamic MR imaging. The algorithm minimizes a linear combination of three terms, a data fitting functional and two regularization functionals corresponding to the nuclear and ℓ_1 norm. The proposed method is tested on simulated and real dynamic datasets. This paper suggests an image reconstruction model that directly induces clinically-relevant informations from partial measurements.

Keywords: low-rank plus sparse model, dynamic MRI, motion, under-sampling, split Bregman-based method

1 Introduction

Dynamic magnetic resonance imaging (MRI) consists of acquiring multiple images (frame by frame) of a dynamic object in time. Since this is a sequential and slow acquisition process, motion artefacts are often present due to unintentional movements of the patient. Faster dynamic MR imaging, by reducing the number of measurements (under-sampling), can minimize the chance of motion affecting a frame, giving a better temporal resolution for dynamic processes, or trading the time saving for higher spatial resolution.

A few years ago, a more efficient signal acquisition than the traditional Shannon sampling theory was introduced for sparse or compressible signals. This theory, called Compressed Sensing (CS), states that one can recover images from only a few random measurements. This is possible providing that (1) the image is sparse in some domain or in its own, (2) sensing and sparsifying matrices satisfies the restricted isometry property and are incoherent, and (3) non-linear reconstruction techniques is used to recover the signal. Since these assumptions can generally be met in medical imaging, CS has been applied in MRI as a rapid imaging technique [1].

Recently, the recovery of a matrix from incomplete information has attracted interest. This research topic is known as low-rank matrix completion [2] and has strong parallels with CS framework. Indeed, one can see the notion of matrices with a low-rank as an equivalent of signals with only a few significant coefficients. Similarly, analogous to ℓ_1 norm minimization promoting sparse signals is the notion of nuclear norm minimization promoting low-rank matrices. Combining low-rank and sparsity constraints for matrix problems has recently been investigated in mathematics and computational science because it has a large spectrum of potential applications. The idea is to recover low-rank and sparse components from a matrix which is supposed to have an underlying low-rank structure [3–5].

In medical imaging, these type of priors have been recently studied. In particular, it has been used by Majumdar and Ward [6] for accelerating MRI, by Lingala et al. for accelerating dynamic MRI [7] and by Gao et al. [8] to reduce radiation dose in computed tomography (CT). While these works mostly focus on achieving better image quality from under-sampled data than state of the art methods, we take a different approach in this paper. The novelty is that regularization is viewed as providing a useful decomposition of dynamic MR images that can be used technically or is shown to be clinically relevant. The algorithm used, a split Bregman based method proposed by Gao et al. in CT [8], has strong links with alternating direction method for solving the low-rank and sparse decomposition problem [4, 5].

The rest of the article is organized as the following. Section 2 provides a brief review of the low-rank and sparse decomposition problem. In section 3, we discuss under-sampling strategies for the proposed method. Reconstruction model and algorithm are explained in section 4. Numerical simulations are shown in section 5 and section 6 concludes this paper.

2 Low-rank and Sparse Decomposition

In this section, we introduce the decomposition from a mathematical and computational perspective. We assume we have a matrix $X \in \mathbf{R}^{n \times m}$ which is the superposition of a low-rank and a sparse component. The goal is to decompose the given matrix into its low-rank L and sparse S components such that $X = L + S$. This can be cast naturally as the following optimization problem,

$$\min_{L,S} \ \operatorname{rank}(L) + \lambda \|S\|_0 \quad \text{such that} \quad X = L + S \ , \tag{1}$$

but reveals to be intractable as it encloses rank and ℓ_0 minimization problems, which both are known to be NP-hard and consequently difficult to solve. From a statistical point of view, this method can be seen as a robust variant of principal component analysis (PCA), where one seeks a low-rank matrix from grossly corrupted measurements.

To make the problem easier to solve, one can reformulate it as a convex one [2–4],

$$\min_{L,S} \|L\|_* + \lambda \|S\|_1 \quad \text{such that} \quad X = L + S \ . \tag{2}$$

Here $\|L\|_*$ and $\|S\|_1$ denote respectively the nuclear norm of L (the sum of its singular values), $\|L\|_* = \sum_i \sigma_i(L)$ with $\sigma_i(L)$ the i^{th} singular value of L, and the ℓ_1

norm of S defined as the sum of the absolute values of all entries, $\|S\|_1 = \sum_i |s_i|$ with s_i the i^{th} entries of S viewed as a vector. λ can be viewed as a trade-off parameter between low-rank and sparse components. Theoretical analysis in [5] leads to the trade-off parameter value $\lambda = \max(n, m)^{-1/2}$ for recovering any low-rank, incoherent matrix with high probability. The convex relaxation approach (2) is usually solved using alternating direction method, an improvement of the augmented Lagrangian method, which exploits the favourable structure appearing in both the objective function and the constraint [4, 5].

3 Dynamic MR Data and Sampling Scheme

In this study, the low-rank and sparse decomposition model operates as a spatio-temporal one. The matrix X to decompose is formed as the concatenation of each image frames $\{x_i\}_{i=1}^{J} \in \mathbf{R}^{N=n\times n}$ casted as column vectors of X, i.e.,

$$X = [x_1, x_2, ..., x_J] \in \mathbf{R}^{N\times J} \ . \tag{3}$$

Hence, columns of X correspond to spatial pixels and rows correspond to temporal intensity variations of the pixels in the image domain. Since each frames x_i exhibits significant correlations, the whole sequence lies in fact in a low-complexity model, an underlying low-rank structure, and thus motivates this decomposition. We highlight that the method relies on an appropriate number of frames since the matrix X can be said low-rank only if $\text{rank}(X) \ll \min(N, J)$.

To accelerate MRI, the idea is to reduce acquisition time by sampling only partially the k-space and reconstruct images from these incomplete data. Creating better random k-space sampling trajectories for under-sampled MRI acquisition has been subject to a lot of research in the CS MRI literature, as in practice it is conditioned by hardware and physiological considerations. Here, the proposed method is more closely related to low-rank matrix completion than CS, since we do not employ any sparsifying transform. Under-sampling is possible because of the spatio-temporal matrix formulation and the use of nuclear norm and ℓ_1 minimization in the model.

Since we do not want to use non uniform Fourier transform in order to avoid longer computational cost, we limit our trajectory choices to Cartesian sampling. Experiments showed that the reconstruction quality is sensitive to the sampling strategy. In this paper, we choose to densely sample the low spatial frequencies and randomly select phase encoding lines elsewhere in each time-frame. This results in a sampling scheme random in time, except for the center of the k-space. We make this choice not only because it is easily done in practice, but also because it is common practice in CS MRI and because we could achieve modest acceleration rate with accurate reconstruction. Here, acceleration rates are computed by dividing the number of k-space points acquired over the total number of points in the k-space. For example, a 2-fold acceleration implies that only 50% of the k-space is used.

4 Reconstruction Model and Algorithm

In this paper, we consider the following unconstrained optimization problem for the reconstruction,

$$\min_{L,S} \frac{1}{2}\|A(L+S)-y\|_2^2 + \mu(\|L\|_* + \lambda\|S\|_1) \tag{4}$$

where $A : \mathbf{R}^{N\times J} \to \mathbf{C}^p$ is the Fourier operator providing a vector y of $p < N \times J$ measurements. The first term in the objective function is a data fitting criterion, and the second term encloses the original decomposition problem.

A slightly different problem has been proposed by Gao et al. in dynamic CT [8] and solved using a split Bregman based method. We rely on this efficient approach to solve (4). The iterative algorithm, described by equations in (5), consists of three major steps : a quadratic problem solved using conjugate gradient, an ℓ_1 problem solved by shrinkage formula and a nuclear norm problem solved by singular value thresholding.

$$\begin{cases}
(L^{n+1}, S^{n+1}) = \arg\min\limits_{L,S} \|A(L+S) - y + f^n\|_2^2 + \alpha\|L - d_L^n + v_L^n\|_2^2 \\
\qquad\qquad + \beta\|S - d_S^n + v_S^n\|_2^2 \\
d_S^{n+1} = \arg\min\limits_{d_S} \frac{1}{2}\|S^{n+1} + v_S^n - d_S\|_2^2 + \lambda\frac{\mu}{\beta}\|d_S\|_1 \\
v_S^{n+1} = v_S^n + S^{n+1} - d_S^{n+1} \\
d_L^{n+1} = \arg\min\limits_{d_L} \frac{1}{2}\|L^{n+1} + v_L^n - d_L\|_2^2 + \frac{\mu}{\alpha}\|d_L\|_* \\
v_L^{n+1} = v_L^n + L^{n+1} - d_L^{n+1} \\
f^{n+1} = f^n + A(L^{n+1} + S^{n+1}) - y
\end{cases} \tag{5}$$

These three major steps have closed form solutions, hence the iterative scheme can be rewritten as described in algorithm 1, where $\mathcal{S}$ and $\mathcal{D}$ are respectively the shrinkage and singular value thresholding operators, defined as

$$\mathcal{S}_\tau(X) = \operatorname{sign}(X)\max(|X| - \tau, 0)\ , \tag{6}$$

$$\mathcal{D}_\tau(X) = U\mathcal{S}_\tau(\Sigma)V^*\ . \tag{7}$$

Here $X = U\Sigma V^*$ represents any singular value decomposition. To ensure good convergence, stopping criterion is met when a maximum number of iteration (typically 500 or 1000 iterations) is achieved or when $\|A(L+S)-y\|/\|y\| \leq 10^{-5}$. α and β are set equal to μ.

We emphasize the main goal of this work is not to compare image reconstruction quality with state of the art methods in dynamic MR reconstruction from under-sampled data. In fact, it is to provide the direct reconstruction of the low-rank and sparse components, yielding the exploitation of the proposed decomposition. Accordingly, we suggest that the parameter λ should be tuned

Algorithm 1 Low-rank and sparse decomposition from partial measurements

```
**Input:** Measurements $y$, parameters $\mu$ (regularization) and $\lambda$ (decomposition)
**Output:** $L$, $S$
$L^0 = S^0 = v_L^0 = v_S^0 = d_L^0 = d_S^0 \leftarrow 0$ ; $\alpha = \beta = \mu$ ; $f^0 \leftarrow 0$ ; $n \leftarrow 0$
**while** stopping criterion is not met **do**
    $S^{n+1} \leftarrow (A^TA + \mu I)^{-1}(A^T(y - f^n) + \beta(d_S^n - v_S^n) - A^TA(L^n))$
    $L^{n+1} \leftarrow (A^TA + \mu I)^{-1}(A^T(y - f^n) + \alpha(d_L^n - v_L^n) - A^TA(S^n))$
    $d_S^{n+1} \leftarrow \mathcal{S}_{\frac{\lambda\mu}{\beta}}(S^{n+1} + v_S^n)$
    $v_S^{n+1} \leftarrow v_S^n + S^{n+1} - d_S^{n+1}$
    $d_L^{n+1} \leftarrow \mathcal{D}_{\frac{\mu}{\alpha}}(L^{n+1} + v_L^n)$
    $v_L^{n+1} \leftarrow v_L^n + L^{n+1} - d_L^{n+1}$
    $f^{n+1} \leftarrow f^n + A(L^{n+1} + S^{n+1}) - y$
    $n \leftarrow n + 1$
**end while**
```

by visual inspection, to obtain the best possible motion and contrast enhancement separation. More precisely, a correct scaling for this parameter should be of order of $\lambda = \max(N, J)^{-1/2}$ given by Candès et al. [5].

5 Numerical Simulations

To evaluate the method, we tested the proposed model on simulated and in vivo datasets by targeting cardiac imaging and dynamic contrast enhanced (DCE) MRI applications. Numerical simulations were implemented on MATLAB R2012a environment and run on a 2.2GHz Intel 8-core processor laptop. Simulated dataset were created in image domain and real datasets were acquired fully-sampled on MRI scanner. Both were then retrospectively under-sampled with a corresponding acceleration rate. The decomposition is computed using algorithm 1 with μ found by empirical study and λ tuned by visual inspection.

5.1 Dynamic phantom

The method is first studied on simulated data. A 2D plus time numerical phantom of size $128 \times 128 \times 40$ is created to mimic three time-varying components in dynamic MRI. In particular, the phantom simulates periodic respiratory motion, periodic local motion and abrupt local changes of intensity.

To our knowledge there is no commonly used method that provides this joint separation and reconstruction procedure. Hence, we test our approach against the zero filling Fourier transform and dynamic MRI acceleration method k-t FOCUSS [9] for the reconstruction stage, followed up by a principal component analysis decomposition for the separation stage. More precisely, the PCA stage is done by taking only the first three principal components to model a component with a low-rank. The difference between reconstructed data and this low-rank component is done to obtain an equivalent of the sparse component of the proposed method. Results in figure 1 show that the suggested approach is able to reconstruct with very good accuracy the original sequence, and provide a more robust decomposition than the classical PCA for time-varying components such as motion and intensity changes. We provide quantitative results in table 1.

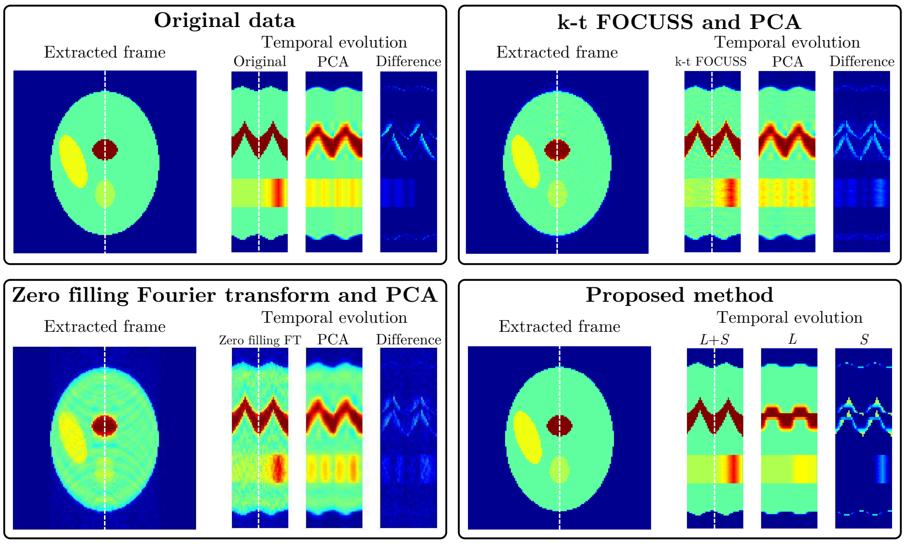

Fig. 1. Dynamic phantom dataset. Original data and different reconstruction methods from partial measurements with a 2-fold acceleration along with PCA decomposition. The sampling scheme used is the one described in section 3. For the proposed method, parameters are set to $\mu = 10$ and $\lambda = 2\max(N, J)^{-1/2}$.

	Zero filling FT	k-t FOCUSS	Proposed method
Reconstruction error	0.1072	0.0449	0.0020
$\|AX - y\|_2^2$	1.5010e-28	0.5869	3.3621e-05
Nuclear norm $\|.\|_*$	291.2141	299.7161	289.1930
Sparsity $\|.\|_1$	1.1675e+04	5.7848e+03	3.5804e+03

Table 1. Quantitative results for phantom reconstruction. Reconstruction error is computed as relative reconstruction error, i.e., $\|\tilde{X} - X\|_2 / \|X\|_2$, where $\tilde{X}$ are reconstructed data.

5.2 In vivo data

Cardiac imaging dataset consists of a cine MRI sequence of the heart with a size of $224 \times 155 \times 50$. The original dataset and its reconstruction/decomposition from partial k-space is presented in figure 2. We tune λ to obtain a rank-1 component, acting as an average of the whole sequence, while completely isolating movement of the heart in the sparse frames. Presentation of these images from this perspective may be useful from a clinical point of view by isolating heart movements that may help detect motion abnormalities.

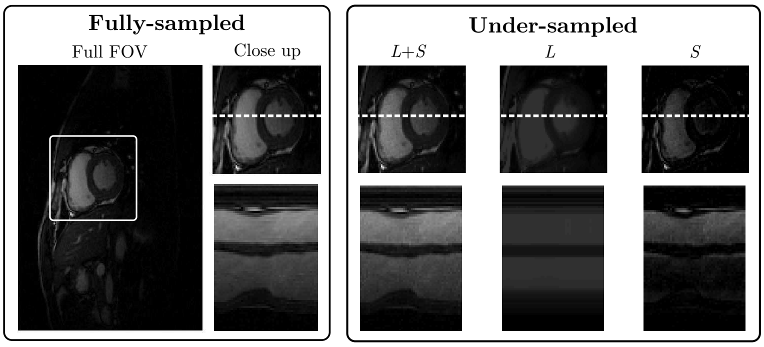

Fig. 2. Cardiac cine MRI dataset. Left figures are fully-sampled data with full field of view, close up and temporal evolution along a dynamic profile (corresponding dashed line). Right figures are reconstructed images from partial measurements. Top figures show specific frame with the separation into low-rank and sparse components. Bottom figures present temporal evolution along corresponding dynamic profiles. Acceleration rate is 2, parameters are set to $\mu = 10$ and $\lambda = \frac{1}{2}\max(N, J)^{-1/2}$. Relative reconstruction error is 0.0792.

In DCE MRI, acquisition of multiple MR images are taken before, during, and after the administration of an MR contrast agent. As in dynamic MRI, artefacts due to patient movements (such as breathing, heartbeat, etc.) can appear during the acquisition. A common approach is to register images to reduce important misalignments. Here, dataset is of size 256 × 256 × 10 with respiratory motion. The decomposition from partial k-space, shown in figure 3, is able to isolate contrast enhancement in the heart through the sparse component. Since the contrast uptake and washout is clearly separated in this decomposition, it has been shown that it could help in the registration of the time frames of the low-rank component to correct for respiration-induced motion [10].

6 Conclusion

We have proposed reconstruction of low-rank and sparse components of dynamic MR data from partial k-space measurements. While providing faster dynamic MR imaging, this method leads to a flexible separation of motion and contrast enhancement that can be exploited in different ways.

More generally, this approach suggests a joint reconstruction model with a clinically-relevant separation process. This is an interesting direction for fur-

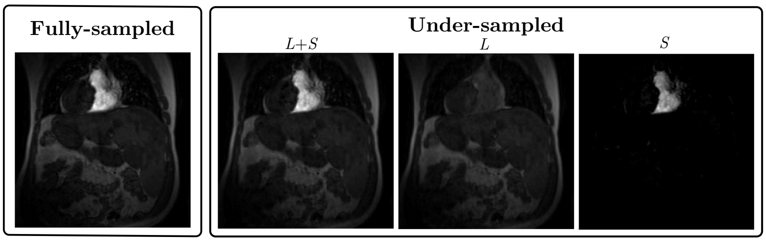

Fig. 3. DCE MRI dataset. Left figure is fully-sampled extracted frame from the sequence. Right figures present extracted frames of under-sampled reconstructed sequence along with low-rank and sparse decomposition. 2-fold acceleration, parameters are set to $\mu = 10$ and $\lambda = 2\max(N, J)^{-1/2}$. Relative reconstruction error is 0.0587.

ther research, where reconstruction models would extract informations related directly to clinically-relevant measures. This might be possible through incorporation of appropriate priors and by targeting specific applications in medicine.

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