Constrained magnetic resonance image reconstruction from incomplete frequency measurements

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CONSTRAINED MAGNETIC RESONANCE IMAGE RECONSTRUCTION FROM INCOMPLETE FREQUENCY MEASUREMENTS

A Thesis

Submitted to the School of Electrical and Electronic Engineering
of the Nanyang Technological University

by

Deng Jun

in Partial Fulfilment of the Requirements
for the Degree of Doctor of Philosophy

December 3, 2014

Statement of Originality

This thesis is submitted to the School of Electrical and Electronic Engineering, College of Engineering, Nanyang Technological University in partial fulfillment of the requirements for the degree of Doctor of Philosophy. I hereby certify that the work embodied in this thesis is the result of original research done by me and has not been submitted for a higher degree to any other University or Institute.

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Date

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Author

*To Dad and Mom,
for their encouragements and love.*

Contents

Abstract	v
Acknowledgments	vii
List of Figures	x
List of Tables	xx
List of Abbreviations	xxi
List of Notation	xxii
1 Introduction	1
1.1 Overview of Magnetic Resonance Imaging	1
1.1.1 Overview of MRI Hardware and Imaging Physics	1
1.1.2 Image Reconstruction and k-space Sampling	5
1.1.3 FOV and Aliasing	6
1.2 Challenges in Practical Applications of MRI and MRI Reconstructions	8
1.3 Thesis Outline	12
2 Orthonormal Expansion ℓ_1-Minimization for MRI Reconstruction	14
2.1 Introduction	14
2.1.1 Compressed Sensing	16
2.2 Sparse Sampling	18
2.3 Preliminary: Soft-thresholding Operator	19

2.4	ONE- ℓ_1 Algorithm	20
2.4.1	Orthonormal Expansion of Measurement Matrix	20
2.4.2	Augmented Lagrangian Multiplier Formalism	20
2.4.3	An Alternating Minimization Method	21
2.5	Experiments and Results	24
2.5.1	Experiment Setup	24
2.5.2	Performance Evaluation	27
2.6	k-t ONE- ℓ_1 : An Accurate and Fast Compressed Sensing Algorithm for Dynamic Cardiac MRI Reconstruction	28
2.6.1	Sparsity of Dynamic Cardiac MR Images	32
2.6.2	Experiments and Results	32
2.6.3	Performance Evaluation	35
2.7	Discussion and Conclusion	37
3	Motion-compensated Orthonormal Expansion ℓ_1-Minimization for Reference- driven MRI Reconstruction Using Augmented Lagrangian Methods	44
3.1	Introduction	44
3.2	Theory	47
3.2.1	Problem Formulation	47
3.2.2	Preliminary: Augmented Lagrangian Method	48
3.2.3	Inter-frame Motion	49
3.2.4	Dynamic Cardiac MRI Reconstruction	50
3.3	Proposed Method	51
3.3.1	The Proposed Model	51
3.3.2	Equivalent Model Conversion	51

3.3.3	Augmented Lagrangian Formalism	53
3.3.4	Alternating Direction Minimization	53
3.3.5	Empirically Improved Proposed Algorithm	56
3.4	Experiments and Results	56
3.4.1	Experiment Setup	56
3.4.2	Implementation Details	58
3.4.3	Performance Evaluation	61
3.5	Discussion and Conclusion	69
3.5.1	Computational Complexity	70
3.5.2	Choice of Parameters	71
3.5.3	Effect of Motion Estimation and Compensation	72
3.5.4	Source of Improvements	73

4 Compressive SEMAC: Reconstruction of MR Images with Metallic Implants by POCS-based Parallel Imaging and Noise 77

4.1	Introduction	77
4.2	Theory	79
4.2.1	SEMAC Overview	79
4.2.2	Sparsity of SEMAC-encoded Slices	84
4.2.3	Compressive SEMAC Sampling	84
4.2.4	Reconstruction of Compressed SEMAC-encoded Slice	85
4.2.5	Combination of Compressive SEMAC-encoded Slices	91
4.3	Experimental Methods	93
4.3.1	SNR Quantification	93
4.3.2	In Vivo Studies	93

4.4	Results	94
4.4.1	SNR Quantification	94
4.4.2	In Vivo Studies	94
4.5	Discussion and Conclusion	96
4.5.1	Compressive SEMAC Sampling	100
4.5.2	Comparisons to Denoising-only Methods	101
5	Conclusion and Future Work	102
	Publication	107
	References	109

Abstract

Prolonged scan time hampers the practical application of Magnetic Resonance Imaging (MRI). Skipping part of the phase encodings reduces scan time while producing reconstruction aliasings. In this thesis, we develop constrained reconstructions methods to reconstruct high quality MR images from down-sampled k-space data by exploiting sparsity of MR images under the theory of Compressed Sensing (CS). CS makes it possible to reconstruct MR images from incomplete k-space data with a constrained ℓ_1 -optimization problem.

To solve the low computational efficiency of ℓ_1 constrained optimization-based methods, in the first work we propose an iterative optimization method. The key idea behind it is to equivalently convert the original ℓ_1 optimization to a convex constrained problem with the help of expanding the measurement matrix to an orthonormal matrix. By doing this, the original problem can be tackled by a joint framework of Augmented Lagrange multipliers (ALM) and alternating direction method (ADM). In-vivo brain and dynamic cardiac studies demonstrate that the proposed method converges faster and provides comparable reconstruction accuracy compared to the commonly used and state-of-the-art optimization techniques.

Reconstruction with prototypical Compressed Sensing can fail when either the number of samples or level of sparsity is insufficient. Meanwhile there are many applications where a reference image is readily available. In the second work, we explore the recon-

struction problem with the help of two constraints: sparsity and prior information from a reference image. A novel method for motion-compensated reference-driven MR image reconstruction is presented. The target image is directly reconstructed by solving a ℓ_1 - ℓ_2 convex minimization problem which prompts ℓ_1 -norm sparsity of the target and the motion-compensated difference images. An efficient algorithm is proposed to solve the minimization problem with joint application of Augmented Lagrangian method and alternating direction minimization method. Numerical experiments demonstrate that the proposed framework provides more accurate reconstructions especially in high undersampling ratios when comparing with commonly used and state-of-the-art methods.

Sparsity constraint has been combined with parallel MRI techniques for better reconstruction performance. In the third work, we focus on a significant practical problem: reconstruction of MR images of parts of the body that have metallic implants. Field inhomogeneity near metallic implants causes severe susceptibility artifacts in MR images, which renders MRI non-diagnostic. A recent imaging technique, SEMAC (Slice Encoding for Metal Artifact Correction), enables full correction of metal-induced artifacts by augmenting a spin-echo (SE) view-angle-tilting (VAT) sequence with phase encodings in z direction. However, there are two main problems hampering the clinical utility of SEMAC, namely prolonged scan time and relatively low signal-to-noise ratio (SNR). To address both problems, the second work incorporates SEMAC with recent advances in CS and parallel imaging (PI). We propose a projection on convex set (POCS) technique in which the reconstruction of a down-sampled SEMAC-encoded slice alternates between sequential in-plane PI reconstruction at each k_z location and joint noise suppression across multiple coils. Phantom and in-vivo results show that the proposed method not only greatly reduces scan time incurred to fully correct metal artifacts but also leads to the improved SNR of SEMAC-corrected results.

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List of Figures

1.1	Comparison between CT and MRI in visualizing brain tumors: a) only one tumor (pointed out with arrow) is detected in the CT scan; b) two tumors are detected in the MRI scan.	2
1.2	Demonstration of spin precessing under static magnetic field B_0 and the effect of radio frequency pulse B_1 . Under B_0 all spins precess with Larmor frequency and produce a net magnetization M in alignment of B_0 . A radio frequency (RF) pulse with magnetic field strength B_1 is applied, which tilts the magnetization away from the longitudinal direction, generating a net transverse magnetization M_{xy}	3
1.3	Demonstration of k-space sampling and image reconstruction.	6
1.4	Demonstration of aliasing caused by k-space down-sampling. a) fully sampled k-space; b) MR image reconstructed from a); c) half k_y sampled k-space; d) MR image reconstructed from c).	7

1.5	Connection and continuity of the three works presented in this thesis. Outside the dotted box are three constraints of interest in this thesis. Sparsity threads together the three works. Work 1 considers sparsity constraint only while Work 2 and Work 3 explore extra constraints to improve reconstruction performance. Work 2 improves the performance in Work 1 and Work 1 is essentially the noise suppression step in Work 3.	12
2.1	Regular Cartesian sampling results in coherent overlying of images which are supposed to be lying in neighboring field of view. Random sampling causes interference to be incoherent and noise like.	19
2.2	Comparison of reconstruction results given 5 seconds running time. a) and b) are ground-truth for test 1 and test 2, respectively. d) and g), e) and h), f) and i) are reconstructed results from the proposed method, IST and NCG, respectively; c) shows radial sampling pattern in our tests — 24 equally spaced radial lines, which corresponds to approximate 10 times acceleration (90% undersampling).	25
2.3	Comparison of convergence rate for test 2. To arrive at a relative distance of 10^{-10} , the proposed method used 18 seconds while IST used 172 seconds and NCG used as much as 2083 seconds.	28
2.4	Comparison of reconstruction accuracy for test 1, given sufficient time to converge to the final solution. Reconstruction accuracy was exhibited in a function of acceleration factors.	29
2.5	Comparison of reconstruction accuracy for test 2, given sufficient time to converge to the final solution. Reconstruction accuracy was exhibited in a function of acceleration factors.	29

2.6	Diagrammatic exhibition of transformational relation of $\mathbf{x}$, $\mathbf{b}$, $\mathcal{F}_\Omega$ and Ψ . The purple cube on the left represents dynamic images that we desire; the right top black cube represents k-t measurements $\mathbf{b}$, where orange dots represent sampled locations while others black area represent unsampled locations; the right bottom blue cube is the sparse coefficients cube; the central top and bottom dashed box represent $\mathcal{F}_\Omega$ and Ψ , respectively. . .	31
2.7	Spatial-temporal sparsity in dynamic cardiac MR images: a) shows three image frames selected from one image sequence comprised of 25 image frames, with different phases of one same heart being outlined with dotted boxes; b) shows temporal sparsity by taking one-dimensional Fourier transform along temporal direction.	33
2.8	Sampling pattern utilized: fully-sampled k-t space data was decimated to a desired sampling pattern. At each k_x location, we undersampled $k_y - t$ domain using a random 2D Cartesian sampling mask with densely sampling central area and random sparsely sampling in the other areas. .	34
2.9	Comparison of reconstruction results using 20% of full k-t space data at $t = 15$ temporal point: A region of interest (ROI) was zoomed in and is shown on the top right corner. Difference images constructed by subtracting ROI of each method from the original ROI were shown. It can be seen that k-t FOCUSS had more structured contents in its difference images as indicated by the white arrows, which implied loss of information in the reconstructed images. Structured noise as shown in difference images of k-t FOCUSS were significantly reduced in results of k-t SPARSE and k-t ONE- ℓ_1	37

2.10	Comparison of reconstruction results using 20% of full k-t space data at $t = 25$ temporal point: A region of interest (ROI) was zoomed in and is shown on the top right corner of each reconstructed image. Difference images constructed by subtracting ROI of each method from the original ROI were shown. It can be seen that k-t FOCUSS had more structured contents in its difference images as indicated by the white arrows, which implied loss of information in the reconstructed images. Structured noise as shown in difference images of k-t FOCUSS were significantly reduced in results of k-t SPARSE and k-t ONE- ℓ_1	38
2.11	Comparison of reconstruction results by the three methods in $y - t$ plain at $x = 128$ and $x = 140$. Difference images constructed by subtracting reconstructed images of each method from the original are shown. Compared to k-t SPARSE and k-t ONE- ℓ_1 , k-t FOCUSS failed to follow the temporal variations in certain regions as pointed out by the red arrows.	39
2.12	Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 4$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.	40
2.13	Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 8$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.	41

2.14	Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 10$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.	42
2.15	regularized mean squared errors (RMSE) of the three methods for a range of acceleration factors. It can be seen that k-t SPARSE and k-t ONE- ℓ_1 provided comparable RMSE while k-t FOCUSS provided higher RMSE in our experiments.	43
3.1	Exhibition of target and reference images for general phantom and in-vivo MR brain image. First column from top to bottom: reference phantom image, target phantom image, difference image of reference and target images without motion compensation, difference image with motion compensation. Second column from top to bottom: reference in-vivo image, target in-vivo image, difference image without motion compensation, difference image with motion compensation. Third column: sampling pattern comprised of 24 equally spaced radial lines which corresponds to approximate 10 times acceleration (90% undersampling).	59
3.2	Exhibition of reference image and one sample target for in-vivo cardiac MR images. Sampling mask in k_y - t domain is shown on the right: fully-sampled central regions and random sparsely sampled in other regions . .	60

3.3	Comparisons of phantom brain reconstructions from 5% of full-sampled k-space data. Top: a) and d) by SparseMRI; b) and e) by SparseMRINC; c) and f) by Proposed. Bottom: one-dimensional line profile across red dotted arrow line. d), e) and f) are difference images of each method constructed by subtracting reconstructed images from ground-truth. Red arrows indicate remaining presence of feature displacements from reference image. Dotted white circles highlight reconstruction artefacts in the reconstructed image.	62
3.4	Comparisons of in-vivo brain reconstructions from 10% of full-sampled k-space data. Top: a) and d) by SparseMRI; b) and e) by SparseMRINC; c) and f) by Proposed. Bottom: one-dimensional line profile across red dotted arrow line. d), e) and f) are difference images of each method constructed by subtracting reconstructed images from ground-truth. Red arrows indicate remaining presence of feature displacements from reference image.	64
3.5	Quantitative comparisons of phantom (top) and in-vivo (bottom) brain reconstructions for a range of acceleration factors.	65

3.6	Comparison of cardiac cine reconstructions from 10% of full k-t space data: sample ROI reconstructions in spatial x - y domain. First column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 1$ time point. Second column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 17$ time point. Third column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 24$ time point. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructed images. Red arrows indicate remained aliasing. Structured “noise” in difference images imply either undesirable aliasing or loss of essential details.	66
3.7	Comparison of cardiac cine reconstructions from 10% of full k-t space data: sample ROI reconstructions in spatial-temporal y - t domain. Left: sample ground-truth at $x = 120, 128, 150$ spatial positions. Right-first column (top-to-bottom): k-t Sparse, k-t FOCUSS-MEMC, and the proposed at $x = 120$. Right-second column (top-to-bottom): k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $x = 128$. Right-third column (top-to-bottom): k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $x = 150$. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructions. Solid red arrows indicate undesirable remained aliasings. Dotted white arrows point out places where temporal variations were flattened.	67
3.8	Quantitative comparison of cardiac cine reconstructions for a range of acceleration factors.	68

3.9	Exhibition of effect of motion estimation and compensation on the proposed method. From left to right of the top, reconstructions from $\times 20$ accelerated data by SparseMRINC, ProposedNC and Proposed respectively are shown. Quantitative comparison from a range of acceleration factors is shown in the bottom.	74
3.10	Exhibition of effect of motion estimation and compensation on SparseMRINC. Reconstuction from (a) SparseMRINC, (b) SparseMRIMEMC, (c) Proposed2 are shown.	75
4.1	Frequency-position mapping exhibit: in the absence of filed inhomogeneity, precession frequency of one excited spin and its spatial location is linearly mutually mapped (dotted line). When field inhomogeneity (dashed line) exists, the mapping becomes non-linear (solid curve) causing through-plane (in-plane) displacement (dark grey regions) and through-plane (in-plane) pile-ups (light grey regions).	81
4.2	Exhibition of SEMAC technique. (a) imaging sequence of SEMAC; (b) steps of corrections of through-plane distortions. During the image acquisition stage, distorted excitation profiles of each slice are resolved with extra slice direction encodings. In the image reconstruction stage, resolved spins from all slices in one certain voxel are combined together to correct the through-plane distortions in that voxel.	83
4.3	Sample SEMAC-encoded distorted excitation profiles in y - z plane. The image is highly sparse: only a few large-magnitude elements while most areas only contains background noise.	85

4.4	Center-filled Poisson sampling pattern. Top: three-dimensional down-sampling with a center-filled Poisson disk on k_y - k_z plane at each k_x direction. Bottom: sample subsequently formed sampling pattern on k_x - k_y plane. Pictures have been resized for better rendering.	86
4.5	Calculation of the synthesizing weight of each coil. Left corresponds to $\mathbf{x}_i$ in Eq. 4.4. Middle matrix represents neighbouring measurements of $\mathbf{x}_i$. Right corresponds to the weights of interest. Values of the synthesizing weights could be obtained by solving the over-determined system.	88
4.6	Flowchart of the reconstruction process of the proposed method. The full-sampled k-space data is first under-sampled by the carefully designed sampling pattern. Reconstruction of under-sampled k-space iterates between parallel MRI reconstruction at each k_z position in k-space domain and noise suppression in the image domain	92
4.7	Comparison of sample phantom SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b) reconstruction in x - y plane by Compressive SEAMC, (d) reconstruction in x - y plane by CS-SEMAC, (d) reconstruction in reformatted cross-sectional y - z plane by Compressive SEMAC, (e) reconstruction in reformatted cross-sectional y - z plane by C-SEMAC, (f,g,h,i) difference images constructed by subtracting reconstructed images above from corresponding ground-truth images. A dashed-box in (a) indicates an uniform region for SNR quantification. The most right shows the titanium shoulder prosthesis used in the phantom study.	95
4.8	Comparison of a typical view of SEMAC-encoded slices in x - z and x - y planes: (a) standard SEMAC, (b) CS-SEMAC, and (c) Compressive SEMAC.	97

4.9	Comparison of sample in-vivo knee SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b)reconstruction in x - y plane by Compressive SEAMC, (d) reconstruction in x - y plane by CS-SEMAC, (c) and (e) difference images constructed by subtracting reconstructed images on their left from (a). White arrows in (d) and (e) point out regions where CS-SEMAC encounters noticeable loss of image details.	98
4.10	Comparison of sample in-vivo spine SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b)reconstruction in x - y plane by Compressive SEAMC, (d) reconstruction in x - y plane by CS-SEMAC, (c) and (e) difference images constructed by subtracting reconstructed images on their left from (a).	99
5.1	Approximation to absolute sparsity prior: smaller p brings about better approximation	105

List of Tables

2.1	Comparison of CPU time of each iteration	24
2.2	Comparison of k-t ONE- ℓ_1 with state-of-the-art methods.	36
3.1	Comparison of performance given different sets of parameters	72

Abbreviation

ADM	Alternating Direction Method
ALM	Augmented Lagrangian Multiplier
BPDN	Basis Pursuit Denoising
CoSaMP	Compressive Sampling Matching Pursuit
CS	Compressed Sensing
CT	Computed Tomography
DFT	Discrete Fourier Transform
FOV	Field of View
GRAPPA	Generalized Autocalibrating Partially Parallel Acquisitions
IST	Iterative Soft-Thresholding
MC	Motion Compensation
ME	Motion Estimation
MRI	Magnetic Resonance Imaging
NCG	Non-linear Conjugate Gradient
OMP	Orthogonal Matching Pursuit
ONE	OrthoNormal Expansion
POCS	Projection onto Convex Sets
RF	Radio Frequency
RMSE	Regularized Mean Square Error
ROI	Region of Interest
SE	Spin Echoes
SEMAC	Sensitivity Encoding for Metal Artefacts Correction
SENSE	Sensitivity Encoding for Fast MRI
SPIRIT	Iterative Self-consistent Parallel Imaging Reconstruction
TV	Total Variation (Transform)
VAT	View Angle Tilting

List of Notation

$(\cdot)'$	Matrix or vector conjugate transpose
$\langle \mathbf{x}, \mathbf{y} \rangle$	Inner product of two vectors $\mathbf{x}$ and $\mathbf{y}$
$\ \mathbf{x} - \mathbf{y}\ _0$	ℓ_0 quasi-norm or Number of non-zero elements in the support of the difference between $\mathbf{x}$ and $\mathbf{y}$
$\ \mathbf{x} - \mathbf{y}\ _1$	ℓ_1 norm or sum of absolute value of the difference between $\mathbf{x}$ and $\mathbf{y}$
$\ \mathbf{x} - \mathbf{y}\ _2$	ℓ_2 norm or Euclidian distance between $\mathbf{x}$ and $\mathbf{y}$
$S_\lambda(\mathbf{x})$	Element-wise soft thresholding operation on $\mathbf{x}$ with a threshold value λ .

Chapter 1

Introduction

1.1 Overview of Magnetic Resonance Imaging

MRI is a widely used medical imaging modality to see the inside of a human body in a clinic. The mechanism in which MRI works is completely different from that of computed tomography (CT) X-ray in terms of physics. The radiation of a standard CT scan passes through the human body. The signal is received and processed by a computer to obtain a cross sectional image. An MRI, on the contrary, makes use of a magnetic field and radio wave. Wire coils receive signal discharged due to microscopic transitions from one energy level to another. Images are obtained by taking the Fourier transform of the signal received.

Among many advantages of MRI over CT, the most significant is MRI provides excellent soft tissue contrast, as illustrated in Fig. 1.1. In Fig. 1.1, the same part of a patient's brain was scanned by both CT (Fig. 1.1a) and MRI (Fig. 1.1b).

1.1.1 Overview of MRI Hardware and Imaging Physics

A standard MRI scanner mainly consists of three components, the magnet, the radio frequency coil and the gradient magnets. The magnet, known as the most important component of an MRI machine, provides a powerful static magnetic field. Gradient

Figure 1.1: Comparison between CT and MRI in visualizing brain tumors: a) only one tumor (pointed out with arrow) is detected in the CT scan; b) two tumors are detected in the MRI scan.

magnets which gives magnetic field of much smaller magnitude create a variable magnetic field to allow scanning of different parts of the body. The radio frequency coil transmits radio frequency waves of a carefully-calculated range, which select layers of the body to be imaged via “resonance” with the so-called Larmor frequency, with which atoms precess under the magnetic environment established by the magnet and the gradient magnets.

An MRI machine obtains the image of the selected parts of the patient through a sophisticated physical process. To understand the physics of MRI, we first have to know what is a spin. Some atoms have an odd number of protons and/or neutrons, and when putting in an external magnetic field, those nucleons will precess along the magnetic field with a prescribed angle like a spinning top does in the gravitational field. Those nucleons are so called spins. MRI normally uses ^1H nuclei (protons) as the spin of choice due to the biological abundance of hydrogen in human body and high sensitivity of the proton towards the external magnetic field. Every ^1H proton itself is viewed as a microscopic magnet. Suppose we have an external static magnetic field B_0 , this static magnetic

field would polarize the spins as demonstrated in Fig.1.2. On the transverse plane, the magnetization cancel each other; while in the longitude direction, there are slightly more parallel precessing spins than anti-parallel precessing ones, thus generating a net magnetization with strength M aligned to B_0 . The spins would precess at a frequency called Larmor frequency which is equal to $\gamma \times B_0$ where γ is a prescribed proportionality constant which depends on the kind of nucleus and the chemical environment of the nucleus.

Figure 1.2: Demonstration of spin precession under static magnetic field B_0 and the effect of radio frequency pulse B_1 . Under B_0 all spins precess with Larmor frequency and produce a net magnetization M in alignment of B_0 . A radio frequency (RF) pulse with magnetic field strength B_1 is applied, which tilts the magnetization away from the longitudinal direction, generating a net transverse magnetization M_{xy} .

This equilibrium will be on until a radio frequency (RF) pulse with magnetic field strength B_1 tuned to the Larmor frequency is applied to excite the spins of interest. This B_1 effectively applies a torque to rotate the longitudinal M by a prescribed angle dependent on the strength of B_1 and its application duration. The tilted net magnetization will have a transverse component denoted as M_{xy} . The magnetization would return back to equilibrium. According to Faraday's law of induction, an electromotive force will be

produced and can be collected with the same coils for emitting the RF pulse. This time series signal is known as FID (free induction decay). Each time of excitation we are able to collect one time series signal or one view.

The transverse magnetization M_{xy} can present many different physical properties of the tissue. In this work, we only discuss M_{xy} as the proton density. Other properties such as longitudinal magnetization recovery time T_1 and transverse magnetization decay time T_2 are not our focus in this thesis. In other words, the imaging objective is to obtain the spatial distribution of M_{xy} .

The third indispensable component of an MRI scanner are gradients magnets. After the superposition of a multi-dimensional gradient fields, the precessing frequency of certain spin at position $\mathbf{r} = (\mathbf{x}, \mathbf{y}, \mathbf{z})$ will be

$$w(\mathbf{r}) = \gamma \cdot (B_0 + \mathbf{x} \cdot \mathbf{G}_x + \mathbf{y} \cdot \mathbf{G}_y + \mathbf{z} \cdot \mathbf{G}_z) \quad (1.1)$$

As a matter of fact, spins with distinctive spatial locations and their precessing Larmor frequency are unambiguously one-to-one mapped. All spins now emit electronic magnetic radiation that the RF receiver can detect with a frequency corresponding to their spatial positions and intensity proportional to the proton density. The signal received at any given time is a mixture of harmonic oscillations with different frequencies (decided by its spatial positions) and magnitudes. Thus, taking a Fourier transform of the signal received, we have the MRI image of interest. We have the following mathematical expression of the relationship between the raw signal $S(k_x, k_y, k_z)$ and the MRI image to be reconstructed $M(x, y, z)$.

$$S(k_x, k_y, k_z) = \iiint M(x, y, z) e^{-i2\pi(k_x \cdot x + k_y \cdot y + k_z \cdot z)} dx dy dz, \quad (1.2)$$

where (k_x, k_y, k_z) are the coordinates of raw signal space, known as k-space. The changing transverse magnetization which is the source of the signal measured in MRI is a vector that is described by the complex quantity $e^{-iw(\mathbf{r}) \cdot t}$. This quadrature detection results in two data streams with a 90° phase difference. The digitised values from these signals become the real part and the imaginary part of the k-space. By taking a Fourier transform of the complex k-space data, the MRI image reconstructed will be also complex. Therefore, reconstructions must be appropriate for complex data.

1.1.2 Image Reconstruction and k-space Sampling

Thus far, the k-space we are discussing is continuous but in practice, they are sampled as shown in Fig. 1.3. For the sake of simplicity, herewith we consider two-dimensional MRI problems and we denote (k_x, k_y) , in place of $(k_x(t), k_y(t))$, as a particular spatial frequency in k-space. Sampled k-space data $\tilde{S}(k_x, k_y)$ is expressed as

$$\tilde{S}(k_x, k_y) = S(k_x, k_y) \cdot \sum_{m,n=-\infty}^{m,n=+\infty} \delta(k_x - m\Delta k_x, k_y - n\Delta k_y) \quad (1.3)$$

where Δk_x and Δk_y are sampling intervals along k_x and k_y direction, respectively; $\delta(x, y)$ is a 2D sampling function which satisfies

$$\delta(x, y) = \begin{cases} 1 & x = 0, y = 0 \\ 0 & \text{others} \end{cases}$$

Sampling in k-space amounts to periodic repetition in image domain. By taking 2D discrete Fourier transform of $\tilde{S}(k_x, k_y)$, in image domain, we have

$$\widetilde{M}_{10}(x, y) = \left(\frac{1}{\Delta k_x \Delta k_y} \right) \sum_{m,n=-\infty}^{m,n=+\infty} M_{10}\left(x - \frac{m}{\Delta k_x}, y - \frac{n}{\Delta k_y}\right) \quad (1.4)$$

Note $M_{10}(x, y)$ is the original MR image, shown as the central image constrained within $(\text{FOV}_x, \text{FOV}_y)$ in Fig. 1.3. The reason why no one under-samples in the read direction,

is in practice it is very challenging to move from one readout position to another without passing through the intervening positions. Therefore, under-sampling is not performed in the frequency encoding direction but only phase-encoding directions.

Figure 1.3: Demonstration of k-space sampling and image reconstruction.

1.1.3 FOV and Aliasing

Field of view (FOV) is a very important notion in k-space sampling and MRI analysis. For an effective MRI scan, FOV should be larger than the size of the object of interest. FOV relates to sampling intervals in k-space as

$$\begin{aligned} \text{FOV}_x &= \frac{1}{\Delta k_x} = \text{sampling rate along } k_x \\ \text{FOV}_y &= \frac{1}{\Delta k_y} = \text{sampling rate along } k_y \end{aligned} \tag{1.5}$$

Figure 1.4: Demonstration of aliasing caused by k-space down-sampling. a) fully sampled k-space; b) MR image reconstructed from a); c) half k_y sampled k-space; d) MR image reconstructed from c).

Eq. (1.3) and Eq. (1.5) reveal that FOV is a measurement of the distance between two adjacent reconstructed images as shown in Fig. 1.3. It follows that an insufficiently large FOV due to large sampling intervals (fewer k-space samples) causes aliasing in the form of overlapping of adjacent images. Fig. 1.4 shows the aliasing incurred when FOV_y (k-space samples along k_y) decreases by half. This phenomenon seems to be a

paradox: on the one hand, acquiring fewer k-space samples reduces the scan time; on the other hand, aliasing arises when k-space samples are insufficient. The following three chapters discuss efficient algorithms posed to reconstruct MR images from down-sampled frequency measurements.

1.2 Challenges in Practical Applications of MRI and MRI Reconstructions

Prolonged scan time hampers the practical utility of MRI. Lying still in the machine tube in a noisy environment for long makes the patients uncomfortable, and even causes fear or recalls psychic trauma in serious cases. Any severe motions during the scan can render obtained MR images non-diagnostic. Early stage of effort to reduce scan time mainly relied on fast data collection by utilizing fast imaging sequences, increased gradient magnitude or strengthened slew rates (rates of changes of gradients) or combinations thereof. However, those techniques are limited by physical and physiological constraints as there is a limit that normal human being is not able to endure in a magnetic environment [1–6].

In a very intuitive manner, the scan time is proportional to the number of phase encodings collected. It is very natural to think of the idea that collecting less data will accordingly reduce the scan time. Nonetheless, from the perspective of signal processing, increased sampling interval in the frequency domain causes repetitions of the original image to overlay with their neighbours. Successful reconstruction is impossible unless there is other prior information available to fill up the lost information carried by the un-sampled k-space data. Those methods that take advantage of any prior information to complement the loss of information are known as constrained reconstruction methods [7, 8]. In Liang’s review paper [7], constrained methods were classified into four kinds: they are Fourier reconstruction methods, phase-constrained methods, non-parametric

constrained methods and parametric modelling methods. In this thesis, we develop constrained MRI reconstruction methods and we have our focus on three sources of prior information: sparsity, coil sensitivity and prior information from a reference image.

Coil Sensitivity

There is one significant category of MRI reconstruction methods: parallel MRI methods which reconstruct MR images by incorporating prior information from inherent correlation between k-space data or images across coils. In parallel MRI, a signal is received with multiple coils carefully designed and located around the part of body to be scanned. An individual image received by each coil is the same original image after being modulated with different sensitivity maps; therefore individual images received are related to each other in certain mathematically solvable way. Alike the existence of correlation in the image domain, k-space measurements within a neighbouring area across coils are also correlated, and theoretically the value of one location can be linearly expressed by its neighbouring locations across coils. The most popular parallel MRI methods are SMASH [9, 10], SENSE [11] and GRAPPA [12, 13]. There are also other parallel MRI techniques among which the most well-known methods are AUTO-SMASH [14], PILS [15], SPACE RIP [16], VD-AUTO-SMASH [17], Generalized SMASH [18] and POCSENSE [19]. SENSE, SMASH and methods derived based on them are image-based reconstruction methods in the sense that reconstruction is performed in image space. GRAPPA, PILS and methods derived based on them are data-based reconstruction in the sense that reconstruction is based on the correlation of the k-space data. Those methods usually require the sampling pattern to be regular Cartesian. There are advanced parallel MRI reconstruction methods that are able to reconstruct MR images from arbitrary sampling patterns such as KSPA [20], PRUNO [21] and SPIRiT [22].

Sparsity

Compressed sensing theory states that under certain conditions with sufficient samples, it is highly possible that a sparse signal can be exactly recovered from incomplete measurements [23–27]. Sparsity is the key to the successful reconstruction. The advent of CS has advanced the development of fast MRI to a revolutionary height. CS has been applied to MRI reconstruction and enables reasonable reconstruction of MR images from only a small fraction of k-space samples by exploiting the sparsity or compressibility of the MR images [24, 28–37]. In standard CS-MRI reconstruction methods, the sparsity prior represents itself with the ℓ_1 norm of the sparse coefficients in certain sparsifying domain. Successful reconstruction is achieved by prompting the sparsest solution while complying with other constraints such as data fidelity condition.

Prior Information from a Reference

In some applications such as interventional MRI, longitudinal MRI and dynamic cardiac MRI, a pre-scanned reference image can be readily obtained. By taking advantage of prior information from the reference image which shares anatomical similarity with the target image to be reconstructed, many research works have shown that reconstruction can be greatly improved [38–48]. Previous works generally fall into two categories: the first is to break the reconstruction into two steps — first reconstruct the residual image, and then linearly combine the reconstructed residual image and the reference image (with or without motion compensation) to obtain the target image [39–42]; the other category is to directly reconstruct on the target image by restricting the solution space with various constraints such as sparsity constraint, support constraint or energy distribution constraint that incorporate prior information from the reference image [43, 44].

In our first work, we consider the sparsity-only constraint and make improvements to

the existing sparsity-only-constrained MRI reconstruction methods. A novel iterative algorithm, dubbed as “ONE- ℓ_1 ”, for CS in MRI reconstruction is presented. The proposed method is accurate, computationally efficient and converges quickly. In-vivo brain and cardiac cine studies demonstrate that the proposed method converges faster and provides reconstruction accuracy comparable to commonly used and state-of-the-art optimization techniques.

Sparsity-only-constrained methods could fail in cases when there are insufficient samples or the sparsity level is low. In the second work, we explore the reconstruction by integrating sparsity constraint with prior information from a reference. Numerical experiments demonstrate that the proposed framework provides more accurate reconstructions especially in high undersampling ratios compared to commonly used and state-of-the-art methods.

In the third work, sparsity constraint has been combined with coil sensitivity for better reconstruction performance. We focus on a significant practical problem: reconstruction of MR images of parts of the body that have metallic implants. Field inhomogeneity near metallic implants causes severe susceptibility artifacts in MR images, which renders MRI non-diagnostic. We propose a projection on convex set (POCS) technique in which the reconstruction alternates between in-plane parallel MRI reconstruction and joint noise suppression using sparsity constraint across multiple coils. Phantom and in-vivo results show that the proposed method not only greatly reduces scan time incurred to fully correct metal artifacts but also leads to the improved signal-to-noise ratio (SNR) of existing state-of-the-art methods.

To sum up, in this thesis we develop constrained MRI reconstruction methods to reconstruct high-quality MR images from incomplete frequency measurements. Sparsity constraint is the theme of our thesis, and it threads together the three works presented.

The second work complements the first work with better reconstruction performance by introducing one more prior information constraint from a reference image. The third work complements the first work by introducing extra prior information from coil sensitivity with a specific challenging application. Fig. 1.5 delineates the continuity and connection of the three works with a flow chart.

Figure 1.5: Connection and continuity of the three works presented in this thesis. Outside the dotted box are three constraints of interest in this thesis. Sparsity threads together the three works. Work 1 considers sparsity constraint only while Work 2 and Work 3 explore extra constraints to improve reconstruction performance. Work 2 improves the performance in Work 1 and Work 1 is essentially the noise suppression step in Work 3.

1.3 Thesis Outline

The remaining of this report is organized as follows:

Chapter 2 presents the first work, “Orthonormal Expansion ℓ_1 Minimization for Compressed Sensing in MRI”. We propose an iterative optimization technique to efficiently solve the prototypical CS-based method in MRI reconstruction.

Chapter 3 describes the second work: MRI reconstruction in the presence of a reference image. A novel method for motion-compensated reference-driven MR image reconstruction is presented.

Chapter 4 is devoted to our third work. In this work, Sparsity constraint has been combined with parallel MRI techniques for better reconstruction performance. We focus on a significant practical problem: reconstruction of MR images of parts of the body that have metallic implants.

Chapter 5 gives a conclusion of the works done and provides some insights to possible future work.

Chapter 2

Orthonormal Expansion ℓ_1 -Minimization for MRI Reconstruction

2.1 Introduction

Magnetic Resonance Imaging (MRI) is a very commonly-used imaging modality in clinical practice because of its superior soft-tissue contrast and absence of ionizing radiation. However, in practical applications, the utility of MRI is hampered by the long scanning time. Staying in a noisy environment for a long time can cause patients uncomfortable. Meanwhile any movements incurred during imaging might render the obtained MR images non-diagnostic with motion artefacts. Attempts to reduce imaging time by utilizing fast imaging sequences, increased gradient magnitude or strengthened slew rates (rates of changes of gradients) or combinations thereof is limited by physical and physiological constraints [1–6]. From signal processing perspective of view, scanning time is proportional to the number of acquired data-space samples (k-space). Therefore, imaging process can be accelerated by skipping portion of k-space samples. Seeking for methods to reduce the scan time without degrading the image quality becomes the top issue in the MRI community.

After collecting fewer samples, we have the following under-determined problem:

$$\mathbf{b} = \mathcal{F}_\Omega \mathbf{x} \quad (2.1)$$

where $\mathbf{x} \in \mathbb{C}^N$ is the vectorized MR image to be reconstructed and $\mathbf{b} \in \mathbb{C}^n$, $n < N$ contains the vectorized measurements. $\mathcal{F}_\Omega$ is the partial Fourier transform corresponding to under-sampling the Fourier coefficients of $\mathbf{x}$ (*i.e.*, k-space) according to the sampling index set Ω .

It is impossible to have a unique solution for $\mathbf{x}$ unless certain prior information is imposed on the problem to constrain the solution space. One prior information often taken advantage of is the “minimum energy”, which states that a unique $\mathbf{x}$ can be derived from the following constrained problem:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \{\|\mathbf{x}\|_2 : \mathcal{F}_\Omega \mathbf{x} = \mathbf{b}\}, \quad (2.2)$$

Solving Eq. (2.2) corresponds to letting values in those un-sampled locations be zero, followed by taking an inverse Fourier Transform to the zero-padded k-space. The obtained image will suffer from severe aliasing.

Another powerful prior information is the sparsity information of MR images. It's noted that most MR images have sparse representations under certain sparsifying transforms, *e.g.*, discrete cosine transform (DCT), wavelet transforms of various basis [49–51], curvelet transform [52], total variational transform (TV) [28, 53–56]. In strict sense, a K-sparse signal is the one with only K non-zero elements in its support. Under sparsity constraint, a unique solution can be theoretically derived by seeking for the sparsest solution while adhering to the data consistency:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \{\|\Psi \mathbf{x}\|_0 : \mathcal{F}_\Omega \mathbf{x} = \mathbf{b}\}, \quad (2.3)$$

where the ℓ_0 quasi-norm returns the cardinality of the support of the operand and Ψ is the sparsifying transform. However, solving (2.3) can be challenging because it leads to a non-convex problem.

2.1.1 Compressed Sensing

Compressed sensing theory states that under certain conditions, the above impractical ℓ_0 quasi-norm problem can be approximated with solvable ℓ_1 norm problem at the cost of a certain degree of over-sampling [23–27, 57, 58]. With a sufficient number of samples, it is highly possible that certain sparse signals can be exactly recovered from a small number of measurements. By exploiting the implicit sparsity of MR images, CS has been found with successful application in the reconstruction of MR images from incomplete frequency measurements [24, 28–37], thus reducing the scan time to a large extent. The basic formulation for CS reconstruction in MRI is known as a basis pursuit denoising (BPDN) problem as follows:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \{ \|\Psi \mathbf{x}\|_1 : \mathcal{F}_{\Omega} \mathbf{x} = \mathbf{b} \}, \quad (2.4)$$

By selecting a proper positive regularization parameter μ , (2.4) can be formulated into the following unconstrained form, both of which lead to the same solution [59]:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \|\Psi \mathbf{x}\|_1 + \frac{\mu}{2} \|\mathcal{F}_{\Omega} \mathbf{x} - \mathbf{b}\|_2^2. \quad (2.5)$$

Existing linear programming algorithms to accurately solve Eq. (2.5), such as conjugate gradient method (NCG) [29], interior point method [60, 61] and fixed point method [62] suffer from burdensome computational complexity and slow convergence rate, especially when dealing with MR images of a large size [35, 63]. There are a few methods being proposed to improve the computational complexity performance of the aforementioned methods but at the cost of reconstruction accuracy [63, 64].

One category of algorithms to tackle (2.4) is the greedy-based algorithms which identify one or multiple sparsifying basis in each step and accordingly update support of the solution, such as OMP [65], Stage-wise OMP [66] and CoSaMP [67]. However greedy algorithms are less preferable than convex optimization methods aforementioned in terms of reconstruction accuracy, especially in the recovery of noise-contaminated signal.

On the other hand, there are many fast iterative algorithms [62, 64, 68–71] being proposed to efficiently solve (2.4). A popular algorithm is iterative soft thresholding (IST) method, well known for its low computational complexity as in the following form:

$$\mathbf{x}_{t+1} = \mathbf{S}_\lambda \left(\mathbf{x}_t + \Psi F_\Omega' \mathbf{z}_t \right), \quad \mathbf{z}_t = \mathbf{b} - F_\Omega \Psi' \mathbf{x}_t, \quad (2.6)$$

where S_λ is a soft-thresholding operator with a threshold λ and $'$ denotes the transpose operator. Although fast iterative algorithms are favoured because of their low computational complexity, few of them can have the same sparsity-undersampling tradeoff as convex optimization algorithms [63]. Note “ $\mathbf{x}$ ” in (2.6) and the rest of the chapter denote vectorized sparse representation of the image of interest.

In this chapter, we present a computationally efficient iterative algorithm for MRI reconstruction in the framework of CS. The proposed algorithm is optimal from the perspective of CS. The key idea behind the proposed method is to equivalently transfer the original ℓ_1 optimization in (2.4) into a convex constrained problem with the help of expanding the measurement matrix to an orthonormal matrix. By doing this, the original problem can be solved by a joint framework of Augmented Lagrange multipliers (ALM) and alternating direction method (ADM). The efficacy of the proposed method, dubbed as ONE – ℓ_1 , is demonstrated by comparing with NCG and IST methods, with both simulated and in-vivo MRI studies which demonstrate that the proposed method converges faster and provides comparable reconstruction accuracy compared to the commonly used

and state-of-the-art optimization techniques.

Section 2 and Section 3 introduce sparse sampling and soft-thresholding operator, respectively. Section 4 describes the $ONE - \ell_1$ algorithm for MRI reconstruction; Section 5 demonstrates the efficacy of the proposed method with simulated and in-vivo MRI brain studies. Section 6 explores our core algorithm to dynamic cardiac MRI reconstruction. A discussion and conclusion is drawn in Section 7.

2.2 Sparse Sampling

Two elements of successful application of Compressed Sensing are sparsity and incoherence. The incoherence requirement states that sparse sampling in the sampling domain should render incoherent interference in the sparse domain [23, 24]. This interference could be quantitatively measured with point spread function (PSF) [29] which calculates the contribution of a unit-intensity pixel to other pixels under certain sampling pattern. A small PSF value indicates low coherence produced by the sampling pattern. Fig. 2.1 shows that regular Cartesian sparse sampling causes the interference to be coherent in the form of clear overlying of images while random sampling produces incoherent interference. Although the image obtained from random sampling infers much lower resolution, it is possible to remove the incoherent interference while the co-hinged images obtained from regular sparse sampling could be unfolded by no means. In practice, the center of k-space is more densely sampled than the other region as the central low frequency region carries most energy. There are two popular sampling patterns which not only render incoherent interference but also inherently over-sample the central area; they are radial sampling and spiral sampling.

Figure 2.1: Regular Cartesian sampling results in coherent overlying of images which are supposed to be lying in neighboring field of view. Random sampling causes interference to be incoherent and noise like.

2.3 Preliminary: Soft-thresholding Operator

Consider a simple optimization problem:

$$\min_{\mathbf{x}} \lambda \|\mathbf{x}\|_1 + \frac{1}{2} \|\mathbf{x} - \mathbf{y}\|_2^2 \quad (2.7)$$

Closed-form solution for $\mathbf{x}$ is obtained with an element-wise soft-thresholding operator S_λ ,

$$\mathbf{x}(i) = S_\lambda(\mathbf{y}(i)) = \text{sgn}(\mathbf{y}(i)) \cdot (|\mathbf{y}(i)| - \lambda)^+$$

where $(\cdot)^+ = \max(\cdot, 0)$ and

$$\text{sgn}(\delta) = \begin{cases} \delta/|\delta|, & \delta \neq 0 \\ 0, & \delta = 0 \end{cases}$$

2.4 ONE- ℓ_1 Algorithm

2.4.1 Orthonormal Expansion of Measurement Matrix

We define a matrix $A \in \mathbb{C}^{n \times N}$ being partial-orthonormal if it consists of a subset of rows of an orthonormal matrix $\Phi = \begin{bmatrix} A \\ B \end{bmatrix}$, where $B \in \mathbb{C}^{(N-n) \times N}$ is another partial orthonormal matrix, whose rows together with those of A form an orthonormal matrix.

Denote $A = F_\Omega \Psi'$, (2.4) can be expressed as:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \{ \|\mathbf{x}\|_1 : A\mathbf{x} = \mathbf{b} \} \quad (2.8)$$

In the context of MRI acquisition and reconstruction, A is inherently partial orthonormal: F_Ω is partial orthonormal as under-sampling the k-space corresponds to selecting rows from the orthonormal full Fourier encoding matrix; multiplying F_Ω with another orthonormal matrix Ψ' keeps the partial orthonormal property. Therefore, the sensing matrix A which is partial orthonormal can be expanded to an orthonormal matrix Φ , leading (2.8) to the following form:

$$(\mathbf{x}, \mathbf{p}) = \arg \min_{\mathbf{x}, \mathbf{p}} \{ \|\mathbf{x}\|_1 : \Phi\mathbf{x} = \mathbf{p}, P_\Omega(\mathbf{p}) = \mathbf{b} \} \quad (2.9)$$

where ω is the index set of sampled locations. $\mathbf{p}$ denotes the “imaginary” fully sampled k-space data consisting of acquired k-space data in ω and missed k-space data in other sampling locations. $P_\Omega : \mathbb{C}^N \rightarrow \mathbb{C}^n$ is an operator which retains only the elements indexed by sampling index set Ω .

2.4.2 Augmented Lagrangian Multiplier Formalism

Augmented Lagrangian method (AL) was originally proposed for solving constrained optimization problem. It turns the constrained optimization problem into an unconstrained one comprising three parts: the cost function, the Lagrange multiplier term and

a quadratic regularization to satisfy the constraints. AL Minimises it iteratively under a fixed flow to solves the original problem [72, 73] and is well known for its superior convergence property [74].

With ALM framework, we have its corresponding AL function of (2.9) as follows

$$\mathcal{L}(\mathbf{x}, \mathbf{p}, \mathbf{y}, \mu) = \|\mathbf{x}\|_1 + \langle \mathbf{p} - \Phi\mathbf{x}, \mathbf{y} \rangle + \frac{\mu}{2} \|\mathbf{p} - \Phi\mathbf{x}\|_2^2 \quad (2.10)$$

where $\mathbf{y} \in \mathbb{C}^N$ is the Lagrange multiplier and μ is a positive scalar. $\langle \mathbf{a}, \mathbf{b} \rangle$ represents the inner product of two vector operands.

Since the minimization of $\mathcal{L}(\mathbf{x}, \mathbf{p}, \mathbf{y}, \mu)$ is element-wise, Eq. (2.10) can be further derived to the following form:

$$\mathcal{L}(\mathbf{x}, \mathbf{p}, \mathbf{y}, \mu) = \|\mathbf{x}\|_1 + \frac{\mu}{2} \|\mathbf{p} - \Phi\mathbf{x} + \mu^{-1}\mathbf{y}\|_2^2 - \frac{1}{2\mu} \|\mathbf{y}\|_2^2, \quad (2.11)$$

Note the constraint $P_\Omega(\mathbf{p}) = \mathbf{b}$ is implicitly satisfied when updating $\mathbf{p}$ in each iteration as will be shown in Exhibit 2.

An AL framework for solving Eq. (2.10) is shown below:

Exhibit 1: AL algorithmic framework:

Given $\mu^{(0)}$, $\mathbf{y}^{(0)}$, $\mathbf{b}$, initial guess $\mathbf{x}^{(0)}$, $k = 0$

Repeat

1. $\mathbf{x}^{(k+1)} = \arg \min_{\mathbf{x}} \mathcal{L}(\mathbf{x}, \mathbf{y}^{(k)}, \mu^{(k)})$
2. $\mathbf{y}^{(k+1)} = \mathbf{y}^{(k)} + \mu^{(k)} (A\mathbf{x}^{(k+1)} - \mathbf{b})$
3. $\mu^{(k+1)} > \mu^{(k)}$

Until stopping criterion is met

2.4.3 An Alternating Minimization Method

Directly tackling Eq. (2.11) can be very challenging, we would rely on an alternating direction method [75–77]. We alternatively minimize $\mathcal{L}(\mathbf{x}, \mathbf{p}, \mathbf{y}, \mu)$ with respect to one

variable at a time. Specifically, at the $(k+1)$ th iteration,

$$\begin{cases} \mathbf{x}^{(k+1)} = \arg \min_{\mathbf{x}} \mathcal{L}(\mathbf{x}, \mathbf{p}^{(k)}, \mathbf{y}^{(k)}, \mu^{(k)}) \\ \mathbf{p}^{(k+1)} = \arg \min_{\mathbf{p}} \mathcal{L}(\mathbf{x}^{(k+1)}, \mathbf{p}, \mathbf{y}^{(k)}, \mu^{(k)}) \end{cases} \quad (2.12)$$

1. Minimization with respect to $\mathbf{x}$

$$\begin{aligned} \mathbf{x}^{(k+1)} &= \arg \min_{\mathbf{x}} \mathcal{L}(\mathbf{x}, \mathbf{p}^{(k)}, \mathbf{y}^{(k)}, \mu^{(k)}) \\ &= \arg \min_{\mathbf{x}} \|\mathbf{x}\|_1 + \frac{\mu}{2} \|\mathbf{p} - \Phi \mathbf{x} + \mu^{-1} \mathbf{y}\|_2^2 \\ &= \arg \min_{\mathbf{x}} \|\mathbf{x}\|_1 + \frac{\mu}{2} \|\Phi'(\mathbf{p} + \mu^{-1} \mathbf{y}) - \mathbf{x}\|_2^2 \\ &= \arg \min_{\mathbf{x}} \|\mathbf{x}\|_1 + \frac{\mu}{2} \|\mathbf{x} - \Phi'(\mathbf{p} + \mu^{-1} \mathbf{y})\|_2^2 \end{aligned} \quad (2.13)$$

The last two steps of Eq. (2.13) hold due to the fact that Φ is an orthonormal matrix.

Thanks to the orthonormal expansion, $\mathbf{x}$ can be exactly solved with an element-wise soft-thresholding operator:

$$\begin{aligned} \mathbf{x}^{(k+1)}(i) &= \mathbf{S}_{1/\mu^{(k)}}(\mathbf{U}^{(k)}(i)) \\ &= \begin{cases} 0, & \text{if } |\mathbf{U}^{(k)}(i)| \leq 1/\mu^{(k)} \\ \left(\frac{|\mathbf{U}^{(k)}(i)| - 1/\mu^{(k)}}{|\mathbf{U}^{(k)}(i)|} \right) \mathbf{U}^{(k)}(i), & \text{if } |\mathbf{U}^{(k)}(i)| > 1/\mu^{(k)} \end{cases} \end{aligned} \quad (2.14)$$

where $\mathbf{U}^{(k)} = \Phi'(\mathbf{p}^{(k)} + \frac{1}{\mu^{(k)}} \mathbf{y}^{(k)})$, $|\cdot|$ takes the magnitude of the operand, $i = 1, 2, \dots, N$.

2. Minimization with respect to $\mathbf{p}$

$$\begin{aligned} \mathbf{p}^{(k+1)} &= \arg \min_{\mathbf{p}} \mathcal{L}(\mathbf{x}^{(k+1)}, \mathbf{p}, \mathbf{y}^{(k)}, \mu^{(k)}) \\ &= \arg \min_{\mathbf{p}} \|\mathbf{p} - \Phi \mathbf{x} + \mu^{-1} \mathbf{y}\|_2^2 \end{aligned} \quad (2.15)$$

Therefore the minimum of Eq. (2.15), together with the constraint $P_{\Omega}(\mathbf{p}) = \mathbf{b}$, we have

$$\mathbf{p}^{(k+1)} = \begin{bmatrix} P_{\Omega}(\mathbf{p}^{(k+1)}) \\ P_{\bar{\Omega}}(\mathbf{p}^{(k+1)}) \end{bmatrix} = \begin{bmatrix} \mathbf{b} \\ P_{\bar{\Omega}}\left(\Phi \mathbf{x}^{(k+1)} - \frac{1}{\mu^{(k)}} \mathbf{y}^{(k)}\right) \end{bmatrix}$$

where $P_{\bar{\Omega}} : \mathbb{C}^N \rightarrow \mathbb{C}^{N-n}$ is the complementary operator of P_{Ω} which keeps the elements outside the sampling set Ω . μ^{k+1} is updated with a multiplier r which is larger than 1. Note $\mathbf{y}^{k+1}$ is updated in a standard way prescribed by ALM framework.

The outline of our algorithm is described in Exhibit 2 below. In practice, the inner iterations comprising of Step 1 and Step 2 in Exhibit 2 are executed once and terminated before inner convergence which is outlined in Exhibit 3. Theoretically the accelerated algorithm brings in a trade-off between reconstruction accuracy and computational efficiency. Empirically, executing the inner iteration once produces comparative results as using the steps prescribed in Exhibit 2 [63].

Exhibit 2: Outline of ONE - ℓ_1 fast algorithm:

Input: $\mathbf{y}^{(0)} = 0$, $\mu^{(0)} > 0$, $\mathbf{b}$, Ω , $\mathbf{p}^{(0)} = \begin{bmatrix} \mathbf{b} \\ 0 \end{bmatrix}$, r ;

Repeat

While not converged **do**

// Step 1 solves $\mathbf{x}^{(k+1)} = \arg \min L(\mathbf{x}, \mathbf{p}^{(k)}, \mathbf{y}^{(k)}, \mu^{(k)})$

Step 1: $\mathbf{x}^{(k+1)} = S_{1/\mu^{(k)}}(\Phi^{-1}(\mathbf{p}^{(k)} + \frac{1}{\mu^{(k)}}\mathbf{y}^{(k)}))$

// Step 2 solves $\mathbf{p}^{(k+1)} = \arg \min_{\mathbf{p}} L(\mathbf{p}, \mathbf{x}^{(k+1)}, \mathbf{y}^{(k)}, \mu^{(k)})$

Step 2: $\mathbf{p}^{(k+1)} = \begin{bmatrix} b \\ P_{\bar{\Omega}}(\Phi \mathbf{x}^{(k+1)} - \frac{1}{\mu^{(k)}}\mathbf{y}^{(k)}) \end{bmatrix}$

end

Step 3: $\mathbf{y}^{(k+1)} = \mathbf{y}^{(k)} + \mu^{(k)}(\mathbf{p}^{(k+1)} - \Phi \mathbf{x}^{(k+1)})$

Step 4: $\mu^{(k+1)} = r \times \mu^{(k)}$

Step 5: $k = k + 1$

end if converged

Output: $\mathbf{x}^{(k)}$, $\mathbf{p}^{(k)}$

Exhibit 3: Outline of accelerated $ONE - \ell_1$ fast algorithm:

Input: $\mathbf{y}^{(0)} = 0$, $\mu^{(0)} > 0$, $\mathbf{b}$, Ω , $\mathbf{p}^{(0)} = \begin{bmatrix} \mathbf{b} \\ 0 \end{bmatrix}$, r ;

Repeat

// Step 1 solves $\mathbf{x}^{(k+1)} = \arg \min L(\mathbf{x}, \mathbf{p}^{(k)}, \mathbf{y}^{(k)}, \mu^{(k)})$

Step 1: $\mathbf{x}^{(k+1)} = S_{1/\mu^{(k)}}(\Phi^{-1}(\mathbf{p}^{(k)} + \frac{1}{\mu^{(k)}}\mathbf{y}^{(k)}))$

// Step 2 solves $\mathbf{p}^{(k+1)} = \arg \min_{\mathbf{p}} L(\mathbf{p}, \mathbf{x}^{(k+1)}, \mathbf{y}^{(k)}, \mu^{(k)})$

Step 2: $\mathbf{p}^{(k+1)} = \begin{bmatrix} b \\ P_{\Omega}(\Phi\mathbf{x}^{(k+1)} - \frac{1}{\mu^{(k)}}\mathbf{y}^{(k)}) \end{bmatrix}$

Step 3: $\mathbf{y}^{(k+1)} = \mathbf{y}^{(k)} + \mu^{(k)}(\mathbf{p}^{(k+1)} - \Phi\mathbf{x}^{(k+1)})$

Step 4: $\mu^{(k+1)} = r \times \mu^{(k)}$

Step 5: $k = k + 1$

end if converged

Output: $\mathbf{x}^{(k)}$, $\mathbf{p}^{(k)}$

2.5 Experiments and Results

2.5.1 Experiment Setup

The proposed method was evaluated with one 256×256 T1-weighted MR simulated from Brainweb database, dubbed as test 1 and one 512×512 T1-weighted in-vivo MR brain image, dubbed as test 2. Although the proposed method doesn't rely on specific sampling patterns, in our experiments the fully-sampled k-space data was down-sampled with equally spaced radial lines on a Cartesian grid to mimic accelerated acquisition, as seen in Fig 2.2(c). Discussion of optimal sampling pattern is beyond the scope of this thesis, however some hints can be found in reference [78].

Algorithms	Test #1	Test #2
NCG	0.81	1.95
IST	0.25	0.60
Proposed	0.23	0.60

Table 2.1: Comparison of CPU time of each iteration

We compared the proposed method with commonly used Non-linear Conjugate Gradient method (NCG) [29] and Iterative Soft Thresholding method (IST). Ground-truth

Figure 2.2: Comparison of reconstruction results given 5 seconds running time. a) and b) are ground-truth for test 1 and test 2, respectively. d) and g), e) and h), f) and i) are reconstructed results from the proposed method, IST and NCG, respectively; c) shows radial sampling pattern in our tests — 24 equally spaced radial lines, which corresponds to approximate 10 times acceleration (90% undersampling).

was obtained by taking an inverse Fourier transform of the fully-sampled k-space data. Table 3.1 shows the CPU time per outer iteration for the three methods. Two metrics were compared, the convergence rate $\kappa(\cdot)$ and the reconstruction accuracy. We quantified convergence rate of each method as the evolution rate of the solution after each iteration towards the eventually converged solution. Specifically, it is expressed as the relative ℓ_2 distance between the solution of j th iteration and the converged solution as follows:

$$\kappa^{(j)} = \left(\frac{\|\mathbf{x}^{(j)} - \mathbf{x}^{(\infty)}\|_2^2}{\|\mathbf{x}^{(\infty)}\|_2^2} \right),$$

where $\mathbf{x}^{(\infty)}$ is the converged solution. As only the three methods might not converge to the same solution, we simply calculated $\mathbf{x}^{(\infty)}$ for each algorithm by running thousands of iterations of the algorithm to derive $\mathbf{x}^{(\infty)}$. Since the algorithms to be compared have different computational complexities for each iteration, we evaluated $\kappa^{(j)}$ as a function of iteration running time $t^{(j)}$. Reconstruction accuracy was quantified as $\|\mathbf{x} - \mathbf{x}^*\|_2^2 / \|\mathbf{x}^*\|_2^2$, where $\mathbf{x}^*$ is the ground-truth.

The penalty parameter μ in the proposed method was geometrically increased as $\mu^{(k+1)} = r \times \mu^{(k)}$. Specifically, $r = 1.2$ for both tests. Given $Q_\alpha(\cdot)$ is an α -quartile operator, we set $\mu^{(0)} = 1/Q_{0.99}(|\Phi' \mathbf{p}^{(0)}|)$, in other words, we initialize the first threshold value to be the largest 1% of the magnitude of $\Phi' \mathbf{p}^{(0)}$. We selected the threshold λ such that it provided the smallest relative error for IST implementation. Specifically, $\lambda = 0.01, 0.015$ for test 1 and test 2, respectively. We followed the parameter settings of [29] for NCG implementation (MATLAB code available on Dr. Michael Lustig's home page). The stopping criteria was satisfied when $\|A\mathbf{x} - \mathbf{b}\|_2^2 / \|\mathbf{b}\|_2^2 < 1e - 8$ for all algorithms.

All experiments were implemented in MATLAB, running on a WINDOWS desktop equipped with 3.1 GHz Intel Core i5 CPU and 8 GB RAM.

2.5.2 Performance Evaluation

To examine the computational efficiency, we allowed a certain running time for all three methods and compared their reconstruction performance. Fig. 2.2 shows reconstructed results for 5 seconds for all three methods, where the k-space data was under 80% undersampling (x5 acceleration).

Fig. 2.2(e) and (h) show the reconstruction results of IST for test 1 and test 2, respectively. Fig. 2.2(f) and (i) delineates the reconstruction by the NCG for test 1 and test2, respectively. It can be seen that both IST and NCG suffered from severe streaking artefacts, as pointed by red arrows. The artefacts were considerably reduced by the proposed method as seen in Fig. 2.2(d) for test 1 and (g) for test 2.

Fig. 2.3 plots evolution of $\kappa^{(j)}$ of test 2 for all three methods as a function of $t^{(j)}$, where the k-space was under 85% undersampling ($\times 6$ acceleration). It can be noticed that the proposed method in red solid lines converged much faster than both the IST method in black dashed lines and the NCG method in blue dotted lines. Specifically, to obtain a $\kappa^{(j)} = 10^{-10}$, the proposed method used 18 seconds while the IST and the NCG method used 172 seconds and 2083 seconds, respectively. In other words, the proposed method converged 10 times faster than IST and more than 100 times faster than NCG.

Fig. 2.4 and 2.5 plot the reconstruction accuracy of test 1 and test 2 for all three methods as a function of acceleration factors. Both cases show that the proposed method achieved comparable reconstruction accuracy with NCG while both the proposed and NCG provided higher reconstruction accuracy than IST. The advantage over IST becomes more obvious as acceleration factors increased.

Figure 2.3: Comparison of convergence rate for test 2. To arrive at a relative distance of 10^{-10} , the proposed method used 18 seconds while IST used 172 seconds and NCG used as much as 2083 seconds.

2.6 k-t ONE- ℓ_1 : An Accurate and Fast Compressed Sensing Algorithm for Dynamic Cardiac MRI Reconstruction

Dynamic cardiac Magnetic Resonance Imaging (MRI) uses MRI to monitor dynamic processes of cardiac motions in the form of a series of image frames representing dynamic heart phases. Imaging time is very important in practical applications of dynamic cardiac MRI. Reduced-data acquisition techniques speed up imaging process by undersampling

Figure 2.4: Comparison of reconstruction accuracy for test 1, given sufficient time to converge to the final solution. Reconstruction accuracy was exhibited in a function of acceleration factors.

Figure 2.5: Comparison of reconstruction accuracy for test 2, given sufficient time to converge to the final solution. Reconstruction accuracy was exhibited in a function of acceleration factors.

the data space, known as k-t space. However, fewer samples than required by Nyquist rate result in undesirable aliasing. Therefore, seeking for high quality image reconstructions from undersampled k-t space data becomes the top issue in the community.

Compressed sensing theory states that under some mild conditions, if the signal of interest has sparse representation in some basis, exact recovery is possible from fewer measurements than the Nyquist limits theory requires [23, 24, 79]. By exploiting the implicit sparsity of cardiac MR images, CS has been found successful in the applications of dynamic cardiac MR images reconstructions from reduced acquisitions [33, 34, 80]. k-t SPARSE [34, 80] shows that basic formulation for CS-based cardiac MRI reconstructions is essentially a basis pursuit denoising (BPDN) problem as follows:

$$\mathbf{u} = \arg \min_{\mathbf{u}} \{ \|\Psi \mathbf{u}\|_1 : \mathcal{F}_\Omega \mathbf{u} = \mathbf{b} + \mathbf{e} \}, \quad (2.16)$$

where $\mathbf{u} \in \mathbb{C}^N$ is vectorized cardiac MR images with all frames stacked on top of each other; $\mathbf{b} \in \mathbb{C}^M$, $M < N$ represents acquired k-t space data; $\mathbf{e} \in \mathbb{C}^M$ is measurement noise; Ψ denotes sparsifying transform; here $\mathcal{F}_\Omega$ is the sensing matrix which corresponds to down-sampling Fourier coefficients of $\mathbf{u}$ according to the sampling index set Ω . (2.4) can be formulated into the following form with a proper positive penalty parameter μ :

$$\mathbf{u} = \arg \min_{\mathbf{u}} \|\Psi \mathbf{u}\|_1 + \frac{\mu}{2} \|\mathcal{F}_\Omega \mathbf{u} - \mathbf{b}\|_2^2. \quad (2.17)$$

Fig. 2.6 provides a diagrammatic exhibition of transformational relations of $\mathbf{x}$, $\mathbf{b}$, $\mathcal{F}_\Omega$ and Ψ .

k-t SPARSE provides optimal reconstructions from the perspective of CS. However, the principal disadvantage of k-t SPARSE is its low computational efficiency. k-t FOCUSS [33] used an iterative re-weighted minimum norm algorithm called FOCUSS [81, 82] and it partially solved the computational inefficiency problem of k-t SPARSE. The implementation of k-t FOCUSS involves inverse of a very large weighting matrix, which is

Figure 2.6: Diagrammatic exhibition of transformational relation of $\mathbf{x}$, $\mathbf{b}$, $\mathcal{F}_\Omega$ and Ψ . The purple cube on the left represents dynamic images that we desire; the right top black cube represents k-t measurements $\mathbf{b}$, where orange dots represent sampled locations while others black area represent unsampled locations; the right bottom blue cube is the sparse coefficients cube; the central top and bottom dashed box represent $\mathcal{F}_\Omega$ and Ψ , respectively.

challenging in practice. Instead, matrix inversion was circumvented using a conjugate gradient method, which in return sacrifices the computational efficiency. In the k-t FOCUSS journal paper [33], the authors discussed the superiority of CS-based methods over non-CS based methods, for instance UNFOLD [83], k-t BLAST and k-t SENSE [84] in terms of reconstruction accuracy. There are also methods which combines UNFOLD with parallel MRI reconstruction techniques such as UNFOLD-SENSE[85], UNFOLD-SMASH[86]. However, those methods all require the exact knowledge of the spatial-spectrum support which can be very difficult to obtain in practice.

Motivated by [87], which proposed a theoretical algorithm for CS with simulated signal and impractical simulated sampling pattern, we consider a novel reconstruction problem for dynamic cardiac MRI. This problem is very important in clinic practice but challenging especially because of motion artefacts involved and large size of data. The proposed method, dubbed as k-t ONE- ℓ_1 , first casts the original model to an equivalent one by expanding the sensing matrix to an orthonormal matrix. We then solve the new model in an Augmented Lagrangian (AL) framework using an alternating direction minimization method, which can be implemented easily and computationally efficiently. Efficacy of the proposed method is validated via comparing with k-t SPARSE and k-t FOCUSS using an in-vivo cardiac dataset.

2.6.1 Sparsity of Dynamic Cardiac MR Images

Fig. 2.7(a) shows several image frames from an in-vivo cardiac image sequence. It can be seen that except areas outlined by dotted boxes, most areas of the images are highly similar because of their static background. The similarity indicates that sparsity in dynamic cardiac MR images are twofold: spatial sparsity revealed by taking sparsifying transform such as Wavelet transform to spatial domain at each temporal point; temporal sparsity via taking one-dimensional Fourier transform along temporal direction, as shown in Fig.2.7(b). The implicit sparsity lying within guarantees the application of CS to the reconstruction of dynamic cardiac MR images.

2.6.2 Experiments and Results

2.6.2.1 Experiment Setup

The core algorithm of k-t ONE- ℓ_1 has been discussed in Exhibit 2 and Exhibit 3. Fig. 2.6 prescribes the steps to extend ONE- ℓ_1 algorithm to dynamic cardiac MRI reconstruction.

Figure 2.7: Spatial-temporal sparsity in dynamic cardiac MR images: a) shows three image frames selected from one image sequence comprised of 25 image frames, with different phases of one same heart being outlined with dotted boxes; b) shows temporal sparsity by taking one-dimensional Fourier transform along temporal direction.

In our application, the accelerated ONE- ℓ_1 was used. The proposed method was evaluated with one in-vivo short-axis MRI scan dataset of size $256 \times 256 \times 25$, corresponding to coordinates $k_x \times k_y \times t$. Dataset was provided by Dr. Jong Chul Ye [33]. Imaging acceleration is simulated by retrospectively decimating fully-sampled k-t space data to a desired sampling pattern. At each k_x location, we undersampled $k_y - t$ domain using a random 2D Cartesian sampling mask with densely sampling the central area and randomly sparsely sampling in other areas. Fig. 2.8 shows the sampling pattern utilized in our experiments.

Figure 2.8: Sampling pattern utilized: fully-sampled k-t space data was decimated to a desired sampling pattern. At each k_x location, we undersampled $k_y - t$ domain using a random 2D Cartesian sampling mask with densely sampling central area and random sparsely sampling in the other areas.

We compared the proposed method with state-of-the-art CS-based k-t SPARSE and k-t FOCUSS. We implemented k-t SPARSE with off-the-shelf non-linear conjugate gradient (NCG) solver provided in [29]. The NCG solver in [29] was also used to handle the matrix inverse in k-t FOCUSS with 8 and 16 iterations of line search, dubbed as "k-t FOCUSS-8"

and "k-t FOCUSS-16", respectively. σ started with a very small value and geometrically increased with $r = 1.5$. Stopping criteria was satisfied when $\|P\mathbf{x} - \mathbf{b}\|_2^2 / \|\mathbf{b}\|_2^2 < 1e-8$ for all algorithms. We quantitatively evaluated the performance in terms of regularized mean-square-errors (RMSE),

$$\text{RMSE} = \frac{\|\mathbf{u} - \mathbf{u}^*\|_2^2}{\|\mathbf{u}^*\|_2^2}, \quad (2.18)$$

where $\mathbf{u}$ represents images reconstructed and $\mathbf{u}^*$ represents the ground-truth obtained from fully-sampled k-t space data.

All experiments were implemented in MATLAB, working on a WINDOWS desktop equipped with 3.1 GHz Intel Core i5 CPU and 8 GB RAM.

2.6.3 Performance Evaluation

Table 2.2 shows quantitative comparison results of k-t ONE- ℓ_1 with k-t SPARSE, k-t FOCUSS-8 and k-t FOCUSS-16, with $\times 5$ and $\times 10$ accelerated data. For both cases, k-t FOCUSS-16 offered lower RMSE than k-t FOCUSS-8 but using nearly double CPU time. In both cases k-t SPARSE provided even lower RMSE than both k-t FOCUSS-8/16. In terms of computational efficiency, however, k-t FOCUSS-8/16 took less total time than k-t SPARSE. k-t ONE- ℓ_1 not only had comparable reconstruction accuracy with k-t SPARSE, but also greatly reduced total reconstruction time used by the other methods. Specifically, k-t ONE- ℓ_1 was nearly 30 times faster than k-t SPARSE and 23 times faster than k-t FOCUSS-16. Time/iteration was calculated by dividing total CPU time by total number of outer iterations of each method.

Fig. 2.9 and Fig. 2.10 show reconstruction results of k-t FOCUSS-16, k-t SPARSE and k-t ONE- ℓ_1 against the original fully sampled images at $t = 15$ and $t = 25$ respectively. A region of interest (ROI) was zoomed in and shown on the top right corner of each reconstructed image. Difference images constructed by subtracting ROI of each method

from the original ROI were shown. Comparisons revealed by Fig. 2.9 and Fig. 2.10 are consistent with results in Table 2.2. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable reconstructions as seen from reconstructed. It can be seen that k-t FOCUSS has more structured contents in its difference images as indicated by the white arrows, which implies loss of information in the reconstructed images. Structured noise as shown in difference images of k-t FOCUSS has been significantly reduced in results of k-t SPARSE and k-t ONE- ℓ_1 .

Fig. 2.11 depicts reconstruction results by the three methods in $y-t$ plain at $x = 128$ and $x = 140$. Difference images obtained by subtracting reconstructed images of each method from the original are shown. Compared to k-t SPARSE and k-t ONE- ℓ_1 , k-t FOCUSS failed to follow the temporal variations in certain regions as pointed out by the red arrows.

	Methods	Total time(s)	Time/iteration	RMSE
$\times 5$	k-t SPARSE	126.8	12.68	0.8%
	k-t FOCUSS-8	50	25	1.5%
	k-t FOCUSS-16	101	50.5	1.07%
	k-t ONE- ℓ_1	4.27	0.28	0.74%
$\times 10$	k-t SPARSE	133	13.3	1.74%
	k-t FOCUSS-8	57.78	28.9	2.5%
	k-t FOCUSS-16	97.5	48.75	2%
	k-t ONE- ℓ_1	4.29	0.29	1.72%

Table 2.2: Comparison of k-t ONE- ℓ_1 with state-of-the-art methods.

Fig. 2.12, Fig. 2.13 and Fig. 2.14 plot comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 4$ acquisition acceleration, $\times 8$ acquisition acceleration and $\times 10$ acquisition acceleration respectively. Results shown in Fig. 2.12, Fig. 2.13 and Fig. 2.14 are consistent: k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.

Figure 2.9: Comparison of reconstruction results using 20% of full k-t space data at $t = 15$ temporal point: A region of interest (ROI) was zoomed in and is shown on the top right corner. Difference images constructed by subtracting ROI of each method from the original ROI were shown. It can be seen that k-t FOCUSS had more structured contents in its difference images as indicated by the white arrows, which implied loss of information in the reconstructed images. Structured noise as shown in difference images of k-t FOCUSS were significantly reduced in results of k-t SPARSE and k-t ONE- ℓ_1 .

Fig. 2.15 shows regularized mean squared errors (RMSE) calculated with Eq. (2.18) of the three methods for a range of acceleration factors. It can be seen that k-t SPARSE and k-t ONE- ℓ_1 provided comparable RMSE while k-t FOCUSS provided higher RMSE in our experiments.

2.7 Discussion and Conclusion

One desirable advantage about the proposed method is easy parameter tuning. The only parameter to be tuned is r , which geometrically scales the regularization scalar μ . Selec-

Figure 2.10: Comparison of reconstruction results using 20% of full k-t space data at $t = 25$ temporal point: A region of interest (ROI) was zoomed in and is shown on the top right corner of each reconstructed image. Difference images constructed by subtracting ROI of each method from the original ROI were shown. It can be seen that k-t FOCUSS had more structured contents in its difference images as indicated by the white arrows, which implied loss of information in the reconstructed images. Structured noise as shown in difference images of k-t FOCUSS were significantly reduced in results of k-t SPARSE and k-t ONE- ℓ_1 .

tion of r offers a trade-off between computational efficiency and reconstruction accuracy. A larger r will result in a faster convergence but sacrifice the recovery accuracy. Normally, setting r between the range $[1.2, 1.5]$ helps converge fast to a reasonable reconstruction.

In this work, we have only considered the wavelet sparsity regularization while there is increasing interest in imposing total variation regularization (TV) to improve image quality [29, 30]. Incorporating the TV regularization is not straightforward in our framework as finite difference transform is not unitary as the Fourier or wavelet transforms. This will be in the research scope of our future work. One possible trial is to integrate

Figure 2.11: Comparison of reconstruction results by the three methods in $y-t$ plane at $x = 128$ and $x = 140$. Difference images constructed by subtracting reconstructed images of each method from the original are shown. Compared to k-t SPARSE and k-t ONE- ℓ_1 , k-t FOCUSS failed to follow the temporal variations in certain regions as pointed out by the red arrows.

variable splitting technique [77, 88, 89] with alternating direction minimization method as explored in [56, 90].

Figure 2.12: Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 4$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.

Good computational efficiency comes from two factors: (1) Orthonormal expansion circumvents the inverse problem of an ill-posed system leading to solutions with iterative soft-thresholding form, which is very easy to implement and runs fast; (2) Augmented Lagrangian method framework guarantees fast convergence of the proposed method [74]. Take the application of ONE- ℓ_1 on dynamic MRI reconstruction as an instance, main computational burden at each iteration comes from two 1D Fast Fourier transforms along temporal direction and two 2D Fast Fourier transform for each frame. Running on a PC with configurations mentioned above, it took 0.28 seconds to run each iteration, and normally the algorithm would converge within 20 iterations.

Recently, researchers have proposed some motion-adaptive algorithms for even better reconstructions than those replying on compressed sensing alone, at the cost of computa-

Figure 2.13: Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 8$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.

tional efficiency [45, 46]. Those methods required a separate CS-based reconstruction in the beginning to perform motion estimation. k-t FOCUSS or k-t SPARSE were used to perform the separate CS reconstruction. Accurate motion estimation is essential to those methods, and because data size in practical applications of dynamic cardiac MRI reconstruction can be very large, it is important to have a computationally efficient method to perform the separate reconstruction for accurate motion estimation. k-t ONE- ℓ_1 can be naturally embedded in those advanced methods and help improve their performance in terms of reconstruction accuracy and computational efficiency.

To conclude, in this chapter we proposed a fast and accurate reconstruction method based on Compressed Sensing. On the one hand, it solved the problems of computational efficiency of linear programming based methods which render optimal reconstruction ac-

Figure 2.14: Comparison of relative errors of each reconstructed frame against the corresponding original frame of the three methods under $\times 10$ acquisition acceleration. k-t SPARSE and k-t ONE- ℓ_1 achieved comparable frame relative errors while k-t FOCUSS incurred relatively higher frame relative errors compared to its counterparts.

curacy; on the other hands, it solved the reconstruction accuracy issues of those methods that aimed to improve the computational efficiency of linear programming methods.

Expanding the sensing matrix into an orthonormal matrix via introducing an extra variable plays an essential role in the success of our proposed method. The expanded orthonormal problem was then formulated into an unconstrained optimization problem with Augmented Lagrangian Multiplier method. Multiple variables were alternatively updated with an alternating direction algorithm. Specifically, each time one variable was updated while keeping the rest variables constant with values calculated from previous alike steps.

The proposed method was first validated with 2D noise-corrupted general images by comparing with commonly used non-linear conjugate method and iterative soft-thresholding method. In this chapter, we also explored the reconstruction problem in

Figure 2.15: regularized mean squared errors (RMSE) of the three methods for a range of acceleration factors. It can be seen that k-t SPARSE and k-t ONE- ℓ_1 provided comparable RMSE while k-t FOCUSS provided higher RMSE in our experiments.

dynamic cardiac image reconstruction. We proposed an algorithm dubbed as “k-t ONE- ℓ_1 ” which was based on the aforementioned core algorithm. “k-t ONE- ℓ_1 ” was tested with an in-vivo cardiac dataset by comparing with commonly used k-t SPARSE and state-of-the-art k-t FOCUSS.

The proposed method could either be applied to the direct reconstruction of MR images or be embedded into a more advanced reconstruction framework for higher accuracy and lower computational complexity concerns.

Chapter 3

Motion-compensated Orthonormal Expansion ℓ_1 -Minimization for Reference-driven MRI Reconstruction Using Augmented Lagrangian Methods

3.1 Introduction

Compressed Sensing (CS) theory breaks the restraint of Nyquist limit theory by stating that under some mild conditions, one signal which has sparse representation in some domain can be exactly recovered from highly incomplete measurements [23, 24, 27, 79]. Signals are reconstructed by solving a constrained optimization problem which prompts sparsity of the signal. By exploiting the sparsity in MR images, CS has been applied to MR image reconstructions to reduce the imaging time [28–31, 36, 91–93].

However, when the signal of interest is not sufficiently sparse or the number of acquired measurements is not sufficiently large, reconstructions from Compressed Sensing would still fail. Meanwhile, in some applications such as interventional MRI, longitudinal MRI and dynamic cardiac MRI, a pre-scanned reference image can be readily obtained. Many research works have shown that reconstruction can be greatly improved by taking

advantage of prior information from the reference image. Previous works generally fall into two categories. One is to break the reconstruction into two steps: first reconstruct the residual image, and then linearly combine the reconstructed residual image and the reference image (with or without motion compensation) to obtain the target image [39–42]. The other category is to directly reconstruct on the target image by restricting the solution space with various constraints such as sparsity constraint, support constraint or energy distribution constraint that incorporate prior information from the reference image [43, 44]. Prior information from the reference has also been proven helpful in reconstructions of dynamic cardiac MRI, which monitors motion process of a beating heart with a series of MR images. In [45], each frame image was estimated from its left and right neighbouring frames with motion estimation and compensation. In [46, 47], one fully-sampled reference image was acquired and a series of residual images were constructed by subtracting the motion-compensated reference image from all frames, which was then reconstructed with a reweighted minimum norm algorithm called FOCUSS [81].

In view of the availability of a reference image in many applications and its great potential in improving the performance of reconstruction of the target image, we present a novel framework for reference-driven MR image reconstruction. Our preliminary work can be found in [48]. Inspired by modern video compression techniques, we consider the reference and target images as two consecutive video frames. Inter-frame motion is estimated with motion estimation and compensation method. One motion-compensated residual image is derived by subtracting the motion-compensated reference image from the target image. The target image is directly reconstructed by solving a ℓ_1 - ℓ_2 convex minimization problem which is composed of three components: two ℓ_1 -norm regularization terms for prompting spatial sparsity of the target and motion-compensated residual images and one ℓ_2 -norm regularization for enhancing consistency with k-space data ac-

quired.

The proposed constrained optimization problem is then solved with an efficient and easy-to-implement algorithm. We first re-formulate the original model to an equivalent new model by expanding the sensing matrix into an orthonormal matrix and decoupling effects of regularization term via introducing an auxiliary variable. We then solve the new model with the joint application of AL framework and an alternating direction minimization method.

Main contributions of this work can be summarized as follows:

- (i) It enables visually and quantitatively more accurate reconstructions than its counterparts especially in high undersampling ratios.
- (ii) It is popular to reconstruct the residual image first and combine the reconstructed residual image and the reference image to obtain the target image. However, the reconstruction of the residual image in existing methods usually falls back to a prototypical CS-only problem, which can still fail when the residual image is not sufficiently sparse or the number of measurements is not sufficiently large. Instead of separating the reconstruction process into two steps, we propose a novel model that directly reconstructs the target image by prompting sparsity of the target and sparsity of the motion-compensated residual image in the same objective function simultaneously. The additional sparsity constraint in the objective function essentially provides additional prior information from the reference image and further restricts the solution space of the target image to the true subspace where it belongs to.
- (iii) It exploits the scenario when there are obvious local feature displacements between the target and reference images, which hasn't been investigated much by existing

methods.

We demonstrate efficacy of the proposed method using three datasets, two are MR brain images including phantom and in-vivo images and the other is cardiac cine MR images. In the MR brain image studies, we compare the proposed method with commonly-used sparse MRI method [29] and reference-driven sparse MRI method [39]. In the cardiac cine image study, we compare with state-of-the-art k-t SPARSE [34] and k-t FOCUSS-MEMC [47].

The rest of this chapter is organized as follows: Section 2 provides backgrounds and some preliminary remarks to this work; Section 3 describes the algorithm in details; Section 4 demonstrates efficacy of the proposed method with numerical experiments; A discussion about the proposed method and a conclusion are delivered in Section 5.

3.2 Theory

3.2.1 Problem Formulation

Consider the following inverse problem

$$\mathbf{b} = A\mathbf{u} + \mathbf{e} \quad (3.1)$$

where $\mathbf{u} \in \mathbb{R}^N$ is the signal of interest, $A \in \mathbb{R}^{M \times N}$ with $M < N$ is the sensing matrix, $\mathbf{b} \in \mathbb{R}^M$ represents the measurements and $\mathbf{e}$ is measurement noise. Eq. (3.1) is an under-determined problem. Suppose $\mathbf{u}$ has a sparse representation in certain basis, specifically in the form of

$$\mathbf{x} = B\mathbf{u},$$

where B is the sparsifying transform (for instance wavelet transform), $\mathbf{x}$ is sparse coefficients of $\mathbf{u}$. A k-sparse signal $\mathbf{u}$ suggests there are only k non-zero elements in $\mathbf{x}$.

The Compressed Sensing theory suggests that a unique solution of the inverse problem in (3.1) can be obtained by solving the following tractable ℓ_1 -norm convex optimization problem:

$$\mathbf{u} = \arg \min_{\mathbf{u}} \{ \|\Psi \mathbf{u}\|_1 : \mathcal{F}_\Omega \mathbf{u} = \mathbf{b} + \mathbf{e} \}, \quad (3.2)$$

where $\mathbf{u} \in \mathbb{C}^N$ is vectorized MR image to be reconstructed; $\mathbf{b} \in \mathbb{C}^M$, $N < M$ denotes vectorized acquired k-space data; $\mathbf{e} \in \mathbb{C}^M$ is measurement noise; Ψ , similar as B , is the sparsifying transform; $\mathcal{F}_\Omega$, similar as A , is the partial Fourier transform corresponding to under-sampling Fourier coefficients of $\mathbf{u}$ according to the sampling index set Ω .

Denote $\mathbf{x} = \Psi \mathbf{u}$ to be sparse coefficients of $\mathbf{u}$, and $P = F_\Omega \Psi'$, where $'$ represents the adjoint operator. (3.2) can be restated as:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \{ \|\mathbf{x}\|_1 : P\mathbf{x} = \mathbf{b} + \mathbf{e} \}, \quad (3.3)$$

3.2.2 Preliminary: Augmented Lagrangian Method

Augmented Lagrangian method (AL) was originally proposed for solving constrained optimization problem. It transfers the constrained optimization problem into unconstrained one comprising three parts: the cost function, the Lagrange multiplier term and a quadratic regularization to satisfy the constraints. Minimising it iteratively under a fixed flow to solves the original problem [72, 73]. AL is well known for its superior convergence property [74].

Consider the constrained optimization problem in (3.2), its corresponding AL function is constructed as

$$\mathcal{L}(\mathbf{u}, \mathbf{y}, \mu) = \|\Psi \mathbf{u}\|_1 + \mathbf{y}^H (\mathcal{F}_\Omega \mathbf{u} - \mathbf{b}) + \frac{\mu}{2} \|\mathcal{F}_\Omega \mathbf{u} - \mathbf{b}\|_2^2 \quad (3.4)$$

where $\mathbf{y} \in \mathbb{R}^M$ denotes the Lagrange multiplier vector, and right quadratic term represents the penalty term associated with the constraint $\mathcal{F}_\Omega \mathbf{u} = \mathbf{b} + \mathbf{e}$, with a positive

penalty parameter μ .

An AL framework for solving (3.2) is shown below:

AL algorithmic framework:

Given $\mu^{(0)}$, $\mathbf{y}^{(0)}$, $\mathbf{b}$, initial guess $\mathbf{u}^{(0)}$, $k = 0$
Repeat
 1. $\mathbf{u}^{(k+1)} = \arg \min_{\mathbf{u}} \mathcal{L}(\mathbf{u}, \mathbf{y}^{(k)}, \mu^{(k)})$
 2. $\mathbf{y}^{(k+1)} = \mathbf{y}^{(k)} + \mu^{(k)} (\mathcal{F}_{\Omega} \mathbf{u}^{(k+1)} - \mathbf{b})$
 3. $\mu^{(k+1)} > \mu^{(k)}$
Until stopping criterion is met

3.2.3 Inter-frame Motion

One remarkable concept from modern video compression techniques for instance, MPEG and H.264, is that one frame can be predicted from one another by exploiting temporal redundancies between frames [94]. Motion estimation and motion compensation constitute two key elements in video compression process. Motion estimation is to derive a collection of coordinate shifts $(\Delta u, \Delta v)$, known as motion vector, that matches one small neighbour of location (u, v) in the target frame $\mathbf{I}_t$ to another neighbour of location $(u + \Delta u, v + \Delta v)$ in the reference frame $\mathbf{I}_r$ with minimum mean absolute values (MAD). Motion compensation is to relocate pixels in reference frame according to the motion vector derived from motion estimation process. Therefore, the target frame can be predicted from motion-compensated reference frame and a difference image as follows:

$$\mathbf{I}_t(\mathbf{r}) = \mathbf{I}_r(T(\mathbf{r})) + \mathbf{I}_d, \quad (3.5)$$

where $\mathbf{r}$ and $T(\mathbf{r})$ represent the collection of (u, v) and the collection of $(u + \Delta u, v + \Delta v)$, respectively. If motion is estimated and compensated reasonably, the difference image $\mathbf{I}_d$ is expected to be sparse in image space. (3.5) can be simplified with a motion-adaptive

transform f ,

$$\mathbf{I}_t = f\mathbf{I}_r + \mathbf{I}_d, \quad (3.6)$$

To obtain accurate motion estimation, full-resolution both reference and target frames should be known, which is challenging in MRI applications as we only have under-sampled target frame. One solution is to first reconstruct the target frame with conventional CS and motion is estimated using reconstructed images as studied in [45, 46]. Alternatively, motion can initially be estimated using low-resolution target and reference frames reconstructed from zero-padded undersampled k-space. The latter method is applied in our implementation. Looking for optimal motion-adaptive transform is beyond the scope of this paper, commonly used motion-adaptive transforms are motion-model registration based methods [40–44], block-matching based methods [46, 47] and phase-based methods [45, 95].

3.2.4 Dynamic Cardiac MRI Reconstruction

Dynamic cardiac MRI is the imaging technique that uses MRI to monitor dynamic processes of cardiac motions. Inter-frame anatomical similarity existing in dynamic cardiac image sequence governs consistency and redundancy between two frames of interest while displacements of features in space appear as inter-frame motions. Unlike general reference-driven MRI reconstruction issues, there is generally more than one image to be reconstructed from the reference image.

Consider a dynamic image sequence $\mathbf{I}_t$ composed of T frames. In the context of dynamic cardiac MRI reconstruction, $\mathbf{b}$ in (3.1) and $\mathbf{I}$, f in (3.6) are specified in a slightly different form as following,

$$\mathbf{I}_t = \begin{bmatrix} \mathbf{I}_{t,1} \\ \vdots \\ \mathbf{I}_{t,T} \end{bmatrix}, f = \begin{bmatrix} f_1 \\ \vdots \\ f_T \end{bmatrix}, \mathbf{b} = \begin{bmatrix} \mathbf{b}_1 \\ \vdots \\ \mathbf{b}_T \end{bmatrix}.$$

3.3 Proposed Method

3.3.1 The Proposed Model

Inspired by modern video compression techniques, we consider the target and reference images as two consecutive frames. Anatomical similarity governs consistency between the two frames while displacements of features in space appear as inter-frame motions. Therefore, the target image can be predicted by the reference image as in (3.6).

Many existing methods first reconstructed the difference image and added back reconstructed difference image to motion-compensated reference to obtain final reconstructed target image. In contrast, we directly reconstruct the target image itself by exploiting ℓ_1 -norm sparsity of target image $\mathbf{I}_t$ and compensated difference image $\mathbf{I}_d$ with the following model,

$$\mathbf{I}_t = \arg \min_{\mathbf{I}} \{ \lambda_1 \|\Psi \mathbf{I}\|_1 + \lambda_2 \|\mathbf{I} - f \mathbf{I}_r\|_1 : \mathcal{F}_\Omega \mathbf{I} = \mathbf{b} + \mathbf{e} \} \quad (3.7)$$

where Ψ , $\mathcal{F}_\Omega$, $\mathbf{b}$, f and $\mathbf{e}$ were defined previously. λ_1 , λ_2 are two positive regularization parameters.

Solving Eq. (3.7) with linear programming methods [29, 61, 62] can be computationally challenging. Alternatively, we provide an efficient algorithm to solve (3.7).

3.3.2 Equivalent Model Conversion

Directly attacking the original model is challenging as the sensing matrix $\mathcal{F}_\Omega$ is not invertible and the two regularization terms in the cost function of (3.7) are coupled with respect to $\mathbf{I}$. Therefore, some "tricks" are played to convert the original model to an

equivalent model to accurately solve the original problem but with improved computational efficiency.

3.3.2.1 Orthonormal Expansion

A matrix $P \in \mathbb{C}^{M \times N}$ is defined to be partial-orthonormal if it comprises a subset of rows from an orthonormal matrix $\Phi = \begin{bmatrix} P \\ Q \end{bmatrix}$, where $Q \in \mathbb{C}^{(N-M) \times N}$ is another partial orthonormal matrix [35, 48, 63].

Denote $\mathbf{x} = \Psi \mathbf{I}$ to be sparse coefficients of $\mathbf{I}_t$ in some basis, and $P = \mathcal{F}_\Omega \Psi'$, (3.7) can be expressed as:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \left\{ \begin{array}{l} \lambda_1 \|\mathbf{x}\|_1 + \lambda_2 \|\Psi' \mathbf{x} - f \mathbf{I}_r\|_1 \\ s.t. \ P \mathbf{x} = \mathbf{b} + \mathbf{e} \end{array} \right\}, \quad (3.8)$$

where $'$ represents the adjoint operator.

Sensing matrix $\mathcal{F}_\Omega$ is partial orthonormal as under-sampling the k-t space corresponds to selecting rows from the orthonormal full Fourier encoding matrix, and multiplying $\mathcal{F}_\Omega$ with another orthonormal matrix Ψ' keeps the partial orthonormal property. Therefore, P is inherently partial orthonormal and can be expanded to an orthonormal matrix Φ , leading (3.8) to the following equivalent form:

$$\mathbf{x} = \arg \min_{\mathbf{x}} \left\{ \begin{array}{l} \lambda_1 \|\mathbf{x}\|_1 + \lambda_2 \|\Psi' \mathbf{x} - f \mathbf{I}_r\|_1 \\ s.t. \ \Phi \mathbf{x} = \mathbf{p} + \mathbf{e}, \ H_\Omega(\mathbf{p}) = \mathbf{b} \end{array} \right\}, \quad (3.9)$$

where $\mathbf{p}$ is nominal fully sampled k-space data, $H_\Omega : \mathbb{C}^N \rightarrow \mathbb{C}^M, N < M$ is a sampling operator which keeps the elements indexed by sampling index set Ω while ignores the others.

3.3.2.2 Variable Splitting

In order to decouple mutual effects of the two sparsity-promoting regularization terms in the cost function of (3.9), we replace $(\Psi' \mathbf{x} - f \mathbf{I}_r)$ with an auxiliary variable $\mathbf{z}$. Then (3.9) is equivalently converted to a new constrained problem where the cost function is

minimized with respect to $(\mathbf{x}, \mathbf{z})$, subject to the original constraint and a new constraint that equals $\mathbf{z}$ with $\Psi'\mathbf{x} - f\mathbf{I}_r$. Specifically we can obtain the following form:

$$(\mathbf{x}, \mathbf{z}) = \arg \min_{\mathbf{x}, \mathbf{z}} \left\{ \begin{array}{l} \lambda_1 \|\mathbf{x}\|_1 + \lambda_2 \|\mathbf{z}\|_1 \\ s.t. \Phi\mathbf{x} = \mathbf{p} + \mathbf{e}, H_\Omega(\mathbf{p}) = \mathbf{b}, \\ \mathbf{z} = \Psi'\mathbf{x} - f\mathbf{I}_r \end{array} \right\} \quad (3.10)$$

Introducing an auxiliary variable or "variable splitting" has been used in applications of for instance image deconvolution, in-painting image reconstruction and restoration [56, 77, 88, 89, 96, 97].

3.3.3 Augmented Lagrangian Formalism

Utilizing AL framework, we have the AL function of (3.10) as:

$$\begin{aligned} \mathcal{L}(\mathbf{x}, \mathbf{z}, \mathbf{p}, \mathbf{u}, \mathbf{v}, \beta_1, \beta_2) \\ = \lambda_1 \|\mathbf{x}\|_1 + \mathbf{v}^H(\mathbf{p} - \Phi\mathbf{x}) + \frac{\beta_1}{2} \|\mathbf{p} - \Phi\mathbf{x}\|_2^2 + \lambda_2 \|\mathbf{z}\|_1 \\ + \mathbf{u}^H(\mathbf{z} - (\Psi'\mathbf{x} - f\mathbf{I}_r)) + \frac{\beta_2}{2} \|\mathbf{z} - (\Psi'\mathbf{x} - f\mathbf{I}_r)\|_2^2 \end{aligned} \quad (3.11)$$

where $\mathbf{u} \in \mathbb{C}^M$ and $\mathbf{v} \in \mathbb{C}^M$ are Lagrangian multiplier vectors for constraints $\Phi\mathbf{x} = \mathbf{p} + \mathbf{e}$ and $\mathbf{z} = \Psi'\mathbf{x} - f\mathbf{I}_r$, respectively; $\beta_1, \beta_2 > 0$. Note the constraint $H_\Omega(\mathbf{p}) = \mathbf{b}$ is satisfied when updating $\mathbf{p}$ in each iteration.

3.3.4 Alternating Direction Minimization

Solving (3.11) can be computationally challenging, as we have to minimize $\mathcal{L}$ with respect to multiple unknowns. Instead we minimize $\mathcal{L}$ in terms of one unknown each time as described in the alternating direction minimization method (AMD) [35, 76, 77].

Specifically, at $(k+1)$ th iteration:

$$\begin{aligned} \mathbf{x}^{(k+1)} &= \arg \min_{\mathbf{x}} \mathcal{L}(\mathbf{x}, \mathbf{z}^{(k)}, \mathbf{p}^{(k)}, \mathbf{u}^{(k)}, \mathbf{v}^{(k)}, \beta_1^{(k)}, \beta_2^{(k)}) \\ \mathbf{z}^{(k+1)} &= \arg \min_{\mathbf{z}} \mathcal{L}(\mathbf{z}, \mathbf{x}^{(k+1)}, \mathbf{p}^{(k)}, \mathbf{u}^{(k)}, \mathbf{v}^{(k)}, \beta_1^{(k)}, \beta_2^{(k)}) \\ \mathbf{p}^{(k+1)} &= \arg \min_{\mathbf{p}} \mathcal{L}(\mathbf{p}, \mathbf{x}^{(k+1)}, \mathbf{z}^{(k+1)}, \mathbf{u}^{(k)}, \mathbf{v}^{(k)}, \beta_1^{(k)}, \beta_2^{(k)}) \end{aligned}$$

$\mathbf{u}^{(k+1)}, \mathbf{v}^{(k+1)}, \beta_1^{(k+1)}, \beta_2^{(k+1)}$ are updated standardly according to AL framework.

3.3.4.1 Minimization with Respect to $\mathbf{x}$

After some derivations and simplifications,

$$\begin{aligned} \mathcal{L}_{\mathbf{x}} = & \lambda_1 \|\mathbf{x}\|_1 + \frac{\beta_1 + \beta_2}{2} \left\| \mathbf{x} - \frac{\beta_1}{\beta_1 + \beta_2} \Phi'(\mathbf{p} + \beta_1^{-1} \mathbf{v}) - \right. \\ & \left. \frac{\beta_2}{\beta_1 + \beta_2} \Psi(f\mathbf{I}_r + \mathbf{z} + \beta_2^{-1} \mathbf{u}) \right\|_2^2 + c \end{aligned} \quad (3.12)$$

where c represents constants to $\mathbf{x}$.

$\mathbf{x}$ can be exactly solved with element-wise soft-thresholding as described previously.

$\mathbf{x}^{(k+1)}$ is updated as follows:

$$\begin{aligned} \mathbf{x} = & \mathbf{S}_{\lambda_1(\beta_1 + \beta_2)^{-1}} \left(\frac{\beta_1}{\beta_1 + \beta_2} \Phi'(\mathbf{p} + \beta_1^{-1} \mathbf{v}) + \right. \\ & \left. \frac{\beta_2}{\beta_1 + \beta_2} \Psi(f\mathbf{I}_r + \mathbf{z} + \beta_2^{-1} \mathbf{u}) \right) \end{aligned} \quad (3.13)$$

where $\mathbf{S}_{\lambda}$ is soft-thresholding operator with threshold λ .

3.3.4.2 Minimization with Respect to $\mathbf{z}$

After some derivations and simplifications,

$$\mathcal{L}_{\mathbf{z}} = \lambda_2 \|\mathbf{z}\|_1 + \frac{\beta_2}{2} \left\| \mathbf{z} - (\Psi' \mathbf{x} - f\mathbf{I}_r) + \beta_2^{-1} \mathbf{u} \right\|_2^2 + c \quad (3.14)$$

where c represents constants to $\mathbf{z}$. Similarly, $\mathbf{z}$ can also be exactly solved with element-wise soft-thresholding. Specifically,

$$\mathbf{z} = \mathbf{S}_{\lambda_2 \beta_2^{-1}} (\Psi' \mathbf{x} - f\mathbf{I}_r - \beta_2^{-1} \mathbf{u}) \quad (3.15)$$

3.3.4.3 Minimization with Respect to $\mathbf{p}$

$$\mathcal{L}_{\mathbf{p}} = \frac{\beta_1}{2} \left\| \mathbf{p} - \Phi \mathbf{x} + \beta_1^{-1} \mathbf{v} \right\|_2^2 + c \quad (3.16)$$

Similarly, c is an constant to $\mathbf{p}$. Therefore,

$$\mathbf{p} = \Phi \mathbf{x} + \beta_1^{-1} \mathbf{v} \quad (3.17)$$

Together with the constraint $H_\Omega(\mathbf{p}) = \mathbf{b}$, $\mathbf{p}$ has the following solution,

$$\mathbf{p} = \begin{bmatrix} H_\Omega(\mathbf{p}) \\ H_{\bar{\Omega}}(\mathbf{p}) \end{bmatrix} = \begin{bmatrix} \mathbf{b} \\ H_{\bar{\Omega}}(\Phi\mathbf{x} - \beta_1^{-1}\mathbf{v}) \end{bmatrix} \quad (3.18)$$

where $\bar{\Omega}$ is the complementary set of Ω .

For simplicity, denote $\mathbf{I}_{rc} = f\mathbf{I}_r$ outline of the proposed algorithm for solving the model in (3.7) is shown in the following table.

Algorithm I: Outline of Proposed Algorithm

Initialization:

$\mathbf{I}_{rc}, \mathbf{x}^{(0)}, \mathbf{z}^{(0)}, \mathbf{p}^{(0)}, \mathbf{u}^{(0)}, \mathbf{v}^{(0)}, \beta_1^{(0)}, \beta_2^{(0)}, \mathbf{b}, \Omega, r_1, r_2, k = 0;$

Repeat

1. Update $\mathbf{x}^{(k+1)} =$

$$\mathbf{S}_{\lambda_1(\beta_1^{(k)} + \beta_2^{(k)})^{-1}} \left(\frac{\beta_1^{(k)}}{\beta_1^{(k)} + \beta_2^{(k)}} \Phi'(\mathbf{p}^{(k)} + \beta_1^{(k)-1}\mathbf{v}^{(k)}) + \frac{\beta_2^{(k)}}{\beta_1^{(k)} + \beta_2^{(k)}} \Psi(\mathbf{I}_{rc} + \mathbf{z}^{(k)} + \beta_2^{(k)-1}\mathbf{u}^{(k)}) \right)$$

2. Update $\mathbf{z}^{(k+1)} =$

$$\mathbf{S}_{\lambda_2\beta_2^{(k)-1}} \left(\Psi'\mathbf{x}^{(k+1)} - \mathbf{I}_{rc} - \beta_2^{(k)-1}\mathbf{u}^{(k)} \right)$$

3. Update $\mathbf{p}^{(k+1)} =$

$$\begin{bmatrix} \mathbf{b} \\ H_{\bar{\Omega}} \left(\Phi\mathbf{x}^{(k+1)} - \frac{1}{\beta_1^{(k)}}\mathbf{v}^{(k)} \right) \end{bmatrix}$$

4. Update $\mathbf{v}^{(k+1)} =$

$$\mathbf{v}^{(k)} + \beta_1^{(k)} (\mathbf{p}^{(k+1)} - \Phi\mathbf{x}^{(k+1)})$$

5. Update $\mathbf{u}^{(k+1)} =$

$$\mathbf{u}^{(k)} + \beta_2^{(k)} (\mathbf{z}^{(k+1)} - (\Psi'\mathbf{x}^{(k+1)} - \mathbf{I}_{rc}))$$

6. Update $\beta_1^{(k+1)} = r_1 \times \beta_1^{(k)}$

7. Update $\beta_2^{(k+1)} = r_2 \times \beta_2^{(k)}$

8. $k = k + 1.$

Until stopping criterion is met.

Output: $\mathbf{x}^{(k+1)}, \mathbf{p}^{(k+1)}, \mathbf{z}^{(k+1)}$

3.3.5 Empirically Improved Proposed Algorithm

In the algorithm described above, motion was estimated using low-resolution target image and reference image from acquired undersampled k-space with zero-padding unacquired locations. Motion compensated reference image I_{rc} was remained unchanged. We find helpful re-estimating the motion using reconstructed high-resolution target image, as motion re-estimated gets closer to the true motion field. Therefore, we have an improved algorithm where motion is iteratively refined using reconstructed target image obtained in inner iteration with the original algorithm. Normally, after re-estimating the motion twice, the algorithm will converge with a pre-set stopping criterion. Algorithm 2 shows outline of the improved algorithm.

3.4 Experiments and Results

3.4.1 Experiment Setup

Two categories of datasets were used to evaluate the performance. One is MR brain images including phantom and in-vivo images and the other is cardiac cine MR images. We simulated imaging acceleration by retrospectively decimating fully-sampled k-space data to a desired sampling pattern, though our method is not limited to specific sampling patterns.

3.4.1.1 General MR images

- (i) Simulated phantom dataset. We generated a reference image using MATLAB embedded function with default parameter values. The target image was constructed by adjusting certain parameter values such that ellipses in the reference were non-linearly scaled or rotated by certain angles. Random Gaussian noise of zero means

Algorithm II: Improved Proposed Algorithm

Initialization:

$\mathbf{I}_{rc}^{(0)}, \mathbf{x}^{(0)}, \mathbf{z}^{(0)}, \mathbf{p}^{(0)}, \mathbf{u}^{(0)}, \mathbf{v}^{(0)}, \beta_1^{(0)}, \beta_2^{(0)}, \mathbf{b}, \Omega, r_1,$
 $r_2, k = 0;$

Repeat

A. Repeat:

1. Update $\mathbf{x}^{(k+1)} =$

$$\mathbf{S}_{\lambda_1(\beta_1^{(k)} + \beta_2^{(k)})^{-1}} \left(\frac{\beta_1^{(k)}}{\beta_1^{(k)} + \beta_2^{(k)}} \Phi'(\mathbf{p}^{(k)} + \beta_1^{(k)-1} \mathbf{v}^{(k)}) \right. \\ \left. + \frac{\beta_2^{(k)}}{\beta_1^{(k)} + \beta_2^{(k)}} \Psi(\mathbf{I}_{rc} + \mathbf{z}^{(k)} + \beta_2^{(k)-1} \mathbf{u}^{(k)}) \right)$$

2. Update $\mathbf{z}^{(k+1)} =$

$$\mathbf{S}_{\lambda_2 \beta_2^{(k)-1}} \left(\Psi' \mathbf{x}^{(k+1)} - \mathbf{I}_{rc} - \beta_2^{(k)-1} \mathbf{u}^{(k)} \right)$$

3. Update $\mathbf{p}^{(k+1)} =$

$$\begin{bmatrix} \mathbf{b} \\ H_{\bar{\Omega}} \left(\Phi \mathbf{x}^{(k+1)} - \frac{1}{\beta_1^{(k)}} \mathbf{v}^{(k)} \right) \end{bmatrix}$$

4. Update $\mathbf{v}^{(k+1)} =$

$$\mathbf{v}^{(k)} + \beta_1^{(k)} (\mathbf{p}^{(k+1)} - \Phi \mathbf{x}^{(k+1)})$$

5. Update $\mathbf{u}^{(k+1)} =$

$$\mathbf{u}^{(k)} + \beta_2^{(k)} (\mathbf{z}^{(k+1)} - (\Psi' \mathbf{x}^{(k+1)} - \mathbf{I}_{rc}))$$

6. Update $\beta_1^{(k+1)} = r_1 \times \beta_1^{(k)}$

7. Update $\beta_2^{(k+1)} = r_2 \times \beta_2^{(k)}$

8. $k = k + 1.$

Until stopping criterion is met.

B. Update $\mathbf{I}_{rc}^{(k+1)}$ and set $k = 0.$

Until stopping criterion is met.

Output: $\mathbf{x}^{(k+1)}, \mathbf{p}^{(k+1)}, \mathbf{z}^{(k+1)}$

and 0.01 standard deviation was then added to both target and reference images to simulate practical scanning. Data size is 256×256 .

- (ii) In-vivo brain dataset. We selected two slices from an in-vivo three-dimensional brain dataset and used one of them as reference and the other as target. We intentionally increased reconstruction difficulty by selecting two slices which have obvious features differences. Data size is 256×256 .

Radial sampling pattern was applied to undersample the k-space. We simulated radial sampling with equispaced radial lines on a Cartesian grid, as shown in Fig. 3.1 which guarantees densely sampling in the central low-frequency area.

3.4.1.2 Dynamic Cardiac MR images

The proposed method was also evaluated with one in-vivo short-axis MRI scan dataset of size $256 \times 256 \times 25$ corresponding to coordinates $k_x \times k_y \times t$. At each k_x location, we undersampled k_y - t domain using a random two-dimensional Cartesian sampling mask with fully-sampled central areas and random sparsely sampled regions otherwise as shown in Fig. 3.2.

Fig. 3.1 and 3.2 show reference and target images used in our experiments. Difference images with and without motion compensation into consideration are exemplified to show feature displacements existing between reference and target images. Visual comparison between the difference images imply that motion estimation and compensation result in higher level of structural spatial sparsity in difference images.

3.4.2 Implementation Details

We applied Dr. Liu’s off-the-shelf optical flow method as the motion estimation and motion compensation transform [98]. Motion was initially estimated and compensated using low resolution images obtained from acquired k-space data. The penalty parameters β_1, β_2 started with very small value and geometrically increased. Incremental length control parameters r_1, r_2 were set equally to be 1.1. Stopping criteria was met when $\|P\mathbf{x} - \mathbf{b}\|_2^2 / \|\mathbf{b}\|_2^2 < 1e - 8$.

In the MR brain image studies, we compare the proposed method with commonly-used sparse MRI method [29], dubbed as SparseMRI, and reference-driven sparse MRI

Figure 3.1: Exhibition of target and reference images for general phantom and in-vivo MR brain image. First column from top to bottom: reference phantom image, target phantom image, difference image of reference and target images without motion compensation, difference image with motion compensation. Second column from top to bottom: reference in-vivo image, target in-vivo image, difference image without motion compensation, difference image with motion compensation. Third column: sampling pattern comprised of 24 equally spaced radial lines which corresponds to approximate 10 times acceleration (90% undersampling).

Figure 3.2: Exhibition of reference image and one sample target for in-vivo cardiac MR images. Sampling mask in k_y - t domain is shown on the right: fully-sampled central regions and random sparsely sampled in other regions

method [39], dubbed as SparseMRINC. In the cardiac cine image study, we compare with state-of-the-art k-t SPARSE [34] and k-t FOCUSS-MEMC [47].

In practice, we find helpful re-estimating the motion using reconstructed high-resolution target image and run the proposed algorithm iteratively. For simplicity, we name the original proposed method “Proposed 1” and the proposed method with motion refinement “Proposed 2”. If not mentioned explicitly, reconstruction results shown are obtained with Proposed 2.

We quantitatively evaluate the performance in terms of relative error defined as,

$$\text{Relative Error} = \frac{\|I - I^*\|_2^2}{\|I^*\|_2^2}, \quad (3.19)$$

where I represents reconstructed image and I^* denotes original image obtained from full-sampled data. All experiments were implemented in MATLAB, working on a WINDOWS desktop equipped with 3.1 GHz Intel Core i5 CPU and 8 GB RAM.

3.4.3 Performance Evaluation

3.4.3.1 General MR images

Fig. 3.3 shows comparison of reconstructions of phantom brain with 5% of full-sampled k-space measurements. Fig.3.3(a)-3.3(c) depict reconstructions by SparseMRI, SparseMRINC and the proposed, respectively. Fig.3.3(d)-3.3(f) show difference images constructed by subtracting reconstructed images from ground-truth for the three methods accordingly. Fig.3.3(a) reveals that SparseMRI suffers from severe streaking aliasing and artefacts. SparseMRINC significantly suppressed streaking aliasing and other artefacts noticed in Fig.3.3(a), but red arrows in Fig.3.3(b) indicate remaining presence of feature displacements from reference image. Dotted white circles highlight remaining reconstruction artefacts in the reconstructed image by SparseMRINC. The proposed method provides better reconstruction in terms of suppressing both artefacts and residual presence of feature displacements. Fig.3.3 also exemplifies one-dimensional line profiles across reconstructed images at the bottom. It is not difficult to notice that the proposed method follows the original line profile much more closely than its counterparts, especially in locations where intensities rise or fall sharply.

Fig. 3.4 shows comparison of in-vivo brain reconstructions using 10% of full-sampled k-space measurements. Figs. 3.4(a) and 3.4(d) are the reconstruction result by SparseMRI.

Figure 3.3: Comparisons of phantom brain reconstructions from 5% of full-sampled k-space data. Top: a) and d) by SparseMRI; b) and e) by SparseMRINC; c) and f) by Proposed. Bottom: one-dimensional line profile across red dotted arrow line. d), e) and f) are difference images of each method constructed by subtracting reconstructed images from ground-truth. Red arrows indicate remaining presence of feature displacements from reference image. Dotted white circles highlight reconstruction artefacts in the reconstructed image.

Figs. 3.4(b) and 3.4(e) exemplify the result by SparseMRINC. Fig. 3.4(c) and 3.4(f) correspond to the reconstruction from the Proposed method. Reconstruction by SparseMRI incurred severe artefacts and loss of details. SparseMRINC plausibly provided higher image quality in terms of resolution. However, central area of Fig. 3.4(b), pointed by red arrows, indicate obvious residual presence of feature displacements between target and reference images. Both artefacts and feature mismatch were significantly mitigated with the Proposed method as seen in Fig. 3.4(c). Comparison of the difference images indicates the same result. At the bottom of Fig. 3.4, one-dimensional profiles at the same position across reconstructed images are compared against original profile. Consistently, the proposed method matched the original more precisely than its counterparts.

Fig. 3.5 shows quantitative comparisons for both phantom and in-vivo brain studies in terms of relative errors from a range of acceleration factors. Top and bottom figures correspond to phantom and in-vivo experiments, respectively. Proposed 1 and Proposed 2 prevail over their counterparts in both studies for all accelerations. Constant lower relative errors brought by Proposed 2 than Proposed 1 indicate updating motion with previously reconstructed image improves reconstruction accuracies.

3.4.3.2 Dynamic Cardiac MR Images

Fig. 3.6 compares cardiac cine reconstructions on spatial x - y plain of k-t Sparse, k-t FOCUSS-MEMC and the proposed method with 10% of full-sampled k-t space measurements. First row exemplifies sample ground-truth region of interest (ROI) at three different temporal points corresponding to three different phase of a beating heart. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructions. Red arrows in reconstructions by k-t Sparse and k-t FOCUSS-MEMC indicate undesirable remaining aliasings. Noticeable

Figure 3.4: Comparisons of in-vivo brain reconstructions from 10% of full-sampled k-space data. Top: a) and d) by SparseMRI; b) and e) by SparseMRINC; c) and f) by Proposed. Bottom: one-dimensional line profile across red dotted arrow line. d), e) and f) are difference images of each method constructed by subtracting reconstructed images from ground-truth. Red arrows indicate remaining presence of feature displacements from reference image.

Figure 3.5: Quantitative comparisons of phantom (top) and in-vivo (bottom) brain reconstructions for a range of acceleration factors.

structured “noise” in difference images imply k-t Sparse and k-t FOCUSS-MEMC incurred either undesirable aliasings or missed essential details. The proposed method was

Figure 3.6: Comparison of cardiac cine reconstructions from 10% of full k-t space data: sample ROI reconstructions in spatial x - y domain. First column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 1$ time point. Second column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 17$ time point. Third column (top-to-bottom): ground-truth, k-t Sparse, k-t FOCUSS-MEMC, and Proposed at $t = 24$ time point. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructed images. Red arrows indicate remained aliasing. Structured “noise” in difference images imply either undesirable aliasing or loss of essential details.

Figure 3.7: Comparison of cardiac cine reconstructions from 10% of full k - t space data: sample ROI reconstructions in spatial-temporal y - t domain. Left: sample ground-truth at $x = 120, 128, 150$ spatial positions. Right-first column (top-to-bottom): k - t Sparse, k - t FOCUSS-MEMC, and the proposed at $x = 120$. Right-second column (top-to-bottom): k - t Sparse, k - t FOCUSS-MEMC, and Proposed at $x = 128$. Right-third column (top-to-bottom): k - t Sparse, k - t FOCUSS-MEMC, and Proposed at $x = 150$. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructions. Solid red arrows indicate undesirable remained aliasings. Dotted white arrows point out places where temporal variations were flattened.

able to give cleaner difference images. The proposed method followed temporal variations more closely with the original than its counterparts.

Fig. 3.7 shows comparison of sample cardiac cine reconstructions in spatial-temporal y - t domain with 10% of full k - t space measurements. Left part of Fig. 3.7 depicts sample

Figure 3.8: Quantitative comparison of cardiac cine reconstructions for a range of acceleration factors.

ground-truth at $x = 120, 128, 150$ spatial positions. The right part show reconstructions from k-t Sparse, k-t FOCUSS-MEMC, and the Proposed method from top to bottom at those spatial positions. Difference images constructed by subtracting reconstructed images from ground-truth are shown to the right of corresponding reconstructions. Solid red arrows in reconstructions by k-t Sparse and k-t FOCUSS-MEMC indicate undesirable remained aliasings. Dotted white arrows point out places where temporal variations were flattened. The proposed method significantly suppressed the aliasings and followed temporal variations more closely with the original than its counterparts.

Fig. 3.8 shows quantitative comparison for cardiac cine study in terms of relative errors

from a range of acceleration factors. The four methods provided close performance at low accelerations. But at higher accelerations, Proposed 1 and Proposed 2 offered noticeable lower relative error reconstructions than k-t Sparse and k-t FOCUSS-MEMC. Similarly, constant lower relative errors brought by Proposed 2 than Proposed 1 indicate updating motion with previously reconstructed image improves reconstruction accuracies.

3.5 Discussion and Conclusion

By exploring the sparsity of MR images, Compressed Sensing theory has been found with successful reconstructions of MR images from a small number of measurements. Research works have shown even better reconstructions by taking advantage of prior information from a reference image which has anatomical similarity with the target image. Compared to conventional CS methods, many existing reference-driven methods structure reconstructions of the target image as the addition of one reference image (either motion-compensated or not) and one sparse difference image. The difference image is then reconstructed by the conventional CS prototype. However, instead of reconstructing the target image as combination of one reference and one residual image, in this work, a novel method for motion-compensated reference-driven MR image reconstruction is presented. The target image is directly reconstructed by solving a ℓ_1 - ℓ_2 convex minimization problem which prompts ℓ_1 -norm sparsity of the target and the motion-compensated difference images. An efficient algorithm is proposed to solve the minimization problem with joint application of Augmented Lagrangian method and alternating direction minimization method. Numerical experiments demonstrate that the proposed framework provides more accurate reconstructions especially in high undersampling ratios when comparing with commonly used and state-of-the-art methods.

One significant contribution of this work is that it innovatively reconstruct the target

image directly. It is popular to reconstruct the residual image first and combine the reconstructed residual image and the reference image to obtain the target image. However, the reconstruction of the residual image in existing methods usually falls back to a prototypical CS-only problem, which can still fail when the residual image is not sufficiently sparse or the number of measurements is not sufficiently large. Instead of separating the reconstruction process into two steps, we have proposed a novel model that directly reconstructs the target image by prompting sparsity of the target and sparsity of the motion-compensated residual image in the same objective function simultaneously. The additional sparsity constraint in the objective function essentially provides additional prior information from the reference image and further restricts the solution space of the target image to the true subspace where it belongs to.

3.5.1 Computational Complexity

Main computational burden comes from the process of motion estimation and compensation. Take the cardiac cine dataset of size $256 \times 256 \times 25$ for example. Running on a PC with configurations mentioned before, each time of motion estimation and compensation cost 35 seconds taking up 67% of total time. Excluding time for motion estimation and compensation, main computational cost of each iteration falls on two discrete Fast Fourier transforms and two sparsifying transforms:

$$\text{Fourier Transform :} \quad \mathcal{F}\mathbf{x}$$

$$\text{Inverse Fourier Transform :} \quad \mathcal{F}'(\mathbf{p} + \beta_1^{-1}\mathbf{v})$$

$$\text{Sparsifying Transform :}$$

$$\Psi(\mathcal{F}'(\mathbf{p} + \beta_1^{-1}\mathbf{v}) + f\mathbf{I}_r + \mathbf{z} + \beta_2^{-1}\mathbf{u})$$

$$\text{Inverse Sparsifying Transform :} \quad \Psi'\mathbf{x}$$

While $\mathcal{F}$ and $\mathcal{F}'$ are Fourier transform and inverse Fourier transform respectively for both brain datasets and cardiac cine dataset, which can be executed efficiently with fast Fourier transform, Ψ and Ψ' are different in the two cases. For brain case, Ψ and Ψ' are two-dimensional wavelet transform and we obtained the sparse representation with off-the-shelf WaveLab toolbox [99]. For cardiac cine case, Ψ and Ψ' are one-dimensional Fourier and inverse Fourier transform along time and frequency direction, respectively. It took 0.25 and 0.45 seconds to run one iteration of inner loop in the proposed algorithm for brain and dynamic cardiac datasets, respectively. Desirable computational efficiency mainly comes from two factors:

- (i) Orthonormal expansion and variable splitting lead to solutions with iterative point-wise soft-thresholding form, which is very easy to implement and runs fast.
- (ii) Joint application of Augmented Lagrangian method and alternative direction minimization method guarantee the proposed framework converges with only a few iterations [74, 100].

3.5.2 Choice of Parameters

Performance of the proposed method is affected by values of $\beta_1^{(0)}$, $\beta_2^{(0)}$, r_1 and r_2 . $\beta_1^{(0)}$ and $\beta_2^{(0)}$, which are initial values of β_1 and β_2 , control how much of the largest sparse coefficients are cut off initially in deriving the solution of $\mathbf{x}$. Smaller the value of $\beta_1^{(0)}$ and $\beta_2^{(0)}$, the larger the percentage we cut off. r_1 and r_2 control the increment of β_1 and β_2 .

The following table compares performances of the proposed method with the $\times 6$ accelerated cardiac cine dataset when different sets of parameters are tested. The top half shows reconstruction performance with various $\beta_1^{(0)}$ and $\beta_2^{(0)}$ such that certain percentage of largest sparse coefficients are thrown away initially while keeping r_1 and r_2 fixed.

The bottom half depicts the performance when 99% of the largest sparse coefficients is thrown away and different pairs of r_1, r_2 are considered. We find that smaller r_1, r_2 and keeping smaller percentage of sparse coefficients initially lead to higher reconstruction accuracy but at the cost of computational efficiency in terms of numbers of iterations needed for converge. Normally r_1, r_2 within the range of $[1.05, 1.5]$ and the cut-off percentage within the range of $[75\%, 99\%]$ can produce good reconstruction.

	Parameters	RMSE	# Iter. to converge
$r_1 = 1.1$ $r_2 = 1.1$	20%	4.53%	17
	50%	0.94%	23
	75%	0.32%	27
	85%	0.32%	30
	99%	0.32%	50
99%	$r_1 = r_2 = 1.05$	0.31%	80
	$r_1 = r_2 = 1.1$	0.32%	50
	$r_1 = r_2 = 1.5$	0.35%	18
	$r_1 = r_2 = 2$	0.52%	13
	$r_1 = r_2 = 5$	1.31%	8

Table 3.1: Comparison of performance given different sets of parameters

3.5.3 Effect of Motion Estimation and Compensation

To exploit the effect of motion estimation and compensation, we consider two cases, one is when no motion estimation and compensation is applied to the proposed method and the other one is when motion estimation and compensation is applied to its counterpart.

- (i) When no motion estimation and compensation is applied to the proposed method, the motion-adaptive transform f in Eq. (3.7) becomes an identity matrix. We test this scenario, dubbed as “ProposedNC”, on the phantom brain dataset with various acceleration factors and compare with SparseMRINC and the original proposed method. Fig. 3.9 shows quantitative comparisons from various accelerations and

one visual performance comparison for $\times 20$ acceleration. From the visual comparison, it can be noted that ProposedNC suffers from slight feature displacements as indicated by red arrows. Likewise but more obviously, feature displacements can be seen in the reconstruction from SparseMRINC. However, ProposedNC successfully suppresses undesirable artefacts shown in SparseMRINC seen from white dotted circles. Quantitative comparison demonstrate that motion estimation and compensation improve performance of the proposed method, but even without motion estimation and compensation the proposed method still surpasses its counterpart for a range of acceleration factors.

- (ii) When motion estimation and compensation is applied to SparseMRINC. For simplicity, the method in this case is dubbed as “SparseMRIMEMC”. In practice, the motion-compensated reference images used by SparseMRIMEMC and the Proposed 2 are identical. Fig. 3.10 compares reconstructions of SparseMRINC, SparseMRIMEMC and the Proposed2 from $\times 20$ accelerated data acquisition. It can be seen that artefacts in Fig. 3.10(a) is reduced in Fig. 3.10(b) as indicated by white dashed circles in Fig. 3.10(a). However, both Fig. 3.10(a) and Fig. 3.10(b) incur motion misalignments indicated by red arrows and streaking aliasing. Those artefacts are completely suppressed in Fig. 3.10(c). Relative errors are 0.0032, 0.0022, 0.00089 for SparseMRINC, SparseMRIMEMC and the Proposed, respectively.

3.5.4 Source of Improvements

Some well-known regularizations can be naturally embedded in our proposed model in (3.7) for even better reconstructions, such as total variation (TV) regularization [28, 56, 90]. Off-the-shelf solvers for instance, nonlinear-conjugate-gradient (NCG) [29] can

Figure 3.9: Exhibition of effect of motion estimation and compensation on the proposed method. From left to right of the top, reconstructions from $\times 20$ accelerated data by SparseMRINC, ProposedNC and Proposed respectively are shown. Quantitative comparison from a range of acceleration factors is shown in the bottom.

be readily used for solving the expanded model, if reconstruction time is not a main consideration.

This work offers a framework for reference-driven MRI reconstruction which is not limited to any specific sampling scheme or motion estimation and motion compensation

Figure 3.10: Exhibition of effect of motion estimation and compensation on SparseMRINC. Reconstruction from (a) SparseMRINC, (b) SparseMRIMEMC, (c) Proposed2 are shown.

method. In other words, more effective sampling schemes and motion estimation and motion compensation methods proposed in the future can be naturally embedded into the proposed framework and make even better reconstruction performance.

In some scenarios, the target and reference images might have obvious contrast variations. Authors in [38, 41] modulated the contrast variations using contrast modulation functions with a generalized-series model. Therefore, (3.7) is rephrased as,

$$\mathbf{I}_t = \mathbf{C} \odot (f \cdot \mathbf{I}_r) + \mathbf{I}_d, \quad (3.20)$$

where $\mathbf{C}$ is the contrast modulation functions and $\odot$ represents a point-wise multiplication operator. Further discussion about this issue will be studied in the future.

In this chapter, we presented a novel method for reference-driven MR image reconstruction. The proposed method enables reasonable reconstructions from highly under-sampled k-space. We have shown efficacy of the proposed method by both simulated phantom and in-vivo datasets. We also provide an algorithm for the proposed model, although its computational efficiency and fast convergence property hasn't been investigated in details in this paper. The proposed method should prove useful in image

reconstructions in contrast-enhanced MRI, interventional MRI, longitudinal MRI, dynamic cardiac MRI and other applications where a reference is available.

Chapter 4

Compressive SEMAC: Reconstruction of MR Images with Metallic Implants by POCS-based Parallel Imaging and Noise

4.1 Introduction

Metallic implants are commonly used to treat orthopedic disorders, such as total knee replacement and spinal fixation in orthopedic surgery. Magnetic resonance imaging (MRI) providing excellent soft-tissue contrast is potentially the best modality for post-surgical examination of patients surgically treated with metallic implants. However, metal induces severe susceptibility artifacts in MR images, which often render MRI non-diagnostic.

While many methods have been proposed to suppress metal-induced artifacts in MRI [101–105], only two recently proposed spin-echo methods, MAVRIC (Multi-Acquisition Variable Resonance Image Combination) [106] and SEMAC (Slice Encoding for Metal Artifact Correction) [107], provide full correction of metal artifacts.

MAVRIC excites metal-effect affected spins into multiple overlapping frequency bands, while SEMAC features a view-angle-tilting compensation (VAT) [101] with a z-direction phase encoding after a spin echo sequence, as seen in Figure 4.2(a). While effective

in correcting metal-induced artifacts in MR images, both techniques incur significantly prolonged scan times by an order of 20.

SEMAC and MAVRIC involve combining multiple data elements in each voxel to correct metal artifacts. MAVRIC combines overlapping frequency bands with a sum-of-squares, which effectively suppresses noise by doubling the magnitudes however it also amplifies the differences among data elements, penalizing those containing relatively small signals. In contrast, SEMAC combines SEMAC-encoded slices with a complex sum to generate distortion-free MR images. However, SEMAC-corrected images can produce undesirably low (SNR) because many resolved voxels principally contain noise only [107].

The prolonged scan times incurred by the additional z -phase encoding and the low signal-to-noise ratio (SNR) due to the combination of SEMAC-encoded slices are the two main problems hampering the clinical utility of SEMAC. Hargreaves [108] proposed accelerating SEMAC acquisition by incorporating parallel imaging and partial- k imaging. However, the scan times are reduced at the cost of further loss of SNR. In scenarios inherently with SNR trade-off, loss in SNR can be even more problematic [109] such as some application of MRI for fat suppression. Koch [110] sequentially applied Compressed Sensing and data-driven parallel imaging to achieve acceleration. Lu exploited the redundancy in SEMAC-encoded slices received by multiple coils to enhance the SNR of SEMAC-corrected results via singular value decomposition [111] and compressed sensing [112].

In this work, we propose a new method to address both prolonged scan times and relatively low SNR of SEMAC without affecting the correction of metal-induced artifacts. Our preliminary work can be found in [113]. The new method, dubbed as Compressive SEMAC, is developed to exploit the compressibility of SEMAC-encoded slices. Specifically, the resolved distorted excitation profiles are highly sparse: field inhomogeneities in

each voxel are only dispersed to a limited frequency range. The proposed Compressive SEMAC performs center-filled Poisson random acquisition in the k_y - k_z phase encoding directions. The reconstruction of down-sampled SEMAC-encoded slices is performed with a *Projection Over Convex Set* (POCS) algorithm, which iterates between in-plane parallel imaging reconstruction at each k_z location and through-plane joint noise suppression across multiple coils. This POCS-based procedure is repeated for all slices to reconstruct resolved distorted excitation profiles, which are then summed up to correct the through-plane distortions as in standard SEMAC post-processing procedure. Phantom and in-vivo experiment results show that the proposed Compressive SEMAC fully corrects metal-induced artifacts in MR images, while incurring much shorter scan times and providing higher SNR as compared to the standard SEMAC and accelerated SEMAC with Compressed Sensing [112].

4.2 Theory

4.2.1 SEMAC Overview

MRI near metallic implants incurs severe artifacts, causing obtained image non-diagnostic. This is largely due to metal-induced field inhomogeneities artifacts which is responsible for most of the metal artifacts [114–116]. These metal artifacts are reflected in MR images in the following forms.

Signal Loss

Steep field gradients near metal surfaces leads to B_0 (externally supplied field) inhomogeneities: spins at different locations are not exposed to exactly the same B_0 , which yields a range of Larmor frequencies. The phenomenon that spins precess at different rates is known as “dephasing” in the transverse plain. Since the signal recorded is the

net magnetization in the transverse plane, dephasing causes cancellation of signal, namely signal loss.

Through-plane and In-plane Distortions

Nonlinear frequency-position mapping during the slice-selective excitation is the main reason for through-plane distortions. Normally, the thickness of one excited slice has a linear one-to-one mapping relationship with the bandwidth of the RF pulse, as depicted by the dotted line in Fig. 4.1. However, the field is twisted to be nonlinear around the metal objects, resulting in a nonlinear frequency-position mapping, as illustrated by the solid curve in Fig. 4.1. This nonlinearity leads to through-plane displacement (dark grey regions) and through-plane pile-ups (light grey regions).

Let $\Delta f(x, y, z)$ denotes the field inhomogeneities at a spatial location (x, y, z) , the spatial shift along z-axis, Δz , can be quantified as [107]:

$$\Delta z = -\frac{\Delta f(x, y, z)}{BW_{RF}}s \quad (4.1)$$

where BW_{RF} is bandwidth of the RF pulse, s is the nominal slice thickness centered at location (x, y, z) . Eq. (4.1) depicts the through-plane distorted excitation profiles caused by metal-induced inhomogeneities, $\Delta f(x, y, z)$.

In-plane distortions can be understood in the same way as through-plane distortions once replacing slice-selective gradient with readout gradient.

Consider the same location (x, y, z) . Denote BW_{read} as the readout bandwidth, Δz to be through-plane displacement defined as Eq. (4.1), N_x to be the number of samples along readout direction, G_s and G_x to be the slice-selective gradient and readout gradient, respectively. In-plane shift can be measured as follows [107]:

$$\Delta x = \frac{G_s}{G_x}\Delta z \quad (4.2)$$

Figure 4.1: Frequency-position mapping exhibit: in the absence of filed inhomogeneity, precession frequency of one excited spin and its spatial location is linearly mutually mapped (dotted line). When field inhomogeneity (dashed line) exists, the mapping becomes non-linear (solid curve) causing through-plane (in-plane) displacement (dark grey regions) and through-plane (in-plane) pile-ups (light grey regions).

And maximum in-plane shift is bounded by

$$\Delta x_{\max} = BW_{RF}/2BW_P \quad (4.3)$$

where $BW_P = 2BW_{read}/N_x$ is the readout bandwidth allocated on each k-space sample. Note that there are no distortions along y-axis [108].

4.2.1.1 SEMAC Technique

SEMAC is an imaging technique that completely corrects the signal loss and distortions due to metal-induced field inhomogeneities by applying an VAT compensation sequence following the spin-echo sequence with third dimensional phase encodings in z direction, as demonstrated in Fig. 4.2(a). The spin echoes in SEMAC address the signal loss resulting from intra-voxel dephasing, and in-plane distortions is cured by the VAT compensation gradient. Additional z -phase encoding in SEMAC resolves through-plane distortions. SEMAC essentially performs 2D excitation of spins subject to metal-induced field inhomogeneities into non-overlapping slabs. The slabs are 3D encoded into SEMAC-encoded slices, which contain the distorted excitation profiles at the corresponding nominal z locations. As illustrated in Fig. 4.2(b), the SEMAC-encoded slices are positioned such that the spins are placed back to their actual spatial locations. Eventually metal-induced artifacts is corrected via adding up the SEMAC-encoded slices with a linear complex sum.

Eliminate Signal Loss

Recall that signal loss is mainly caused by intra-voxel dephasing resulted from field inhomogeneities near the metal objects. As illustrated in Fig. 4.2(a), SEMAC is de facto a spin echo method: manipulating another 180° radio frequency (RF) pulse after the initial 90° , which refocuses the dephased spins. This “trick”, however, effectively addresses the signal loss problem in metal MRI.

Figure 4.2: Exhibition of SEMAC technique. (a) imaging sequence of SEMAC; (b) steps of corrections of through-plane distortions. During the image acquisition stage, distorted excitation profiles of each slice are resolved with extra slice direction encodings. In the image reconstruction stage, resolved spins from all slices in one certain voxel are combined together to correct the through-plane distortions in that voxel.

Correct In-plane and Through-plane Distortions

Most in-plane distortions can be suppressed by including a VAT compensation gradient along slice-selective direction G_{slice} in Fig. 4.2(a) during readout [101].

SEMAC corrects through-plane distortion by following a SE sequence with VAT with slice direction phase encodings (light grey region along G_{slice} in 4.2(a)). Since through-plane distortions appear as through-plane displacement and through-plane pile-ups. Additional encoding along z-axis resolves the through-plane distorted excitation profiles for each slice, which explicitly positions the excited spins in certain ROI to their actual spatial positions. Adding up the resolved spins from all slices in one certain voxel corrects the through-plane distortions. Fig. 4.2(b) illustrates the correction of through-plane distortions.

4.2.2 Sparsity of SEMAC-encoded Slices

Fig. 4.3 shows three sample SEMAC-encoded distorted excitation profile on y - z plane. It can be seen that the distorted excitation profile is highly sparse. On one hand, as most resolved data elements only contain background noise, combining sparse distorted excitation profiles to correct through-plane distortions results in relatively low SNR of the SEMAC-corrected results. On the other hand, the sparsity of distorted excitation profiles, when properly exploited, presents a great opportunity to accelerate the SEMAC acquisition.

4.2.3 Compressive SEMAC Sampling

The acceleration of SEMAC imaging is achieved by random down-sampling k_y - k_z domain with a center-filled Poisson disk, as shown in Fig. 4.4. The center-filled Poisson sampling disk is designed to meet two objectives: (1) full sampling of central k_y lines for all k_z locations and, (2) uniform Poisson random down-sampling in outer k_y - k_z plane. The fully-sampled central k_y lines are used for the calibration of interpolation kernels in parallel imaging, which involves the estimation of k -space correlations between coils.

Figure 4.3: Sample SEMAC-encoded distorted excitation profiles in y - z plane. The image is highly sparse: only a few large-magnitude elements while most areas only contains background noise.

Note that the auto-calibration of the interpolation kernels is done for each k_z location. This is important to ensure that the reconstruction of down-sampled SEMAC-encoded slices does not affect the performance of the additional z -phase encoding in resolving through-plane distortions.

The Poisson random down-sampling, which renders aliasing artifacts highly incoherent, can be implemented by scheduling the skipping of k_y and k_z phase encoding steps. The incoherent down-sampling in outer k_y - k_z space is important for Compressive SEMAC: both aliasing artifacts and background noise can be effectively suppressed by exploiting the compressibility of distorted excitation profiles.

4.2.4 Reconstruction of Compressed SEMAC-encoded Slice

The reconstruction is realized via a *projection over convex set* (POCS) algorithm, which iterates between in-plane k_x - k_y parallel imaging reconstruction at each k_z location and noise suppression by exploiting the joint sparsity of SEMAC-encoded slices across coils. The reconstruction algorithm is outlined in Exhibit 1. Parallel imaging relies on the

Figure 4.4: Center-filled Poisson sampling pattern. Top: three-dimensional down-sampling with a center-filled Poisson disk on k_y - k_z plane at each k_x direction. Bottom: sample subsequently formed sampling pattern on k_x - k_y plane. Pictures have been resized for better rendering.

correlation of spatial sensitivities between coils to interpolate missing in-plane k -space samples, while denoising is performed in the image domain where joint sparsity of distorted excitation profiles can be exploited to differentiate signals from noise.

4.2.4.1 Parallel Imaging Reconstruction

With the center-filled Poisson-disk sampling pattern in k_y - k_z plane, the in-plane k_x - k_y parallel imaging reconstruction is to fill in missing k -space readout lines at irregular k_y locations. Fig. 4.4 shows an in-plane k_x - k_y sampling pattern at one k_z location. As the missing k -space lines reside at irregular Cartesian locations, auto-calibrating recon-

struction for regular Cartesian down-sampling, such as ARC and GRAPPA [12, 117, 118], cannot be directly applied in our case. Instead, we perform the in-plane parallel imaging reconstruction by imposing k -space self-consistence constraint, as explored in the data-driven parallel MRI reconstruction methods, SPIRIT and PRUNO [21, 22].

Similar to GRAPPA, the self-consistence constrained in-plane parallel imaging reconstruction estimates the calibration kernel $\mathbf{g}$ from the the central fully-sampled $k_x - k_y$ region. The kernel $\mathbf{g}$ contains the reconstruction weights which captures the spatial correlations of k -space samples in a local neighborhood. The key observation of the self-consistence parallel imaging reconstruction is the kernel $\mathbf{g}$, once estimated, is spatially invariant and independent from the actual k -space sampling pattern. Hence, the kernel $\mathbf{g}$ can be readily imposed on both acquired and missing k -space samples.

Auto-calibration The calibration kernels are derived based on the idea of self-consistence which states that value of any point (acquired or missed) synthesized from its entire neighbour should be consistent with itself or mathematically expressed as follows:

$$x_i(j) = \langle N(x_i(j)), g_i \rangle \quad (4.4)$$

where $x_i(j)$ denotes the j -th pixel of the i -th coil, $N(x_i(j))$ denotes the entire neighbourhood of $x_i(j)$ across all coils, g_i is the synthesizing weights for the i -th coil. The coefficients of the linear combination are the synthesizing weights g_i for the i -th coil.

Full-sampled central region in k_x - k_y plane is used as the calibration area, which provides both $x_i(j)$ and $N(x_i(j))$. Kernel for the i -th coil g_i is obtained by solving the following least square problem:

$$g_i = \arg \min_{g_i} \sum_{j \in \Omega} \|x_i(j) - \langle \mathcal{N}(x_i(j)), g_i \rangle\|_2^2 \quad (4.5)$$

where Ω is the support of data of i -th coil which are “synthesized” from their neighbourhoods in the calibration stage. Fig. 4.5 exhibits the scheme of calculating the synthesizing weights for each coil.

Figure 4.5: Calculation of the synthesizing weight of each coil. Left corresponds to $\mathbf{x}_i$ in Eq. 4.4. Middle matrix represents neighbouring measurements of $\mathbf{x}_i$. Right corresponds to the weights of interest. Values of the synthesizing weights could be obtained by solving the over-determined system.

Reconstruction Let $\mathbf{x}$ be the vectorized entire k -space data across all coils, $\mathbf{G}$ denotes a matrix having coil synthesizing kernels g_i in appropriate locations. It is convenient to express the self consistency in matrix form.:

$$\mathbf{x} = \mathbf{G}\mathbf{x} \quad (4.6)$$

where the matrix $\mathbf{G}$ effectively performs convolution of the calibration kernels over the entire k -space samples $\mathbf{x}$. Note that Eq. 4.6 is equivalent to $(\mathbf{G} - \mathbf{I})\mathbf{x} = \mathbf{N}\mathbf{x} = 0$, where

$\mathbf{N}$ is referred to as null kernel [21]. By splitting $\mathbf{x}$ into the acquired samples $\mathbf{x}_a$ and the missing samples $\mathbf{x}_m$, we have

$$\mathbf{N}_m \mathbf{x}_m = -\mathbf{N}_a \mathbf{x}_a, \quad (4.7)$$

where $\mathbf{N}_a$ and $\mathbf{N}_m$ are the columns of $\mathbf{N}$ corresponding to the acquired and missing samples, respectively. The missing samples $\mathbf{x}_m$ can then be effectively found by solving (4.7) with Conjugate Gradient (CG) descent [21, 29]. Note that the computationally intensive PI reconstruction using CG (4.7) only needs to be invoked once to fill in the missing k -space values prior to the POCS iteration. During the POCS iteration, the parallel imaging reconstruction is carried out by executing the convolution of $\mathbf{G}$ (4.6).

4.2.4.2 Noise Suppression via Exploiting Joint Sparsity

With the aid of incoherent Poisson-disk sampling along k_y - k_z phase encoding directions, the noise amplified by the in-plane parallel imaging reconstruction are rendered highly incoherent in the image domain. Given the *a priori* knowledge that distorted excitation profiles are highly sparse, three-dimensional Fourier Transform of the parallel imaging reconstructed SEMAC-encoded slices serves as an effective sparsifying transform: distorted excitation profiles are mostly sparse along the z axis. Furthermore, the distorted excitation profiles are jointly sparse across coils, as phased-array coils receive the same distorted excitation profile modulated with different coil sensitivities. The joint sparsity across coils can be leveraged by a sum-of-squares combination of the sparsified coefficients.

The noise suppression is modelled into the following constrained minimization problem:

$$\begin{aligned} \min_{\mathbf{w}} \quad & \sum_{c=1}^n \|\mathcal{S}_c \mathbf{w}\|_1^2 \\ \text{s.t.} \quad & \mathcal{F}_\Omega \mathcal{S}_c \mathbf{w} = \mathbf{x}_{a,c}, \forall c = 1, \dots, n \end{aligned} \quad (4.8)$$

where the distorted excitation profile $\mathbf{w}$ in three-dimensional image domain is modulated with the coil sensitivity S_c for n coils. The data consistency is enforced for the acquired k -space samples $\mathbf{x}_{a,c}$ over the sampling support $\mathcal{F}_\Omega$. The optimization problem in Eq. 4.8 is often re-formulated into a unconstrained Lagrangian form,

$$\arg \min_{\mathbf{w}} \sum_{c=1}^n \|S_c \mathbf{w}\|_1^2 + \lambda \|\mathcal{F}_\Omega S_c \mathbf{w} - \mathbf{x}_{a,c}\|_2^2, \quad (4.9)$$

where the parameter λ controls the data consistency. This optimization problem can be easily solved by soft-thresholding with λ [29]. Note that no elaborate sparsifying transform is required in this case.

Eq. (4.9) can be efficiently solved by iteratively executing joint soft-thresholding and data fixing which enforces data consistency. Let $w(\rho) = [w_1(\rho), w_2(\rho), \dots, w_{N_c}(\rho)]$ represents the vector comprising of distorted excitation profiles at certain position ρ across N_c coils. Denote β to be the threshold and $i = 1, 2, \dots, N_c$, the joint soft-thresholding operator $JS(\cdot)$ is implemented as

$$JS(w_i(\rho)) = \frac{w_i(\rho)}{\|w(\rho)\|_2} \max(\|w(\rho)\|_2 - \beta, 0),$$

The reconstruction algorithm is outlined in Exhibit 1.

Intuitively, the sum-of-squares combination of distorted excitation profiles received by multiple coils exploits the joint sparsity such that the sparsified coefficients of signals can be more easily differentiated from noise. The reconstruction of a SEMAC-encoded slice in Compressive SEMAC iterates between successive in-plane parallel imaging reconstruction and noise suppression via exploiting joint sparsity. The parameter β starts with a large value to perform aggressive denoising at the early stage of the iteration, while the potential of loss in image details is mitigated with the data consistency constraint and the parallel imaging reconstruction. Over the iterations, the parameter β gradually reduces to match the noise level estimated from high k -space edges.

Exhibit 1: Proposed Reconstruction Algorithm

- 1: **Initialization**
 - 2: Estimate in-plane correlation kernel $\mathbf{G}$ from central k -space;
 - 3: Perform in-plane parallel imaging reconstruction by solving Eq. 4.7;
 - 4: Estimate background noise variance σ^2 from outer k -space;
 - 5: Set soft-threshold $\beta = n\sigma$ (e.g.; $n = 20$)

 - 6: **Repeat POCS while $\beta > \sigma$**
 - 7: Denoising of distorted excitation profiles:
 - 8: Perform the joint soft-thresholding with β
 - 8: Impose the constraint of data consistency:
 - 9: Set data with the acquired samples in k -space;
 - 10: Convolute k -space data with the correlation with kernel $\mathbf{G}$;
 - 11: Set data with the acquired samples in k -space;
 - 12: $\beta \leftarrow \beta - \sigma$ and go to 6
-

4.2.5 Combination of Compressive SEMAC-encoded Slices

The reconstruction algorithm is repeated to reconstruct all SEMAC-encoded slices. The reconstructed compressive SEMAC-encoded slices are then combined to correct through-plane distortions. To ensure coherent combination of resolved signals in each voxel, phase variations between the SEMAC-encoded slices are carefully eliminated during acquisition. In addition, the SEMAC-encoded slices are phase-modulated such that their corresponding distorted excitation profiles are positioned in the center of field-of-view (FOV) along the slice-select dimension. Subsequently, the compressive SEMAC-encoded slices are positioned at their nominal z locations and combined to correct through-plane distortions.

Fig. 4.6 shows the reconstruction flowchart of the proposed method. The full-sampled k -space data is first under-sampled by the carefully designed sampling pattern. Reconstruction of under-sampled k -space iterates between parallel MRI reconstruction at each k_z position in k -space domain and noise suppression in the image domain.

Figure 4.6: Flowchart of the reconstruction process of the proposed method. The full-sampled k-space data is first under-sampled by the carefully designed sampling pattern. Reconstruction of under-sampled k-space iterates between parallel MRI reconstruction at each k_z position in k-space domain and noise suppression in the image domain

4.3 Experimental Methods

For the following studies, the performance of Compressive SEMAC is evaluated through comparison with the standard SEMAC where k -space is full-sampled and Compressed Sensing SEMAC (CS-SEMAC) proposed by Lu in [112]. Imaging acceleration is simulated by retrospectively decimating fully-sampled k -space data to the center-filled Poisson-disk sampling, which can be incorporated in the SEMAC imaging sequence by skipping the corresponding k_y - k_z phase encodes. The reconstruction algorithms were implemented in MATLAB (Mathworks, Natick, MA) on a Windows machine equipped with Intel Core i5-2400 Processor 3.10 GHz and 8 GB RAM.

4.3.1 SNR Quantification

To quantify the comparison of different methods in terms of SNR improvement, we performed quantitative SNR measurements on a phantom study — images of a titanium shoulder prosthesis positioned in gel. The size of the dataset is $384 \times 192 \times 11 \times 28$. Dataset was shared by Dr. Wenmiao Lu and specific scan parameters could be found out in [107]. The full-sampled SEMAC data were retrospectively down-sampled by 3 in this phantom study.

SNR was calculated with the “pseudo multiple replica” method [119]. Detailed procedures of quantifying the SNR had been explored by [107].

4.3.2 In Vivo Studies

We scanned two volunteer human subjects with metallic implants. The first volunteer with stainless steel screws in his knee and the second volunteer with a metallic fixation device in his spine. The experiment datasets were provided by Dr. Wenmiao Lu and the scan parameters for both in-vivo studies can be found out in his journal [107].

4.4 Results

4.4.1 SNR Quantification

Fig. 4.7 shows sample SEMAC-corrected phantom images by standard SEMAC, CS-SEMAC and Compressive SEMAC. Fig. 4.7(a) and (b) depict the sample image by standard SEMAC reconstructed from full-sampled k-space data in x - y plane and reformatted cross-sectional image in y - z plane. Fig. 4.7(c) and (e) show corresponding reconstructed sample images by CS-SEMAC. Fig. 4.7(g) and (i) show corresponding reconstructed images by the proposed Compressive SEMAC. Fig. 4.7(d), (f), (h) and (j) show difference images constructed by subtracting reconstructed images above them from corresponding standard SEMAC images. It can be seen that both Compressive SEMAC and CS-SEMAC significantly reduce the noise in standard SEMAC images. Structured noise in difference images highlighted by white arrows imply that CS-SEMAC incurred severe loss of details.

One uniform region with the same coordinates across all slices was selected for SNR evaluation as indicated by the dashed box in Figs. 4.7(a), (c) and (g). The SNR value for standard SEMAC is 12 and this value is boosted to 30 and 35 by Compressive SEMAC and CS-SEMAC, respectively.

4.4.2 In Vivo Studies

Fig. 4.8 shows sample SEMAC-encoded slices (known as distorted excitation profiles) for the in-vivo knee study by standard SEMAC, CS-SEMAC and Compressive SEMAC in x - z and x - y planes. Views in x - z plains indicate that the distorted excitation profiles are highly sparse. Fig. 4.8 also shows that noise incurred by standard SEMAC in both x - z and x - y planes was significantly suppressed by CS-SEMAC and Compressive SEMAC.

Figs. 4.9 exemplifies one sample SEMAC-corrected image of in-vivo knee study in

Figure 4.7: Comparison of sample phantom SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b) reconstruction in x - y plane by Compressive SEMAC, (d) reconstruction in x - y plane by CS-SEMAC, (d) reconstruction in reformatted cross-sectional y - z plane by Compressive SEMAC, (e) reconstruction in reformatted cross-sectional y - z plane by C-SEMAC, (f,g,h,i) difference images constructed by subtracting reconstructed images above from corresponding ground-truth images. A dashed-box in (a) indicates an uniform region for SNR quantification. The most right shows the titanium shoulder prosthesis used in the phantom study.

x - y plane by standard SEMAC, Compressive SEMAC and CS-SEMAC. Figs. 4.9(a), (b), (d) show reconstruction by Standard SEMAC, Compressive SEMAC and CS-SEMAC, respectively. Fig. 4.9(c) shows the difference image of Compressive SEMAC constructed by subtracting Fig. 4.9(b) from Fig. 4.9(a). Fig. 4.9(e) shows the difference image of CS-SEMAC constructed by subtracting Fig. 4.9(d) from Fig. 4.9(a). It can be seen that noise was greatly suppressed by Compressive SEMAC and CS-SEMAC. Both methods retained the correction ability of Standard SEMAC. By examining the difference images, it can be seen that Compressive SEMAC preserved more image details while its counterpart incurred severe loss of details, as implied by the white arrows in Fig. 4.9 (d) and (e). Fig. 4.10 show SEMAC-corrected reconstructions of in-vivo spine study. Comparisons in Fig. 4.10 show consistent results with phantom and in-vivo knee studies.

4.5 Discussion and Conclusion

Severe metal-induced artifacts often render MR images non-diagnostic. SEMAC is an imaging technique that removes metal-induced artifacts in MR images but there are two main problems hampering the clinical utility of SEMAC, namely prolonged scan times and relatively low signal-to-noise ratio (SNR). To address both problems, this work incorporates SEMAC with the advances in compressive sensing to exploit the compressibility of SEMAC-encoded slices. The proposed technique, dubbed as Compressive SEMAC, employs a center-filled Poisson disk to perform vast down-sampling of SEMAC-encoded slices along k_y - k_z phase encoding directions. The reconstruction of a down-sampled SEMAC-encoded slice is performed with a *Project Over Convex Set* (POCS) algorithm, which iterates between in-plane reconstruction at each k_z location using parallel MRI technique and joint noise suppression across multiple coils. Phantom and in-vivo experiment results validate that the proposed Compressive SEMAC not only greatly reduces

Figure 4.8: Comparison of a typical view of SEMAC-encoded slices in x - z and x - y planes: (a) standard SEMAC, (b) CS-SEMAC, and (c) Compressive SEMAC.

Figure 4.9: Comparison of sample in-vivo knee SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b) reconstruction in x - y plane by Compressive SEAMC, (d) reconstruction in x - y plane by CS-SEMAC, (c) and (e) difference images constructed by subtracting reconstructed images on their left from (a). White arrows in (d) and (e) point out regions where CS-SEMAC encounters noticeable loss of image details.

Figure 4.10: Comparison of sample in-vivo spine SEMAC-corrected images. (a) ground-truth by full-sampled standard SEMAC, (b) reconstruction in x - y plane by Compressive SEAMC, (d) reconstruction in x - y plane by CS-SEMAC, (c) and (e) difference images constructed by subtracting reconstructed images on their left from (a).

scan times incurred to fully correct metal artifacts but also leads to the improved SNR of SEMAC-corrected results.

The key idea of Compressive SEMAC is to alternatively perform parallel imaging reconstruction and noise suppression via exploiting the sparsity of SEMAC-encoded slices.

Parallel imaging reconstruction and noise suppression fix disadvantages of the other: parallel imaging reconstruction enables successful reconstruction of down-sampled SEMAC-encoded slices but further degrading the SNR; noise suppression by prompting the joint sparsity of three-dimensional distorted excitation profiles remarkably suppresses noise, but inevitably incurs potential loss of details. Compressive SEMAC leverages these two procedures with a POCS manner. Note Compressive SEMAC exploits multiple-coils joint sparsity instead of single coil sparsity, as the phase-array coils receive the same image information modulated with different coil sensitivities. Intuitively, in joint soft-thresholding, it is the sum-of-squares of sparsified coefficients across all coils that is essentially being thresholded, therefore sparsified coefficients in sensitivity-low area can be well preserved, as long as their sum-of-square magnitude across all coils is larger than the threshold. The proposed method can be incorporated with other reconstruction techniques to achieve further acceleration of acquisition, such as partial Fourier reconstruction method [108, 120, 121].

4.5.1 Compressive SEMAC Sampling

Compressive SEMAC consists of a practical sampling strategy which provides necessary acceleration factor but also incoherence for effective denoising. Uniform sampling provides good noise property or low g -factor. However, aliasing brought by uniform sampling is coherent and can be difficult to unfold. On the other hand, purely random sampling offers incoherent aliasing but incurs frequently occurring large gaps between samples which enlarges the g -factor and increases the noise. Compressive SEMAC consists of a center-filled Poisson disk sampling, which integrates advantages from both uniform sampling and random sampling: it renders incoherent aliasings and noise while provides uniform distance between samples.

Center-filled region provides enough measurements to construct an over-determined system of linear equation for performing parallel imaging calibration in k_x - k_y plane to calculate the convolution kernels. Uniform random Poisson sampling in the high-frequency area in k_y - k_z plane makes sure the noise and aliasing is incoherent and can be suppressed in the noise suppression stage.

4.5.2 Comparisons to Denoising-only Methods

Denoising-only method [112] relies on the advanced results from Compressed Sensing. It accelerates the imaging process of SEMAC meanwhile boosts the SNR as it is essentially a basis pursuit denoising (BPDN) problem. However, denoising-only methods can incur loss of image details. To preserve image details, Compressive SEMAC complements noise suppression with parallel imaging reconstruction in a POCS manner. Specifically, after noise suppression, the signal of interest is subject to data consistence and self-consistence constraints so as to compensate possible signal loss by noise suppression.

Although not explicitly discussed in the paper, another significant advantage over CS-SEMAC is reduction of reconstruction time. Take the knee study for example, CS-SEMAC took as much as 7 hours to reconstruct all 32 SEMAC-encoded slices while Compressive-SEMAC took 1.5 hours to complete the whole reconstruction process.

To conclude, Compressive SEMAC addresses the problems of significantly prolonged scan time and low SNR of SEMAC with full correction of metal-induced artefacts.

Chapter 5

Conclusion and Future Work

Conclusion

Sampling less data reduces scan time to a significant extent but causes undesirable aliasings. Developing efficient methods to reconstruct the MR image from incomplete measurements becomes our main concern. Sparsity or compressibility of MR images is the theme of this thesis, connecting the three individual works.

In the first work, we investigated the application of CS in MRI reconstruction. A method, dubbed as “ONE- ℓ_1 ”, was proposed to address low computational efficiency and slow convergence problems in commonly-used and state-of-the-art methods while delivering a comparable recovery accuracy, as demonstrated with in-vivo brain and in-vivo dynamic cardiac studies. Orthonormal expansion plays an very important role in our method, specifically the measurement matrix is expanded to an orthonormal matrix so that the solution of x can be updated with a closed form.

In light of the limitation of sparsity-only constrained reconstruction methods and the availability of a reference in many applications, we explored the reconstruction problem with the help of sparsity and the presence of a reference image. A novel method for motion-compensated reference-driven MR image reconstruction is presented. The target image is directly reconstructed by solving a ℓ_1 - ℓ_2 convex minimization problem which

prompts ℓ_1 -norm sparsity of the target and the motion-compensated difference images. An efficient algorithm is proposed to solve the minimization problem with joint application of Augmented Lagrangian method and alternating direction minimization method.

In the third work, sparsity constraint has been combined with coil sensitivity for better reconstruction performance. We focus on a significant practical problem: reconstruction of MR images of parts of the body that have metallic implants. Field inhomogeneity near metallic implants causes severe susceptibility artefacts in MR images, which renders MRI non-diagnostic. We propose a POCS technique in which the reconstruction alternates between in-plane parallel MRI reconstruction and joint noise suppression using sparsity constraint across multiple coils. Phantom and in-vivo results testify that the proposed reconstruction technique not only greatly reduces scan time incurred to fully correct metal artifacts but also leads to the improved SNR of existing state-of-the-art methods.

To conclude, the sparsity of MR images, if exploited properly, enables reasonable reconstruction from highly down-sampled k-space samples, which in turn reduces the scan time incurred to achieve high-quality images using traditional imaging techniques. Reconstruction performance could be further improved by incorporating appropriate extra prior information such as coil sensitivity and anatomical similarity between the target and reference images.

Future Work

- (i) Sparsity plays an important role in MRI reconstruction. The sparser an MR image is, the larger the acceleration we can achieve. Traditional sparsifying transforms might fail to sparsify the image to a desirable level, especially when the image contains lots of details such as the brain image or when the measurements are significantly noisy. Designing the optimal sparsifying transform is a very promising research direction. Preliminary works suggest the “optimal” transform should be adaptive and data-specific. Elad *et al.* [122] and Mairal *et al.* [123–125] provided a nice direction to follow.
- (ii) In our first and second works, we mainly concerned sparsity in the wavelet domain. It is very popular to impose a sparsity constraint in the finite difference domain; in other words, adding a ℓ_1 -norm total variation (TV) penalty to the objective function will produce a better reconstruction result in recovery accuracy, especially helpful in preserving high frequency information such as the image details. Therefore, how to incorporate this TV penalty into the model will be an interesting topic to work on. Indeed, in our reference-driven MRI reconstruction work, incorporating TV regularization is very straightforward. However, how to solve the expanded constraint problem efficiently is more challenging.
- (iii) Iterative soft thresholding in noise suppression is quite straightforward and easy to implement. Though it achieves reasonable performance, we doubt that there are still chances for useful information being removed together with noise by this simple denoising method. In light of the efficacy of the ONE- ℓ_1 method and the fact that ONE- ℓ_1 involves aggressive continuation reconstruction, we are inspired to incorporate “ONE- ℓ_1 ” with “Compressive SEMAC” to achieve even superior

reconstruction performance.

- (iv) It is true that given certain sparsity level and number of samples, directly solving (P_p) will produce better performance than solving (P_1) in terms of reconstruction accuracy, where $0 < p < 1$. This superiority can be demonstrated in Fig. 5.1, which shows that as a sparseness prior, ℓ_p ($0 < p < 1$) better approximates ℓ_0 than ℓ_1 does. There are many works related to solving (P_p) and some of them have already been applied to the field of MRI reconstruction [31, 126–131]. Modelling a (P_p) ($0 < p < 1$) and solving the resulted nonconvex problem attract great interest from us.

Figure 5.1: Approximation to absolute sparsity prior: smaller p brings about better approximation

- (v) It is promising and interesting to apply what we've achieved to other significant problems in MRI. One possible application is metabolic MRI. Metabolic imaging provides direct information about tissue metabolism. Magnetic Resonance Spectroscopic Imaging (MRS) is the most commonly used imaging tool in metabolic MRI technique and it could be easily incorporated into standard MRI machine. One of

the drawbacks of standard MRI techniques when applied to metabolic MRI is that limited signal detected is not desired to image metabolic events: The external static magnetic field B_0 polarize spins and generates a net magnetization with the same direction as B_0 . This net magnetization can be too small as spins of two energy states cancel out each other. To address the limited signal problem, a sophisticated imaging concept was proposed, dubbed as “hyperpolarization” [132, 133].

Hyperpolarization technique drives nuclei temporarily into a different re-distribution such that the net magnetization amplifies by a factor of 10,000. However, there are several concerns. First, this state is highly unstable, generating massive polarization decays to equilibrium exponentially with a constant time T_1 . To image metabolic events in real time, we desire the hyperpolarized states to be long enough, in other words, looking for spins with long T_1 (such as C^{13}). At the same time, imaging time should be reduced, and this is where MRI reconstruction techniques come into the picture. There are already some works exploring the reconstruction problems in MRSI and had very promising results [134–136]. Take C^{13} as an example of spins. Because C^{13} has a very large chemical shift and C^{13} in the parent molecule and its metabolites are only sparsely detected in a few spectrum locations, we are very keen to explore this level of sparsity in order to improve the special reconstruction problems in MRS.

Publication

- (i) Zai Yang, Cishen Zhang, Jun Deng and Wenmiao Lu, “Orthonormal Expansion ℓ_1 -Minimization Algorithms for Compressed Sensing”, IEEE TRANSACTIONS ON SIGNAL PROCESSING, VOL. 59, NO. 12, 2011
- (ii) Jun Deng, Zai Yang, Cishen Zhang and Wenmiao Lu, “Orthonormal Expansion ℓ_1 -Minimization for Compressed Sensing in MRI”, Proceeding of IEEE International Conference in Image Processing (ICIP) 2011, pp. 2297-2300
- (iii) Jun Deng, Yap-Peng Tan and Wenmiao Lu, “Motion-compensated Orthonormal Expansion ℓ_1 -Minimization for Reference-driven MRI Reconstruction Using Augmented Lagrangian Method”, submitted to Journal of Visual Communication and Image Representation, under minor revision
- (iv) Jun Deng, Yap-Peng Tan and Wenmiao Lu, “Motion-adaptive ℓ_1 -Minimization for Reference-driven MRI Reconstruction”, accepted by IEEE International Conference on Image Processing (ICIP) 2013, *oral presentation* (paper withdrawn for visa issue)
- (v) Jun Deng, Wenmiao Lu, Yi Lu and Yap-Peng Tan, “Compressive SEMAC: Reconstruction of MR Images with Metallic Implants by POCS-based Parallel Imaging and Noise Suppression”, submitted to Magnetic Resonance in Medicine, under revision

- (vi) Wenmiao Lu, Jun Deng, Yi Lu, Garry E. Gold and Brian Hargreaves, “POCS-based Compressive Slice Encoding for Metal Artifact Correction”, Proceeding of International Society of Magnetic Resonance in Medicine 2011

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