

PONTIFICIA UNIVERSIDAD CATOLICA DE CHILE SCHOOL OF ENGINEERING

## MOTION CORRECTED 3D LIVER UNDERSAMPLED MRI

### FELIPE ANDRÉS YÁÑEZ LANG

Thesis submitted to the Office of Research and Graduate Studies in partial fulfillment of the requirements for the degree of Master of Science in Engineering

Advisor: PABLO IRARRÁZAVAL M.

Santiago de Chile, May 2014

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O MMXIV, Felipe Andrés Yáñez Lang

Gratefully to my family and Hana S. D. G.

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As the author of this thesis I am extremely proud to let you know that the page you are reading is indisputably the most valuable one I wrote.

Felipe Yáñez Paris, France, January 2014

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#### ABSTRACT

The emergence of sparse reconstruction methods for undersampled data in Magnetic Resonance Imaging (MRI), such as Compressed Sensing (CS), have been valuable tools to accelerate data acquisition while preserving accurate image reconstruction. However, sparse reconstruction methods, including CS, are not easy to apply when there is intra-frame motion. Such is the case of free-breathing dynamic MRI in the liver. It is difficult to avoid non-rigid motion artifacts, even more so in volumetric acquisitions. To avoid these kind of artifacts, we propose a new reconstruction technique tailored for dynamic liver imaging by estimating the motion between frames to correct inconsistencies in k-space measurements. In this work, we describe how the proposed method addresses an increase in image efficiency for free-breathing dynamic 3D liver MRI. Our approach produced results that demonstrate it is feasible to achieve a 10x speedup in acquisition time and remove motion artifacts without diminishing image quality. The proposed method produced gains up to 6 dB with respect of traditional CS framework.

**Keywords:** compressed sensing; undersampling; sparse reconstruction; motion; motion correction; non-rigid registration; liver.

#### RESUMEN

La aparición de métodos ralos de reconstrucción de imágenes para datos submuestreados en formación de Imágenes por Resonancia Magnética (IRM), como Compressed Sensing (CS), han sido herramientas valiosas para acelerar la adquisición de datos, preservando una reconstrucción precisa de la imagen. Sin embargo, los métodos ralos de reconstrucción de imágenes, incluyendo CS, no tienen una aplicación simple cuando hay movimiento intra-cuadro. Tal es el caso de IRM dinámicas en el hígado, adquiridas en respiración libre. Es difícil evitar artefactos producto de movimientos no rígidos del hígado, más aún en adquisiciones volumétricas. Para evitar este tipo de artefactos, proponemos una nueva técnica de reconstrucción de imágenes adaptada para imágenes dinámicas de hígado, mediante la estimación del movimiento entre cuadros para corregir inconsistencias en las mediciones del espacio-k. En este trabajo se describe cómo el método propuesto aumenta la eficiencia de la imagen en aplicaciones de IRM dinámicas en el hígado, adquiridas en respiración libre. Nuestro método produce resultados que demuestran que es factible aumentar 10 veces el tiempo de adquisición y eliminar artefactos de movimiento sin disminuir la calidad de la imagen. El método propuesto produce ganancias de hasta 6 dB con respecto a la técnica tradicional.

Palabras Claves: *compressed sensing*; submuestreo; reconstrucción; movimiento; corrección de movimiento; registro no rígido; hígado.

#### **1. INTRODUCTION**

Image efficiency in Magnetic Resonance Imaging (MRI), i.e. the trade-off between acquisition time and image quality (Figure 1.1), has been widely studied in the MRI community. In the past, image efficiency improvements were shown to be directly related to hardware development, e.g. acquiring multiple lines in the readout after a single excitation to speed up data collection (Wright, 1997). Nowadays, we are at the point where physical and physiological restrictions are the main reasons for limiting the speed while scanning (Lustig, Donoho, & Pauly, 2007). In this sense, the emergence of new approaches handling the imaging problem with less data as required by the Nyquist-Shannon rate seem to provide an answer for further improvements in image efficiency.



FIGURE 1.1. Image efficiency in MRI, i.e. the trade-off between acquisition time and image quality, can be related to two sources of improvement. The first one is producing higher quality results in a fixed time acquisition scheme  $(A_1 \rightarrow B)$ ; and the second one is speeding up acquisition time without diminishing image quality  $(A_2 \rightarrow B)$ .

These new approaches, also known as sparse reconstruction methods, rely on the idea of compressibility, which assumes redundancy in an image (Candes, Romberg, & Tao,

2006a, 2006b). One sparse reconstruction method for undersampled data of high impact in MRI is Compressed Sensing (CS) (Candes et al., 2006a, 2006b; Candes & Tao, 2006; Donoho, 2006). Previous work has shown that CS is a relatively new concept in signal processing used to speed up MRI scanning time (Lustig et al., 2007). CS enables reliable image recovery for severely undersampled random measurements, if the desired signal is compressible in a known domain and the aliasing artifacts due undersampling are incoherent in the measurement domain (Candes et al., 2006a, 2006b; Candes & Tao, 2006; Donoho, 2006; Lustig et al., 2007). The CS framework is used in different MRI applications, e.g. brain imaging (Lustig, Donoho, Santos, & Pauly, 2008), diffusion spectrum imaging (Bilgic et al., 2012), quantitative susceptibility mapping (Yanez et al., 2013), and multi-contrast reconstruction (Bilgic, Goyal, & Adalsteinsson, 2011).

CS has also been applied in dynamic MRI, where most reconstruction methods use temporal correlations in the signal. A common approach is to exploit the sparsity of the residual signal after subtraction of an initial estimate (Jung, Sung, Nayak, Kim, & Ye, 2009; Jung & Ye, 2010). In this way, the signal has a sparse representation, and it is possible to achieve more accurate results. A similar problem has also been widely studied in the field of video compression, where video images are compressed using the similarities between different frames to achieve high efficiency. Some ideas from video compression algorithms are also used in dynamic MRI reconstructions (Jung & Ye, 2010).

In MRI applications, dealing with motion is also an important issue for reconstruction methods, because during an exam, i.e. while scanning, unwanted or involuntary motion from the patient may lead to motion artifacts in the reconstructed images (Lustig et al., 2008; Usman et al., 2012). The presence of motion may also reduce the sparsity of the images (Usman et al., 2012). In this sense, a generalized motion correction framework was developed to correct non-rigid motion in the reconstructed images (Batchelor et al., 2005). The motion correction framework models a matrix equation that produces motion-corrupted images from the ideal image. The inversion has been demonstrated in (Batchelor et al., 2005), where it was shown that it is possible to reconstruct a motion-corrected image from numerical matrix inversion algorithms.

In liver MRI, it is critical to have high spatial and temporal resolution to identify small structures for clinical interpretation, even more so in volumetric acquisitions where poor-resolution images are usually obtained in patients with end-stage liver diseases because of breath-hold limitations (Chandarana, Block, Stepancic, Sodickson, & Otazo, 2012). Small structures such as tumor nodules up to 20 mm and tumor thrombi in small vessels (macro-scopic angioinvasion) are frequently hard to identify in low-quality images (Chandarana et al., 2011). Increasing spatial and temporal resolution can help detect tumors in early stages, thereby avoiding surgery and instead treating the patient with curative therapy, which provides the best possible long-term survival at a lower cost (Lee et al., 2011; Naugler & Sonnenberg, 2010).

Herein, we propose a compressed sensing framework tailored for free-breathing 3D liver MRI with high spatial and temporal resolution. The proposed dynamic framework incorporates a generalized non-rigid motion registration between frames (Myronenko, 2010; Hill, Batchelor, Holden, & Hawkes., 2001) to correct inconsistencies in k-space and increase the number of samples to recover a motion corrected image under a CS reconstruction method (Usman et al., 2012). At each frame, the number of measurements is severely below the Nyquist-Shannon rate. Parallel imaging was used in this work, where the proposed method was applied independently to each coil. We performed this approach in 3D in-vivo experiments using various undersampling factors, and obtained improved ratios with respect to traditional CS technique.

#### 2. THEORY

We organize this section into three parts: first we present the imaging problem to solve, we compare different schemes to tackle the problem, and finally we present the proposed technique.

#### 2.1. Imaging

In traditional dynamic MRI, acquisition techniques sample data according to a regular breathing position to avoid motion artifacts (Figure 2.1 (a)). Instead, we will consider sampling through different breathing positions, i.e. the acquired data in a respiratory cycle of T possible motion states (frames) delivers a collection of T images, as illustrated in Figure 2.1 (b). We assume that at a particular discrete time  $t \in \{1, ..., T\}$ , all acquired coefficients are consistent, i.e. each frame is free of motion artifacts.



FIGURE 2.1. Representation of two acquisition approaches employed in dynamic MRI, considering measurements at different translational displacement positions across time. (a) Traditional acquisition technique, the acquired data in a respiratory cycle of T possible frames delivers a collection of few images ( $\ll T$ ). (b) Proposed acquisition technique, the acquired data in a respiratory cycle of T possible frames delivers a collection of few images ( $\ll T$ ). (b) Proposed acquisition technique, the acquired data in a respiratory cycle of T possible frames delivers a collection of T severely undersampled images.

Let us define  $\mathbf{m}_t \in \mathbb{C}^N$  as the underlying vector form of the ideal *N*-samples sequence of 3D MR images in the canonical domain at discrete times  $t \in \{1, ..., T\}$ ,  $\mathbf{b}_t \in \mathbb{C}^P$  as the vector form of the *P* k-space noisy measurements of  $\mathbf{m}_t$  ( $P \ll N$ ), and  $\mathbf{e}_t \in \mathbb{C}^P$  as the corresponding acquisition noise. To facilitate notation, we will drop the subindex *t*, and will assume that it represents the vector form at all discrete times  $t \in \{1, ..., T\}$ . With this, the imaging capture procedure can be written as

$$\mathbf{b} = \mathbf{SFm} + \mathbf{e},\tag{2.1}$$

where  $\mathbf{F}$  is the 3D Fourier transform operator that transforms independently each image to k-space, and  $\mathbf{S}$  is the sampling operator that randomly undersamples the k-space data from each frame.

Now, we can also describe **m** from a reference frame  $\mathbf{m}_{t_0} \in \mathbb{C}^N$  by using the motion information between each frame and the reference. We denote **V** as a motion operator that warps the pixels from an arbitrary reference image  $\mathbf{m}_{t_0}$  to the positions at all possible times. In operator form, this can be written as

$$\mathbf{m} = \mathbf{V}\mathbf{m}_{t_0},\tag{2.2}$$

such that Equation (2.1) is

$$\mathbf{b} = \mathbf{SFVm}_{t_0} + \mathbf{e}. \tag{2.3}$$

As k-space has been severely undersampled ( $P \ll N$ ), the system in Equation (2.3) is ill-posed, i.e. it does not satisfy the Nyquist-Shannon sampling rate. To measure the degree of undersampling, we define the acceleration factor as R = N/P.

For image recovery, we need additional information to formulate a regularized version of Equation (2.3), and in this sense, the structure of the true images is key.

#### 2.2. Approaches

We propose to address the reconstruction of a motion corrected image by solving an optimization problem for a reference image  $\mathbf{m}_{t_0} \in \mathbb{C}^N$ , chosen from any of the *T* possible frames in the respiratory cycle.

A first approximation for image recovery can be made with a least squares method. Considering the model in Equation (2.3), one minimizes the residual of data consistency

$$\hat{\mathbf{m}}_{t_0} = \underset{\mathbf{m}_{t_0}}{\arg\min} \frac{1}{2} \left| \left| \mathbf{SFVm}_{t_0} - \mathbf{b} \right| \right|_{\ell_2}^2,$$
(2.4)

where  $||\mathbf{u}||_{\ell_p} = (\sum_{i=1}^n |u_i|^p)^{1/p}$  denotes the *p*-norm of vector  $\mathbf{u} \in \mathbb{R}^n$ , letting  $p \ge 1$  be a real number, and the motion operator **V** is known. The solution of this problem is well-known and has a closed form, but the main problem is the stability of the solution because of small perturbations in the measurements. The solution's stability is directly related to the large condition number of the encoding matrix, **SFV**.

A comprehensive theory to tackle this problem was proposed by Tikhonov and Arsenin (Tikhonov & Arsenin, 1977), where information of the underlying signals was incorporated to the model. This information is the so-called regularization or penalization

$$\hat{\mathbf{m}}_{t_0} = \arg\min_{\mathbf{m}_{t_0}} \frac{1}{2} ||\mathbf{SFVm}_{t_0} - \mathbf{b}||_{\ell_2}^2 + \tau \frac{1}{2} ||\Psi \mathbf{m}_{t_0}||_{\ell_2}^2, \qquad (2.5)$$

where  $\tau$  is the regularization parameter that weights the trade-off between the data consistency and the penalization, and  $\Psi$  is an operator that ensures smoothness in the underlying image. The solution of this problem is also known and has a closed form (Tikhonov & Arsenin, 1977). The main problem with the  $\ell_2$ -regularization method is that the smoothness assumption is not always true in medical imaging.

A new approach was introduced in 2006, Candès et al. (Candes et al., 2006a, 2006b; Candes & Tao, 2006) and Donoho (Donoho, 2006) proposed a reliable image reconstruction based on compressibility of the signals. In medical imaging,  $\ell_1$ -regularization fits very well since medical images can be represented in a sparse domain. Comparing to Tikhonov and Arsenin's regularization, sparse reconstruction methods also have the advantage of achieving more accurate results with high acceleration factors (Ng, 2004). The  $\ell_1$ -regularization method does not have a closed form solution, but it can be solved using efficient first-order optimization methods (Lustig et al., 2007; Becker, Bobin, & Candes, 2011; Boyd & Vandenberghe, 2004).

#### 2.3. Recovery

For an accurate motion corrected image reconstruction, we propose a second-order cone program that minimizes the regularized version of Equation (2.3), i.e. the  $\ell_1$  norm of a sparse representation of  $\mathbf{m}_{t_0}$ , with the data consistency constraints (Candes & Tao, 2005)

$$\begin{array}{l} \underset{\mathbf{m}_{t_0}}{\text{minimize}} & \left|\left|\Phi\mathbf{m}_{t_0}\right|\right|_{\ell_1} \\ \text{subject to} & \frac{1}{2} \left|\left|\mathbf{SFVm}_{t_0} - \mathbf{b}\right|\right|_{\ell_2}^2 < \sigma, \end{array}$$

$$(2.6)$$

where  $\Phi$  is a sparsifying operator, e.g. wavelet, or total variation, and  $\sigma$  is a small number that controls data fidelity, usually determined by the noise level.

Prior to solving the problem of minimization (2.6), we illustrate the procedure to obtain the motion operator  $\mathbf{V}$  employed in this recovery.

- First, we compute an initial reconstruction using a CS framework.
- Next, we define a reference frame and estimate the motion vectors by registering these images to the reference.
- Finally, we define **V** using this registration to align frames to the reference, and the inverse registration function is used to warp the reference to all possible frames.

#### 2.3.1. Initial reconstruction

For a preliminary estimation, we exploit temporal correlations assuming sparsity of the residual signal after subtraction of an initial estimate of the mean (Jung et al., 2009). We first compute the mean of the measurements, denoted as  $\bar{\mathbf{b}}$ .

Now, the zero-mean measurements are computed as

$$\mathbf{b}_t' = \mathbf{b}_t - \bar{\mathbf{b}}, \ \forall t \in \{1, \dots, T\}.$$

$$(2.7)$$

A zero-mean CS recovery is applied independently to the residual of each frame  $\mathbf{b}'_t$ . Because of the sparsity of the residual image, we select the canonical domain as the sparse domain. The zero-mean CS reconstruction is defined as follows:

$$\hat{\mathbf{m}}' = \underset{\mathbf{m}'}{\arg\min} \ \frac{1}{2} ||\mathbf{SFm}' - \mathbf{b}'||_{\ell_2}^2 + \beta ||\mathbf{m}'||_{\ell_1}, \tag{2.8}$$

where  $\beta$  is the regularization parameter that weights the trade-off between the data consistency and the penalization.

The initial reconstruction is computed by adding the mean image in the canonical domain to each residual estimation,

$$\hat{\mathbf{m}}_t = \hat{\mathbf{m}}_t' + \mathbf{F}^H \bar{\mathbf{b}}, \ \forall t \in \{1, \dots, T\},$$
(2.9)

where  $\mathbf{F}^{H}$  is the Hermitian transpose of  $\mathbf{F}$ , i.e. the 3D inverse Fourier transform operator that transforms independently each to k-space frame to the image domain.

#### 2.3.2. Motion vectors estimation

The reconstructed images allow us to select a reference image. The reference frame is usually chosen at end expiration when the liver is moving less. Each preliminary estimation is registered to the reference frame using a fast and efficient adaptive regularization approach for non-rigid image registration (Myronenko, 2010).

Our registration method relies on a Bayesian formulation, where we estimate the prior distribution on parameters assuming that it is close to some given model distribution. We constrain the prior distribution to be a Gauss-Markov random field, which allows us to solve for the prior distribution analytically and provides a fast optimization algorithm (Myronenko, 2010),

$$\mathbf{V}_{t} = \underset{\mathbf{v}_{t}}{\arg\min} D(\hat{\mathbf{m}}_{t}, \hat{\mathbf{m}}_{t_{0}} | \mathbf{v}_{t}) + w \left| \left| \mathbf{k}^{T} \mathbf{Q} \mathbf{v}_{t} \right| \right|_{\ell_{1}}, \ \forall t \in \{1, \dots, T\},$$
(2.10)

where  $D(\hat{\mathbf{m}}_t, \hat{\mathbf{m}}_{t_0} | \mathbf{v}_t)$  is a similarity measure, e.g. Mutual Information (MI) (Viola & Wells, 1997), Sum of Squared Differences (SSD), or Sum of Absolute Differences (SAD), w is the weight between data consistency and penalization,  $\mathbf{k}$  are the squared-rooteigenvalues of the model distribution,  $\mathbf{Q}$  is a matrix containing the eigenvectors of the inverse covariance shift-invariant matrix. In a prior distribution constrained to be a Gauss-Markov random field, the eigenvalues and eigenvectors have a known form (Myronenko, 2010). Motion operator  $\mathbf{V}$  is defined by the motion vectors  $\mathbf{V}_t$  obtained from the proposed registration algorithm. The motion vectors are obtained pixel-wise for every frame.

#### 2.3.3. MC-CS recovery

To recover the motion corrected image,  $\hat{\mathbf{m}}_{t_0}$ , the acquired data from all the motion states (frames) **b** and the estimated motion vectors operator **V** are needed as shown in Equation (2.6). Considering the noise level in the  $\lambda$  regularization parameter, the unconstrained version of the minimization problem in Equation (2.6) is the following convex problem

$$\hat{\mathbf{m}}_{t_0} = \arg\min_{\mathbf{m}_{t_0}} \frac{1}{2} ||\mathbf{SFVm}_{t_0} - \mathbf{b}||_{\ell_2}^2 + \lambda ||\Phi \mathbf{m}_{t_0}||_{\ell_1}.$$
(2.11)

#### 3. MATERIALS AND METHODS

The goal of the proposed technique is to reconstruct a motion corrected 3D liver image from undersampled pseudorandom measurements. The main contribution is employing motion-corrected inconsistent k-space samples from different frames into a CS reconstruction framework to estimate a single higher quality image (Figure 2.1). To correct motion, we estimate the motion vectors between different frames. To compute the motion vectors we perform a preliminary CS reconstruction to each frame, and then, we register those reconstructed images to a reference frame. The obtained motion vectors generate the motion operator **V**, which is an invertible matrix (Batchelor et al., 2005). Figure 3.1 shows a block diagram with the proposed algorithm steps.

#### 3.1. Imaging protocol

A conventional 3D T1-weighted fast field echo sequence was performed in the liver of healthy volunteers to generate the in-vivo dataset. Previously, a low-resolution image was acquired as a prescan. Informed consent was obtained from volunteers prior to imaging. A four-element body coil was used for all imaging, and images were obtained using a Philips Achieva 1.5 T scanner (Philips Healthcare, Best, The Netherlands).

#### **3.2. Reconstruction protocol**

To solve Equations (2.11) and (2.8), two different  $\ell_1$ -norm penalized non-linear conjugate gradients with fast & cheap backtracking line-search reconstruction were implemented in Matlab (R2011a, The MathWorks, Inc., Natick, MA) (Lustig et al., 2007). A pseudo-code of both algorithms can be found in the Appendix.

To run the algorithms, we used a computer with an Intel(R) Core(TM) i7-3770 CPU @ 3.40 GHz and a memory (RAM) capacity of 32.0 GB. In both reconstructions, we performed a maximum of 150 conjugate gradient iterations. Equation (2.11), for computational efficiency, was solved using the Hermitian-symmetric form for data consistency:



FIGURE 3.1. Block diagram of the proposed free-breathing dynamic 3D liver MRI reconstruction framework. (1) From the acquired undersampled motion corrupted samples, the mean of the data is subtracted. A CS recovery is performed to the residual, independently for each of the T frames. The estimation of each image is computed as the sum of the corresponding CS recovery with the mean image in the canonical domain. (2) The reconstructed images allows us to select a reference frame, usually chosen at end expiration where the liver is moving less. The T reconstructed frames are registered to the reference image, to compute the corresponding motion vectors. (3) The undersampled motion corrupted k-space acquisitions and the previously computed motion vectors are used to perform a motion corrected CS reconstruction to obtain a high resolution 3D liver image.

$$\mathbf{V}^{H}\mathbf{F}^{H}\mathbf{S}^{H}\mathbf{S}\mathbf{F}\mathbf{V}\mathbf{m}_{t_{0}}=\mathbf{V}^{H}\mathbf{F}^{H}\mathbf{S}^{H}\mathbf{b}.$$

For Equations (2.11) and (2.8), we selected optimal  $\lambda$  and  $\beta$  respectively via the computation of the L-curve criterion (Hansen, 2000). In this case, optimal regularization parameters lie on the corner of the L-curve (Hansen, 1992), but sometimes it is difficult to distinguish the operating point that lies on the corner. Because of this difficulty, Hansen and O'Leary proposed the criteria of choosing the point with maximum curvature to be the optimal point (Hansen & O'Leary, 1993).

In Equation (2.11), the sparse representation is obtained via wavelet transformation, where the wavelet transform operator  $\Phi$  is an especially effective and computationally efficient biorthogonal wavelet: Cohen-Daubechies-Feauveau 9/7 (CDF 9/7) wavelet transform<sup>1</sup>, which was reported to yield high quality sparse approximations for simulated diffusion propagators (Merlet, Paquette, Deriche, & Descoteaux, 2012). In Equation (2.8), the sparse representation is in the canonical domain.

#### 3.3. In-vivo experiments

We performed a conventional breath-held 3D T1-weighted fast field echo sequence with fully sampled cartesian trajectory in the liver of four healthy volunteers to generate the in-vivo dataset. During data collection, we acquired different frames in one respiratory cycle. For liver imaging, a four-element body coil was used, and the measurements were obtained with the following parameters: pulse repetition time = 4.1 ms, echo time = 1.95 ms, field of view =  $160 \times 224 \times 150$  mm<sup>3</sup>, flip angle =  $10^{\circ}$ , slice thickness = 10 mm, dynamic scans = 16, spatial resolution = 2 mm isotropic, scan time = 222 s.

The coil sensitivity maps were estimated by preliminarily acquiring a fully-sampled low-resolution image prior to the 3D T1-weighted fast field echo sequence. Both acquisitions had identical previously defined scan parameters. Secondly, a smoothing filter was applied to the low-resolution images from each coil. Finally, the estimated maps were found to be the normalization of each smoothed low-resolution image by computing the sum-of-squares of all coil images.

Undersampled k-space data were obtained by multiplying the acquired measurements from each coil with the sampling pattern. The sampling pattern is different for each frame, and it is generated using a Monte Carlo algorithm with minimum peak interference according to a particular acceleration factor (R) (Lustig et al., 2007). The random sampling

<sup>&</sup>lt;sup>1</sup>Matlab code available online at http://www.getreuer.info/home/waveletcdf97

pattern is based on a polynomial variable density function, i.e. the low-frequency regions are more dense than the higher frequency regions (Figure 3.2 ). The number of samples from each frame is determined by the probability density function and the sampling factor (R). We also enabled a sampling pattern that does not require a probability density function (results not shown). In-vivo experiments were performed at various sampling factors (R).



FIGURE 3.2. Sampling patterns at R = 5. Each sampling pattern was generated using a polynomial variable density function, where the order of the polynomial can vary. For image display we show 2D slices crossing the center of k-space. The sampling pattern is a binary matrix, which represents if a sample is acquired (white) or not (black). In our experiments we use a polynomial of order 6 to generate the sampling pattern.

To apply the proposed technique, we previously constructed the motion operator V using motion information between frames. A CS recovery is applied within each frame to ultimately compute the motion vectors. The underlying initial CS reconstruction is defined as follows: we subtract the mean data across frames (mean image); estimate the residual for each frame via CS recovery; and add them to the mean image in the canonical domain. The CS reconstructions from each receiver coil are combined using the sum of squares prior to registration. The reference image (frame) is chosen from previous combined reconstructions. We set as the reference the most common respiratory motion state at end expiration when the liver is moving less. All CS estimations are non-rigidly registered to the reference using an adaptive image registration algorithm (Myronenko, 2010). We used this registration to align frames to the reference, and the inverse registration function to warp the reference to all possible frames. Motion operator V is constructed with these two functions.

We performed the registration algorithm that solves Equation (2.10) using the Mutual Information (MI) (Viola & Wells, 1997) similarity measure. We considered 250 iterations of a single hierarchical level with a mesh window size of 16 voxels.

We used the motion operator V and undersampled k-space data to reconstruct the underlying motion corrected 3D liver image using the proposed technique. To test accuracy in reconstructions, we considered the signal-to-error ratio (SER)

$$SER = 20 \log_{10} \left( \frac{\|\mathbf{y}\|_{\ell_2}}{\|\mathbf{x} - \mathbf{y}\|_{\ell_2}} \right),$$
(3.1)

and the complex wavelet structural similarity (CW-SSIM) index (Sampat, Wang, Gupta, Bovik, & Markey, 2009) defined as

$$CW-SSIM = \frac{2\left|\sum_{i=1}^{n} c_{x,i} c_{y,i}^{*}\right| + K}{\sum_{i=1}^{n} |c_{x,i}|^{2} + \sum_{i=1}^{n} |c_{y,i}|^{2} + K},$$
(3.2)

where in both cases  $\mathbf{x} \in \mathbb{R}^m$  and  $\mathbf{y} \in \mathbb{R}^m$  are the vector representation of the estimated image and the true image, respectively. In the *CW-SSIM* index,  $\mathbf{c}_x \in \mathbb{C}^n$  and  $\mathbf{c}_y \in \mathbb{C}^n$  represent the wavelet coefficients of images  $\mathbf{x}$  and  $\mathbf{y}$ ; ()\* represents the complex conjugation operation; and K represents a small positive constant to achieve accurate performance in local low contrast regions (Sampat et al., 2009). SER and CW-SSIM are measures quantified in dB and %, respectively.

#### 4. RESULTS

The proposed technique was tested on the in-vivo dataset with breath-held 3D liver MRI data simulating 5 different motion states. The performance of the proposed motion-corrected CS technique (MCCS), tailored for free-breathing acquisitions, was compared against a traditional CS reconstruction (CS), from free-breathing data without motion estimation and motion correction.



FIGURE 4.1. Optimal parameter selection for the traditional CS method. The L-curve was computed on the left, where the X-axis represents the data consistency term  $\frac{1}{2} ||\mathbf{SFVm}_{t_0} - \mathbf{b}||_{\ell_2}^2$ , and the Y-axis represents the regularization term  $||\Phi \mathbf{m}_{t_0}||_{\ell_1}$ . We solved Equation (2.11) for 15 values of fixed  $\lambda$ . Setting fixed  $\lambda$  as defined in (a) yielded to an under-regularized recovery, whereas using (c) resulted in an over-regularized reconstruction. On the right, we illustrate the computation of the curvature as function of the regularization parameter. Point  $\lambda$  as defined in (b) is the operating point that maximizes the curvature. Therefore,  $\lambda$  as defined in (b), is the optimal regularization parameter  $\lambda_{opt}$ .

#### 4.1. Regularization parameters

We selected optimal settings for the MCCS and CS frameworks. Computations of the L-curve were performed on the in-vivo dataset using several reduction factors (*R*), and selecting the operating point with maximum curvature. Figures 4.1 and 4.2 illustrate the L-curve and curvature of the regularization parameters for Equations (2.11) and (2.8) with 5-fold acceleration. For both cases, setting  $\lambda = 0.01$  and  $\beta = 0.002$ , defined in Figures 4.1 (a) and 4.2 (a), yield to an under-regularized image reconstruction, whereas using  $\lambda = 0.5$  and  $\beta = 0.2$ , as in Figures 4.1 (c) and 4.2 (c), result in an over-regularized image reconstruction.



FIGURE 4.2. Optimal parameter selection for the traditional CS method. The Lcurve was computed on the left, where the X-axis represents the data consistency term  $\frac{1}{2} ||\mathbf{SFm'} - \mathbf{b'}||_{\ell_2}^2$ , and the Y-axis represents the regularization term  $||\mathbf{m'}||_{\ell_1}$ . We solved Equation (2.8) for 15 values of fixed  $\beta$ . Setting fixed  $\beta$  as defined in (a) yielded to an under-regularized recovery, whereas using (c) resulted in an over-regularized reconstruction. On the right, we illustrate the computation of the curvature as function of the regularization parameter. Point  $\beta$  as defined in (b) is the operating point that maximizes the curvature. Therefore,  $\beta$  as defined in (b), is the optimal regularization parameter  $\beta_{opt}$ .

For both cases, the second column in Figures 4.1 and 4.2 illustrates the computation of the curvature as function of the regularization parameter, where  $\lambda$  and  $\beta$  as defined in Figures 4.1 (b) and 4.2 (b) are the operating point that maximizes the curvature. Therefore,  $\lambda_{opt} = 0.1$  and  $\beta_{opt} = 0.04$  as defined in Figures 4.1 (b) and 4.2 (b), are the optimal regularization parameters. All MCCS and CS reconstructions are performed with these optimal settings.

#### 4.2. Image recovery

The proposed technique was tested on the in-vivo dataset with breath-held 3D liver MRI data simulating 5 different motion states. The ground truth, fully-sampled image is illustrated in Figure 4.3 displaying a coronal cut. The first out of sixteen frames is set as



FIGURE 4.3. Results obtained using the MCCS and CS methods at different R.

# Ground truth image







Transversal

Coronal

Sagittal

# Traditional CS reconstruction



Transversal

(in)



Sagittal

# Proposed MCCS technique

Coronal



Transversal





Coronal

Sagittal

FIGURE 4.4. Body planes obtained using the MCCS and CS methods at different R.

the reference. The performance of the proposed motion-corrected CS technique (MCCS), tailored for free-breathing acquisitions, was compared against a traditional CS reconstruction (CS), applied just the reference frame free-breathing data. In our experiments, we downsampled the data according to different sampling patterns (S) using acceleration factors from R = 4 to R = 20. Figure 4.3 presents also the traditional CS and proposed MCCS reconstructions at reduction factors of 4, 5, 6.7, 10 and 20. For the CS reconstructions, motion artifacts due to severely undersampling k-space become more evident as R increases. Preservation of sharp edges and correction of motion artifacts can be observed in the MCCS reconstructions.

We also display the three body planes obtained by the MCCS and CS recostrucions at R = 6.7. The ground truth image, the traditional CS reconstruction and the proposed MCCS technique are illustrated in Figure 4.4, considering the transversal, coronal and sagittal planes from left to right. We can appreciate that the proposed method recovers an accurate image, whereas the CS reconstruction could not avoid the presence of artifacts because of the few measurements.



FIGURE 4.5. Computation of the reconstruction SER for the proposed motioncorrected CS recovery (MCCS) and traditional CS framework (CS) at different acceleration factors (R) using the 3D-liver in-vivo dataset.

#### 4.3. Computation of ratios

The proposed motion-corrected CS image reconstruction method with optimal settings at different acceleration factors was compared against a traditional CS framework. Figure 4.5 illustrates the signal-to-error ratio as function of R. Reconstructions obtained with the proposed technique reported more accurate results, with SER gains up to 6 dB compared to the traditional CS framework.



FIGURE 4.6. Computation of the reconstruction CW-SSIM index using the MCCS technique for the 4 volunteers of the dataset at different acceleration factors (R). The mean CW-SSIM index of the 4 MCCS reconstructions is illustrated as a function of R, with its respective standard deviation.

Four different volunteers were scanned to create the underlying dataset. To test the robustness of the proposed technique, the complex wavelet structural similarity index between the ground truth and each reconstruction was performed for several reduction factors. Figure 4.6 illustrates a plot of the mean and standard deviation of the index as a function of R. Reported results show that the proposed technique is stable under high reduction factors (up to R = 10). At higher reduction factors, the motion information estimation is poor because of the few samples, leading to unstable MCCS reconstructions.

#### 5. DISCUSSION

We proposed a motion corrected reconstruction technique tailored for dynamic 3D liver undersampled MRI. The main contribution is to employ motion-corrected inconsistent k-space samples from different motion states (frames) of the liver into a CS reconstruction framework to estimate a motion corrected image (Usman et al., 2012). As shown in the results, this technique achieved accurate and reliable reconstructions in the in-vivo experiments (Figures 4.3, 4.4, 4.5 and 4.6).

To correct motion, we estimated the motion vectors between different motion states (frames) by using CS to reconstruct each frame and by registering these images to a reference. The CS framework recovers structured images by relying on compressibility, i.e. high contrast components are chosen over low contrast (Figures 4.3 and 4.4). In addition, registration also favors high contrast samples, which leads to decreased signal-toerror ratios outside the liver (higher contrast region) (Usman et al., 2012; Asif, Hamilton, Brummer, & Romberg, 2012). We have used an adaptive non-rigid registration algorithm (Myronenko, 2010) to estimate the inter-frame motion between different frames. A source of improvement to the current theory may be to estimate motion vectors within neighboring frames in the form of a linear dynamical system instead of estimating them with respect to a single reference motion state (Asif et al., 2012).

The main limitations of this work can be grouped as follows: architecture and implementation. As shown in Figure 3.1, the architecture of the proposed technique is a sequential process. Even though each step is robust, if a poor initial CS reconstruction is performed, it will lead to inexact motion vectors and finally to a low resolution motion corrected image. A comprehensive approach to avoid this kind of limitation may be to merge the three separate steps into a single optimization algorithm (Asif et al., 2012; Odille, Vuissoz, Marie, & Felblinger, 2008). On the other hand, the implementation of the proposed technique over a traditional CS framework is computationally more expensive, because three steps must be performed. We used a computer with an Intel(R) Core(TM) i7-3770 CPU @ 3.40 GHz and memory (RAM) capacity of 32.0 GB to run the proposed technique, with the algorithm taking approximately 100 minutes. Speeding up the reconstruction time may be possible by parallel computing techniques.

The proposed method can be extended to 3D CINE liver MRI as an approach for applications where the respiratory signal can be used as a motion surrogate signal, such as is done in coronary MR angiography (Stuber, Botnar, Danias, Kissinger, & Manning, 1999; Spuentrup & Botnar, 2006). In coronary MR angiography, spatial resolution is bounded by breath-hold acquisition (15–20 s) (Spuentrup & Botnar, 2006), but with the emergence of navigator techniques, the spatial resolution is improved by correcting free-breathing acquisitions (Stuber et al., 1999). Using motion corrupted data (avoiding external navigator), a 3D CINE liver MR image may be generated from the motion corrected image obtained in this work. As previously discussed, to reconstruct the motion corrected image  $\hat{\mathbf{m}}_{t_0}$ , we need to solve Equation (2.11). By employing the acquired data from all the frames **b** and the estimated motion vector operator, the proposed 3D CINE liver is defined as follows:

$$\hat{\mathbf{m}} = \mathbf{V}\hat{\mathbf{m}}_{t_0}.\tag{5.1}$$

Equation (5.1) shows how to generate the whole time series, where an accurate estimation of the respiratory signal may be obtained through rigid registration in the head-feet (H-F) direction of a region of interest (ROI) including the liver.

#### 6. CONCLUSION

We have presented a recovery algorithm tailored for free-breathing dynamic 3D liver MRI, which demonstrated an increase in imaging efficiency while reducing acquisition time and removing non-rigid motion artifacts. In addition, the recovery algorithm does not sacrifice image quality. In the in-vivo experiments, our framework produced improved signal-to-error ratios and complex wavelet structural similarity indexes in comparison with the ground truth, demonstrating that it is feasible to achieve a 10x speedup in acquisition time and remove motion artifacts without diminishing image quality.

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**APPENDICES** 

#### **APPENDIX A. PSEUDO-CODE**

In this section we present the pseudo-code of the proposed we present the pseudo-code of the proposed Motion Corrected Compressed Sensing framework for free-breathing 3D liver MRI. Prior to solve Equation (2.11), we need to compute the motion operator  $\mathbf{V}$  using the acquired k-space undersampled data **b**. The pseudo-code is illustrated in Algorithm 1.

#### Algorithm 1: Pseudo-code of the computation of motion operator V.

Data: K-space undersampled data b

Result: Motion operator V

Initialization;

for each of the T frames do

Initial reconstruction: 
$$\hat{\mathbf{m}}_t \leftarrow \left( \underset{\mathbf{m}'}{\arg\min \frac{1}{2}} ||\mathbf{SFm}' - \mathbf{b}'||_{\ell_2}^2 + \beta ||\mathbf{m}'||_{\ell_1} \right)_t + \mathbf{F}^H \bar{\mathbf{b}};$$

end

Select reference frame  $\hat{\mathbf{m}}_{t_0}$ ;

for each of the T frames do

Motion vectors estimation:  $\mathbf{V}_t \leftarrow \underset{\mathbf{v}_t}{\arg\min} D(\hat{\mathbf{m}}_t, \hat{\mathbf{m}}_{t_0} | \mathbf{v}_t) + w ||\mathbf{k}^T \mathbf{Q} \mathbf{v}_t||_{\ell_1};$ 

end

Using the k-space measurements **b** and the previously computed motion operator **V**, we are able to solve Equation (2.11) as illustrated in Algorithm 2.

Algorithm 2: MC-CS recovery.

Data: K-space undersampled data b and motion operator V

**Result**: Motion corrected 3D Liver image

Initialization;

while Stopping criteria not reached do

Pre-computation of parameters for line-search;

Line-search for optimal stepsize:

 $t^{\star} \leftarrow \arg\min_{t} \left| \frac{1}{2} \left| \left| \mathbf{SFV} \left( \mathbf{m}_{t_0} + t\Delta \mathbf{m}_{t_0} \right) - \mathbf{b} \right| \right|_{\ell_2}^2 + \lambda \left| \left| \Phi \left( \mathbf{m}_{t_0} + t\Delta \mathbf{m}_{t_0} \right) \right| \right|_{\ell_1};$ 

Motion corrected image update:  $\mathbf{m}_{t_0} \leftarrow \mathbf{m}_{t_0} + t^* \Delta \mathbf{m}_{t_0}$ ;

Gradient computation:  $g_{new} \leftarrow \mathbf{V}^H \mathbf{F}^H \mathbf{S}^H (\mathbf{SFVm}_{t_0} - \mathbf{b}) + \lambda \Phi^H |\Phi \mathbf{m}_{t_0}|;$ 

Search direction:  $b \leftarrow ||g_{new}||^2_{\ell_2}/||g_{old}||^2_{\ell_2}$ ;

Gradient update:  $g_{old} \leftarrow g_{new}$ ;

Conjugate gradient update:  $\Delta \mathbf{m}_{t_0} \leftarrow -g_{new} + b\Delta \mathbf{m}_{t_0}$ ;

end