REDUCTION OF DISTORTIONS IN MRSI USING A NEW SIGNAL MODEL

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ABSTRACT

We propose a new reconstruction scheme for magnetic resonance spectroscopic imaging (MRSI) signal based on minimizing the spatial total variation (TV) integrated with the $\ell_1$-norm of the spectral data. Furthermore, we propose to represent the MRSI signal as a linear combination of polynomials and spikes to capture the baseline and metabolite peaks. The proposed signal model provides a sparser representation of the spectral data, which enables us to suppress the field inhomogeneity induced line shape distortions and losses as well as reduce noise. We also take advantage of high resolution field map and anatomical prior derived from additional 3-D MRI scan to model system imperfections.

Index Terms— $B_0$ inhomogeneity, magnetic resonance spectroscopic imaging (MRSI), total variation, $\ell_1$-minimization

1. INTRODUCTION

MR Spectroscopic Imaging (MRSI) serves as a useful means to measure the concentrations of various in vivo metabolites, which are crucial in diagnosis and treatment of a variety of diseases including cancer. Reconstruction of the MRSI data is, however, challenging due to a number of issues.

The lack of a homogeneous magnetic field in the MR scanner also termed as $B_0$ inhomogeneity degrades the quality of the spectral lines in the MRSI data. This often leads to the broadening of the spectral lines as well as losses. The effect of inhomogeneity is more pronounced when the MRSI signal is acquired at low resolution.

Another important issue is the spectral fat and water leakage. The broad spatial point spread functions (PSF) in standard Fourier reconstructions, along with the strong signals from unsuppressed water and fat (stronger than metabolites by x100), results in considerable cross-talks between spatial regions. This is referred to as spectral leakage; the intense signals from extra-cranial fat regions and residual water will leak to all pixels in the image.

Several constrained schemes were proposed to overcome the above mentioned distortions [7], [8]. However, all of these schemes model the spatial-spectral signal as a linear combination of very few basis functions; they are too constrained to be applied to in vivo applications. The work of [1] is also related. However, their model cannot effectively account for non-idealities such as field inhomogeneity induced intra-voxel distortions, spectral leakage from lipids, baseline variations, and residual water peaks.

In our previous work [2] we attempted to address the first issue by taking advantage of a 3-D field map extracted from a higher resolution multi-slice water-referenced scan to better model the scanner.

In this paper we extend our work and propose to improve the reconstruction of the MRSI signal in several ways:

- We model the spectral signal as a sparse linear combination of spikes and polynomials. The spikes capture the metabolite peaks, while the polynomials account for the smooth baseline due to macromolecules, fat and residual water leakage. This results in more uniform peaks in the reconstruction.
- We incorporate 3-D high-resolution anatomical priors in order to alleviate spectral leakage. Further, the proposed reconstruction scheme exploits 3-D high-resolution field map and $T_2^*$ decay from a 3-D, high-resolution water scan similar to our previous work.
- Moreover, we formulate the reconstruction problem as a regularized $\ell_1$-minimization scheme. In addition to the data consistency term, we penalize the TV norm of the spectral data within the different spatial compartments, along with the $\ell_1$-norm of the signal. This approach is similar to schemes introduced in [6], [3].

Notations: In the discrete domain we denote spatial indices by $n = (n_x, n_y, n_z)$ and the frequency index as $n_f$ corresponding to $r = (x, y, z)$ and $f$ in the continuous domain. We denote the corresponding $k$-space indices as $k = (k_x, k_y, k_z)$ and $k_f$ (or $k$ and $t$ in the continuous domain), where $k_f$ corresponds to the discrete time index. By default, we assume a signal is in the spatial-spectral domain, thus, we represent the MRSI signal as $s[n, n_f]$ in the spectral and $s_f[k, k_f]$ in the time domain, where $s_f[k, k_f] = \mathcal{F}_f[s]$. In general, we indicate the indices in the $k$-space by a subscript; e.g. $s_{(\omega)}[k_x, k_y, n_x, n_z] \in \mathcal{S}$ is the 2-D DFT of $s$ along $n_x$ and $n_z$. We also adopt the simpler notation of $\hat{s}$ to represent a signal in the $k$-space $\hat{s} = s_{(\omega)}[k_x, k_y, k_z, k_f]$.

2. MRS IMAGE FORMATION

We use the echo-planar spectroscopic imaging (EPI) sequence to scan the object on a Cartesian grid. We assume the time elapsed to acquire each $k_f$ line is zero. We correct for the shift between even and odd lines [2]. Ignoring the $T_1$ relaxation time, we model the MRSI acquisition scheme as

$$\hat{s}(k, t) = \int_{\mathbb{R}^3} \int_{\mathbb{R}} \rho(r, f) e^{-\alpha_0 (r_f)} e^{-\gamma T_2^* (r_f) t} e^{-2\pi i (kr + \nu t)} \, df \, dr,$$  \hspace{1cm} (1)

where $\alpha_0 = 2\pi f_0 = \gamma \Delta B_0(r)$ represents the field map in which $\Delta B_0(r) = \gamma \Delta B_0(r)$ is the field inhomogeneity and $\gamma$ denotes the gyromagnetic ratio. Eq. (1) implies that the inhomogeneity $\Delta B_0(r)$ degrades the magnetization signal $\rho$ (the signal of interest to reconstruct) as a phase term $e^{-\alpha_0 (r_f)}$ or equivalently as a frequency shift in the spectral domain.

In the discrete domain we express (1) as
\[
\hat{s}[k,f] = \sum_{n=0}^{N-1} \sum_{k_f=0}^{N_f-1} e^{-j \omega_0[n] k_f} e^{-2 \pi \omega_0[n] k_f} v[n,n_f].
\] (2)

Using accompanying MRI scan, we propose to estimate the high-resolution field map and \( T_2^* \) decay. These parameters are estimated using the Dixon scheme, where MRI data is collected at multiple delay times to estimate the field map and fat/water concentrations.

In this paper we consider the MRSI data \( \hat{s}[k,k,k_f] \) to be at resolution \((M_i,M_i,N_f)\) and the water-referenced (MIR) data \( q[n] \) at a higher resolution \( N = (N_i,N_i,N_i) \). Note that we assumed same spectral and temporal resolution; i.e., \( N_f = N_i \).

3. MRSI Reconstruction

3.1. Forward (or System) Model

To exploit the high resolution MRSI priors, we propose to reconstruct the MRSI data at the same grid size as the MRI data. Thus, having the scanned MRSI data \( \hat{s}[k,k,k_f] \) in one slice at resolution \((M_i,M_i,N_f)\), we would like to reconstruct \( v[n,n_f] = v[n_i,n_i,n_i,n_f] \) at a finer grid \( (N,N_f) \), which has the same spatial resolution as the estimated field map and \( T_2^* \) decay. As a result, we need to solve

\[
\mathcal{A} = \hat{s},
\]

where \( \mathcal{A} \) indicates the forward (or system) model shown in (2).

As explained in Section 2, in the MR scanner, inhomogeneity and \( T_2^* \) decay affect the desired signal in the temporal domain, \( v(i) \), through a multiplication by an exponential term. Therefore, to implement \( \mathcal{A} \) we first define the operator \( \mathcal{B} \) as

\[
\mathcal{B}_{v_i}[k,k_f] = B_{\hat{s}}[n,n_f] = \mathcal{F}(\mathcal{F}^{-1}v[n] \cdot \mathcal{F}(\mathcal{F}^{-1}v[n_f]))
\]

\( \mathcal{F} \) indicates the Fourier transform, \( \mathcal{F}^{-1} \) the inverse Fourier transform, and \( \cdot \) the multiplication.

Due to the fact that the MR measurements are noisy, a better reconstruction criterion is the one that accounts for the noise as

\[
\|\mathcal{A} v - \hat{s}\| \leq \varepsilon.
\] (3)

To exploit the spatial correlation of the MRSI data and to make the reconstruction at a finer grid well-posed, we minimize total variation (TV) of \( v[n,n_f] \) subject to the criterion (3),

\[
\tilde{v} = \arg \min_v \{TV_v(v)\}, \quad \text{s.t.} \quad \|\mathcal{A} v - \hat{s}\| \leq \varepsilon,
\] (4)

where \( TV_v(\cdot) \) denotes the discrete spatial (so the subscript \( n \)) total variation and is defined as the \( \ell_1 \)-norm of the spatial gradients

\[
TV_v(v) = \|D_v v\|_{\ell_1} = \sum_{n,n_f} \sqrt{\|D_v v\|^2 + \|D_v v\|^2},
\]

with \( D_v v = v[n_i+1,n_i,n_i,n_f] - v[n_i,n_i,n_i,n_f] \) and similarly for \( D_{\hat{s}} \) and \( D_v \). We can also express (4) as

\[
\tilde{v} = \arg \min_v \left\{ \|\mathcal{A} v - \hat{s}\|^2 + \lambda TV_v(v) \right\}.
\] (5)

We define the reconstruction error as \( e = \varepsilon\|\tilde{v}\| \). Hence, we optimize the regularizing parameter(s) to achieve a desired reconstruction error.

3.2. Signal Model

In our current model of (5), we reconstruct the MRSI data without using any anatomical prior and also prior knowledge of the spectral data. If we penalize all the finite differences, this will lead to cross talks between regions of different spectral content. Hence, we propose to use the anatomical priors which we can extract from the high-resolution water scan \( q[n] \). We also model the spectral signal using a dictionary of bases yielding an improved reconstruction. We address these topics below.

3.2.1. Anatomical Prior

Spectral fat and water leakage is an important issue in MRSI reconstruction, where the intense signals from extra-cranial fat regions and residual water will leak to all pixels in the image. To alleviate this problem, we constrain \( v \) to a mask that covers the field of view \( \Omega \) and also constrain the TV norm into two regions of fat \( (\Omega_f) \) and water \( (\Omega_w = \Omega - \Omega_f) \) using the high-resolution scan \( q[n] \). (Recall that we also used \( q[n] \) to estimate the field map.) In general we can add more regions such as CSF etc. depending on the anatomy of the object. Thus, we segment the field of view to \( K \) non-overlapping regions \( \Omega = \bigcup_{i=1}^{K} \Omega_i \).

In this setting, we update the forward model as

\[
\mathcal{A}_i = \mathcal{V}_i B_{\hat{s}} M_{\Omega_i},
\] (6)

where \( M_{\Omega_i} \) denotes the masking operator to constrain the reconstruction to the field of view:

\[
v_{\Omega_i} = M_{\Omega_i} v[n,n_f] = \begin{cases} v[n,n_f], & n \in \Omega_i; \\ 0, & \text{else} \end{cases}
\]

and to avoid cross talks between different spatial regions we update the TV norm as

\[
TV_{\hat{s}}(v) = \sum_{i=1}^{K} \lambda_{\Omega_i} TV_{\Omega_i}(v),
\]

where \( \Omega_i = \{\Omega_1,\ldots,\Omega_K\} \) and each constrained gradient (here we show the \( x \)-gradient) is expressed as

\[
\Delta_{\Omega_i}^x = \begin{cases} v[n+(1,0,0),n_f] - v[n,n_f], & n+n+(1,0,0) \in \Omega_i; \\ 0, & \text{else} \end{cases}
\]

Hence we define the TV norm only within regions. The modified reconstruction criterion is stated as

\[
\tilde{v} = \arg \min_v \left\{ \|\mathcal{A}_i v - \hat{s}\|^2 + \lambda TV_{\hat{s}}(v) \right\},
\] (7)

with the updated forward model given in (6).

3.2.2. Union of Bases

We can add the \( \ell_1 \)-norm of the signal \( \|\cdot\|_{\ell_1} \), in addition to the TV norm to the reconstruction formula of (7),

\[
\tilde{v} = \arg \min_v \left\{ \|\mathcal{A}_i v - \hat{s}\|^2 + \lambda_1 TV_{\hat{s}}(v) + \lambda_2 \|\cdot\|_{\ell_1} \right\}.
\] (8)

By adding this term, and choosing an appropriate parameter \( \lambda_2 \), we reduce the baseline and noise but preserve the peaks similar to a soft-thresholding denoising.

A typical MRSI spectrum, however, is composed of (a) a few metabolite peaks and (b) a baseline due to residual water and fat.
leakage, and the existence of macromolecules. Fig. 1(a) depicts an example of such spectral line of brain in vivo data reconstructed using (7). The shaded area shows the region of interest. (b) The spectrum at the same voxel used in (a), reconstructed using the proposed scheme of (10). 

\[ w = (w_1, w_2)^T \] represents the coefficients, \( \psi = I \) is the Euclidean (or Dirac) basis that efficiently captures the peaks \( w_d \) while the polynomials \( \varphi \) can represent the baseline. As a consequence, using (9), we propose the new reconstruction scheme as

\[ \hat{v} = \arg \min_w \left\{ \left\| A_1 w - \lambda_1 \right\|_2 + \lambda_2 \left\| T_v^\Omega (w) + \lambda_2 \left\| \right\|_2 \right\}, \] (10)

and we can write the updated forward model as \( A_2 = \forall \Phi M_{\Omega} \). In this setting another reason to include the last \( \ell_2 \) term is to make the problem well-posed.

The proposed constrained model opposed to most previous studies [3], [5] exploits the spectral line shapes (peaks and baseline) in the reconstruction and provides a sparse representation of the MRSI signal. In this framework the proposed \( \ell_1 \)-minimization could be regarded as an efficient deconvolution scheme that reduces perturbations in the MRSI data caused by several factors such as inhomogeneity, fat leakage, and noise.

To achieve baseline decomposition with lower-degree polynomials, we limit their support to a region of interest (ROI) where we exclude the water peak. The shaded region in Fig. 1 shows an example of the ROI.

To represent the baseline, we employ Chebyshev polynomials of the first kind defined as

\[ T_0(x) = 1, \quad T_1(x) = x, \quad T_{i+1}(x) = 2xT_i(x) - T_{i-1}(x), \]

for \( x \in [-1,1] \). Fig. 2 shows a few of these polynomials. We define the discrete version of the polynomials with a support limited to \( \Lambda = [n_a, n_b] \) as

\[ R_i[n] = T_i \left( \frac{2n - n_a - n_b}{n_b - n_a} \right), \quad n \in \Lambda, \]

and normalize them with their \( \ell_2 \)-norm. Thus, we use \( N_p \) polynomials \( 0 \leq i \leq N_p - 1 \) with limited support as basis functions of \( \varphi \).

As a result, we can express (10) as

\[ v[n, n_f] = \Phi w = w_d[n, n_f] + \sum_{i=0}^{N_p-1} w_i[n, i]R_i[n_f], \]

where \( w_d \) represents the Dirac coefficients and has the same size as \( v \), whereas \( w_i[n, i] \) with size \( (N, N_p) \) denotes the polynomial coefficients using polynomials \( R_i[n] \) of order \( N_p - 1 \) and length \( N_f \).

Fig. 1(b) shows the reconstructed spectrum (same point as the one shown in (a) of Fig. 1) using the proposed scheme of (10). As seen, the baseline is captured by the polynomials. The TV norm in (10) regularizes the resulting baseline-removed signal \( w_d \) in order to make the line shapes and peaks uniform. This is not attainable by first reconstructing the MRS signal by using e.g. (7) and then removing the base line from each spectral line. Note that the TV norm in (7) applies to the MRS signal \( v \), which includes the baseline. Subtracting the varying baseline from the reconstructed \( \hat{v} \) leads to non-uniformity in the metabolite peaks magnitudes in uniform regions.

Distortions such as residual water and fat leakage appear as baseline perturbations in the spectral domain which are varying voxel to voxel. Spectral fat leakage not only appears as a broad peak, but also distorts the whole baseline and spectra resulting in oscillatory variations in metabolite peak images. In the conventional methods, baseline is removed after MRSI reconstruction using e.g. polynomials [10]. Although our approach is qualitatively equivalent to the conventional schemes [9], it can remove peaks amplitude variations due to distorted baselines, whereas removing the baseline after reconstruction fails to suppress the distortion.

An issue in finding the proper solution in regularized minimization schemes is setting the appropriate regularizing parameters, here \( \lambda_1 \) and \( \lambda_2 \). Here we attempt to find the appropriate parameters to achieve a desired reconstruction error. Hence, we have one degree of freedom in choosing \( \lambda_1 \) and \( \lambda_2 \). In our experience, the parameter \( \lambda_2 \) plays the major role in making the problem well-posed. Using a smaller value of \( \lambda_2 = 0.1\lambda_1 \) is often sufficient to ensure the decomposition of \( v \) into baseline and metabolites components and provide reasonable suppression of artifacts.

4. EXPERIMENTAL RESULTS

We tested our approach for the in vivo brain data and compared it to the standard scheme [9] integrated with the Papoulis-Gerchberg (PG) algorithm [4]. We acquired the water-suppressed MRSI data in a single 10mm-slice with resolution \( (M_x, M_y, N_f) = (64,32,256) \) where we used 10 measurements to improve SNR. We chose \( TR = 2 \) sec and \( TE = 40 \) msec (echo time for the first acquisition) resulting in a total scan time of 10.7 min. We also acquired a water-referenced MRSI data at this resolution to be employed in the standard reconstruction scheme and also the PG algorithm for comparison. We extracted the field map and \( T_2^* \) decay from a higher-resolution \( (N_x, N_y, N_f) = (128,64,4) \) water data \( q[n] \) scanned at the same volume as the MRSI scan. For our proposed reconstruction scheme

![Fig. 1. (a) A typical spectrum (zoomed version) of the brain reconstructed using (7). The shaded area shows the region of interest. (b) The spectrum at the same voxel used in (a), reconstructed using the proposed scheme of (10).](image1)

![Fig. 2. Some examples of Chebyshev polynomials.](image2)
of (10), we employed polynomials of order 7 \((N_p = 8)\). We used \(\lambda_1 = 0.1\) and \(\lambda_2 = 0.002\) in (10), which led to a reconstruction error of \(e = 5\%\).

For the PG algorithm we applied spatial and spectral apodization resulting in a reconstruction error of \(e = 3.2\%\). Additionally, we reconstructed the MRSI signal using (7) and (8) to show the advantage of employing \(\ell_1\)-norm of the spectral signal as well as using the proposed signal model.

Fig. 3(a) and (c) show a few reconstructed spectra at different locations of imaged brain using the proposed scheme and the PG method. While the metabolite peaks in all spectra when using the proposed method are reconstructed in high quality, the reconstructed spectra resulting from the PG algorithm show degraded (sometimes lost) peaks and very noisy line shapes. Note that fat leakage is significantly reduced when the proposed scheme is used.

In Fig. 4 we demonstrated the reconstructed NAA peak using different schemes. The proposed method (see Fig. 4(a)) yields the most uniform result. The PG algorithm (see Fig. 4(d)) shows some magnitude variation inside the brain due to uncorrected inhomogeneity and fat leakage. We also see some variation when TV reconstruction is used in Fig. 4(c). Using a broader mask would reduce these artifacts. The scheme given in (8) (see Fig. 4(b)) performs better than TV reconstruction. Using a union of Diracs and polynomials as a proper MRSI signal model, the NAA peak in Fig. 4(b) is less uniform than the peak reconstructed using (10), which confirms the use of Diracs and polynomials as a proper MRSI signal model.

5. CONCLUSION

In this paper we proposed a new reconstruction scheme for MRSI data in which we benefited from the sparsity of the spectroscopic data where we minimized the TV-norm integrated with the \(\ell_1\)-norm of the signal. We also proposed a better signal model for the MRSI signal based on the union of Diracs and polynomials, which incorporated in our reconstruction scheme. Capturing baseline variations by the polynomials part enabled us to reduce spectral perturbations due to distortions such as fat leakage.

6. REFERENCES