

Automatic Model Recovery for MRSI Reconstruction

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Background

Magnetic Resonance Spectroscopic Imaging (MRSI) holds great potential within the clinical community in its ability to furnish spatially-localized spectral information for a wide array of surveyed metabolites. Nonetheless, MRSI is seldom espoused outside of the MR research community, due to a number of practical limitations. One stems from the fact that in the current gold-standard implementation, Chemical Shift Imaging (CSI)¹, a FID must be acquired at each position in k -space, hence only the central phase encodes are typically acquired in order to curb acquisition times. This restricted measurement process ultimately results in a broadened pointspread function (PSF), leading to spectral contamination artifacts once the data are inverse Fourier transformed. Such effects confound straightforward interpretation, and thus numerous alternatives have been proposed seeking to overcome these shortcomings. One such approach consists of modeling the measurement process, whereby *a priori* information is used to construct the forward signal model. One drawback of this method, however, is that a criterion for selecting the most appropriate model remains elusive, and generated solutions will reflect this initial choice. **In this work**, we propose a data-driven approach where the signal model is estimated directly from the MRSI data, given a general framework that prescribes the functional form and the class of the sample geometry, and requires only a high-resolution static B_0 profile as an additional measurement.

Methods

In a SLIM-type approach^{2,3}, the spatio-spectral distribution of the sample is modeled as a sum of K spectrally-homogenous compartments times the associated spectrum. Following propagation through the imaging equation, the measured signal at k -space position \mathbf{k}_i and time t_m can be expressed as the linear system: $s[\mathbf{k}_i, t_m] = \sum_{k=1}^K K_k[\mathbf{k}_i] Q_k[t_m]$ (1). Here K_k are spatial weightings defined by the geometry of compartment k , and Q_k the corresponding FID. However, a robust method for determining the optimal number and geometry of the compartments is lacking, and a mismatch between the selected and “true” model will result in additional artifacts. We note that a similar decomposition to (1) can be achieved via principal component analysis (PCA), which can be implemented as a singular value decomposition (SVD) of the measurement matrix, i.e., $s[\mathbf{k}_i, t_m] = \sum_{k=1}^K \sigma_k u_k[\mathbf{k}_i] v_k[t_m]$ (2), where $v_k[t_m]$ can be considered as the “eigen-FIDs” and $u_k[\mathbf{k}_i]$ as “eigen-maps.” For our purposes, we would like to define high-resolution maps, $\tilde{u}_k[\mathbf{x}_n]$, on the same spatial grid as an acquired B_0 profile. As this problem is ill-posed, we spatially regularize using the total generalized variation (TGV)⁴, which introduces penalties based on first and second derivatives and promotes piecewise linear solutions. Next, as the components in (2) will reflect the experimental conditions (primarily B_0 effects), an additional static field inhomogeneity compensation step is performed, where the \tilde{u}_k are un-shifted along the chemical shift dimension by means of an acquired static inhomogeneity profile, $\Delta f[\mathbf{x}_n]$, such that $\hat{h}_k[\mathbf{x}_n, f_i] = \tilde{u}_k[\mathbf{x}_n](1 - (T/F_s)|\Delta f[\mathbf{x}_n] + f_i|)$, and setting all non-positive terms to zero. Here, T is the number of FID sample points, and F_s the temporal sampling rate. We then generate the kernel matrix, $\hat{H}_k[\mathbf{k}_i, t_m] = \text{FFT}_t^{-1}\{\mathcal{A}\{\hat{h}_k\}\}$, with sampling operator, \mathcal{A} , and re-synthesize the measurement matrix: $s'[\mathbf{k}_i, t_m] = \sum_{k=1}^K \sigma_k \hat{H}_k[\mathbf{k}_i, t_m] v_k[t_m]$. A subsequent SVD should yield static inhomogeneity-compensated components, v'_k and u'_k . Furthermore, a final application of the TGV-based spatial regularization will yield high-resolution spatial maps, \tilde{u}'_k .

Data Acquisition

CSI data were acquired from a two-compartment phantom using a 3.0 Tesla Siemens Trio (Siemens Healthcare, Erlangen, Germany). The inner compartment (a 8.7 cm diameter sphere) was filled with a solution of 50 mmol/L N-acetyl-aspartate (NAA, ~2.0ppm) and 50 mmol/L creatine (Cr, ~3.0/3.9ppm). The outer cylindrical compartment (height: 13.5 cm, diameter: 10.5 cm) contained corn oil (~1.2/1.6ppm). The VOI for H₂O-suppressed CSI was a 5 mm thick slice positioned at the center of the inner compartment (CSI parameters: FOV 160 x 160 mm, TR 1700 ms, TE 288 ms, grid size 32 x 32, bandwidth 1.2 kHz, T 2048). A static B_0 map (grid size 256 x 256) using the CSI FOV was also acquired during the same session using two spoiled gradient echo sequences, with ΔT_E chosen such that water and fat were in phase. Pre-processing consisted of 1 Hz Gaussian line broadening, and k -space apodization using a Hanning window (Fourier reconstruction only).

Results and Discussion

The results for the first three components (corresponding to the largest singular values) in Figure 2 represent clear advantages over their standard inverse Fourier counterparts (Figure 1). Not only are the metabolite peaks located at their expected resonance positions, but also exhibit considerably reduced contamination and off-resonance effects near the compartment interfaces. Moreover, the phantom geometry can be clearly discerned using the proposed method, whereas improved spectral integrity due to the Hanning window in the Fourier reconstructions has been achieved at the expense of spatial specificity. Though the second component (middle column) stymies the ideal scenario, i.e., where only the first and third components fully describe the measurements, it is likely due to the presence of higher-order field perturbations such as residual eddy currents or B_1 effects which can be further taken into consideration during the analysis. Another clear advantage of the proposed method is that it remains independent of the chosen sampling scheme and coil arrangement, enabling its concurrent usage with a variety of existing acceleration techniques such as SENSE⁵ and GRAPPA⁶.

Conclusion

We demonstrate a viable alternative reconstruction method that bypasses some of the limitations associated with both traditional inverse Fourier methods and model-based approaches. We accomplish this through a general, data-driven framework by loosely bounding the functional and geometric form of desired solutions.

References

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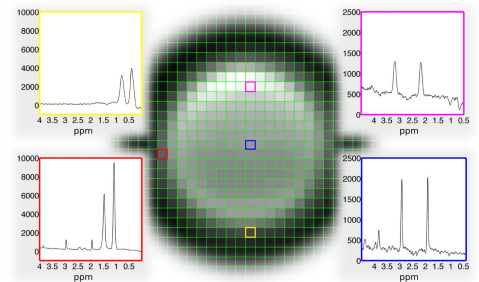


Figure 1: Standard inverse Fourier reconstruction with a few representative spectra (shown as the real part). The chemical shift axis has been windowed in order to focus on the metabolites of interest.

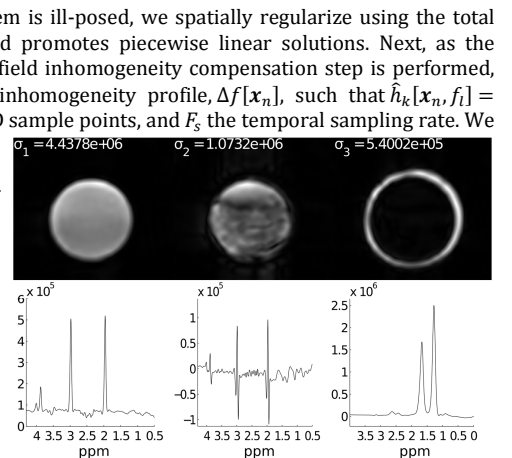


Figure 2: First three components from reconstructions using the proposed method. Images are shown in magnitude (along with their associated singular values), spectra as the real part using the same windowing as in Figure 1. The vertical axis has been scaled to the nominal CSI voxel volume.