A novel parallel sparse MRSI reconstruction scheme

R. Eslami[1], and M. Jacob[2]
[1]Biomedical Engineering, University of Rochester, Rochester, NY, United States, [2]University of Rochester

INTRODUCTION

Low SNR of proton magnetic resonance spectroscopic imaging (MRSI) in vivo data for a small voxel size (e.g., < 0.4cc) necessitates multiple-average acquisition that leads to a long scan time. This issue is even more pronounced when one attempts to acquire J-resolved spectroscopic data using multi-echo acquisition [3] in order to resolve metabolite concentrations such as glutamate and glutamine. Recently, we proposed an efficient MRSI sparse reconstruction technique where we modeled the system using priors such as inhomogeneity, and brain and lipid masks estimated from a companion MR scan for the EPSI sequence using a single channel coil [1]. Here, we propose a fast parallel MRSI acquisition scheme designed on a spiral trajectory. Using a 12-channel head coil, we acquire the in vivo MRSI data at spatial resolution of 44×44 with a single average. We extend our sparse reconstruction scheme to parallel MRSI data on the spiral trajectory. This way, we efficiently reduce measurement noise and other artifacts such as field inhomogeneity and spectral leakage in our proposed reconstruction while we have a fast MRSI acquisition ($\sim$1min for a slice). We show that the proposed scheme could recover the spectral data and outperforms Tikhonov-regularized SENSE reconstruction. We also demonstrate a two-fold acceleration of the acquisition that leads to a comparable reconstruction. This indicates the potential of the proposed scheme for multi-echo MRSI scans.

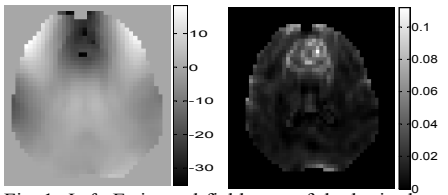

Fig. 1. *Left:* Estimated field map of the brain data in terms of Hz. *Right:* The estimated $1/T_2'$ for brain data (unit is ms^{-1}). The strong field map at the top causes losses in the SENSE scheme.

MATERIALS AND METHODS

We designed a spin echo MRSI sequence based on the analytical spiral trajectory [2] for the $3T$ Tim Trio Siemens scanner. The trajectory covers $N_x \times N_y \times N_f = 44 \times 44 \times 256$ of the k-space data for a FOV of $24 \times 24\text{cm}^2$ and slice thickness of 1cm resulting in a voxel size of $0.55 \times 0.55 \times 1$cc. We used 32 spatial interleaves with $TE = 40$ms and $TR = 2$s, leading to a scan time of 64s for fully sampled data. Each echo covers a spiral-out and the fly-back gradient to return the trajectory to the k-space center, which lasts 1.32ms in total and provides a bandwidth of 758Hz. In our acquisition scheme, we can also achieve acceleration by uniformly downsampling the MRSI data where we skip the spatial interleaves.

In addition to the water-suppressed MRSI data, we also acquire a water reference scan with the same resolution from which we estimate field map, sensitivity maps (for the employed 12-channel head coil), and water and fat masks. We also apply saturation bands to suppress extra-cranial fat. Nevertheless, we still use a fat mask in our reconstruction to reduce leakage from the unsuppressed lipid signals.

To reconstruct the non-Cartesian MRSI data, we propose a novel sparse reconstruction approach in which we incorporate the system model using the estimated MR priors such as sensitivity maps, filed map and T_2' decay, and spatial regions for fat and water in a unified objective function. To make the spatial k-space data on the Cartesian trajectory, we use optimized least squares-nonuniform FFT (OLS-NUFFT) [4] in our system model. We minimize spatial total variation (TV) of the MRSI data, which makes the problem well-posed and results in a piecewise smooth modeling of the MRSI signal in the spatial domain. We restrict the TV norm to water region while using a mask containing both water and fat to confine the MRSI data in our system model. Similar to our previous work [1], we model the spectral MRSI signal as a union of polynomials and spikes. This way, we better sparsify the MRSI data, which makes it a better fit for TV scheme. In addition, we extract the signal of interest which is metabolite peaks expressed by spikes. We use a region of interest (ROI) to exclude the huge water peak and hence, to employ minimum degree of polynomials in the model. To take advantage of the sparsity of the signal in the spectral dimension, we also minimize the ℓ_1 of the MRSI data.

In summary, we propose to solve the following optimization problem:
$\widetilde{w} = \arg\min_w \{\|\mathcal{A}w - \hat{s}\| + \lambda_1 \text{TV}_{\mathbf{n}}^{\Omega_1}(w) + \lambda_2 \|w\|_{\ell_1}\}$. Here, $\hat{s}$ denotes the MRSI k-space raw data and w is the metabolite part of the MRSI signal we wish to reconstruct. $\mathcal{A}$ denotes the system model and $\text{TV}_{\mathbf{n}}^{\Omega_1}$ denotes the spatial TV norm restricted to the region Ω_1 or water region. We have two regularizing parameters. By changing λ_1 we adjust spatial smoothness (metabolite peak integral maps) and a proper selection of λ_2 helps to impose our signal model and remove the spectral noise.

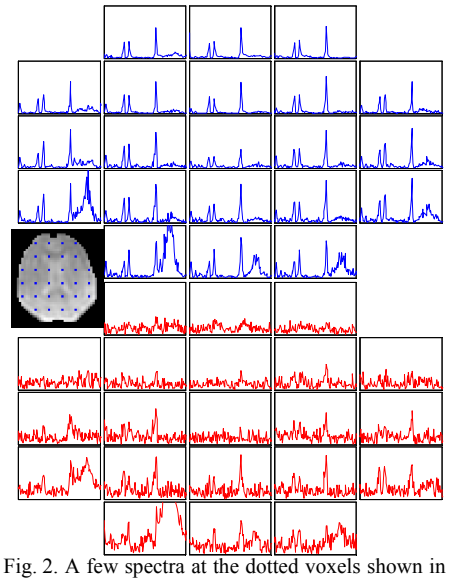

Fig. 2. A few spectra at the dotted voxels shown in the anatomy image using the proposed approach in top and SENSE reconstruction in bottom of the full sampled data.

RESULTS

To test the proposed parallel reconstruction algorithm, we acquired parallel spiral MRSI data on a normal human subject. We compare our reconstruction to a Tikhonov regularized iterative SENSE reconstruction (referred as SENSE henceforth) in which we restricted the MRSI data to the brain mask and used OLS-NUFFT to make the signal on Cartesian grid. In this scheme, we correct for the inhomogeneity and remove the baseline after reconstruction followed by a spatial Gaussian apodization. In both the proposed and SENSE reconstruction schemes, we adjusted the regularizing parameters in order to suppress measurement noise while not oversmoothing the metabolite peak maps.

Fig. 1 shows the estimated field map and $1/T_2' = 1/T_2^* - 1/T_2$ for the brain scan. Here we used $T_2 = 74$ms for the brain tissue. As seen in this figure, there is strong field inhomogeneity in the top region of the brain due to proximity to the frontal sinuses. A few spectra at the voxels indicated by the dots are shown in Fig. 2. The improved reconstruction using the proposed approach leading to less noisy line shapes as well as restoring the spectra in the regions with high inhomogeneity is clear in this figure. Note that we achieve similar results for two times acceleration. In Fig. 3 we depict the peak integral maps of Cho for both reconstruction schemes. Our proposed sparse reconstruction method is capable of recovering the signal even in areas with high inhomogeneity while it can retrieve details such as ventricles in the peak maps. In contrast, the SENSE approach shows losses in the top region of the brain and noisy reconstructions. This is also evident from Fig. 2. In Fig. 3, we also demonstrate the results with 2-fold acceleration. As seen, the proposed approach results in similar reconstructions as in the case of full sampling.

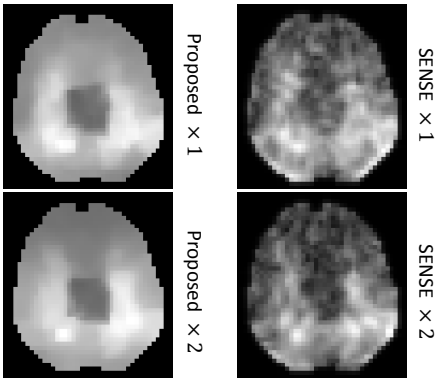

Fig. 3. Reconstructed peak integral maps of Cho using the proposed as well as SENSE schemes at acceleration rates of $\times$ **1** and $\times$ **2**.

REFERENCES

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