Brain metabolite image reconstruction from volumetric MRSI data

Y. Bao[1], A. A. Maudsley[1]

[1]Radiology, University of Miami, School of Medicine, Miami, Florida, United States

Introduction: The quality of in vivo metabolite images obtained using Magnetic Resonance Spectroscopic Imaging (MRSI) is limited by low sensitivity, resulting in low spatial resolution, and artifacts resulting from spectral distortions in regions of increased magnetic field inhomogeneity. These concerns are increased for volumetric MRSI, where the ability to optimize shimming over the whole imaged volume and the ability to obtain high-spatial sampling is further limited. While early reports of improved reconstruction methods have been described for single slice MRSI [1, 2] progress has been limited, in part due to the complexity of MRSI data. It has been demonstrated that statistical methods can provide a method for recovering higher spatial resolution information using high quality structural information from MRI as a prior [3, 4]. In this study, we extended a previously described 2D MRSI model [5, 6] to volumetric MRSI.

Methods: Volumetric MRSI data are viewed as samples from a Gaussian random field that fit a mathematical model from a signal volume, V , sampled over voxels, K_x, K_y, and K_z:

$$S\left(t,k_x,k_y,k_z\right)=\sum_{m}\sum_{V_x=0}^{K_x-1}\sum_{V_y=0}^{K_y-1}\sum_{V_z=0}^{K_z-1}\left(\int_{\substack{(x,y,z)\\ \in V(V_x,V_y,V_z)}} A_m(x,y,z)\,e^{-\frac{t}{T_a(x,y,z)}-\left(\frac{t}{T_b(x,y,z)}\right)^2} e^{\left(-j2\pi\left(\left(f_m(x,y,z)+\gamma\Delta B_0(x,y,z)\right)t+\phi_0(x,y,z)\right)\right)}\,dxdydz\right) e^{-j2\pi\left(\frac{V_xk_x}{K_x}+\frac{V_yk_y}{K_y}+\frac{V_zk_z}{K_z}\right)}+Baseline$$

This model is then reformulated to attribute constant metabolite intensities over local regions for each tissue type, of grey matter, white matter, CSF, and lipid regions. The MRS signal intensities are estimated using knowledge of the fraction of each tissue in each SI voxel, which are obtained by co-analysis with tissue segmentation images obtained from co-registered MRIs. Further, spectral parameters, such as B_0 , linewidth, and phase shift are locally homogeneous and estimated from 0 padding the MRSI data, some estimate errors are allowed since their effects on the MRSI data have been subsided by the exponential function. To address the problem of regions of inadequate spectral quality, regions are excluded based on operator-assessment, guided by generation of quality maps based on the initial estimate of the fitted metabolite resonances, and a modified version of the data obtained by inverse Fourier transform. Using this signal model, the metabolite intensities are then estimated by minimizing the difference between the modeled and acquired data, $S_{acq}(t,k_x,k_y,k_z)$. Using the estimated metabolite intensities, high spatial-frequency content of the acquired MRSI data is extrapolated, to enable reconstruction of higher resolution metabolite images.

Results and Discussions: The proposed method has been applied to simulated volumetric MRSI data (16X16X5 spatial and 512 spectral points) simulated from high resolution tissue maps. MRSI data was then reconstructed at 64X64X5 spatial points. Currently, resolution is only improved in plane, and results are shown in Fig. 1 together with the zero-filled FT reconstructed metabolite images for comparison. The appearance of the reconstructed metabolite images matches well with the high resolution tissue segmentation data used to generate the data. This initial result indicates the potential of applying this algorithm to volumetric MRSI data.

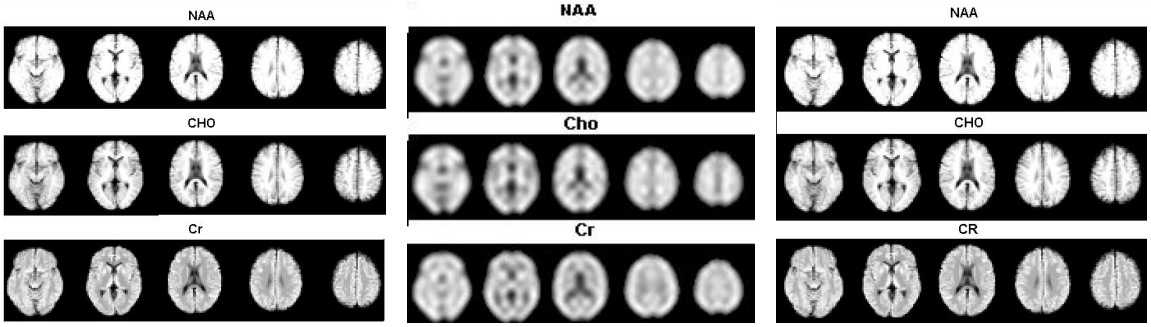

Fig.1. a) Simulated metabolite images at high resolution. b) Metabolite images reconstructed from Fourier transform of the low k-space MRSI data. c) Metabolite images reconstructed using the proposed algorithm.

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