Metabolite Map Estimation from Undersampled Spectroscopic Imaging Data using N-Compartment Model

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TARGET AUDIENCE: Chemical Shift Imaging investigators, Image reconstruction scientists.

PURPOSE: Physiological abnormalities could be detected by irregular change of metabolite concentration in specific brain regions. The combination of fully sampled spectroscopic imaging data and segmented structural image has been used to estimate metabolite value at each voxel [1-4]. This abstract presents an N-compartment-model method with polynomial masks to obtain metabolite maps from undersampled spectroscopic imaging data. The technique assumes that metabolite value within the same tissue type is slowly varying, and the information of tissue boundaries is obtained from segmented structural image. Then, a regularized reconstruction with priors is formulated to reconstruct the metabolite maps. By acquiring only a subset of k-space samples, the acquisition process is sped up, while reconstruction quality is retained via prior knowledge of tissue boundaries.

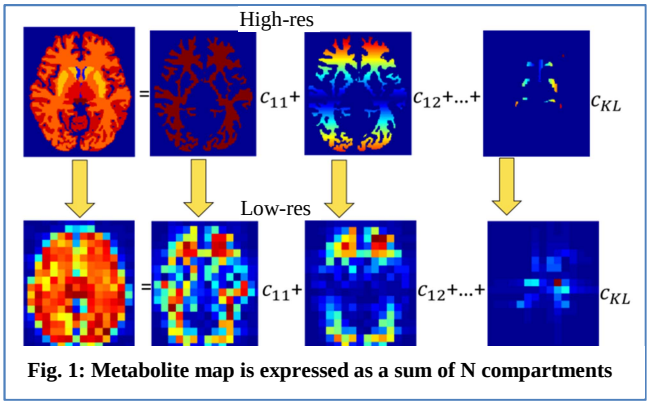

Fig. 1: Metabolite map is expressed as a sum of N compartments

METHODS: In [1-4], each metabolite map is expressed as a superposition of N compartments: $\boldsymbol{x} = \sum_{k=1}^{N} \boldsymbol{m}_k c_k$ where $\boldsymbol{x}$ is metabolite map, $\boldsymbol{m}_k$ is a mask of the k^{th} compartment, c_k is a scaling factor of the k^{th} compartment, N is number of compartments in consideration. This model assumes that metabolite value is constant within the same compartment. In this work, the existing model is extended to accommodate more than one mask per compartment by expressing each metabolite map as $\boldsymbol{x} = \sum_{k=1}^{N}\sum_{p=1}^{L} \boldsymbol{m}_{kl} c_{kl}$ where $\boldsymbol{m}_{kl}$ is the l^{th} mask of compartment k, c_{kl} is the l^{th} scaling factor of compartment k, and L is number of different masks for each compartment. Each mask of a compartment is generated corresponding to each term of the polynomial. For instance, L = 1 means that the 0th order polynomial mask is used, and L = 3 means that the 1st order polynomial mask is used (i.e., $\boldsymbol{m}_{11} = \boldsymbol{m}_1, \boldsymbol{m}_{12} = \boldsymbol{m}_1 \otimes \boldsymbol{x}_{variation}, \boldsymbol{m}_{13} = \boldsymbol{m}_1 \otimes \boldsymbol{y}_{variation}$). The high-resolution $\boldsymbol{m}_{kl}$'s are obtained from the segmented structural image using Freesurfer [5] and FSL[6]. The low-resolution mask, $\boldsymbol{m}_{kl}^{(low)}$, is then obtained from $\boldsymbol{m}_{kl}$ (Fig.1). By stacking $\boldsymbol{m}_{kl}^{(low)}$'s and c_{kl} into a single matrix $\boldsymbol{M}^{(low)}$ and $\boldsymbol{c}$, respectively, the metabolite values are estimated by solving: $\min_{\boldsymbol{c}} \left|\left|\boldsymbol{F}_{us}\boldsymbol{M}^{(low)}\boldsymbol{c} - \boldsymbol{y}\right|\right|_2^2 + \lambda_s \left|\left|\boldsymbol{\psi}\boldsymbol{M}\boldsymbol{c}\right|\right|_1$ where $\boldsymbol{y}$ is the observed k-space low-resolution data, $\boldsymbol{F}_{us}$ is the undersampled Fourier transform, $\boldsymbol{\psi}$ is the sparsifying transform, λ_s is a regularization parameter. For comparison, the least-square (LS) method is applied to obtain the minimum-norm solution.

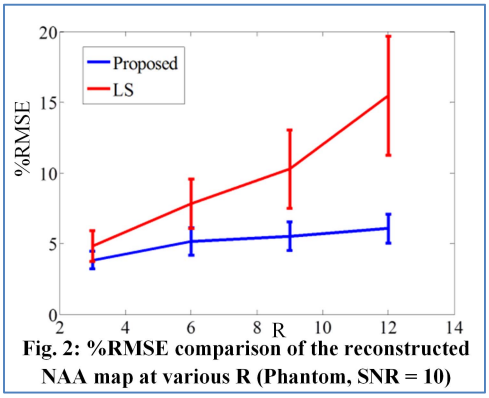

Fig. 2: %RMSE comparison of the reconstructed NAA map at various R (Phantom, SNR = 10)

Experiments were conducted on two data sets: numerical phantom and in vivo data. For the first experiment, the reconstructions were evaluated on the numerical spectroscopic phantom with water suppressed (~ 10 times higher in amplitude than that of NAA peak) and no lipid. The number of compartments N and number of masks per compartment L were chosen to be 9 and 1, respectively. For the second experiment, the water reference and metabolite data were fully sampled at 3 Tesla using LASER sequence [7] with TE/TR = 30/1800 ms and a total scan time of 1minute(1-avg water reference)/8minutes(4-avg metabolite data) to excite a FOV of 24cmx24cmx8cm at 1 cm^3 isotropic. A T1-weighted structural volume at 1 mm^3 isotropic resolution was also acquired in the same orientation. N and L were chosen to be 3 and 3 respectively. The reconstructions were evaluated at an acceleration factor R equal to 6 on the post gridded-data. For both experiments, the Daubechies wavelet of length 2 was used as a sparsifying transform.

RESULTS: Fig. 2 shows the average and standard deviation of root mean square errors (RMSEs) of the reconstructed NAA map with various acceleration factors (R) at SNR = 10 (1st experiment). Fig.3 and Fig.4 depict original data acquired from scanner, reconstructed map from the fully-sampled LS reconstruction (R=1), the proposed method, and the LS reconstruction (R = 6), respectively. RMSEs shown in both figures were computed with respected to the fully-sampled LS reconstruction.

DISCUSSION: As shown in Fig.2, RMSEs at all R of the proposed method is smaller than those obtained from the LS method. This observation is also seen in the in vivo results (Fig. 3 and 4). This is expected because the proposed method includes priors on the data structure. This prior to impose sparsity in the reconstruction is appropriate because the metabolite map has only a few dominating coefficients in the wavelet domain . For the in vivo case, because the metabolite value within the same compartment is slowly varying, we used 1st order polynomial for the mask. One limitation of this study is that undersampling was performed with post-gridded data on a Cartesian grid.

CONCLUSION: By obtaining the knowledge of tissue boundaries from segmented structural image, the metabolite map can be modeled as a composition of values from N compartments. To resemble the real brain, the metabolite value within the same compartment is allowed to be slowly varying by using more than one mask per compartment. With this set-up, there are only a few unknowns to be determined, and the acquisition time could be reduced by undersampling the spectroscopic data. In addition, the sparsity constraint is enforced on the reconstruction process which leads to more accurate reconstruction of spectra compared to that without regularization.

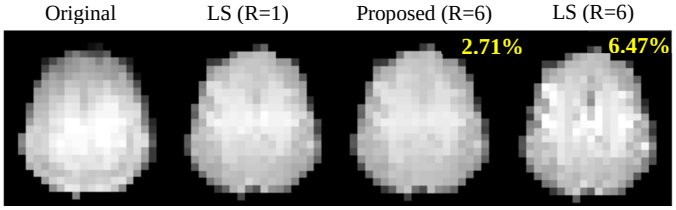

Fig.3: Water maps with corresponding RMSE.
RMSE with respected to the fully-sampled LS reconstruction (R = 1) is shown in the upper right hand corner of each reconstructed map

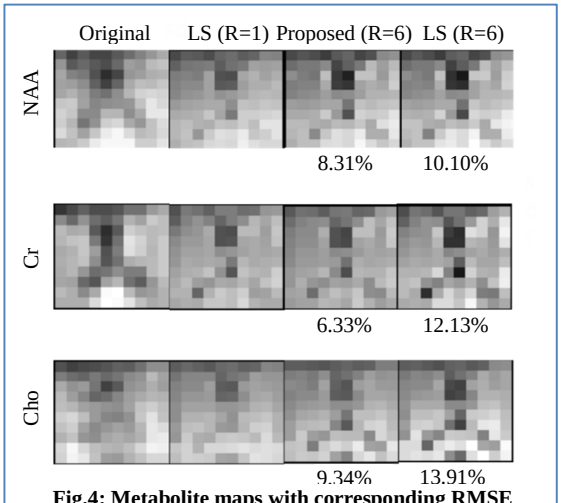

Fig.4: Metabolite maps with corresponding RMSE
RMSE with respected to the fully-sampled LS reconstruction (R = 1) is shown below each reconstructed map

REFERENCES: [1] Hetherington et al MRM 36:21-29 (1996); [2] Lim MRM 37:372-377 (1997); [3] Pfefferbaum et al MRM 41:276-284 (1999); [4] Ratai E AMA 39:889-898 (2008); [5] Fischl et al Neuron. (2002) [6] Zhang et al IEEE TMI (2001); [7] Garwood et al J Magn Reson (2001)