# Undersampled Spectroscopic Imaging with Model-based Reconstruction

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

**PURPOSE:** This abstract presents a two-step, model-based method that leads to an accurate reconstruction from undersampled spectroscopic imaging data. This method takes advantage of a fast water reference scan to estimate a subset of (non-linear) unknowns. Then, a regularized optimization problem with priors is formulated to reconstruct the spectroscopic imaging data. This method reduces acquisition time by undersampling, while preserving high reconstruction quality.

**METHODS:** In [1-4], parametric modeling has been adopted to improve reconstruction accuracy of the spectroscopic data. In this work, the time signal at each voxel is expressed as a sum of K decaying exponentials [1]: $s(t) = \sum_{k=1}^{K} a_k \exp(-t/T_2^{(k)}) \exp\big(j(\omega_0 - \Delta\omega_k)t + (\phi_0 - \Delta\phi_k)\big) + n(t)$ where $a_k$'s are amplitudes, $T_2^{(k)}$'s are decay times, $\omega_0$ and $\phi_0$ are reference frequency and phase, respectively, $\Delta\omega_k$ and $\Delta\phi_k$ are deviations from the reference frequency and phase, K is number of metabolites in the model, and $n(t)$ is white Gaussian noise. $\Delta\omega_k$ and $\Delta\phi_k$ are known constants for $^1$H brain metabolites. In [1,2], the spectrum at each voxel is reconstructed independently by solving a least-square (LS) problem. In this work, the data are undersampled in $k_x$-$k_y$ space, so all spectra must be simultaneously reconstructed. We propose a two-step reconstruction (Fig.1): First, a separate water reference data along with a priori information is used to determine $\omega_0$, $\Delta\omega_k$, $\phi_0$, $\Delta\phi_k$ and $T_2^{(k)}$. Second, $a_k$'s are estimated by solving the following optimization problem: $\min_{\boldsymbol{a}} ||\boldsymbol{F_{us}}\boldsymbol{M}\boldsymbol{a} - \boldsymbol{y}||_2^2 + \lambda_{TV} TV(\boldsymbol{M}\boldsymbol{a})$, where $\boldsymbol{a}$ is a vector consisting of $a_k$'s, $\boldsymbol{M}$ contains bases of each metabolite, $\boldsymbol{y}$ is observed k-space data, $\boldsymbol{F_{us}}$ is the undersampled Fourier transform, $TV(.)$ is total variation operator, $\lambda_{TV}$ is regularization parameter. For comparison, we also applied the LS method that finds a minimum-norm solution: $\min_{\boldsymbol{a}} ||\boldsymbol{a}||_2^2$ subject to $\boldsymbol{F_{us}}\boldsymbol{M}\boldsymbol{a} = \boldsymbol{y}$. In this experiment, spectroscopic spiral CSI were acquired fully sampled at 1.5T with TE/TR = 144/2000 ms with the total scan time of 15:20 minutes and resolution of 1.1cc. The water resonance was suppressed using spin-echo spectral-spatial pulses. Inversion recovery with TI = 170 ms was used for lipid suppression. In post-processing, residual lipids were manually masked out prior to the reconstruction of retrospectively undersampled CSI data. K was chosen to be 3, which represented NAA, Creatine, and Choline. The reconstructions were evaluated for acceleration factors R between 2 and 6 on the post-gridded data.

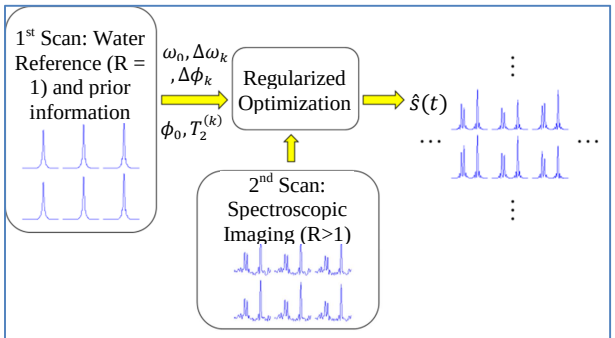


**Fig. 1: A block diagram for the reconstruction**

**RESULTS:** Fig. 2 depicts fully sampled data (top), reconstructed metabolite maps from undersampling with R = 2 via LS (middle), and the proposed method (bottom). Fig. 3 compares spectra at specific locations inside the brain. The fully-sampled observed spectra, reconstructed spectra from the LS method (R=1), and reconstructed spectra from proposed method (R=2) are shown in red, green, and blue, respectively, and difference in magenta. Fig. 4 shows root mean square errors (RMSEs) of each reconstructed metabolite map with respect to the fully-sampled LS reconstruction with various acceleration factors, R.

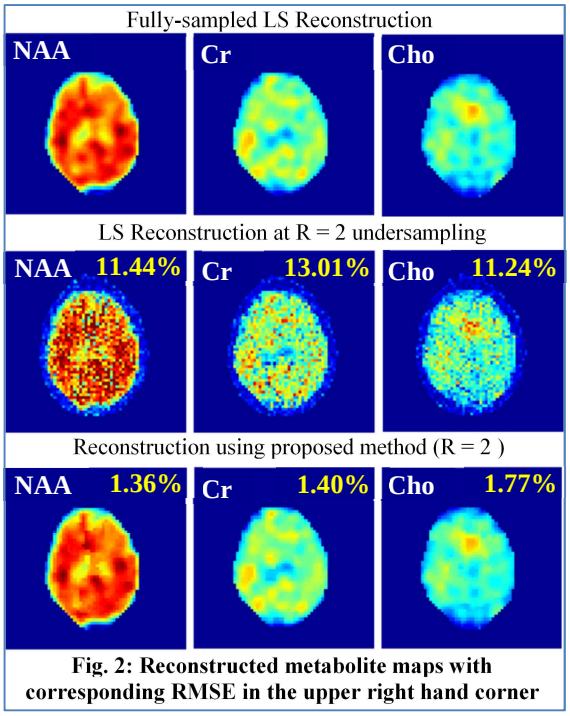


**Fig. 2: Reconstructed metabolite maps with corresponding RMSE in the upper right hand corner**

**DISCUSSION:** The proposed method incorporates prior knowledge by imposing a total variation term. As a result, RMSEs obtained from the proposed method are smaller than those obtained from the LS method even with low R. With higher R, the proposed method significantly reduces RMSE (e.g., from approximately 80% to 3.5% at R = 3). There are some limitations in this study. First, the reconstruction is done on the post-gridded data. Second, lipid was not modeled in our formulation, so undersampling artifacts occurred from the presence of lipid affects the reconstruction accuracy. This problem could be solved using outer-volume suppression (OVS) [5], or alternatively, by adopting and extending the method proposed in [6], where a fast scan of a high-resolution lipid image aids the modeling and reconstruction.

**CONCLUSION:** By representing a time signal at each voxel as a sum of decaying exponentials and taking advantage of a quick water scan, there are only a few, linear unknowns left to be determined. This allows us to undersample the spectroscopic data, which mitigates the limitation on long acquisition times in CSI. In order to tackle with the undersampling artifacts, prior knowledge on the structure of the data is incorporated to the optimization problem via regularization which greatly improves the reconstruction accuracy compared to that without regularization.

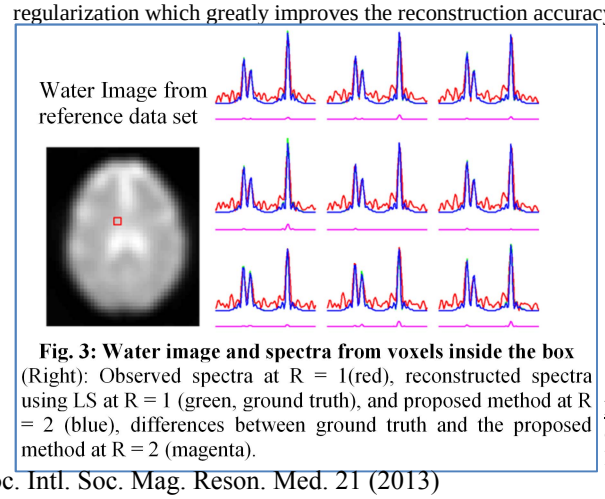


**Fig. 3: Water image and spectra from voxels inside the box** (Right): Observed spectra at R = 1(red), reconstructed spectra using LS at R = 1 (green, ground truth), and proposed method at R = 2 (blue), differences between ground truth and the proposed method at R = 2 (magenta).

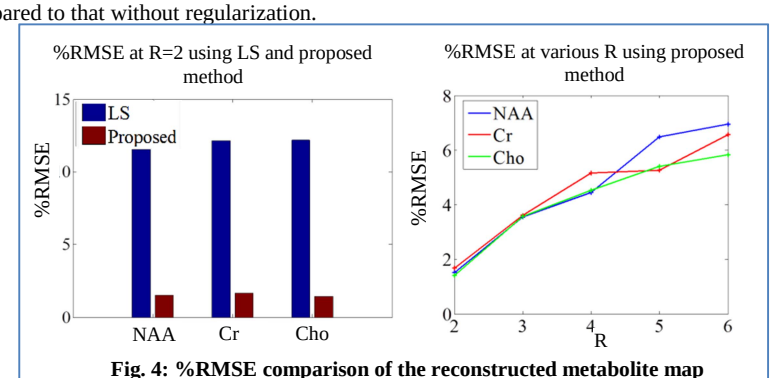


**Fig. 4: %RMSE comparison of the reconstructed metabolite map**

**REFERENCES:** [1] Spielman DM. PhD Thesis (1990); [2] Adalsteinsson et al. MRM 39:889-898 (1998); [3] Eslami R. IEEE TMI (2010); [4] Haldar et al. IEEE ISBI (2006); [5] Duyn et al Radiology (1993); [6] Bilgic B. MRM (2012)