# Removal of Nuisance Lipid Signals from Limited *k*-Space Data in 1H MRSI of the Brain

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**Introduction:** Conventional MRSI experiments often have limited *k*-space coverage due to practical time constraints. Consequently, there is significant leakage of lipid signals from the subcutaneous layer in 1H MRSI of the brain. The spectra of lipid signals from the subcutaneous layer are of little interest, but overlap with other important metabolites in the brain, *e.g.*, lactate and NAA, due to their strong intensities and broad spectral peaks. Such nuisance signals significantly complicate spectrum quantitation in brain MRSI. A variety of techniques have been proposed to address this problem, from those that suppress the lipid signals during data acquisition[1,2] to those that remove the lipid signals in post-processing[3-8]. However, complete removal of nuisance lipid signals from limited MRSI data remains challenging. In this work, we propose a new post-processing method for removal of nuisance lipid signals using a novel spatial-spectral model.

**Methods:** The basic idea of most post-processing methods for lipid signal removal is to reconstruct a high resolution MRSI image of lipids from limited *k*-space data using various prior information of lipids, *e.g.*, spatial support[4,5] and spatial-spectral support[6,7] information. Our approach is using a spatial-spectral model. More specifically, we express the spatial-spectral function (assuming water signals have been removed in advance) as:

$$\rho(\boldsymbol{x},t)=\rho_M(\boldsymbol{x},t)+\rho_L(\boldsymbol{x},t),\ \text{where}\ \rho_M(\boldsymbol{x},t)=W_M(\boldsymbol{x})\sum_{p=1}u_M^p(\boldsymbol{x})\,v_M^p(t)\ \text{and}\ \rho_L(\boldsymbol{x},t)=W_L(\boldsymbol{x})\sum_{p=1}u_L^p(\boldsymbol{x})\,v_L^p(t). \quad (1)$$

In Eq. (1), $\rho_M(\boldsymbol{x},t)$ and $\rho_L(\boldsymbol{x},t)$ denote metabolite and lipid signals, respectively. Each of them is explicitly modeled as a low-rank signal, where $W_*(\boldsymbol{x})$ denotes a spatial support mask, $u_*^p(\boldsymbol{x})$ denotes a spatial basis function and $v_*^p(t)$ denotes a temporal basis function. The support masks and temporal basis functions can be estimated in advance (discussed below). The spatial basis functions are estimated by solving the following optimization problem:

$$\{u_M^{p,o}(\boldsymbol{x}),u_L^{p,o}(\boldsymbol{x})\}=\underset{u_M^p(\boldsymbol{x}),u_L^p(\boldsymbol{x})}{\operatorname{argmin}}\left\|d(\boldsymbol{k},t)-\boldsymbol{\Omega F}\{\Phi(\boldsymbol{x},t)[W_M(\boldsymbol{x})\sum_{p=1}u_M^p(\boldsymbol{x})\,v_M^p(t)+W_L(\boldsymbol{x})\sum_{p=1}u_L^p(\boldsymbol{x})\,v_L^p(t)]\}\right\|_2^2, \quad (2)$$

where $d(\boldsymbol{k},t)$ denotes the measured data, $\boldsymbol{\Omega}$ is a sampling operator, $\boldsymbol{F}$ is a spatial Fourier transform operator and $\Phi(\boldsymbol{x},t)$ is a phase term modeling field inhomogeneity effects. Note that the metabolite signals introduced here are treated as auxiliary variables and the accuracy of its reconstruction is not essential as long as the error does not affect the determination of the lipid signals. The final metabolite signals will be reconstructed after the lipid signals are determined and removed from the MRSI data.

The spatial support masks and temporal basis functions of lipids and metabolites can be easily estimated in three pre-processing steps. First, the spatial support of lipids and metabolites and field map are estimated using a Dixon method from multi-echo GRE data. Second, a high resolution MRSI image is reconstructed from the measured data using zero-padding and conjugate phase reconstruction (for field inhomogeneity correction). Lipid and metabolite signals are then extracted by applying the support masks to the zero-padded data. Third, the temporal basis functions of lipids and metabolites are obtained by applying singular value decomposition to the extracted lipid and metabolite signals, respectively. However, the resulting temporal functions of lipids can still contain leakage of metabolite signals, and *vice versa*. The leakage signals in the temporal basis functions are further removed using HSVD[10] based on prior information of spectral positions of lipid and metabolite signals.

**Results:** The effectiveness of the proposed method was evaluated through *in vivo* experiments at a 3T whole body scanner. A 16×16 brain MRSI data from a healthy volunteer was collected using a CSI sequence with short echo time (30 ms TE) and outer volume suppression. A representative spectrum from a voxel near the fat layer (indicated by the blue box in Fig. 1a) is shown in Fig. 1b, where the leakage of lipid signals is clearly seen. The lipid-removed spectrum obtained by the proposed method is shown in Fig. 1c. Almost complete lipid signal removal was achieved.

**Conclusion:** We have presented a new method for removal of nuisance lipid signals from limited *k*-space data. The proposed method is based on a novel spatial-spectral model of MRSI data and has been shown to be effective for removal of lipid signals in brain 1H MRSI data. The proposed method should prove useful for MRSI studies of the brain.

**References:**

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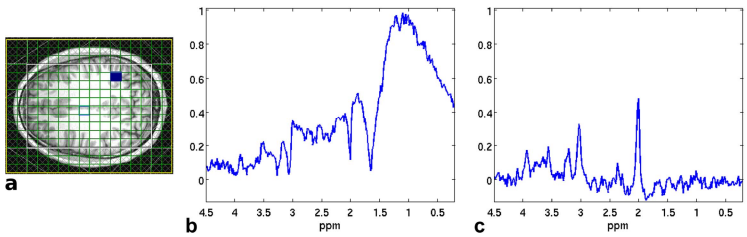


Fig. 1, Experimental results of a human subject at 3T. **a:** Reference image. **b:** Spectrum before removal of lipid signals (magnitude). **c:** Spectrum after removal of lipid signals using the proposed method (real part).