Removal of Lipid Nuisance Signals in MRSI Using a Spatial-Spectral Lipid Model

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INTRODUCTION

Nuisance lipid signals from the subcutaneous lipid layer of the brain often cause significant difficulties for spectral quantification of the brain metabolites. Removal of the lipid signals in brain MRSI data is desirable but challenging because they appear as multiple-peak, broad spectra that overlap with the spectra of important brain metabolites (*e.g.*, lactate and NAA). A variety of techniques have been proposed to address this problem. One approach is to suppress the lipid signals during data acquisition, using, for example, inversion recovery [1], outer-volume suppression [2], selective excitation and extended k-space coverage [3, 4]. Another approach is to remove the lipid signals using post-processing methods, including methods using spatial support information of lipids [5, 6] and methods using spatial-spectral support constraints [7, 8]. In this work, we introduce a model-based post-processing method for effective removal of the lipid signals.

METHODS

The spatial-spectral data acquired in an MRSI experiment can be modelled as $\tilde{\rho}(\boldsymbol{x},t) = \tilde{\rho}_m(\boldsymbol{x},t) + \tilde{\rho}_l(\boldsymbol{x},t)$, where $\tilde{\rho}_m(\boldsymbol{x},t)$ and $\tilde{\rho}_l(\boldsymbol{x},t)$ represent the signals of metabolites and lipids, respectively, all in low spatial resolution. Taking advantages of the priori information of the spatial support and spectral model of lipids, we propose to model the lipid signals as $\tilde{\rho}_l(\boldsymbol{x},t) = \sum_r c_r u_r(\boldsymbol{x}) v_r(t)$. The spatial basis function $u_r(\boldsymbol{x}) = \delta(\boldsymbol{x}-\boldsymbol{x}_r) * h(\boldsymbol{x})$ models the signal linkage from a lipid pixel at $\boldsymbol{x}_r \in \Omega_l$ due to Fourier reconstruction from limited data, where Ω_l denotes the spatial support of lipids. The spectral basis function $v_r(t) = \sum_q a_q \exp\left[-j2\pi(f_q + f_r)\, t - t/T_{2,q}\right]$ models the lipid spectrum at $\boldsymbol{x}_r$, where the parameters f_q, $T_{2,q}$, and a_q are the coefficients of a multiple–peak spectral model of lipids, and f_r incorporates any field inhomogeneity at $\boldsymbol{x}_r$. Assuming that the spatial support and coefficients of the spectral model of lipids and the field map can be estimated in advance, the lipid signals can be estimated by solving the following least-squares problem:

$$\min_{c_r} \|F_t\{\textstyle\sum_r c_r u_r(\boldsymbol{x}) v_r(t)\} - F_t\{\tilde{\rho}(\boldsymbol{x},t)\}\|_W^2, \qquad (1)$$

where F_t denotes the temporal Fourier transform, $\|\cdot\|_W$ denotes a weighted-ℓ_2 norm that is designed to protect significant metabolites by setting weights of 0 for the known frequency ranges of the metabolites [7].

The data processing/acquisition procedure of the proposed method is as follows. First, the spatial support of lipids and field map are simultaneously estimated using a three-point Dixon method [9]. Second, an MRSI dataset is acquired. Third, the BSLIM method is used to reconstruct a high quality lipid spectrum from the MRSI data with the estimated spatial support and field map [10]. Fourth, the parameters of the lipid spectrum are estimated using harmonics retrieval [11]. Finally, the estimated lipid signals are estimated by solving optimization problem in (1) and subtracted from the data to obtain the metabolite signals.

RESULTS

The proposed method has been evaluated using simulation data, for which spectra of four metabolites (NAA, Glu, Cr, and Cho) and a four-peak lipid spectrum were assigned based on different tissue types of a brain dataset [12,13]. A representative field map based on *in vivo* data was also incorporated in the simulation. A representative set of results are shown in Fig. 1. The original spectrum of a pixel close to the lipid layer (Fig. 1b) shows significant lipid signals. The proposed method (Fig. 1d) was compared with the method in [7] (Fig. 1c) that uses spatial-spectral support constraints to remove the lipid signals. Both methods significantly suppressed the lipid signals. However, while there were some residual lipid signals for the method in [7], the proposed method removed the lipid signals almost completely.

CONCLUSION:

We have presented a novel method that can effectively suppress nuisance lipid signals in MRSI data using a spatial-spectral model of the lipid signals. The proposed method should prove useful for 1H MRSI study of the brain.

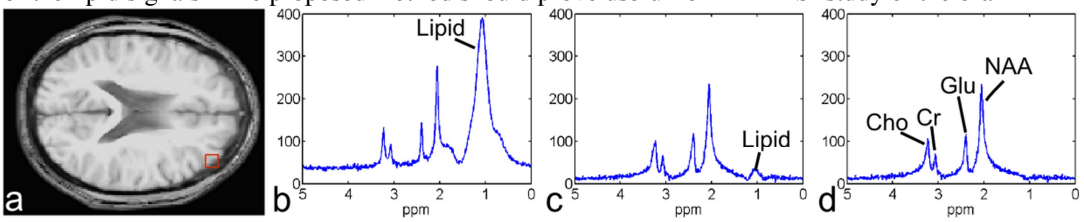

Figure 1. **a:** Anatomical image of the brain dataset [13]. **b:** Spectrum without lipid signal removal. **c:** Spectrum with lipid signal removal using the method in [7]. **d**: Spectrum with lipid signal removal using the proposed method.

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