Removal of Lipid Nuisance Signals in MRSI Using Spatial-Spectral Constraints

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INTRODUCTION

One of the main difficulties for the quantification of metabolites in MRSI data arises from the presence of strong water and lipid signals. While the water signal is well separated in the spectral domain from most metabolites of interest, lipids are more problematic since they typically appear as broad and distorted lineshapes, which overlap with several important metabolite peaks (*e.g.*, lactate and NAA). A variety of data acquisition approaches have been proposed to reduce the intensity of the lipid signal, which includes pulse sequences using long echo times, inversion-recovery, outer volume saturation, or spatially selective excitation. Several postprocessing methods have also been proposed, both in the context of MRSI (taking advantage of the spatially localized origin of lipid signals [1]) as well as in single voxel spectroscopy (typically based on spectral constraints such as the smoothness of lipid lineshapes [2]). Here we introduce a postprocessing method that effectively combines spatial and spectral constraints for removal/reduction of the lipid signals in MRSI data.
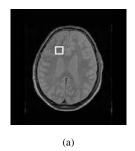
MATERIALS AND METHODS

The signal obtained in an MRSI experiment can be modeled as $\tilde{\rho}(\mathbf{r}, f) = (\rho_l(\mathbf{r}, f) + \rho_m(\mathbf{r}, f)) * h(\mathbf{r}) = \tilde{\rho}_l(\mathbf{r}, f) + \tilde{\rho}_m(\mathbf{r}, f)$, where $\rho_l(\mathbf{r}, f)$ and $\rho_m(\mathbf{r}, f)$ are the spatial-spectral densities of lipids and metabolites, respectively, and $h(r)$ is a broad convolution kernel due to Fourier reconstruction from limited data. Although the lipid signal often originates from a distinct spatial region Ω_l (*e.g.*, a subcutaneous layer in brain MRSI), significant spatial overlap with metabolite signals appears due to the low spatial resolution typical of MRSI data, which combined with the spectral overlap of lipids and metabolites makes the lipid removal problem nontrivial. We propose to use the following spatial-spectral prior information to better constrain the lipid signal estimate: (a) a high-resolution binary map of lipid locations, or "fat mask" M(**r**) which is *1* if $r \in \Omega_l$, and *0* elsewhere, and (b) a field inhomogeneity map. Note that both the fat mask and the field map can be obtained simultaneously with a Dixon-type acquisition [3].
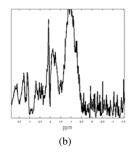
The spatial constraints are applied as follows: $\hat{\rho}_{l,s}(\mathbf{r}, f) = F^{-1} TF \{M(\mathbf{r})\tilde{\rho}(\mathbf{r}, f)\}$, where *F* denotes Fourier transform in the spatial dimensions and *T* is a truncation operator keeping only the measured low-resolution samples. This is similar to one step of the Papoulis-Gerchberg (PG) algorithm [1]. This step produces an estimate of the lipid signal lineshapes for all spatial locations. Next, $\hat{\rho}_{l,s}(\mathbf{r}, f)$ is decomposed spectrally at each voxel into a set of basic lineshapes (*e.g.*, a mixture of Lorentzians using a harmonic retrieval method [4]. Note that the lipid signal generally has non-Lorentzian lineshape but can be adequately approximated by a combination of Lorentzians by the *universal approximation theorem* [5]). Finally, the resulting basic lineshapes at each location are fitted to the original signal $\tilde{\rho}(\mathbf{r}, f)$ using *weighted least squares* to obtain the final lipid signal estimate $\hat{\rho}_l(\mathbf{r}, f)$. The weights are obtained from the field map by estimating at each voxel in the low-resolution dataset the frequency ranges which contain significant metabolite signal contribution, so that these frequency ranges are not fitted (*i.e.*, assigned a weight of *0*). Finally, the lipid estimate is subtracted from the data to obtain the metabolite signal.
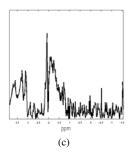
RESULTS AND DISCUSSION

The proposed method has been tested with phantom as well as biological data. A set of representative results obtained from a brain MRSI dataset is shown in Fig 1, with an unprocessed spectrum shown in Fig 1(b). Figures 1(c) and 1(d) show the resulting spectra after lipid removal using PG and the proposed method, respectively, illustrating how the incorporation of spectral constraints helps improve the removal of nuisance lipid signals. Note that the field inhomogeneity map allows consistent prediction of the frequency shift as well as the broadening of metabolite peaks, thus significantly improving the protection of metabolite resonances.

This method has been shown empirically to perform well in most cases. However, under certain conditions, especially in the presence of high field inhomogeneity the decomposition of the lipid signal into Lorentzian lineshapes becomes less parsimonious. This problem can be dealt with by introducing a lineshape correction function into the Lorentzian-based model.
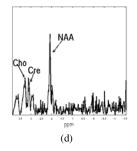

(a) (b) (c) (d)

Figure 1. (a) Brain image; (b) Original spectrum at indicated location, showing significant lipid contamination; (c) PG result; (d) Result of proposed method obtained by removing the estimated lipid signal while protecting choline, creatine and NAA.

CONCLUSIONS

We present a novel method for removal of lipid signals in brain MRSI incorporating both spatial and spectral constraints. Using additional prior information we are able to remove the lipid signal effectively while preserving metabolite signals. This method should allow more accurate quantitation of the metabolites of interest.

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