Reduction of lipid contamination in MR spectroscopic imaging using Signal Space Projection

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Introduction

Lipid contamination originating from the Gibbs ringing artifacts may complicate the metabolite quantification in MR spectroscopic imaging (MRSI). Suppression of lipid signal can be done either by outer volume saturation bands at the perimeter of the brain or by lipid nulling with inversion recovery pulses at the cost of increased SAR, which is particularly challenging at high fields. Alternatively, lipid suppression can be implemented by post-processing methods, such as widening the k-space sampling of lipid signal and therefore diminishing the Gibbs ringing [1] and extrapolating lipid signal to high k-space region to reduce Fourier construction artifacts [2]. Another category of lipid suppression aims to localize lipid signal directly from arbitrarily shaped volume of interest [3].

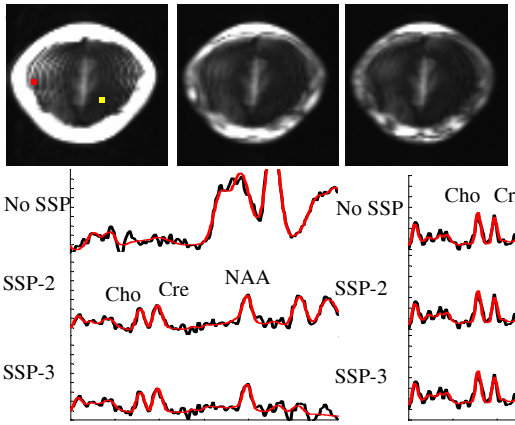
In this study, a new method based on Signal Space Projection (SSP) is introduced to suppress lipid signal in MRSI by data post-processing. SSP is a spatial filtering technique based on the assumption that the spatial patterns of noise (lipid) are uncorrelated with the spatial patterns of signal (metabolites). We describe the SSP method here with a demonstration of high-resolution *in vivo* MRSI experiment at 3T.

Methods

We first express the spectral image in the spatio-spectral domain using a 2-dimentional spatial-spectral matrix $\mathbf{D}_{ori}$ with dimension of [Nx*Ny, Nf], where Nx * Ny is the spatial matrix size, and Nf is the spectral vector size. MRSI spectral data in the range between 1.0 ppm and 1.5 ppm was extracted from $\mathbf{D}_{ori}$ to generate a noise space (lipid) data matrix $\mathbf{D}_{ori\text{-}lipid}$ with the dimension of [Nx*Ny Nlipid], where Nlipid is the size of lipid spectrum centered at the 1.2ppm lipid peak. Singular Value Decomposition of $\mathbf{D}_{ori\text{-}lipid}$ yields spatio-spectral characterizations: $\mathbf{D}_{ori\text{-}lipid}$= **U** x **S** x **V**, where **U** represents the spatial components of the lipid signal, **V** represents the spectral components of the lipid signal, and **S** is a diagonal matrix with singular values. The majority of the lipid signal can be extracted by the first *n*-components of **U**, $\mathbf{U}_n$. Signal Space Projection matrix **P** can thus be constructed as $\mathbf{P} = \mathbf{I} - \mathbf{U}_n \times \mathbf{U}_n$, and lipid suppressed data ($\mathbf{D}_{sup}$) can be obtained by $\mathbf{D}_{sup} = \mathbf{P} \times \mathbf{D}_{ori}$

Proton Echo Planar Spectroscopy Imaging (PEPSI) [4] was performed on a 3 Tesla MR system (Trio, SIEMENS Medical Solutions, Erlangen, Germany) equipped with an 8-channel coil array. PEPSI data were acquired from a para-axial slice at the upper edge of ventricles (matrix size = 64x64, FOV = 220mm, slice thickness= 20mm, TE=35 ms, TR=1500 ms , NEX =8). No outer volume saturations were applied. Even- and odd-echo data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction [4]. Metabolites of N-acetyl-aspartate (NAA), Creatine (Cre) and Choline (Cho) were quantified using the LCModel [5]. The quality of spectra is evaluated by Cramer-Rao Lower Bound (CRLB), which is the lowest bound of the standard deviation of estimated metabolite concentration expressed in % [5].

Results



	NAA	Cre	Cho
No SSP	N/A	N/A	N/A
SSP-2	9/12.4	10/11.3	10/3.8
SSP-3	12/12.0	10/12.6	11/3.7

	NAA	Cre	Cho
No SSP	10/13	9/8.2	9/3.2
SSP-2	6/13.6	8/8.1	7/3.3
SSP-3	5/14.6	7/8.6	7/3.3

Figure 1. Spectral projection images *without* lipid suppression (left), with SSP lipid suppression using 2 components (SSP-2) (middle) and using 3 components (SSP-3) (right). Strong ringing artifacts were significantly reduced by SSP.

Figure 2. Spectra from two representative voxels. One voxel is close to the scalp (left, red marker in Figure 1) and the other one is more central and away from the scalp (right, yellow marker in Figure 1). Spectra are without lipid suppression (upper), with 2-component SSP (SSP-2) lipid suppression (middle) and with 3-component SSP (SSP-3) lipid suppression (lower). The LCModel quantified Cramer-Rao-Lower-Bound (CRLB) (%) and metabolite signal (A.U.) (CRLB/Signal) for NAA, Cre and Cho peaks were listed in the tables bellow. Lipid suppression was successful using SSP to better resolve metabolite peaks and to improve metabolite quantification at peripheral voxel (left), where quantification of metabolites without lipid suppression is not possible because of strong lipid contamination. CRLBs were all less than 10% at brain parenchyma voxel (right) and the quantified metabolite signal was similar before and after SSP. Two component SSP improved lipid suppression as compared to three components SSP without significantly affecting metabolite quantification.

Discussion

Our result demonstrated that the proposed Signal Space Projection (SSP) method can efficiently suppress lipid contamination artifacts. The entire lipid spectrum from the periphery gets deconvolved by the spatial lipid contamination model estimated from the spectral range between 1 and 1.5ppm. MRSI image voxels without serious lipid contamination were not affected by this technique. Spectral quality was improved as a result of successful removal of lipid signal. The LCModel fitting also validated the improved spectral quality by SSP. We calculated only the first 10 SSP components since singular values became very small after the first 10 components. SSP with the first 3 components was sufficient to suppress lipid signal below the level of NAA (Figure 1). This also implies that the computation complexity is very low. In conclusion, fully automatic Signal Space Projection was demonstrated to suppress lipid signal efficiently without intensive computation. SSP can be used alone or be combined with lipid suppression imaging sequences to improve *in vivo* MRSI quality.

Acknowledgements

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