Lipid Suppression in CSI with Highly-Undersampled Peripheral k-space and Spatial Priors

Berkin Bilgic[1], Borjan Gagoski[1], and Elfar Adalsteinsson[1,2]

[1]EECS, Massachusetts Institute of Technology, Cambridge, MA, United States, [2]Harvard-MIT Division of Health Sciences and Technology, MIT, Cambridge, MA, United States

INTRODUCTION: Mapping the concentration of brain metabolites using chemical shift imaging (CSI) is made difficult by the presence of subcutaneous lipid signals, which contaminate the metabolites by ringing due to limited spatial resolution. This problem is further compounded by the narrow spectral separation between the lipid components in the $0.9-1.3$ ppm range and the NAA peak at 2.0 ppm, as well as the spatial proximity of the cortex to the subcutaneous lipid layer. Even though high resolution CSI is not feasible due to SNR constraints on the metabolites, dual-density approach [1,2] exploits the high-SNR property of the lipid layer to generate high-resolution lipid maps and suppress truncation artifacts. Another recent approach for lipid suppression [3] makes use of the fact that the metabolite and the lipid spectra are approximately orthogonal, and seeks sparse metabolite spectra when projected onto lipid-basis functions. Our work combines and extends the dual-density approach and the lipid-basis penalty, while estimating the high-resolution lipid image from single-average k-space data to incur only minimal increase on the total scan time. We demonstrate excellent lipid suppression and a 3-fold decreased reconstruction error in NAA maps relative to [3] *in vivo*. Further, we also exploit the spectral-spatial sparsity of the subcutaneous lipid ring and propose to estimate it from substantially undersampled (acceleration R=10 in the peripheral k-space) single- average *in vivo* data using compressed sensing, and still obtain 2-fold decreased error in NAA maps relative to [3].

METHODS: A healthy volunteer was scanned at Siemens 3T scanner with high spatial resolution, single-slice, constant density spiral CSI (0.16cc, FOV_{xy}=24cm, TE=144ms, TR=2s, N_{avg}=20, t_{acq}=32min, CHESS for water suppression, PRESS-box excites entire FOV, including the skull). The final gridded matrix size was (x,y,f)=(64,64,512). A low resolution, 20-average CSI image was generated by sampling only the center 32-pixel diameter in k_x-k_y plane. The artifact reduction algorithm in [3] was applied on this low-resolution image to solve $\min_x \|\mathbf{F}_{low}\, x - y_{low}\|_2^2 + \lambda \sum_{i \in \mathbf{M}} \|\mathbf{L}\, x_i\|_1$ where $\mathbf{F}_{low}$ is the Fourier transform operator sampling only the center 32-pixel diameter of k-space, y_{low} is the low-resolution data in k-space, $\mathbf{L}$ is the matrix formed by the lipid spectra, $\mathbf{M}$ is a binary mask that marks the metabolite region, x_i is the spectrum at voxel i, and λ is a regularization parameter that was selected empirically. To obtain a gold-standard lipid suppression result, a lipid image was obtained from the high-resolution 20-average data which was masked to retain only the lipid ring, and then combined with the low-resolution 20-average CSI image as per the dual-density approach [1,2]. Iterative reconstruction with lipid-basis penalty [3] was applied to this combined image to yield the gold-standard spectra. For our first proposed method, masked high-resolution lipid image was obtained from single-average data, and combined with the low-resolution 20-average CSI image. Lipid basis penalty reconstruction was then applied to this combined image. For the second proposed method, the high-resolution lipid image was estimated from significantly undersampled single-average data using ℓ_1 norm penalty to promote sparsity. In addition to the fully sampled center 32-pixel diameter k-space, the high k-space region was substantially undersampled (R_{high}=10), from which a high-resolution lipid image was reconstructed using the FOCUSS algorithm [4]. This lipid layer estimate was then combined with the low-res CSI image, and lipid basis penalty was applied to further reduce the ringing artifacts.

Fig 1: Lipid maps without any lipid suppression (a), the gold-standard (b), and the 3 different suppression algorithms (c,d,e)

Fig 2: Comparison between NRMSE values of NAA maps relative to the gold standard

RESULTS: Fig. 1 shows images (in dB scale) obtained by summing over lipid resonance frequencies. In the absence of any lipid suppression, significant lipid contamination is observed (Fig. 1a), as opposed to the clean lipid image obtained with the gold-standard reconstruction (20 avg_{high}, R_{high}=1, shown in Fig. 1b). While Lee et al.'s algorithm [3] significantly reduces the lipid contamination (Fig. 1c), the two proposed methods (1 avg_{high}, R_{high}=1, shown in Fig. 1d and 1 avg_{high}, CS R_{high}=10 in Fig. 1e), provide even further artifact suppression. Fig. 2 validates the observation seen in Fig.1 in terms of normalized root-mean-square error (NRMSE) by comparing the NAA maps estimated using the dataset without lipid suppression and the three artifact reduction methods with the gold-standard NAA map. Fig. 3 shows the performances of the lipid suppression algorithm of Lee et al. [3], the proposed methods and the gold-standard reconstruction by comparing representative spectra in the vicinity of the skull. Fig. 3a, b and c overplot the spectra from the gold-standard with Lee et al.'s method [3], our first proposed method that uses a fully-sampled, 1 average high-resolution data and the second proposed method that uses 1 average high-resolution undersampled data, respectively. The total reconstruction time (FOCUSS & lipid basis penalty) for the proposed method was 14min on a workstation with 48GB memory and 12 processors.

DISCUSSION: The proposed lipid suppression algorithm combines and extends two previously proposed approaches, dual-density sampling and lipid-basis orthogonality, with minimal increase on the total scan time by aggressive undersampling of high frequency k-space. We demonstrated excellent *in vivo* lipid-suppression performance with artifact-free observation of metabolite spectra even in peripheral cortical regions.

REFERENCES: [1] Hu & Stillman, IEEE T. Med. Imaging 1991; [2] Sarkar et al., MRM 2002; [3] Lee & Adalsteinsson, ISMRM 2010: 965; [4] Gorodnitsky and Rao, IEEE T. Signal Proces. 1997

Fig 3a: Spectra in white box using Lee et al.'s [3] method (blue), and gold standard results (black)

Fig 3b: 1st proposed method (1 average high-resolution data) (blue), and gold standard (black)

Fig 3c: 2nd proposed method (1 avg, undersampled by R_{high}=10) (blue), and gold standard (black)