Removal of Nuisance Signal from Sparsely Sampled ^{1}H-MRSI Data Using Physics-based Spectral Bases

Qiang Ning, Chao Ma, Fan Lam, Bryan Clifford, Zhi-Pei Liang

November 11, 2015

1 Synopsis

A novel nuisance removal method is proposed for 1H-MRSI. The method uses spectral bases generated for water and subcutaneous lipids using quantum simulation, and can perform nuisance signal removal directly from (k,t)-space data. Consequently, the proposed method is able to handle sparsely sampled MRSI data, which provides a desirable flexibility for designing accelerated 1H-MRSI data acquisition schemes. Experimental results demonstrate that the proposed method is capable of removing nuisance signals from 1H-MRSI data acquired from the brain without water and lipid suppression.

2 Purpose

Effective removal of nuisance signals (3 or 4 orders of magnitude larger than metabolite signals) is often challenging for practical ^{1}H-MRSI experiments. Conventional methods resort to water and lipid suppression pulses followed by post processing to remove any residual nuisance signals [1, 2, 3, 4]. While these methods perform reasonably well for ^{1}H-MRSI data collected with long T_E, Nyquist sampling of (k,t)-space, and suppression pulses, they cannot handle sparsely sampled ^{1}H-MRSI data collected with short T_E and no suppression pulses. This paper presents a new method to address this problem. A key feature lies in the use of spectral bases generated for water and subcutaneous lipids using quantum simulation (Fig. 1). With these spectral bases, the proposed method can effectively remove water and lipid signals from sparsely sampled ^{1}H-MRSI data acquired without suppression pulses. The method will be particularly useful for accelerated MRSI applications.

3 Method

In order to incorporate prior spectral information for water and subcutaneous lipids into our method, we express the MR signal of water or lipids as

$$\rho(t) = s(t)e(t) = \sum_{n=1}^{N} c_n e^{-t/T_{2n} - j2\pi f_n t} \sum_{p=1}^{P} g_p e^{j2\pi p \Delta f t},$$

where $s(t)$ represents the ideal Lorentzian-shaped spectrum, and $e(t)$ is the generalized series (GS) [5] compensating any line-shape distortions caused by local field inhomogeneity. It is well-known that under ideal conditions, water protons have one spectral component at 4.7ppm, and triglycerides (the principal MR measurable subcutaneous lipids [6, 7]) possess protons experiencing different electron shielding effects and generate multiple resonance components (Fig. 1a). The ideal spectral structures for both water and lipids can be generated through quantum simulation [8]. An example of triglyceride spectrum is shown in Fig. 1b. Note that: 1) the concentration ratios between the different spectral components are not spatially uniform since the saturation of triglycerides varies; 2) different spectral components have different T_2 relaxation constants [7].

Given the spectral bases, the proposed method uses a small set of model parameters denoted as $\boldsymbol{\theta} = \{\{c_n\}, \{T_{2n}, \{g_p\}\}\}$ to ensure that the model matches with a given experimental data. We propose to estimate $\boldsymbol{\theta}$ by solving the optimization problem below and then subtract the estimated nuisance signals from the original signal:

$$\hat{\boldsymbol{\theta}} = \arg\min_{\boldsymbol{\theta}} \|\mathbf{d} - \boldsymbol{\Omega}_{\mathbf{k}t}\mathbf{F}\sum_{m} \boldsymbol{\Omega}_{\mathbf{x}}^{(m)} \boldsymbol{\rho}^{(m)}(\boldsymbol{\theta})\|_2^2 + R(\boldsymbol{\theta}),$$

where $\mathbf{d}$, $\boldsymbol{\rho}$, and $\mathbf{n}$ are each discretized and vectorized, $\boldsymbol{\Omega}_{\mathbf{k}t}$ is the (k,t)-space sampling operator, $\mathbf{F}$ represents the transform from x-space to k-space, $\boldsymbol{\Omega}_{\mathbf{x}}^{(m)}$ is the spatial support for the m-th type of tissue (e.g., fat layer, white matter, gray matter, and CSF, as in the brain), and $R(\boldsymbol{\theta})$ is a regularization term imposing both spatial and spectral constraints on $\boldsymbol{\theta}$.

In practice, the spatial constraints can be obtained from auxiliary anatomical scans. The optimization problem can be efficiently solved by alternatively determining $\boldsymbol{\theta}_1 = \{\{c_n\}, \{T_{2n}\}\}$ and $\boldsymbol{\theta}_2 = \{g_p\}$. Specifically, when $\boldsymbol{\theta}_1$ is fixed, it is a linear least-squares (LS) problem and can be solved by standard convex optimization tools; when $\boldsymbol{\theta}_2$ is fixed, it is a large-scale nonlinear LS problem, and we can resort to quasi-Newton methods such as the limited-memory BFGS algorithm [9].

4 Results

We have evaluated the performance of the proposed method using experimental data acquired from the brain of healthy volunteers on a 3T Siemens Trio MRI scanner. The

acquisition sequence was a 2D bipolar echo-planar spectroscopic imaging (EPSI) sequence, with echo time T_E=20ms, echo-spacing 1.74ms, and in-plane nominal resolution 3.75mm (64x64 matrix size). A corresponding anatomical image was also acquired and segmented into different tissue types (Fig. 2). Note lipid signals were assumed to be generated from the fat layer.

The nuisance removal effect is shown in Fig. 3. As can be seen, the nuisance was removed to a negligible level, even when no suppression pulses were applied in the data acquisition. In nuisance signal removal, it is important that metabolite signals are protected. To demonstrate the ability of the proposed method to preserve metabolite signals during nuisance removal, two sets of MRSI reconstruction results are shown in Fig. 4, 5. The reconstructions were obtained using: 1) the conventional Fourier method, with a hamming window; and 2) the SPICE reconstruction method [10]. As can be seen, the metabolite signals are well-preserved in the reconstruction by the proposed nuisance removal method.

5 Conclusion

A novel method is presented for removing nuisance signals from ^{1}H-MRSI data. The proposed method uses spectral bases for water and lipids generated using quantum simulation. To our knowledge, this is the first time that prior spectral information for water and lipids are used for nuisance signals removal for ^{1}H-MRSI. Experimental results demonstrate that the method can handle sparsely sampled ^{1}H-MRSI data acquired without nuisance suppression pulses. The proposed method will enhance the flexibility and practical usefulness of accelerated ^{1}H-MRSI.

6 Acknowledgement

This work was supported in part by the National Institutes of Health (NIH-1RO1- EB013695 and NIH-R21EB021013-01).

References

[1] Haase A, Frahm J, Hanicke W, Matthaei D, ^{1}H NMR chemical shift selective (CHESS) imaging. Phys Med Biol 1985;30:341–344.

[2] Le Roux P, Gilles R, McKinnon G, Carlier P, Optimized outer volume suppression for single-shot fast spin-echo cardiac imaging. J Magn Reson Imaging 1998;8:1022–1032.

[3] Haupt C, Schuff N, Weiner M, Maudsley A, Removal of lipid artifacts in ^{1}H spectroscopic imaging by data extrapolation. Magn Reson Med 1996;35:678–687.

[4] Ma C, Lam F, Johnson CL, Liang ZP, Removal of nuisance signals from limited and sparse 1h mrsi data using a union-of-subspaces model. Magn Reson Med 2015;.

[5] Liang ZP, Lauterbur PC, A generalized series approach to MR spectroscopic imaging. IEEE Trans Med Imag 1991;10:132–137.

[6] Brix G, Heiland S, Bellemann M, Koch T, Lorenz W, MR imaging of fat-containing tissues: Valuation of two quatitative imaging techniques in comparison with localized proton spectroscopy. Magn Reson Med 1993;11:977–991.

[7] Ren J, Dimitrov I, Sherry A, Malloy C, Composition of adipose tissue and marrow fat in humans by ^{1}H NMR at 7 Tesla. Journal of Lipid Research 2008;49:2055–2062.

[8] Soher BJ, Young K, Bernstein A, Aygula Z, Maudsley AA, GAVA: spectral simulation for in vivo MRS applications. Journal of Magnetic Resonance 2007;185:291–299.

[9] Nocedal J, Wright S, Numerical optimization, series in operations research and financial engineering. Springer, New York, USA 2006;.

[10] Lam F, Liang ZP, A subspace approach to high–resolution spectroscopic imaging. Magn Reson Med 2014;71:1349–1357.

Figure 1: Fig. 1. (a) The multiple spectral components (different microenvironments and corresponding chemical shifts) generated in MR experiments by triglycerides, which is the principal category of MR measurable subcutaneous lipids. (b) A typical spectrum example of lipids.

(a)

Chemical Shift (ppm)	Assignment	Type
5.29	-**C**H=CH-	Olefinic
5.19	-C**H**-O-CO-	Glycerol
4.2	-C$\mathbf{H}_2$-O-CO-	Glycerol
2.75	-CH=CH-C$\mathbf{H}_2$-CH=CH-	Diacyl
2.20	-CO-C$\mathbf{H}_2$-CH_2-	α-Carboxyl
2.02	-C$\mathbf{H}_2$-CH=CH-C$\mathbf{H}_2$-	α-Olefinic
1.6	-CO-CH_2-C$\mathbf{H}_2$-	β-Carboxyl
1.3	-(C$\mathbf{H}_2$)$_n$-	Methylene
0.9	-$(CH_2)_n$-C$\mathbf{H}_3$-	Methyl

(b)

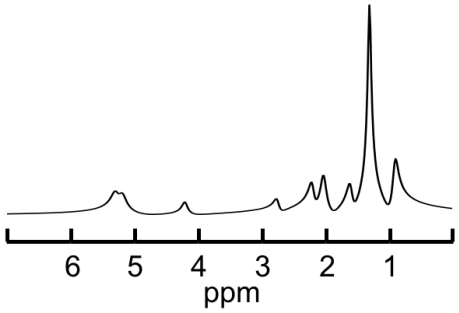

Figure 2: Fig. 2. Segmentation was performed against corresponding anatomical images. The four spatial masks shown below are fat layer, cerebrospinal fluid, white matter, and gray matter, respectively. Note the slight overlap between masks is designed to alleviate the partial volume effect.

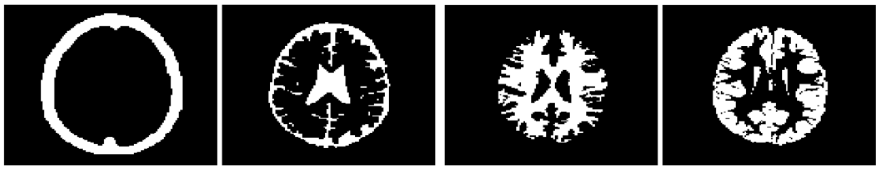

Figure 3: Fig. 3. Whole spectral integral of (a) original signal, (b) estimated nuisance signal, and (c) residual. Note the gray scale difference in (c). The bright area in the outer brain region is a common artifact of EPSI, which can be readily removed in subsequent analysis.

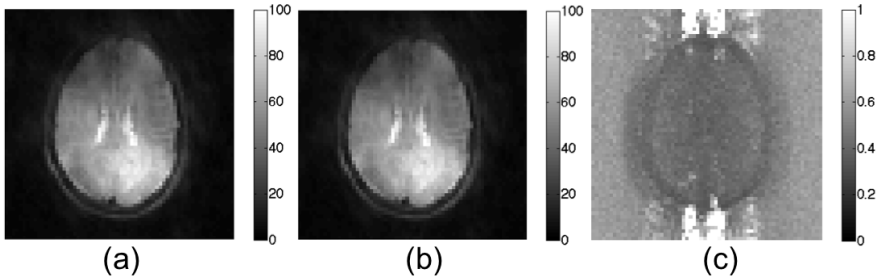

Figure 4: Fig. 4. (a) Whole spectral integral and (b) a typical spectrum after nuisance removal. Outer brain artifacts were masked, and a k-space truncation with a hamming window is applied. A major peak at circa 2ppm can be observed.

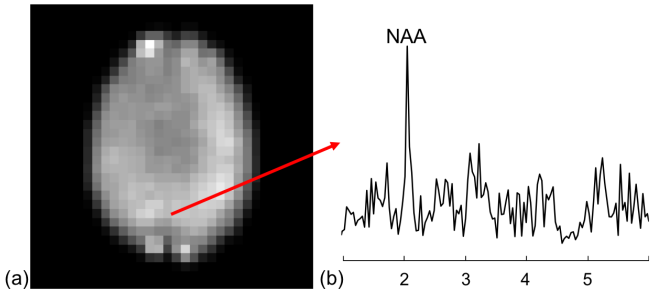

Figure 5: Fig. 5. The SPICE denoising results: (a) spectral integral for NAA (2ppm), and (b) a typical spectrum. Peaks from NAA, Cr, and Cho can be clearly observed, while water/lipid signals are removed to a negligible level.