Low-rank based compartmentalized reconstruction algorithm for high resolution MRSI without lipid suppression methods

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Synopsis

A novel compartmental low rank algorithm and data acquisition method for high resolution MR spectroscopic imaging without the use of any lipid suppression methods is introduced. The field inhomogeneity compensated data is modeled as the sum of a lipid dataset and a metabolite dataset using the spatial compartmental information obtained from the water reference data. These datasets are modelled to be low-rank subspaces and are assumed to be mutually orthogonal. The high resolution spiral acquisition method achieves in plane resolution of upto 1.8x1.8 mm^2 in 7.2 mins. Recovery from these measurements is posed as a low rank recovery problem. Experiments on in-vivo data demonstrates comparable results for both lipid suppressed and lipid unsuppressed data.

Introduction

Spectral leakage from extracranial lipids, whose concentrations are several folds higher than that of the metabolites, causes severe artifacts in MR spectroscopic imaging (MRSI). The effects of spectral leakage are even more aggravated at low resolution due to truncation artifacts. Several methods used for lipid suppression like outer volume suppression, inversion recovery, selective excitation, long echo times etc[1,2,3], result either in signal loss or in partial brain coverage. Improved k-space coverage reduces lipid leakage [4], but at the cost of deteriorated metabolite SNR and increased scan time.

In this work we introduce a novel compartmental low rank algorithm for high resolution MR spectroscopic reconstruction for lipid unsuppressed data. We use the spiral data acquisition scheme introduced in [5], to achieve high spatial resolution MRSI, in a reasonable scan time and with minimal SNR loss. We model the field inhomogeneity compensated data as the sum of two low-rank subspaces for metabolites and lipids which are mutually orthogonal.Experimental results demonstrate the performance of the proposed algorithm with and without the use of lipid suppression methods.

Methods

Variable density multi-shot spirals were used to obtain matrix sixe of 128x128 with the center k-space region of 32x32 averaged 12 times. This achieves an in-plane spatial resolution of upto 1.8x1.8 mm^2 at a scan time of 7.2 mins/slice with TR=1.5 ms. A separate water reference data is acquired in 2.4 mins/slice(TR=0.5 secs) and was processed using [6] to obtain high resolution B_0 map and lipid and brain masks that characterize the spatial compartments. The field inhomogeneity corrected spatio-temporal data is modeled as the sum of low-rank compartments belonging to metabolites (X_M) and lipids (X_L) respectively; $X(r,t) = X_M(r,t) + X_L(r,t)$. These compartments are assumed to be low rank and their spatial support is given by the metabolite and lipid masks. Using a single low-rank subspace to model the entire dataset is not effective because, the massive dynamic range between lipids and metabolites results in the subspace being dominated by the lipid basis functions. We exploit the orthogonality between metabolites and lipids as established in [7] to minimize lipid leakage artifacts. This enables us to recover the subspaces without imposing any prior knowledge of the spectral support. The recovery is formulated as the optimization problem,

$$f(X) = \arg\min_{X_M, X_L} \|\mathcal{A}X - b\| + \lambda_1 \|X_M\|_p + \lambda_2 \|X_L\|_p$$

$$\text{for } p \leq 1 \text{ such that } X_M \perp X_L$$

where $\mathcal{A}$ is the forward model accounting for the non-uniform Fourier transform, field inhomogeneity, and coil sensitivity encoding and b is the measured data. Water is removed as a pre-processing step using HSVD [8]. Equation (2) is solved using iterative reweighted least square algorithm [9].

This work has some conceptual similarities to [10,11]. However what distinguishes the proposed method is the absence of specialized data acquisition and processing steps for estimating the metabolite and lipid basis functions that explicitly account for the spectral support. The subspaces for metabolites and lipids are automatically estimated from the measured data. Hence the proposed method is not sensitive to line broadening of lipids and metabolites; and robust to deviation

from known spectral location which may occur in practical applications with large field variations near the skull. Also in addition these methods employ outer volume suppression or long echo times.

Results

Data is collected on a single axial slice of FOV_{xy} = 24 cm,slice thickness of 1cm at TR/TE = 1500/55 ms. The dataset is once collected without any lipid suppression method and once with 8 OVS bands(lipid suppressed). The datasets are reconstructed on a 96x96 grid size using a standard pipeline of inverse Fourier transform & field inhomogeneity compensation(IFFT Reconstruction) and the proposed method. Fig(1) compares the peak integral NAA maps for both the datasets using both the methods. Maps obtained from IFFT reconstruction shows severe lipid leakage even with the use of OVS bands , whereas the proposed method retains high resolution details and eliminates lipid leakage artifacts. Fig(2) shows the spectra for both the datasets at the pixels marked in the reference image. Spectra from IFFT reconstruction are plotted in blue and the ones from the proposed method in red. Spectra from IFFT reconstruction show lipid leakage and are noisy. The proposed method recovers denoised spectra and lipid leakage is removed. The reconstructed lineshape for both the lipid suppressed and unsuppressed data are comparable.

Conclusion

We introduced a novel low-rank based reconstruction method for high resolution MRSI which is robust to lipid leakage even while recovering from lipid unsuppressed data. We demonstrate comparable reconstructions for lipid suppressed and unsuppressed data using the proposed method.

Acknowledgements

Grant sponsor:American Cancer Society; Grant number:RSG CCE-121672

References

[1] Chu, A., Alger, J. R., Moore, G. J., & Posse, S. (2003). Proton echo-planar spectroscopic imaging with highly effective outer volume suppression using combined presaturation and spatially selective echo dephasing. Magnetic resonance in medicine, 49(5), 817-821.

[2] Bydder, G. M., & Young, I. R. (1985). MR imaging: clinical use of the inversion recovery sequence. Journal of computer assisted tomography, 9(4), 659-675.

[3] Bottomley, P. A. (1987). Spatial localization in NMR spectroscopy in vivo. Annals of the New York Academy of Sciences, 508(1), 333-348.

[4] Ebel, A., & Maudsley, A. A. (2003). Improved spectral quality for 3D MR spectroscopic imaging using a high spatial resolution acquisition strategy. Magnetic resonance imaging, 21(2), 113-120.

[5] Bhattacharya I. , Jacob M.(2015). High Resolution 1H MRSI without lipid suppression at short echo times using variable density spirals;in Proc of ISMRM 2015, #2017.

[6] Cui, C., Wu, X., Newell, J. D., & Jacob, M. (2015). Fat water decomposition using globally optimal surface estimation (GOOSE) algorithm. Magnetic Resonance in Medicine, 73(3), 1289-1299.

[7] Bilgic, B., Gagoski, B., Kok, T., & Adalsteinsson, E. (2013). Lipid suppression in CSI with spatial priors and highly undersampled peripheral k-space. Magnetic Resonance in Medicine, 69(6), 1501-1511.

[8] Barkhuijsen, H., De Beer, R., & Van Ormondt, D. (1987). Improved algorithm for noniterative time-domain model fitting to exponentially damped magnetic resonance signals. Journal of Magnetic Resonance (1969), 73(3), 553-557.

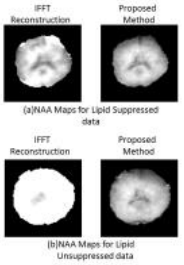
[9] Fornasier, M., Rauhut, H., & Ward, R. (2011). Low-rank matrix recovery via iteratively reweighted least squares minimization. SIAM Journal on Optimization, 21(4), 1614-1640.

[10] Lam, F., & Liang, Z. P. (2014). A subspace approach to high-resolution spectroscopic imaging. Magnetic Resonance in Medicine, 71(4), 1349-1357.

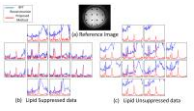
[11] Ma, C., Lam, F., Johnson, C. L., & Liang, Z. P. (2015). Removal of nuisance signals from limited and sparse 1H MRSI data using a union-of-subspaces model. Magnetic Resonance in Medicine.

Abstract ID: 5002

Figures



Fig(1) : NAA maps for (a)lipid suppressed data and (b) lipid unsuppressed data. IFFT reconstruction shows lipid leakage artifacts even with lipid suppression .Proposed method retains high resolution details and eliminates lipid leakage artifacts.



Fig(2) : Spectra at different pixels(see (a)) for (b) lipid suppressed data and (c) lipid unsuppressed data. The spectra from IFFT reconstruction (blue) are noisy and show heavy lipid leakage especially in case of lipid unsuppressed data whereas the spectra from proposed method(red) are

denoised and devoid of lipid leakage.