Fast Data Acquisition and Reconstruction Methods for lipid unsuppressed Metabolic imaging

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Target Audience – Researchers or clinicians interested in fast spectroscopic and metabolic imaging

Introduction – Magnetic Resonance Spectroscopic Imaging (MRSI) is an inherently slow imaging modality, mainly due to the low signal to noise ratio of the metabolites and the additional spectral dimension to acquire. The spatial resolution of classical CSI [1] and more recent non-Cartesian acquisition schemes are often considerably lower than most MR imaging methods; increasing the spatial resolution with current methods will result in prohibitively high scan time and low signal to noise ratio. Another challenge with MRSI methods is the spectral leakage from extra cranial lipids, whose concentrations are several folds higher than the concentration of the metabolites. While several effective methods to suppress lipids do exist [2,3], all of these methods are associated with signal loss or result in partial loss of brain coverage. In addition, methods such as outer volume suppression (OVS) [4] requires considerable time and expertise to position the OVS bands, thus increasing the total preparation time.

We introduce a novel acquisition and compartmentalized low-rank reconstruction pipeline to (a) achieve high spatial resolution MRSI, in a reasonable scan time, and (b) eliminate the need for lipid suppression schemes, thus shortening the total scan time. This acquisition achieves high in plane resolution of up to 1.8x1.8 mm^2 in a scan time of 7.2 mins for a single slice which is considerably faster in comparison to CSI and other high resolution acquisitions. It can be extended to 3D with under sampled spirals further reducing scan time. The saved time could also permit acquiring more slices in 3D acquisition.

Methods - The data acquisition strategy uses a variable density multi-shot spiral[5] to obtain a matrix size of 128x128. We use 288 spatial interleaves to achieve a spectral resolution of 574 Hz (4.6 ppm). The central 32x32 k-space region is fully sampled with 12 averages, while the outer k-space is fully sampled with 1 average. The acquisition was completed in 7.2 minutes/slice with TR=1.5 secs. This implementation of variable density spirals requires lesser number of excitations (which is desirable at higher field strengths) and considerably less scan time in comparison to previous implementations [6]. Also it has the added feature of flexible under sampling of outer k-space. We acquired a separate water reference scan (TR=0.5 secs) in 2.4 minutes/slice; this dataset was processed to obtain high resolution field inhomogeneity maps and lipid and brain masks that characterize the spatial compartments as described in [7].

We model the field inhomogeneity compensated dataset as the sum of low-rank lipid and metabolite compartments, $X(r,t) = X_L(r,t) + X_M(r,t)$, where X_L and X_M belong to lipids and metabolites respectively. Here X_L and X_M are restricted to the lipid and metabolite spatial compartments respectively and are assumed be low-rank. The modeling of the entire dataset as a single low-rank subspace is counter-productive due the huge dynamic range between the lipid and metabolite signals; the subspace will be dominated by lipid basis functions. The compartmental low-rank assumption is valid since there are finite numbers of anatomical regions within each spatial compartment with similar dynamic ranges; the spectra within the compartments can be modeled as a finite linear combination of few basis functions. Inspired by [8], we exploit the orthogonality between metabolites and lipid basis functions to minimize lipid leakage artifacts. This enables us to recover the subspaces without imposing any prior knowledge about the spectral support. We formulate the recovery as the optimization problem:

$$f(X) = \underset{X_L, X_M}{argmin} ||\mathcal{A}X - b||^2 + \lambda_1||X_M||_p + \lambda_2||X_L||_p \quad for\ p \le 1 \quad s.t \quad X_M \perp X_L \qquad -(2)$$

where $\mathcal{A}$ is a forward model accounting for the non-uniform Fourier transform, field inhomogeneity, and coil sensitivity encoding. Water is removed as a pre-processing step using HSVD [9]. Equation (2) is solved using iterative reweighted least square algorithm [10].

This work has conceptual similarities to [11, 12]. However, the distinguishing aspect is the absence of specialized processing steps needed in [11, 12] to estimate the metabolite and lipid basis functions that explicitly account for the spectral support. The proposed approach automatically estimates the lipid and metabolite subspace from the measured data. Hence our approach is robust to line broadening of metabolites and lipids; the explicit use of the spectral location of the metabolite and fat peaks may be violated in practical applications with large field variations near the skull. In addition, the method in [11,12] still requires outer volume suppression and long echo times to reduce lipid leakage.

Results - A single axial slice with FOVxy = 24 cm and slice thickness 1 cm at TR/TE=1500/55 ms is scanned without any lipid suppression method. The datasets are reconstructed at a 96x96 grid size using least squares (LS Recon) and the proposed method. NAA map obtained from the LS Recon is corrupted by severe lipid leakage whereas the proposed method retains high resolution details. Spectra are shown at different locations marked on the water image. The LS Recon spectra show heavy lipid leakage. The proposed method (spectra plotted in black) recovers lipid free metabolite signals. The performance is compared with a lipid suppressed experiment with 8 OVS bands and residual baseline removal. The spectral region marked in the red box is recovered for the fat suppressed data and the spectra are overlaid in red. The proposed method is able to recover metabolite lineshapes of comparable quality to lipid suppressed data.

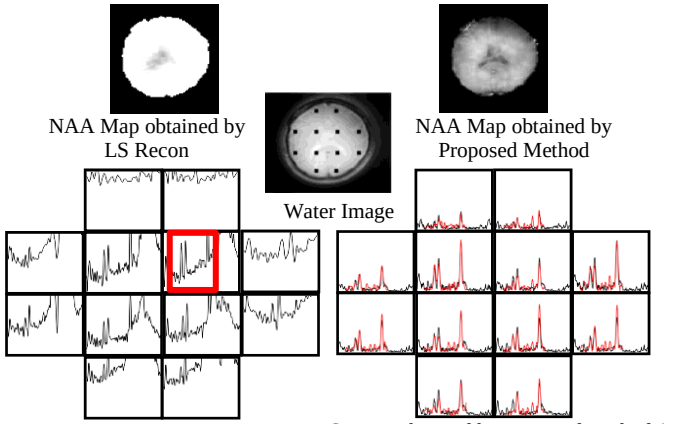

Fig (1) : The top row shows NAA maps reconstructed using least squares and proposed method. The spectra are shown at the pixels marked in the water image. The lipid leakage is severe in LS recon. Spectra from the proposed method(in black) are devoid of lipids. Spectra from a fat suppressed data (using 8 OVS bands and residual baseline removal) are overlaid to compare performance against fat suppressed data.

Conclusion – We have demonstrated a fast data acquisition strategy for high resolution MRSI, which is robust to lipid leakage, even while recovering from lipid unsuppressed data. This can drastically reduce the time for MRSI protocols and will be beneficial for fast multi slice brain metabolite imaging.

References-
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