

HIGH RESOLUTION 1H MRSI WITHOUT LIPID SUPPRESSION AT SHORT ECHO TIMES USING VARIABLE DENSITY SPIRALS

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Target audience – Researchers or clinicians interested in spectroscopic imaging or metabolite mapping of brains

Introduction – The leakage of extra cranial lipids to the brain and unsuppressed water is one of the biggest obstacles in acquiring reliable metabolite estimates in MR spectroscopic imaging (MRSI). Current methods to suppress lipids (e.g. outer volume suppression, selective excitation, using longer echo-time & inversion recovery)^{1,2} require either considerable expertise, provides only partial brain coverage, or result in loss of metabolite SNR. Similarly k-space extrapolation methods³ to suppress lipids are sensitive to the accuracy of lipid masks. We introduce a variable density spiral sequence to considerably improve k-space coverage with minimal loss in metabolite SNR. A two step recovery strategy is used to suppress the nuisance signals and obtain good quality short echo-time MRSI spectra without any fat suppression methods.

Variable density spirals with very long echo times⁴ have been used before, but with our sequence and algorithm we can achieve fat suppression with short TE acquisition.

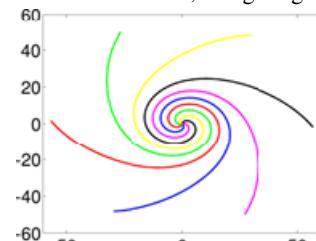


Fig 1: 6 equispaced interleaves out of 24 showing oversampling in the center 32x32 k-space and

Methods – We use a variable density multi-shot spiral sequence to obtain a matrix size of 128x128. The central 32x32 matrix region is acquired at Nyquist rate, while outer k-space is under-sampled by a factor of twelve (Fig 1). 24 spatial interleaves are used to achieve a spectral resolution of 570 Hz (4.7 ppm). In this work, twelve rotations were used to Nyquist sample outer k-space; this corresponds to the central regions being averaged twelve fold. The time to acquire 12 rotations (TR=1.5 s) is around 7.2 mins/slice. We plan to considerably reduce the number of rotations in the future. We also acquired a separate water reference scan with TR=0.5s, corresponding to a scan time of 2.4 mins/slice; this data was processed using the graph-cut based fat-water decomposition algorithm⁵ to obtain high resolution field inhomogeneity maps and lipid and brain masks.

We use a two-step recovery scheme to remove the nuisance signals. We first recover a high-resolution data using quadratic smoothness regularized inversion algorithm. The forward model accounts for field inhomogeneity induced distortions, sensitivity weighting, and non-Cartesian sampling using NUFFT. The residual water signal is removed using HSVD suppression, while the lipid signals are masked out using the brain mask. A fourth order polynomial was estimated and subtracted to account for macromolecular resonances and unaccounted baseline. This signal was then smoothed to the desired point spread function within the brain mask using a quadratic smoothness regularized denoising step within the brain region and was spectrally apodized. To study the utility of the high-resolution strategy, we compare the proposed scheme of 128x128 coverage against three different k-space coverages (32x32, 64x64, 96x96).

Results – The data was acquired on a 3T Siemens scanner. The TR/TE is 1500ms/55ms and no lipid suppression was used. We show the spectra at 3 different locations moving from the center towards the skull. From Fig 2 we observe that the suppression of lipids improves considerably with k-space coverage. Specifically, with no lipid suppression, we observe that the 32x32 coverage yields poor spectra in most regions. By contrast, the 128x128 coverage provides considerably improved lipid suppression.

The NAA maps for different data coverages show that there is a considerable contamination of lipids if we cover less of k-space, thus fat suppression methods cannot be avoided. But for higher k-space coverage the fat contamination reduces and we get good metabolite maps.

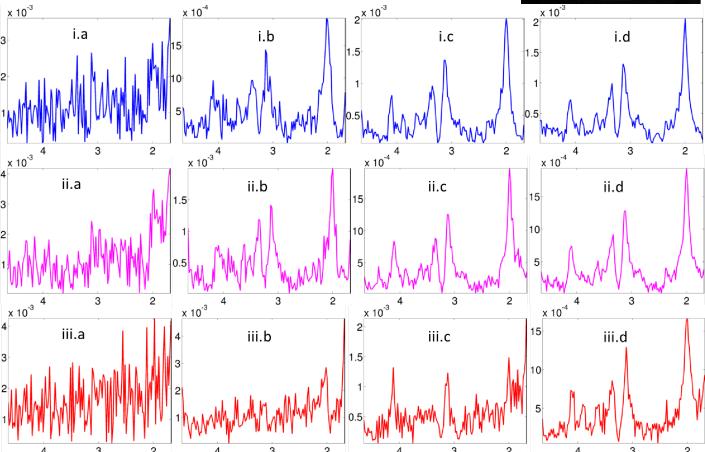


Fig 2: The topmost image shows the high resolution anatomical image of the dataset. The spectra for different k-space coverage a)32, b)64,c)96, d)128 at three different locations i) at the center(in blue) ii)between the center and skull(in magenta) iii) near the skull(in red) are shown

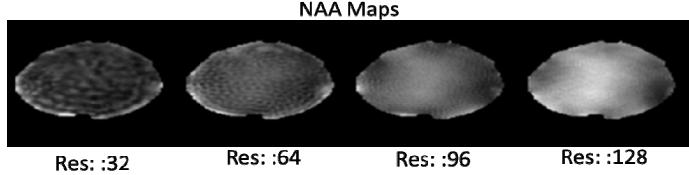


Fig 3: The NAA maps for the different datasets after baseline removal and spatial smoothing. The higher resolution acquisition shows lesser fat contamination of NAA(close to lipid peaks) in comparison to the lower resolution data acquisitions

References – [1]Luo et al MRM '01;45:1095–1102. [2]Ebel et al MRM '03;49:903–908. [3]Haupt et al MRM '96;35:678–687. [4]Sarkar et al MRI '02;20:743–757. [5]Chen et al MRM '14