A Pilot Evaluation of Accelerated Echo-Planar J-Resolved Spectroscopic Imaging in the Human Brain using Compressed Sensing

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Target audience: Researchers interested in Non-uniform Undersampling Acquisition and Compressed Sensing Reconstruction

Purpose/Introduction: Localized J-resolved spectroscopy (JPRESS) has previously been shown to be a powerful tool in the study of metabolism in human brain in vivo [1,2]. To increase the spatial coverage, J-resolved spectroscopy sequence was recently modified with an echo-planar spectroscopic imaging (EPSI) [3-5] readout to yield a novel four-dimensional (4D) spectroscopic imaging (SI) (2 spectral and 2 spatial) called echo-planar J –resolved spectroscopic imaging (EP-JRESI) (6) that allows for the multi-voxel collection of 2D JPRESS spectra in a single experiment. The two remaining dimensions must be incrementally collected, requiring scan times on the order of 20+ minutes, severely limiting clinical applicability. Compressed Sensing (CS) (7), which has been widely used in MRI to speed up acquisition has been implemented successfully to accelerate the collection of the remaining two dimensions and to reduce the scan time of EP-JRESI of human prostate in vivo (8). In this study, we have implemented the novel CS based EP-JRESI acquisition and CS reconstruction in human brain and quantified the metabolites using prior knowledge fitting (ProFit) algorithm (9). ProFit fits the spectra as linear combinations of two-dimensional (2D) basis spectra using a nonlinear least-squares algorithm in combination with a linear least-squares algorithm and incorporates maximum prior knowledge available. In summary, the goals of this study were to implement CS to EP-JRESI in human brain at 3T and to determine the integrity and reproducibility of CS reconstruction quantify the cerebral metabolites using the Profit algorithm.

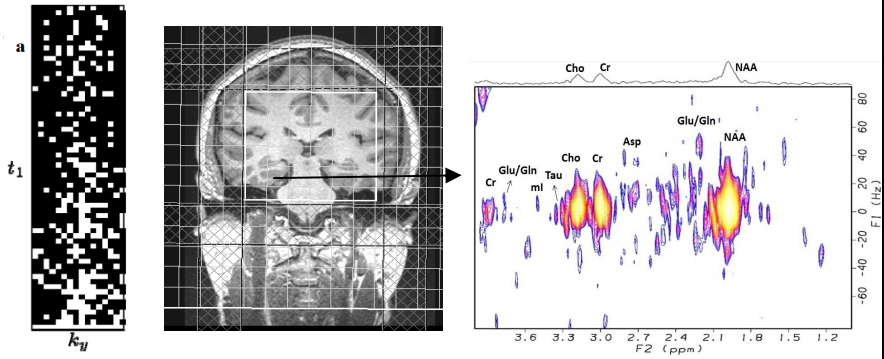
Materials and Methods: The standard echo-planar J-resolved spectroscopic imaging (EP-JRESI) sequence was modified to non-uniformly under-sample 25% of the fully sampled data in the kyt1 plane according to the sampling density shown in Fig. 1a. The CS-modified sequence was tested in the brain of eight healthy volunteers (age of 50.±5 10.6 years) and an Obstructive Sleep Apnea (OSA) patient. All data were collected on a 3T Trio-Tim MRI scanner using the Siemens VB17a compiler. The following parameters were used for CS EPJRESI: TR/TE = 1.5s/30ms, 1.5x1.5x1.5 cm^3 voxel for VOI localization, 64Δt_1 increments, 256 bipolar echo pair, FOV= 16x16cm^2, F1 and F2 bandwidths of 1000 Hz and 1190 Hz, respectively.

The undersampled data was reconstructed using a modified Split Bregman algorithm (10) which solves the unconstrained optimization problem in eqn. (1)

$$\min_m \|\nabla m\|_1 + \lambda \|F_u m - y\|_2 \qquad (1)$$

where ∇ is the gradient operator, m is the reconstructed data, $\|x\|_n$ is the l_n norm, λ is a regularization parameter, F_u is the undersampled Fourier transform, and y is the under-sampled data. Equation 1 removes the artifacts due to the non-uniform under-sampling by minimizing the total variation (TV) while maintaining fidelity with the sampled measurements. Acquired data were post-processed with a custom MATLAB-based program, which applied spatial Hamming and spectral apodization filters to smoothen the data. Modified Profit algorithm was applied to process the extracted data and to calculate metabolite ratio with respect to the 3.0 ppm creatine peak (S/S_{Cr}). The Cramer-Rao Lower Bound (CRLB) values, a measure of the performance of the fitting technique were also calculated. Prior knowledge generated for EP-JRESI included 20 metabolites icluding, creatine (Cr), N-acetylaspartate (NAA), phosphorylcholine (PCh), free choline (Cho), aspartate (Asp), γ-aminobutyric acid (GABA), glucose (Glc), glutamine (Gln), glutamate (Glu), glutathione (GSH), lactate (Lac), myo-inositol (mI), Nacetylaspartylglutamate (NAAG), phosphoethanolamine (PE), and taurine (Tau).

Results and Discussion – Figure 2(b) shows a select spectrum from the right hippocampus region (Fig, 2(a)) of a healthy subject. It shows the quality of the reconstruction with no visible aliasing after the reconstruction. All major metabolites, mI, creatine Cr, Cho, NAA and are visible. Table 1 shows the mean value of various metabolite ratios with respect to creatine over the same region the 8 healthy subjects and a OSA patient. Metabolites with higher physiological concentrations including glutamate/glutamine (Glx), N-acetylaspartate (NAA), myo-inositol (mI), all had acceptable CVs <20%. OSA patient shows difference in Glx compared to healthy subjects which is as expected.



(a) **(b)** **(c)**

Fig. 1: (a) sampling mask used to under-sample the kyt1 plane. (b) T1-weighted coronal localization. (c) select J-resolved spectrum taken from the voxel labeled in (b).

Metabolite/Cr	Healthy Subjects (Mean ± SD)	OSA
NAA	1.63 ±0.16	1.47
Asp	0.59 ± 0.30	0.43
Glc	0.56 ± 0.22	0.49
Gln	0.57 ± 0.16	0.35
Glu	1.15 ± 0.25	0.94
Gly	0.11 ± 0.07	0.14
Asc	0.49 ± 0.15	0.36
mI	0.69 ± 0.13	0.43
PE	0.64 ± 0.25	0.41
Thr	0.48 ± 0.12	0.46
tNAA	1.89 ± 0.27	1.67
tCho	0.35 ± 0.04	0.24
Glx	1.72 ± 0.39	1.28

Table 1: Metabolite ratios in the right hippocampus in healthy subjects and an OSA patient.

Conclusion: This is an exploratory, validation, and feasibility study for CS EP-JRESI in human brain at 3T. We have shown that CS can successfully be applied to the EP-JRESI sequence in the human brain, providing an acceleration factor of at least 4x. Despite only using 25% of the original data, both reconstructed data sets show the expected metabolic features characteristic of both healthy and OSA subject. We were also able to quantify the spectra using a modified version of ProFit algorithm. Initial results indicate that 15 metabolites can be quantified successfully. All these bring EP-JRESI closer to becoming a clinical reality. The optimization of the sampling density as well as reconstruction algorithms is expected to allow for an even greater reduction in the minimum amount of data required for reconstruction.

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