

# Nonuniformly undersampled 5D (3 spatial + 2 spectral) echo planar J-resolved spectroscopic imaging of brain

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**Target Audience:** Those interested in 3D-localized spectroscopic imaging of human brain, localized J-resolved spectroscopy, and nonuniform sampling (NUS) and compressed sensing (CS).

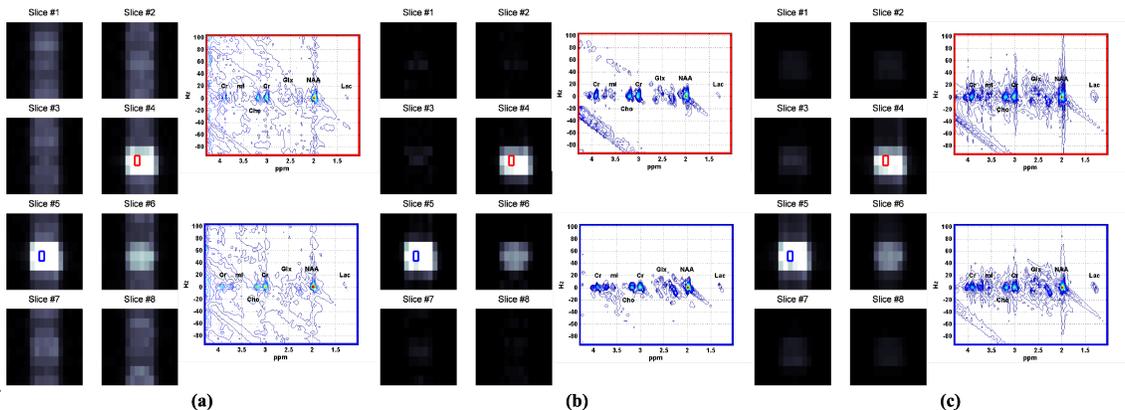
**Purpose:** J-resolved spectroscopy is a multidimensional technique to enhance spectral information by pushing multiplet splittings into a second dimension [1]. Spectroscopic imaging maps metabolic information in up to 3 spatial dimensions. An echo planar (EP) readout allows the acquisition of the  $k_x$  and  $t$  dimensions in a single TR [2], leaving  $k_y$  and  $k_z$  to be incrementally acquired. EP-JRESI combines localized J-resolved spectroscopy with an EP readout for a single slice acquisition ( $k_x, k_y, t_2, t_1$ ) [3]. NUS and CS [4] reconstruction have been applied to the ( $k_y, t_1$ ) plane with a single channel EP-JRESI acquisition and an overall acceleration of 4x in phantom and 2x in vivo [5]. Here, we extend EP-JRESI to include a 3D localization and use NUS on the incrementally-acquired volume ( $k_y, k_z, t_1$ ) to achieve far greater accelerations in scan time for both single and multi channel data.

**Methods:** A physiological gray matter phantom was scanned using a CP extremity transmit/receive coil with the following parameters: TE/TR = 30/1500 ms, FOV = 16x16x16 cm<sup>3</sup>, 1x2x2 cm<sup>3</sup> resolution, 100  $t_1$  increments, spectral bandwidths 1190/1000 Hz in the direct/indirect dimensions, 1 average, total scan time 2 hrs 40 min. Retrospectively, the data was nonuniformly undersampled in the ( $k_y, k_z, t_1$ ) volume by a factor of 16x, simulating a scan time of 10 min.

A healthy human brain (35 years old) was scanned using an 8 channel head receive coil with the following parameters: TE/TR = 30/1200 ms, FOV = 24x24x12 cm<sup>3</sup>, 1.5x1.5x1.5 cm<sup>3</sup> resolution, 64  $t_1$  increments,

BW2/BW1 = 1190/1000 Hz, 1 average, 8x NUS for a total scan time of ~20 min.

NUS consisted of random points from a distribution that followed exponential decay from the origin in  $k_y$  and  $k_z$  as well as in  $t_1$ . Since J-resolved spectra are self sparse, CS reconstruction was performed by minimizing the L1 of the reconstructed data subject to data fidelity. In order to increase sparsity, data outside the spectral region of interest were zeroed. For the multicoil acquisitions, each channel was processed individually before being combined in absolute magnitude.



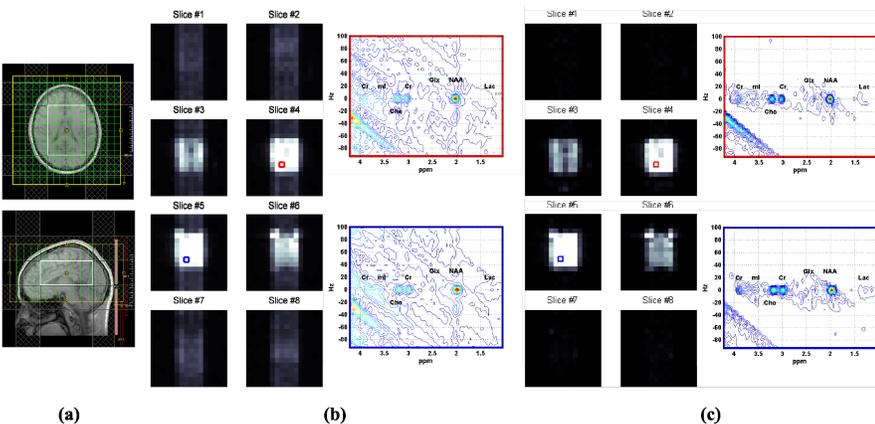
**Figure 1.** NAA metabolite maps (left) and highlighted 4 cm<sup>3</sup> voxel spectra (right) for 16x NUS raw (a), CS reconstructed (b), and fully sampled (c) gray matter phantom data containing 15 brain metabolites at physiological concentrations.

**Results:** Figure 1 shows the results of a 5D EP-JRESI phantom scan, with the raw (minimum energy) reconstruction in (a), the CS reconstruction in (b), and the fully-sampled data in (c). In each grouping, the left image is the metabolite map of NAA over each slice, and the right are the J-resolved spectra of the highlighted voxels from the left. The normalized RMSE between (a) and (c) is 6.4e-3 while it is 8.9e-4 between (b) and (c).

Similarly, Figure 2 shows the raw reconstruction and CS reconstruction of 5D NUS EP-JRESI healthy brain data.

**Discussion:** As shown in Fig. 1, aliasing in the undersampled dimensions is removed in the CS reconstruction compared to the raw data. In addition, the CS reconstruction exhibits denoising relative to the fully-sampled. Singlets such as NAA, creatine (Cr), and choline (Cho) are well resolved as are the multiplets of lactate (Lac), myo-inositol (mI), and glutamate/glutamine (Glx).

**Conclusion:** NUS can be applied to the ( $k_y, k_z, t_1$ ) volume of a 5D EP-JRESI scan to collect data in the same amount of time it would take to fully-sample a single 4D (2 spatial + 2 spectral) slice. CS reconstruction removes aliasing caused by undersampling and denoises, allowing 3D-localized J-resolved spectroscopic imaging data to be collected in a time frame appropriate for a clinical setting for the first time.



**Figure 2.** MRI localization (a) of healthy human brain. NAA metabolite maps (left) and highlighted 3.4 cm<sup>3</sup> voxel spectra (right) for 8x NUS raw data (b) and CS-reconstructed (c).

**References:** [1] Ernst *et al.*, Clarendon Press, Oxford 1987. [2] Posse *et al.*, MRM 1996, 33(1):34-40. [3] Nagarajan *et al.*, ISMRM 2011, p2801. [4] Lustig *et al.*, MRM 2007, 58(6):1182-95. [5] Furuyama *et al.*, MRM 2012, 67(6):1499-1505.

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