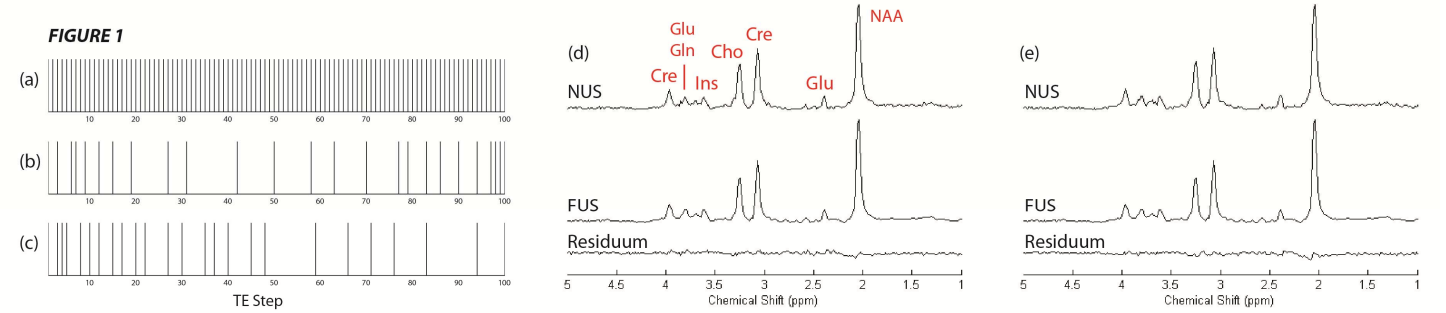
# Accelerated 2D *J*-Resolved MRS through Non-Uniform Sampling and Iterative Soft Thresholding

Andrew Prescot[1], Xianfeng Shi[2], and Perry Renshaw[2,3]
[1]*Department of Radiology, University of Utah, Salt Lake City, UT, United States,* [2]*Department of Psychiatry, University of Utah, Salt Lake City, UT, United States,* [3]*VISN 19 MIRECC, Salt Lake City, UT, United States*

**Target Audience:** Investigators that are interested in normal brain metabolism, psychiatric disorders and neurological disease
**Purpose:** Conventional proton ($^1$H) magnetic resonance spectroscopy (MRS) data acquired from human brain at clinical magnetic field strengths ($B_0$) is characterized by poor spectral resolution and metabolite proton peak overlap, particularly for compounds related to amino acid neurotransmission including γ-amino butyric acid (GABA), glutamate (Glu), glutamine (Gln), and glycine (Gly). Two-dimensional (2D) $^1$H MRS techniques encode a second frequency dimension and enhance the effective spectral resolution by spreading all metabolite proton resonances over a 2D spectral plane.[1] Compared to specific metabolite-edited 1D MRS approaches, the simultaneous measurement of multiple metabolites is the primary alluring feature of *in vivo* 2D $^1$H MRS, and recent significant advances have greatly improved the reliability of 2D spectral quantification by integrating concepts such as prior knowledge fitting.[2] However, the conventional uniform sampling of a second spectral dimension leads to low temporal resolution, rendering 2D MRS techniques as unsuitable for most clinical applications. Biomolecular nuclear magnetic resonance (NMR) has benefitted hugely from the advent of novel sparse non-uniformly sampled (NUS) data acquisition and processing methodologies for accelerating multi-dimensional experiments. For the present study, we have investigated the use of NUS schemes and iterative soft thresholding (IST)[3] for the processing 2D spin-spin coupling (*J*)-resolved $^1$H MRS data recorded from healthy human brain. This combination of data acquisition and post-processing we have termed 2D *J*-RESIST (2D *J*-resolved spectroscopy with iterative soft thresholding).
**Methods:** MRS data were obtained using a 2.89 Tesla Siemens (Erlangen, Germany) Verio™ scanner with a manufacturer-supplied 12-channel phased-array coil used for signal reception. 2D *J*-resolved $^1$H MRS data with full-uniform sampling (FUS; see Figure 1a) were acquired from the parietal-occipital cortex (POC) in ten healthy volunteers (voxel size = 19 mL; TR/TE = 2000/31-229 ms; ΔTE = 2 ms; NEX per TE = 4). FUS data allowed for (i) the judicious selection of NUS schedules (i.e. the nulling and exclusion of specific TE steps), and (ii) the direct quantitative comparison of reconstructed NUS spectra with original FUS data. NUS data of 25% sparsity subsequently were created using Poisson-gap scheduling (PGS), a flexible approach that can yield sampling schemes of desired weightings.[3] PGS with half-sine weighting yielded dense sampling at both the beginning and end of the TE range (see Figure 1b), and a second PGS scheme used quarter-sine weighting to create higher sampling density at the beginning of the TE range (see Figure 1c). The half-sine and quarter-sine NUS data were reconstructed using an iterative amplitude threshold of 0.98, and 2500 iterations per complex point. The modified IST reconstruction process involved gridding of the sparsely-sampled 2D time-domain matrix, fast Fourier transformation (FFT) along the directly-detected frequency dimension (F2), and subsequent IST along the indirectly-detected TE space dimension (F1). **Results and Discussion:** $^1$H MRS data acquired from the POC of a single human subject are presented in Figure 1. The 1D spectra displayed correspond to the central row (F1 = 0 Hz; mathematically equivalent to the TE-averaging approach commonly employed for Glu quantification) extracted from the standard FUS and reconstructed NUS 2D *J*-RESIST spectra.




Data reconstructed using half-sinus and quarter-sinus weighted PGS and IST are presented in Figures 1(d) and 1(e), respectively, with the FUS data and residuals (NUS minus FUS) displayed for both situations. Comparing FUS and NUS data on a complex point-by-point basis, linear regression analysis demonstrates favorable peak amplitude fidelity for sparsely-sampled 2D *J*-RESIST data. Across all 10 subjects (2 scans each) we observed improved regression terms for quarter-sine weighted NUS (slope = 1.01 ± 0.04; intercept = 0.001 ± 0.0004; $R^2$ = 0.98 ± 0.01) compared to half-sine weighted NUS (slope = 1.02 ± 0.04; intercept = 0.002 ± 0.0005; $R^2$ = 0.98 ± 0.0009). **Conclusion:** These retrospective $^1$H MRS data demonstrate a possible fourfold reduction in scan time (i.e. 16 → 4 minutes). Our ongoing studies are addressing several key issues including the relationship of signal-to-noise ratio (SNR) between FUS and NUS 2D MRS data, reconstruction of 2D spectral maps, metabolite peak quantification using established 1D and 2D MRS fitting algorithms, and the analysis of genuinely-acquired NUS 2D $^1$H MRS data. **References:** [1] Ryner et al. J Magn Reson Ser B. 1995;107(2):126-137. [2] Schulte et al. NMR Biomed. 2006;19(2):255-263. [3] Hyberts et al. J Biomol NMR. 2012;52(4):315-327.

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