Accelerating 2D-JPRESS in the Human Brain with Compressed Sensing

Trina Kok[1], Navin Michael[2], and S. Sendhil Velan[1,3]

[1]A*STAR-NUS Clinical Imaging Research Center, Singapore, Singapore, [2]Singapore Institute for Clinical Sciences, Singapore, Singapore, [3]Singapore Bioimaging Consortium, Singapore, Singapore

Introduction: 2D J-resolved experiments allow us to separate the chemical shifts and J couplings in separate dimensions. While localized 2D MRS techniques e.g 2D-JPRESS [1-3] has been demonstrated to successfully improve signal detection of overlapping coupled spins, it carries a penalty in scan time within a clinical setting. 2D JPRESS has been evaluated for several in-vivo applications in single and multi-voxel acquisitions. Exploration of accelerating 2DJ-PRESS via non-uniform under-sampling and reconstruction with compressed sensing (CS) appears promising as 2D spectra are naturally sparse and data sampling along the t_1 encoding direction readily accommodates flexible sampling patterns. Previous works have applied CS to under-sampled L-COSY and 2D JPRESS data to calf [4] and prostate [5] respectively. Here, we apply CS to under-sampled 2D-JPRESS datasets from human brain using an L1-regularized formulation [6] and show that eleven metabolites are recovered with just 30 % of the original data, reducing the scan time by 3.33.

Methods Eleven healthy human subjects were scanned on a 3.0T MRI scanner (Siemens AG, Erlangen, Germany) using a 32-element receive coil. A 2.5 x 2.5 x 2.5 cm^3 voxel was placed in the parietal lobe and data was acquired with maximum echo sampled 2D-JPRESS [7]. Spectral bandwidth was 2000 Hz in f_1 and 500 Hz in f_2, with 100 t_1 increments and 2048 complex t_2 samples. We chose the minimal TE to be 30 ms and took 8 averages for improved SNR, resulting in a total scan time of 26 min. Shimming water line-widths was between 12 - 16 Hz. CHESS was used for water suppression with a bandwidth of 75 Hz. A water scan was acquired at TE = 30ms for coil combination and phase compensation [8].

Data was retrospectively under-sampled in the t_1 dimension so that 30 of the 100 t_1 increments are kept, determined by a random draw from a uniform distribution. Reconstruction of the 2D spectra was obtained via a conjugate gradient algorithm that iteratively minimizes the cost function $||\mathbf{F_u x}-\mathbf{y}||_2 + \lambda \cdot TV(\mathbf{x})$ where $\mathbf{x}$ is the recovered spectral data and $\mathbf{y}$ is the normalized under-sampled data in the t_1-t_2 dimension. $\mathbf{F_u}$ is the under-sampled Fourier Transform operator and $TV(\mathbf{x})$ determines the sum of the absolute variations in the 2D spectrum. λ is an empirical regularization parameter that determines the trade-off between the first data consistency term $||\mathbf{F_u x}-\mathbf{y}||_2$ and the second sparsifying Total Variation (TV) term. To determine an optimal value for λ, the iterative reconstruction was done for all eleven subjects and ten Monte Carlo trials with $\lambda = 10^{-10}$ to 10^{4}. Subsequent reconstructions for the eleven subjects were done for ten random under-sampling realizations using this optimal λ.

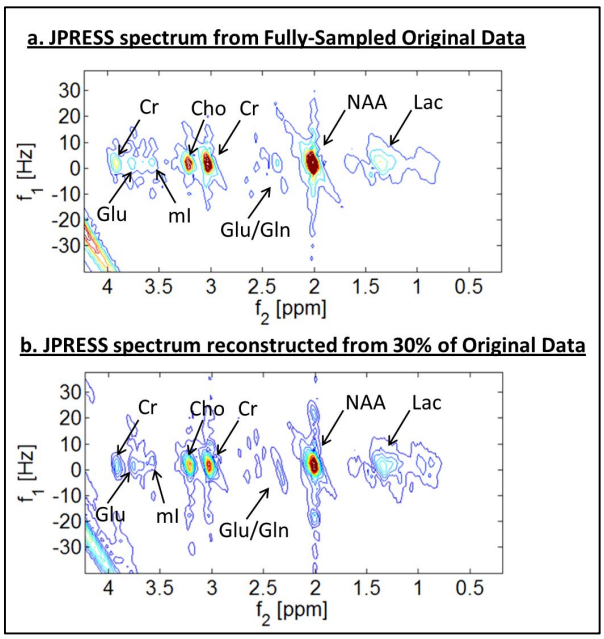

Figure 1. Truncated JPRESS spectra to show metabolites frequency range of interest for a (a) fully sampled dataset and (b) 30% under-sampled data set

	100% Fully-sampled		30% Randomly-Undersampled	
Metabolites	*Mean Cr ratio*	*Mean CRLB*	*Mean Cr Ratio*	*Mean CRLB*
Cr	1.000 ± 0.000	0.761	1.000 ± 0.000	1.391
NAA	1.703 ± 0.206	0.686	1.477 ± 0.235	1.455
PCh/GPC	0.296 ± 0.025	1.088	0.330 ± 0.049	1.970
Ala	0.309 ± 0.177	5.934	0.341 ± 0.186	6.481
GABA	0.317 ± 0.035	6.994	0.320 ± 0.213	11.639
Lac	0.193 ± 0.041	7.708	0.191 ± 0.079	17.451
Glc	0.541 ± 0.091	6.875	0.252 ± 0.277	> 100
Glu	1.165 ± 0.0612	2.733	0.970 ± 0.343	6.397
Gly	0.216 ± 0.024	7.439	0.256 ± 0.065	9.405
Gsh	0.240 ± 0.044	5.224	0.247 ± 0.095	8.413
mI	0.751 ± 0.070	3.490	0.614 ± 0.225	7.819
Scy	0.0579 ± 0.004	9.298	0.0583 ± 0.017	9.762
Asc	0.388 ± 0.072	6.957	0.240 ± 0.243	> 100

Table 1. Mean metabolite ratios and CRLBs for fully sampled dataset and dataset where only 30% of the samples are retained.

Results and Discussion: λ in the range of 5E-5 gave minimal normalized root-mean-square-error (NRMSE). For λ = 5E-5 to 5E-4, the increase in NRMSE is only 3.8% of the minimal. Fig.1a and 1b compares the two 2D JPRESS spectra obtained with the fully-sampled data and under-sampled data respectively. Keeping just 30% of the original data and applying reconstruction via CS, the major peaks of N-Acetylaspartate (NAA), creatine (Cr), PCh/GPC, glutamate (Glu), glutamine (Gln), myo-inositol (mI) and lactate (Lac) can be detected in Fig. 1b. Table 1 compares the mean metabolite Cr ratios and mean CRLB values obtained from the ProFit algorithm using a fully sampled dataset and datasets that are 30% under-sampled. CRLB values of Glucose (Glc) and Ascorbate (Asc) obtained from the under-sampled datasets, are greater than 100, indicating a very poor fit and corresponds to the high error in Cr ratio values of these two metabolites. Taking into account both Cr ratios and CRLB, eleven of the original thirteen metabolites were recovered by applying CS to 30% of the data from the original dataset.

Conclusion: Despite taking just 30% of the original data, the nine metabolites of Cr, NAA, PCh/GPC, Ala, GABA, Glu, Gly, GSH, Lac, mI and Scy are recovered with reasonable ProFit CRLB values. This represents an acceleration factor of about 3.33, potentially bringing the scantime down to 9 min.

References: [1] Dreher et al; MRI 1999; 17:141-150 [2] Thomas et al; JMRI 2005; 6(3):453-459 [3] Thomas et al; NMR in Biomed. 2003; 16(5): 245-141 [4] Furuyama et al; ISMRM 2012; #8 [5] Furuyama et al; MRM. 2012; 67:1499-1505 [6] Lustig et al; MRM 2007; 58:2293-1195 [7] Schulte et al; NMR in Biomed 2006; 19(2):264-270 [8] Michael et al; ISMRM 2012; #1713 [9] Schulte et al; NMR in Biomed 2006; 19(2):255-263