Multi Task Bayesian Compressed Sensing in Sparse 2D Spectroscopy

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Introduction: J-coupling causes spectral splitting and complicated signal modulation that limit the detection of important brain metabolites, such as Glu, in proton spectroscopic imaging. While 2D spectroscopy, e.g. 2DJPRESS [1] and CTPRESS [2], has been demonstrated to successfully improve signal detection of coupled spins, it carries a penalty in scan time and reconstruction complexity. To counter this limitation, Mayer et al [3] exploited the diagonal feature of CTPRESS spectra to achieve four-fold undersampling without adverse aliasing artifacts. Exploration of further undersampling in 2D spectroscopy via compressed sensing appears promising as 2D spectra are naturally sparse and data sampling along the t_1 encoding direction readily accommodates flexible sampling patterns. Here we modeled metabolite spectra for an under-sampled, noisy 2D CTPRESS spectroscopy at 3T, and evaluated the performance of multi-task Bayesian CS [4,5] which incorporated priors for regularization during reconstruction and compared it with Lustig's [6] implementation of conjugate gradient CS and single-task Bayesian CS [7].

Methods Using SPINEVOLUTION [8], 7 brain metabolites [9], (10 mM NAA, 7.9 mM Cr, 1.6 mM Cho, 9.2mM Glu, 4.5mM Gln, 6mM myo-Inositol, 0.4mM Lac) were simulated in a uniformly under sampled, 32-t_1 step CTPRESS experiment with non-interfering aliasing as proposed by Mayer et al [3]. This 32-step 2D experiment is considered the baseline for further undersampling in this study, and was undersampled in the t_1 dimension by factor R as determined by a random draw from a uniform distribution. Gaussian noise was added such that SNR_{NAA} = 15 at full sampling. Reconstruction of the 2D spectra was obtained via three methods: *i)* CS via the non-linear conjugate-gradient solution [6], *ii)* Single-Task Bayesian CS [7], and *iii)* Multi-Task Bayesian CS [4]. The nonlinear conjugate-gradient solution is reproduced as Eq. 1 where y contains under sampled data, Φ is the sparse Fourier Transform , and m is the reconstructed data. λ is chosen as a balance between measurement consistency and enforced sparsity. In the joint Bayesian CS (Eqs. 2, 3 and 4) y_i's represent the under-sampled complex data, and fully sampled individual metabolite magnitude spectra as basis functions. The magnitude spectra were used as basis functions to approximate scanning conditions where phase priors are uncertain. α_0 and **A** are the priors placed across all the spectra, and μ_i is the mean of posterior distribution for m_i and is taken as its best estimate. The log-likelihood expression for α_0 and **A** is conditioned upon all the y_i's and the maximization of this expression leads to evaluating μ_i and Σ_i. In single-task Bayesian CS, the expression for α_0 and **A** is conditioned only on the under sampled spectra.

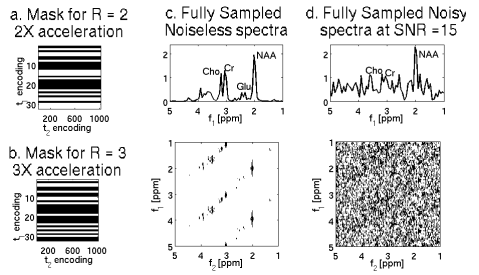

Fig.1. **a.** Mask for undersampling factor R = 2, white lines are sampled **b.** Mask for R = 3. **c**. Fully sampled noise-free CTPRESS data. **d**. Fully sampled noisy data.

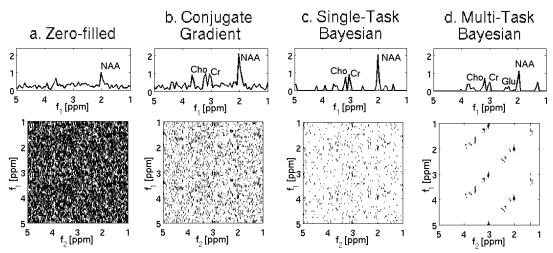

Fig.2. Reconstructed R = 2 spectra on equally-scaled plot **a.** Zero-filling **b.** Conjugate Gradient **c**. Single-task Bayesian **d**. Multi-task Bayesian.

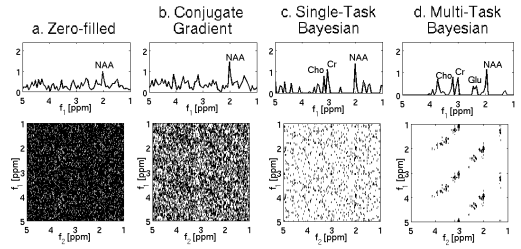

Fig.3. Reconstructed R = 3 spectra on equally-scaled plot **a.** Zero-filling **b.** Conjugate Gradient **c**. Single-task Bayesian **d**. Multi-task Bayesian

$$argmin_m = \| \Phi m - y \|^2_2 + \lambda \| m \|_2 \qquad \text{Eq.1}$$

$$p(m_i \mid y_i, \alpha, \sigma^2) = \frac{p(y_i \mid m_i, \alpha_0) p(m_i \mid \alpha)}{\int dm_i \cdot p(y_i \mid m_i, \alpha_0) p(m_i \mid \alpha)} \qquad \text{Eq.2}$$

$$\mu_i = \alpha_0 \Sigma_i \Phi_i^T y_i \qquad \text{Eq. 3}$$

$$\Sigma_i = (\alpha_0 \Phi_i^T \Phi_i + A)^{-1} \qquad \text{Eq. 4}$$

Results and Discussion: Fig 2 and 3 show the reconstructed 2D spectra and corresponding 1D diagonal spectra for λ= 0.05 and R = 2 and R =3. At R = 2, the three CS methods restore NAA, Cr, Cho peaks in the diagonal spectra that were obscured in the zero-filled reconstruction. In addition Glu peaks were visible in the multi-task Bayesian CS reconstruction. At higher acceleration of R = 3, only NAA peaks were visible in the conjugate gradient CS reconstruction. Multi-task Bayesian CS reconstruction benefited from the prior information of fully sampled metabolite basis spectra, and recovered NAA, Cr, Cho, Glu peaks successfully.

References: : [1] Hurd R et al; MRM 2004; 51:435-440. [2] Dreher et al; MRI 1999; 17:141-150 [3] Mayer D et al; MRM 2005; 54:439–442 [4] Ji et al; IEEE Trans. Sig. Proc 2009; 57;92-106 [5] Bilgic et al; ISMRM 2011 [6] Lustig M et al; MRM 2007; 58:1182-1195 [7] Ji et al; IEEE Trans. Sig. Proc 2008; 56;2346-2356 [8] Veshtort M et al; JMR 2006; 178:248-282 [9] Traber FB et al; JMRI 2004;19:537–545.

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