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 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, 9.2 mM Glu, 4.5 mM Gln, 6 mM myo-Inositol, 0.4 mM Lac) were simulated in a uniformly under sampled, 32-t 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 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, $\Phi$ is the sparse Fourier Transform, and $m$ is the reconstructed data. $\lambda$ 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. $\alpha_{0}$ and $A$ are the priors placed across all the spectra, and $\mu_{i}$ is the mean of posterior distribution for $m_{i}$ and is taken as its best estimate. The log-likelihood expression for $\alpha_{0}$ and $A$ is conditioned upon all the $y_{i}$’s and the maximization of this expression leads to evaluating $\mu_{i}$ and $\Sigma_{i}$. In single-task Bayesian CS, the expression for $\alpha_{0}$ and $A$ is conditioned only on the under sampled spectra.

Results and Discussion: Fig 2 and 3 show the reconstructed 2D spectra and corresponding 1D diagonal spectra for $\lambda = 0.05$ 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.


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