OPTIMIZED RECONSTRUCTION PARAMETERS FOR NOISE MODELING IN MULTI-TASK BAYESIAN COMPRESSED SENSING FOR SPARSE 2D SPECTROSCOPY

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INTRODUCTION: CTPRESS is a homonuclear decoupling method that concentrates J-coupling information within metabolite molecules in a 2D frequency plane (f_1-f_2), and has been shown to successfully detect coupled resonances such as glutamate (Glu) and glutamine (Gln) at the expense of increased total scan time in a 129-step CTPRESS experiment [1]. A 17-step CTPRESS experiment was implemented by Mayer et al [2] considering that all of the signals from a CTPRESS experiment lie close to the a diagonal in the 2D frequency plane, and therefore uniform undersampling in f_1 is possible without aliased signal overlap. Exploration of further under-sampling 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.

Metabolite spectra could be simulated and included as prior spectral information in the reconstruction of under-sampled 2D spectra via Multi-Task (MT) Bayesian CS [3]. We previously showed that MT Bayesian CS successfully reconstructed peaks of Glu and Gln even with imperfect simulated metabolite spectra as priors [4]. Spectroscopy data are intrinsically low SNR and here we extend previous work by incorporating noise modeling parameters for MT Bayesian CS and demonstrate improved reconstruction performance for under-sampled 2D spectra in CTPRESS compared to reconstruction without explicit noise modeling.

METHODS: Using SPINEVOLUTION [5], seven brain metabolites [6], (10.3 mM NAA, 9.95 mM total Cr, 1.63 mM total Cho, 12 mM Glu, 3mM Gln, 6mM myo-Inositol, 0.4mM Lac) were simulated in a uniformly undersampled, 17-t_1 step CTPRESS experiment with non-interfering aliasing as proposed by Mayer et al [2]. This 17-step, 2D experiment is considered the baseline for further undersampling in this study, and was undersampled as determined by a random draw from a uniform distribution in the t_1 dimension by a factor of R. Gaussian noise of $\sigma^2 = 0.0025$ was added such that $SNR_{NAA} = 20$ at full sampling.

The seven brain metabolites were also weighted equally and summed, and the fully sampled spectrum formed the basis function for MT Bayesian CS reconstruction. In Eqs. 1, 2 and 3, y_i's represent the under-sampled complex data and fully sampled metabolite basis function. α_0 is the inverse of the noise variance σ^2; α_0 and $\mathbf{A}$ are 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 evaluation of α_0 and $\mathbf{A}$ results in a log likelihood expression conditioned upon all y_i's and the maximization of this expression leads to evaluating μ_i and Σ_i. Gamma priors (Eqs. 4 and 5) are defined over $\boldsymbol{\alpha}$ and α_0 so that an inverse Gamma prior is introduced on σ^2 and $E[\sigma^2] = b/(a-1)$ and $var[\sigma^2] = b/((a-1)^2(a-2))$.

$$p(\mathbf{m}_i|\mathbf{y}_i, \boldsymbol{\alpha}, \alpha_0) = \frac{p(\mathbf{y}_i|\mathbf{m}_i,\alpha_0)\cdot p(\mathbf{m}_i|\boldsymbol{\alpha})}{\int dm_i\, p(\mathbf{y}_i|\mathbf{m}_i,\alpha_0)\cdot p(\mathbf{m}_i|\boldsymbol{\alpha})} \quad \text{Eq. 1}$$

$$\boldsymbol{\mu}_i = \alpha_0 \boldsymbol{\Sigma} \mathbf{F_u}^T \mathbf{y}_i \quad \text{Eq. 2}$$

$$\boldsymbol{\Sigma}_i = (\alpha_0 \mathbf{F_u}^T \mathbf{F_u} + \mathbf{A})^{-1} \quad \text{Eq. 3}$$

$$\mathbf{A}_i = \text{diag}(\alpha_1 \alpha_2 .. \alpha_i .. \alpha_N)$$

$$p(\boldsymbol{\alpha}|c,d) = \prod \Gamma(\alpha_i|c,d) \quad \text{Eq. 4}$$

$$p(\alpha_0|a,b) = \Gamma(\alpha_0|a,b) \quad \text{Eq. 5}$$

$$\rightarrow E[\sigma^2] = \frac{b}{a-1}, \; Var[\sigma^2] = \frac{b}{(a-1)^2\cdot(a-2)}$$

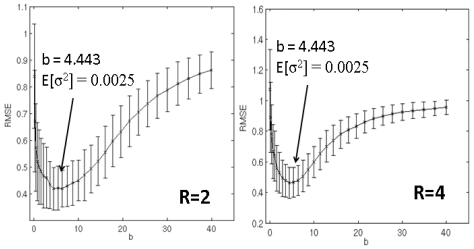

Fig. 1a and b. RMSE evaluated for low-SNR peaks evaluated with different values of *b* for under-sampling factor of R = 2 and R =4 using MT-Bayesian CS with perfectly phased priors.

To include *a priori* noise precision in the reconstruction, we minimize RMSE for the range $a = 2$ to 1E5 and $b = 0.044$ to 40, so that $E[\sigma^2]$ ranges from 2.5E-5 to 0.0225 and $var[\sigma^2]$ ranges from 2.5E-5 to 2.25E-12. Focusing on the low-SNR peaks of Glu, NAA+Gln, and Glx between 2.25ppm-2.35ppm, 2.35ppm-2.47ppm and 3.69ppm-3.80ppm respectively, reconstructed spectra were compared to the fully-sampled baseline spectra and RMSE $||x_{reconstructed}-x_{true}||/||x_{true}$ was calculated. RMSE was evaluated for 20 noise realizations and 5 under-sampling realizations, and for under-sampling factor R = 2, 3 and 4 corresponding to 9, 7 and 5-step CTPRESS experiments respectively. To approximate scanning conditions where phase priors are uncertain, *Abs*(m_i) and *Phase*(m_i) are solved for with MT Bayesian CS using the magnitude prior of the basis function and Single-Task (ST) Bayesian CS [7] respectively.

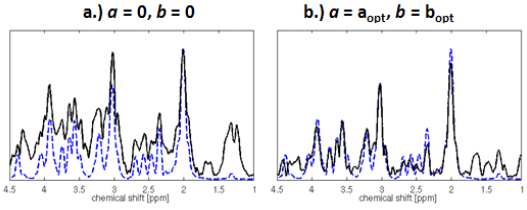

Fig. 2a and b. Diagonal spectra from reconstructed 2D CTPRESS spectra with different values of *a* and *b* for under-sampling factor R = 4. Blue dashed lines indicate the diagonal spectra of simulated noise-free fully sampled data.

RESULTS & DISCUSSION: Fig. 1a and b shows mean RMSE of the low SNR peaks of Glu, NAA+Gln, and Glx taken over 100 random trials for R = 2 and R =4 assuming ideally phased priors. The minimum RMSE is at (a_{opt} = 1778, b_{opt} = 4.443) corresponding to $E[\sigma^2] = 0.0025$ for R =2 and R = 4, which matched the noise of $\sigma^2 = 0.0025$ added to the simulated spectra. Small values of *b* resulted in small values for $E[\sigma^2]$, limiting the de-noising feature of MT Bayesian CS reconstructions. On the other hand, large values of *b* assume more noise than present in the undersampled spectra which lead to dropouts of Glu and Gln peaks in the CS reconstructions. Fig.2a shows the diagonal spectra at R = 4 formed from the reconstructed 2D spectra for $a = 0$ and $b = 0$ without *a priori* noise precision, and Fig 2b demonstrates the successful reconstruction of Glu and Gln peaks in the diagonal spectra formed with the suggested choice of $a = 1780$ and b = 4.443 that best models $\sigma^2 = 0.0025$ added to the simulated spectra.

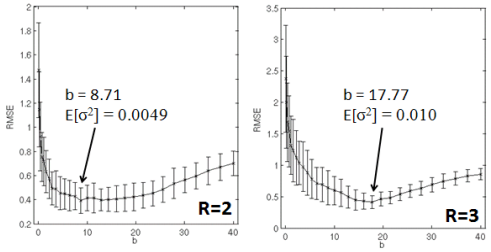

Fig. 3a and b. Fig. 2a and b. RMSE evaluated for low-SNR peaks evaluated with different values of *b* for under-sampling factor of R = 2 and R =3 using MT-Bayesian CS with magnitude priors.

Fig. 3a and b shows mean RMSE of the low SNR peaks taken over 100 random trials for R = 2 assuming non-ideal scanning conditions where phase priors are uncertain. The minimum RMSE corresponds to $E[\sigma^2] = 0.0049$ for R = 2 and to $E[\sigma^2] = 0.010$ for R = 3 which did not model the noise of $\sigma^2 = 0.0025$ added to the simulated spectra. We postulate that this discrepancy is due to insufficient modeling of Rayleigh noise with non-zero mean in the reconstruction of *Abs*(m_i) with MT Bayesian CS.

CONCLUSION: We demonstrated the application of MT Bayesian CS to under-sampled CTPRESS data and the successful recovery of low-SNR peaks with optimized noise modeling parameters, *a* and *b*.

References: [1] Dreher et al; MRI 1999; 17:141-150 [2] Mayer D et al; MRM 2005; 54:439–442 [3] Ji et al; IEEE Trans. Sig. Proc 2009; 57;92-106 [4] Kok et al; ISMRM 2011 #1448 [5] Veshtort M et al; JMR 2006; 178:248-282 [6] Traber FB et al; JMRI 2004;19:537–545. [7] Ji et al; IEEE Trans. Sig. Proc 2008; 56; 2346-2356

This work was supported by Siemens Medical Solutions, NIH R01EB007942