Sparse Reconstruction of Localized Correlated Spectroscopy: From Sub-Sampled Priors to Fast Acquisition

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INTRODUCTION: Despite its successful application to detect many pathological disorders in brain [1, 2], breast [3] and prostate [4], Localized Correlated Spectroscopy (L-COSY) still suffers from long acquisition that prevents this technique to enter clinical studies [5]. Inherent sparse nature of L-COSY can be exploited to accelerate the long acquisition times ensued from iterative sampling along indirect dimension (t_1). In this study, a new reconstruction strategy is presented that takes the advantage of sparsity to reconstruct the whole L-COSY spectrum with less number of acquisitions along the t_1 dimension.

METHOD: The proposed reconstruction strategy consists of two main steps: first finding the location of diagonal and cross peaks from subsampling priors, and then quantifying the spectrum at each peak. Using sparse nature of spectrum, the location of diagonal and cross peaks could be determined from deterministic subsampling along t_1. The amplitude of peaks is calculated through iterative least-square (LS) on those deterministic subsampled t_1 data. The (LS) problem is formulated as follows: The relationship between time domain matrix (T) and spectrum domain matrix (S) is 2D Fourier Transform which is presented is Eq 1.

$$\mathbf{T} = \mathbf{F}_{t_2}^{\mathbf{H}} \times \mathbf{S} \times \mathbf{F}_{t_1}^{\mathbf{H}} \quad \textbf{Eq. 1}$$

$$\tilde{\mathbf{T}}_{\mathbf{v}} = \left(\mathbf{I}_{N_2} \otimes \mathbf{F}_{t_1}\right) \tilde{\mathbf{S}}_{\mathbf{v}} = \boldsymbol{\Psi}\, \tilde{\mathbf{S}}_{\mathbf{v}} \quad \textbf{Eq. 2}$$

$$\boldsymbol{\Gamma} \times \tilde{\mathbf{S}}_{\mathbf{red}} = \mathbf{E} \;\; \textbf{such that} \;\; \boldsymbol{\Gamma} = \boldsymbol{\Psi}_{\mathbf{red}}^{\mathbf{H}}\, \boldsymbol{\Psi}_{\mathbf{red}}\,, \quad \mathbf{E} = \boldsymbol{\Psi}_{\mathbf{red}}^{\mathbf{H}}\, \tilde{\mathbf{T}}_{\mathbf{red}} \quad \textbf{Eq. 3}$$

$$\tilde{\mathbf{S}}_{\mathbf{es}} = \arg\min_{\tilde{\mathbf{S}}} \left\| \mathbf{E} - \boldsymbol{\Gamma}\tilde{\mathbf{S}} \right\|_2 \quad \textbf{Eq. 4}$$

F_{t_2} and F_{t_1} are Fourier Transform matrix along t_2 and t_1 respectively and H is the Hermitian operator. The Eq 1 can be represented in vector notation without loss of generality as presented in Eq 2, where $\otimes$ denotes the Kronecker product, $\tilde{T}_v$, $\tilde{S}_v$ are the vector representation of time domain and spectrum domain data, I_{N_2} is the identity matrix of the order N_2 (number of data points along t_2). The columns in matrix Ψ can be reduced to those columns correspond to known location of peaks. In addition, subsampling of t_1 data is used to reduce rows of Ψ which is denoted as Ψ_{red}. Since the 2D spectrum is highly sparse, with subsampling factor of 2 or so, the resultant equation is still in the form of the LS formulation (Eq 3). $\tilde{S}_{red}$ and $\tilde{T}_{red}$ are the time and spectrum domain data corresponding to Ψ_{red}. Finally the solution is obtained through Eq 4. General Minimum Residual method (GMRES) was employed to solve for this problem. The proposed method was implemented on phantom data and in vivo data from a healthy case both acquired on 3T Siemens Tim-Trio MR scanner with following parameters: TR/TE = 2000ms/30ms, 100 number of Δt_1 increment with 1250Hz spectral window, 2048 complex points along t_2 with 2000Hz spectral window. All fully sampled and reconstructed data were apodized and zero-filled afterward.

RESULT: Figure 1 illustrates the reconstructed spectra for 70%, 60% and 50% subsampling rates. In addition, comparison between original and reconstructed cross peaks for Glx and NAA is depicted in Figure 2. The Structural Similarity Index (SSIM) and Relative RMSE (RRMSE) are used to evaluate reconstruction performance for cross peaks.

DISCUSSION & CONCLUSION: Our preliminary results indicate that the proposed method of reconstruction is able to reduce acquisition time in 2D L-COSY. Spectra for different subsampling rates were successfully reconstructed with negligible deviation from fully sampled spectrum (with RRMSE less than 4%). In addition, SSIM and RRMSE measures for Glx and NAA show that the method can preserve structure of cross peaks. Hence there will be insignificant error after application of post-acquisition processing. Evaluation of the reconstruction method with spectral processing is still needed.

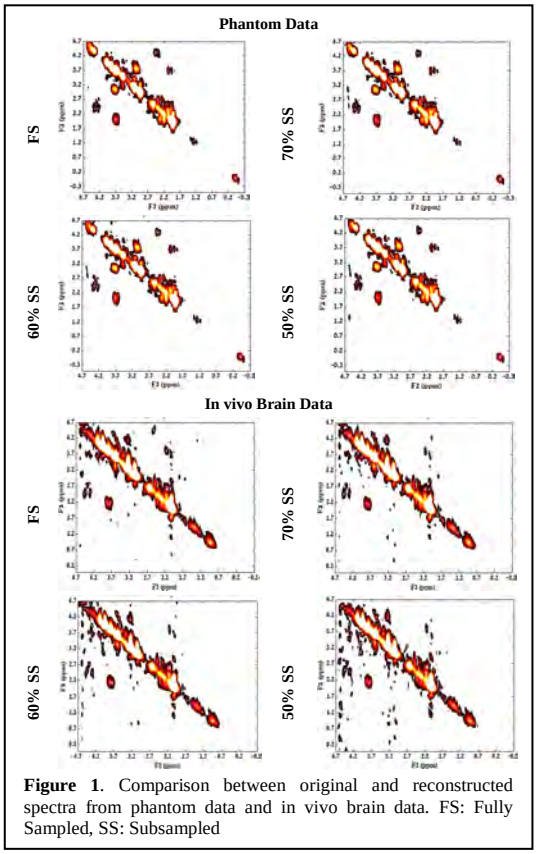

Figure 1. Comparison between original and reconstructed spectra from phantom data and in vivo brain data. FS: Fully Sampled, SS: Subsampled

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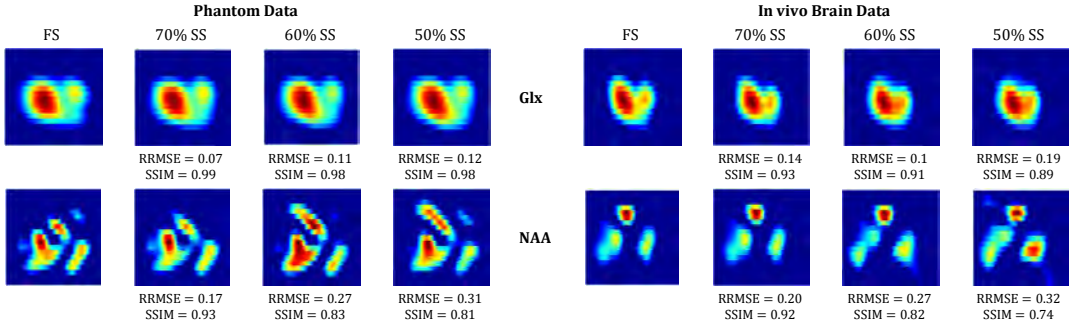

Figure 2. Comparison between original and reconstructed NAA and Glx cross peaks from phantom data (left) and in vivo brain data from healthy subject (right). FS: Fully Sampled, SS: Subsampled