Accurate Compressive Sensing of 1H MR Spectroscopic Imaging in Brain Tumors

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INTRODUCTION: Long acquisition times of 2D and 3D 1H MR Spectroscopic Imaging (1H-MRSI) are a major obstacle to its widespread clinical application. Compressed Sensing (CS) allows accelerated 1H-MRSI acquisitions through reconstruction of non-uniform randomly subsampled k-space [1]. CS can reliably reconstruct the subsampled MRSI data with meaningful selection of regularizers that consider spars and compressible nature of MR spectra. In this study, we implemented CS directly based on the spectral-spatial sparsity of spectra for reconstruction [2]. The efficiency of the CS method was evaluated by calculating the difference in NAA, Creatine (Cr) and Choline (Cho) estimation across all voxels compared to full k-space acquisition as determined by LCModel.

METHOD: 1H-MRSI data from patients with grade II (n=3), grade III (n=2) and grade IV (n=5) glioma were acquired on 1.5T GE scanner with PRESS localization and VSS outer-volume saturation using: TR/TE = 2000ms/30ms, 16×16 Cartesian phase-encoding scheme, FOV = 22cm and slice thickness = 15mm. The fully sampled k-spaces were then non-uniformly subsampled at the rates of 64%, 50%, 42%, 33% and 25%. The reconstruction was formulated as weighted sum of objective functions where the Total Variation (TV) was used for denoising the spatial domain and the L1 norm of MR spectra was also added to preserve their sparsity.

$$\arg\min_{x} \frac{1}{2}\sum_{n=1}^{N}\|\phi.F.x_n - y\|_2^2 + \tau_1\sum_{n=1}^{N}TV(x_n) + \tau_2\sum_{m=1}^{M}\|x_m\|_1$$

ϕ is the subsampling matrix, F is the Fourier Transform along horizontal and longitudinal spatial dimensions, y the subsampled spatial-spectral MRSI data, TV the Total Variation operator, $\|.\|_{l_1}$ the L1 norm, τ_1 and τ_2 are regularization parameters, and M, N are number of voxels and number of spectral points respectively. The Alternating Direction Method of Multipliers (ADMM) [3] scheme was used to solve for the equation. MRSI data was analyzed with LCModel to compare the effect of different CS sampling rates on the metabolite peak areas. For cases with sufficient spatial coverage, radial Cho -NAA index (rCNI) [4] was used to assess how CS affected the spatial distribution of the abnormal tissue region.

	64%	50%	42%	33%	25%
NAA	**0.121**	**0.127**	**0.139**	**0.160**	**0.197**
Cr	**0.154**	**0.129**	**0.151**	**0.181**	**0.231**
Cho	**0.101**	**0.130**	**0.131**	**0.171**	**0.191**

Table 1 RMSE of estimated NAA, Cho and Cr concentration from all 10 cases.

RESULT: Figure 1 shows a heat map of the rCNI of tissue abnormality for fully-sampled MRSI data and CS data with different acceleration rates. These images indicate that CS reconstruction from subsampled data down to 33% could preserve abnormal boundaries. In addition, Table 1 represents the average deviation in NAA, Cho and Cr concentration of all voxels within excitation grid from 10 cases for different subsampling rates. Relative Root Mean Square Error (RRMSE) was used to calculate deviation in concentration of metabolites from fully sampled data in all 10 cases.

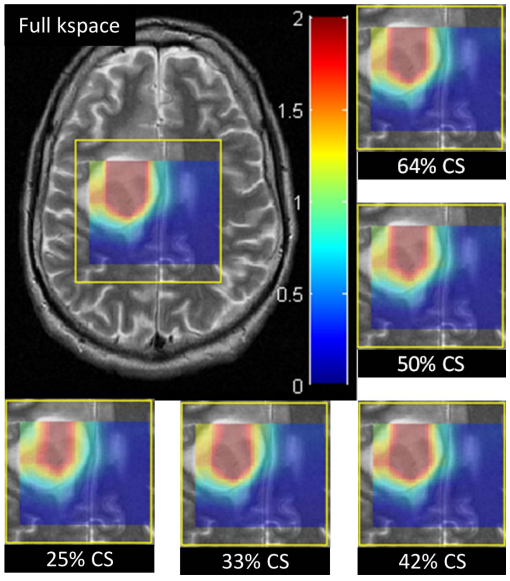

Figure 1. Heat map of radial Cho -NAA index from CS reconstructed MRSI data using different subsampling rates for a grade III glioma.

DISCUSSION & CONCLUSION: The RRMSE and rCNI measures demonstrate that CS method based on meaningful selection of regularizers to exploit spectral-spatial sparsity can accelerate 1H-MRSI acquisition up factor of 3 (33% subsampling) without significantly degrading metabolite information of Cho, NAA and Cr. Further work to evaluate the technique on larger datasets and using analysis techniques such as rCNI to evaluate potential changes in the abnormality boundaries and validation in clinical studies with actual sub-sampling of MRSI data during acquisition is still needed.

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