Accelerated ^{1}H Chemical Shift Imaging of the brain using compressive sensing

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Introduction: Chemical Shift Imaging (CSI) is a non-invasive technique capable of providing specific information about the spatial distribution of metabolites present in the human body. Its ability to quantify therapy and aid in prognosis has been well documented. The advantages of multi-voxel spectroscopy (2, 3 Dimensional) over single voxel spectroscopy are widely established. However, the major disadvantage is the long acquisition time. Therefore there is a strong need for reducing the acquisition time to enable this technology to be more routinely used in the clinic. Reduction in acquisition time is typically accomplished by undersampling k-space. The limiting factor is that the Nyquist criterion is violated when the k-space is undersampled beyond a critical limit, thus giving rise to aliasing artifacts and reducing the Signal to Noise Ratio (SNR). Compressive sensing has been shown to be able to reconstruct data with high SNR from extremely undersampled k-space. An essential study is to implement and validate the approach of such reconstruction methods on compressively sensed 1H CSI data to enable application of this technique in the clinical setting.
Methods: Compressive sensing requires that the data to be reconstructed be sparse in a transform domain. CSI data is sparse in the wavelet domain. Hence application of compressive sensing based reconstruction would enable exploiting this sparsity. A retrospective analysis on previously acquired *in vivo* human brain CSI data sets with dimensions of 16 X 16 X 1024 was performed. The k-space of the data set was undersampled by factors of 2, 3, 5 and 10 and the spectra were reconstructed using compressive sensing as shown in (1). Specifically, k-space data was undersampled in the $k_x - k_f$ space and then the missing k-space data was iteratively filled using the nonlinear conjugate gradient method as was performed in (1). The reconstructed spectra from undersampled k-space and the complete k-space were subject to the following identical post-processing steps in jMRUI (2) : apodization, baseline correction, residual water peak removal, phase correction and quantitation by AMARES (3). Metabolite maps for N-acetylaspartate (NAA), Creatine and Choline for both the full data reconstruction and the undersampled case were also generated using and compared for the 2 CSI brain data sets. The results were quantified by the root mean square error (RMSE) values obtained for the region of interest (ROI) which was a 10 X10 grid in the center of the 16 X 16 grid, for each acceleration factor.

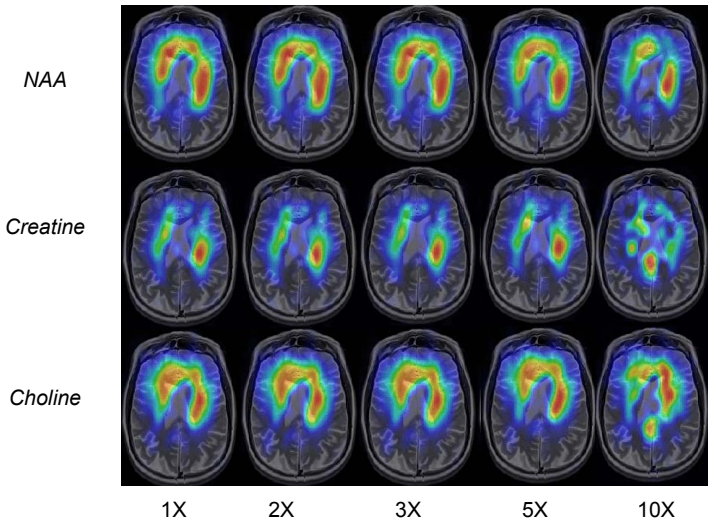

Figure 1: Metabolite maps of NAA, Creatine and Choline in rows 1, 2 and 3 for different acceleration values of 1(no undersampling), 2, 3, 5 and 10.

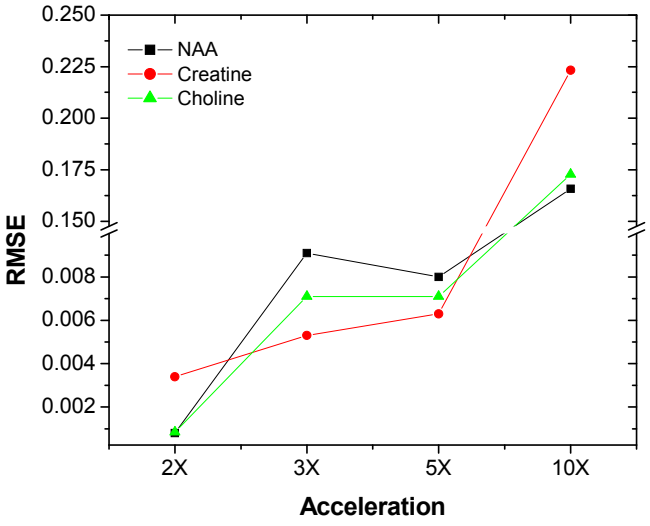

Figure 2: Graph depicting the ROI RMSE values for NAA, Creatine and Choline of the CSI in vivo brain data set as a function of acceleration factor.

Results: The metabolite maps for NAA, Creatine, and Choline for one of the data sets for the 4 values of acceleration have been shown in figure 1.It can be observed that the metabolite maps of the reconstructed data sets preserve most of the morphological information compared to the full k-space reconstruction case (shown in the first column of figure 1) till up to 5X acceleration which is 20% of the k-space data. Figure 2 shows the RMSE values for the corresponding data set for each of the 3 metabolites (shown in figure 1) for the mentioned values of acceleration.
Conclusion: The application of compressed sensing to CSI of *in vivo* human brain data has been performed for the first time. Our results indicate a potential to reduce CSI acquisition times significantly and hence reducing the time spent by the patient in the MR scanner for spectroscopic studies.
The error values and metabolite maps indicate that compressive sensing based reconstruction of the ^{1}H CSI data will aid in reducing the time spent by the patient in the MR scanner or alternately, could be used in obtaining higher resolution spectra in the same period of time. Future work involves quantification of metabolite maps and also the validation of these results by radiologists, so that an optimum level of undersampling could be obtained and application of this technique on breast and prostate *in vivo* human CSI data sets.
Reference:

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