Fast ^{1}H metabolic imaging of cancer

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Introduction: The significance of understanding the metabolic activity in cancer research has been well established. Magnetic resonance spectroscopy (MRSI) is a non-invasive technique capable of providing specific information about the spatial distribution of metabolites. Its ability to quantify therapy and aid in cancer prognosis has been well documented. However, the major disadvantage is the long acquisition time which increases patient discomfort and likelihood of early termination of the study along with increased cost. Therefore there is a strong need for reducing the acquisition time to enable this powerful technology to be more routinely used in the clinic for cancer imaging. A promising solution to this problem would be to reconstruct MRSI data with as few acquisition data as possible which can be achieved by the use of compressive sensing (CS). CS exploits the spectral and spatial sparsity inherent in MRSI data. The study involves implementation and validation of CS based reconstruction methods on compressively sensed ^{1}H MRSI data.

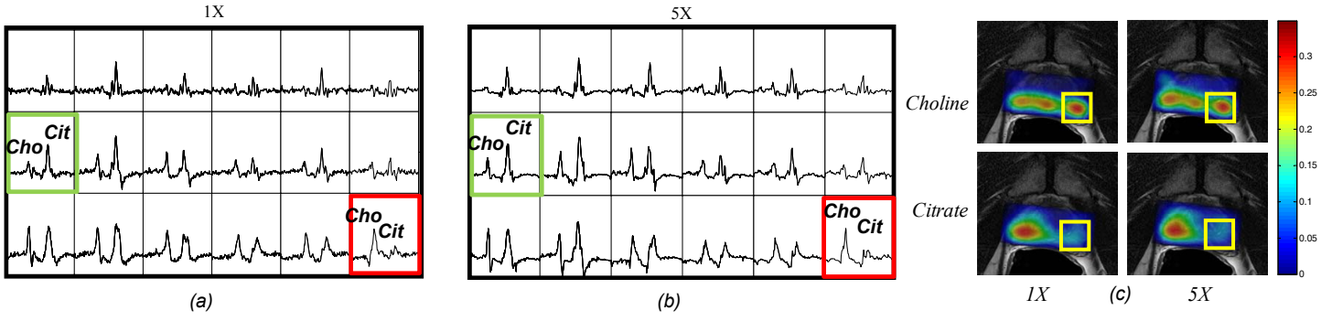

*Figure 1: (a) Plot of the spectra of a representative prostate cancer MRSI at 1X (full k-space reconstruction) and (b) an acceleration factor of 5 as compared to the original MRSI data (1X). Prostate cancer tissue (shown in the red voxel) is characterized by increased choline (**Cho**) and reduced citrate (**Cit**) levels when compared to the metabolic profile of a normal prostate tissue (shown in green). 1(c) shows the Cho and Cit metabolite maps for the prostate cancer data at acceleration factors of 1 and 5. The yellow boxes on the metabolite maps represent the location of the prostate cancer.*

Methods: The reconstruction was applied to ^{1}H MRSI *in vitro* phantom (GE braino, [1]), *in vivo* human brain: normal (N=6), cancer (N=3), and prostate cancer (N=2) data sets for acceleration factors of 2, 3, 4, 5 and 10.Acquisition parameters are summarized in table 1.The reconstruction algorithm described in [2] was used. The error of reconstruction was quantified by the root mean square error metric (RMSE). In order to consistently evaluate the efficacy of the reconstruction, importance was given to minimal post-processing of the original and reconstructed data. The MRSI data sets were subjected to the following processing steps in jMRUI [3]: (a) apodization (b) baseline correction (c) removal of the water peak (d) zero-order phase correction (e) Generation of metabolite maps using the quantitation algorithm available in jMRUI.

Results: Figure 1(a) depicts the full k-space reconstruction of a representative prostate cancer MRSI data set. It can be observed that the reconstructed spectra for the MRSI data set are comparable to the original at 5X shown in 1(b) as well. This is reflected in the similarity between the original and reconstructed metabolite maps for Cho and Cit for both acceleration factors in 1(c). It can also be observed that the reconstructed spectra display lesser noise when compared to the original spectra. This can be attributed to the denoising ability of the wavelets and the smoothing effect of the TV factor in the reconstruction**.** Figure 2 summarizes the performance of the reconstruction for different MRSI data. It can be noted that the RMSE values are less than ~0.03 even at 5X. The 10X case demonstrates the limit of the implemented reconstruction technique.

MRSI data	Scanner	TR(ms)	TE(ms)	# Averages	Grid Size	FOV (mm^3)
In vitro brain phantom	Siemens 3.0T Trio Trim	1700	270	2	16 x 16 x 1024 (8 slices)	160 x 160 x 40
In vivo brain (normal)	Siemens 3.0T Trio Trim	1700	270	4	16 x 16 x 1024	100 x 100 x 15
Brain cancer	Philips 3.0T Achieva	1000	112 112	2 2	16 x 21 x 1024 18 x 21 x 1024 19 x 22 x 1024	80 x110 x 15 180 x 210 x15 190 x 220 x 15
Prostate cancer	Philips 3.0T Achieva	1200 1000	140 140	1 1	14 x 10 x 1024 16 x 12 x 1024 (6 slices each)	25 x 50 x 33 20 x 51 x 26

Table1: MRSI acquisition parameters for the different data types.

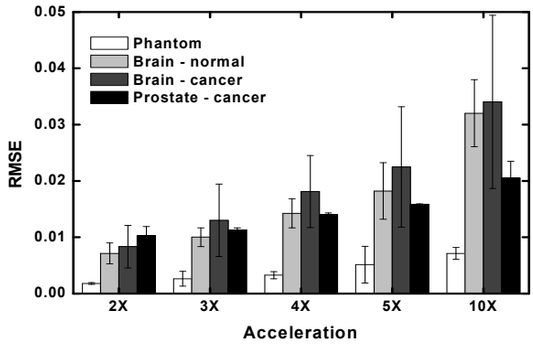

Figure 2: Graph of RMSE values for the different MRSI data used in the study as a function of acceleration factors of 2, 3, 4, 5 and 10

Conclusion: The application of compressed sensing to ^{1}H MRSI has been performed for the first time. We have successfully demonstrated the technique on different types of ^{1}H MRSI data. The quality of the reconstructed data quantified by the reconstruction error and metabolite maps show high fidelity as compared to the original data. Therefore, our results indicate a potential to reduce acquisition times by 80% thus accomplishing the goals of the project and also increasing through-put. This technique could also be used to identify harder-to-detect metabolites by increased averaging which are being characterized as potential biomarkers for brain cancer.

References: 1) Schirmer T., et al., NMR Biomed 13(1): p 28-36 (2000) 2) Geethanath, S., et al., Proc. Intl. Soc. Mag. Reson. Med.18: p 380 (2010). 3) Naressi, A., et al., Comput Biol Med; 31(4):269-286 (2001)

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