The effect of Compressed Sensing reconstruction on the spatial resolution of Magnetic Resonance Spectroscopic Imaging.

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Introduction

Magnetic Resonance Spectroscopic Imaging (MRSI) is a useful tool in the management of disorders affecting the central nervous system. It is however limited by low spatial resolution and long acquisition times restricting its impact in clinical applications. A reduction in k-space sampling could alleviate this issue but at the expense of aliasing artifacts. Compressed sensing (CS) has been shown to be a useful tool for reducing k-space sampling without artifact in MRI [1] and more recently in clinical MRSI [2]; however the effect upon the spatial resolution in MRSI of potential speed up techniques has not been fully investigated.

Aim

The work aims to investigate the effect of CS reconstruction with various k-space sampling strategies on spatial resolution in MRSI by developing novel methodology employing phantom and volunteer datasets.

Methods

Phantom: A phantom consisting of agarose gel in two compartments, one containing N-acetyl aspartate (NAA) and the other creatine, separated by a non-permeable polymer membrane was developed, creating a non-diffusible, flat metabolite edge.

Phantom/Volunteer MRSI Acquisition: The phantom was scanned using an MRSI spin-echo sequence (TE 35ms, TR 2000ms, voxel size 10x10x10mm, 20x20 matrix) in a slice perpendicular to the metabolite edge as shown in Fig 1. An axial slice through the centrum semiovale was scanned in a volunteer, with the same parameters except for TE (144ms), with and without the application of central water and fat saturation slabs to produce a high spatial frequency, high contrast metabolite variation, as shown in Fig 2. No k-space acquisition masks or post-acquisition filtering were applied.

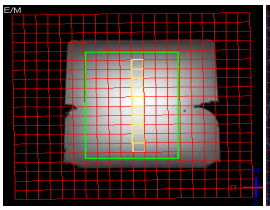


Figure 1-*Phantom MRSI Planning*

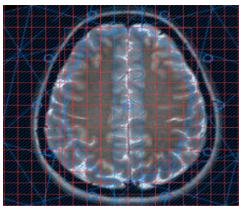
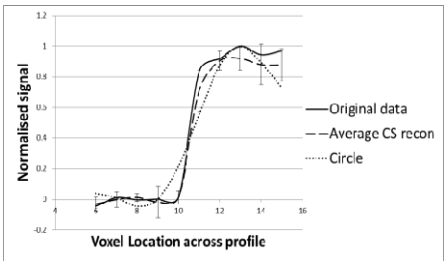


Figure 2-*Volunteer MRSI Planning*

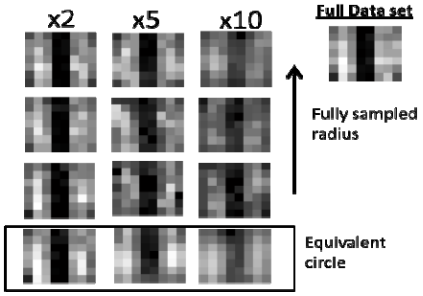
Reconstruction: The MRSI k-space data were randomly under-sampled using a variable-density method in which a variable proportion at the center is fully sampled [1]. Equivalent acceleration factors of x2, x5 and x10 were reconstructed for the volunteer data and for the phantom dataset an acceleration of x4 was also utilized. The implementation of CS utilizing conjugate gradient descent was applied to the 3D MRSI dataset (x,y,f) by software developed in MATLAB [2]. The spectrum itself was utilized as the sparse domain. An equivalently sampled circle at the centre of k-space was also reconstructed without CS for each acceleration factor, along with the fully sampled data set. A profile across the boundary edge within the phantom was defined (Fig 1) and the average normalized area under the NAA peak was plotted for 10 randomly under-sampled CS reconstructions, the slope indicating the spatial resolution. Post reconstruction, the in-vivo data sets were processed in TARQUIN to provide relative metabolite quantification [3]. NAA metabolite maps were produced to indicate the resultant distributions. The RMSE of the voxel-wise NAA measurements relative to the fully sampled dataset and normalized to the mean NAA value without saturation bands (nRMSE) was calculated.

Results

a)



b)



c)

	Normalised RMSE for Area out of Saturation Bands				
% of full radius	x 2	% of full radius	x 5	% of full radius	x 10
50	0.21	30	0.30	20	0.45
40	0.23	20	0.43	10	0.61
30	0.25	10	0.54	5	0.60
Equivalent Circle	0.23		0.23		0.25
	Normalised RMSE for Area in Saturation Bands				
% of full radius	x 2	% of full	x 5	% of full	x 10
50	0.06	30	0.11	20	0.33
40	0.08	20	0.15	10	0.22
30	0.12	10	0.14	5	0.15
Equivalent Circle	0.10		0.22		0.37

Figure 3-a) *Phantom edge profile of NAA signal for x4 CS reconstruction, b) NAA metabolite maps of the volunteer data with the saturation bands for each CS acceleration factor and varying proportions of fully-sampled central k-space and c) the corresponding nRMSE values.*

The phantom profile slopes for the fully-sampled, centrally under-sampled, and CS reconstructions were 0.82, 0.33, 0.70(+/-0.14) respectively. For the in-vivo data, CS reconstruction demonstrates lower bleed through of NAA signal in the saturated region. However, circular under-sampling of k-space appears to produce lower discrepancies in NAA quantitation outside the saturated area.

Discussion/Conclusion

This study demonstrates a suitable method for the assessment of spatial resolution in MRSI. Initial results indicate that substantial speed-up of MRSI acquisition with CS is possible while maintaining spatial resolution, which is important for applications such as delineation of tumour borders. However, testing on a range of volunteer and patient datasets is required to fully optimise the k-space sampling strategy in CS-MRSI and define the trade-off between acceleration factor, spatial resolution and signal-to-noise ratio.

References

[1] Lustig M et al. Mag Reson Med (2007) 58:1182–1195. [2] Geethanath S et al. Radiology (2012) 262:985-994. [3] Wilson M et al. Mag Reson Med (2011) 65:1-12.