The Influence of Macromolecule Baseline on ^{1}H Magnetic Resonance Spectroscopic Imaging Reproducibility

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Introduction

The accurate quantitation of metabolites in MR Spectroscopic Imaging (MRSI) is an important requirement for its clinical use. Poorly characterised macromolecular signals and baseline artefacts (background signals) are known to adversely affect metabolite quantitation during the fitting process due to strong signal overlap. Background signals can be significantly reduced by increasing the echo-time (TE) of the MRS acquisition - potentially improving metabolite quantitation accuracy. However, longer TE's are also associated with an inherent reduction in metabolite signal-to-noise (SNR) and complex dephasing of multiplets - which may result in a reduction in quantitation accuracy. Analysis schemes are also known to play an important role in quantitation accuracy and the most widely used methods incorporate simulated macromolecular signals in the fitting process to improve metabolite determination[1]. However, it has been shown previously for single voxel MRS that the incorporation of an experimentally determined macromolecular baseline into the fitting process may offer improvements in accuracy due to a greater level of prior knowledge being incorporated into the analysis[2]. Therefore, the aim of this study was to measure the influence of echo-time and two different macromolecular analysis schemes on the reproducibility of MRSI metabolite quantitation.

Methods

MRSI data was collected from 6 healthy volunteers (aged between 23 and 30); all scans were performed on a 3T Philips Achieva TX MR system with a 32 channel head coil. 2D MRSI 15x13 voxel grids with PRESS excitation (VOI 6x6 equating to a 5x5 region with a 1/2voxel margin) were manually placed for two different regions: 1) Above the corpus callosum for volunteers 1-3 and 2) in line with the basal ganglia volunteers 4-6 . Scans were acquired in triplicate for TE's of 35ms (volunteers 1 and 4), 80ms (volunteers 2 and 5) and 144ms (volunteers 3 and 6) and TR=2s (all). Water reference data was collected during the first scan for each volunteer in order to obtain absolute concentrations. A healthy volunteer experimental MM baseline (Ex.BL) was extracted by placing a single voxel over left and right white parietal matter using a metabolite nulling inversion recovery (IR) sequence with TI=750ms. The Ex.BL is then manually fitted using TARQUIN MRS Quantitation software then averaged and incorporated into a basis set for use in the fitting of the MRSI metabolite spectra. All MRSI spectra were zero filled in the fitting process. Data analysis was performed in the python programming language. Metabolite Coefficients of Variance (COV's) were calculated to assess the short term reproducibility for each TE and region comparing two macromolecular analysis schemes; using 1) a simulated baseline (Si.BL) and 2) an experimentally acquired baseline (Ex.BL).

Results

A TE=80ms was found to be the most reproducible overall with COV's<13% for total (t) NAA, tCr and tCho (Table 1 and 2). The metabolites tNAA, tCr and tCho were found to be the most stable with COV<15% for all TE's for region 1 (above the Corpus Callosum) as expected due to their higher signal (Table1). At region two (level with the basal ganglia) a large increase in variability ~x5 for TE=35ms was observed (Table 2) when using the Si.BL MM analysis scheme due to poor data quality. Ex.BL reduced this variation by over half for tNAA (Table 2) and overall had the best results with the higher level metabolites; it also had a higher impact when data quality is low particularly for poorly shimmed data suggesting less well-defined spectra are more susceptible to error from MM contribution.

Table 1 Mean metabolite Coefficients of Variance for TE=35ms, 80ms and 144ms for region1 above the corpus callosum, comparing simulated baseline (Si.BL) and experimental baseline (Ex.BL) analysis schemes.

	TE=35ms		TE=80ms		TE=144ms	
	Si.BL	Ex.BL	Si.BL	Ex.BL	Si.BL	Ex.BL
Metabolite	**COV %**	**COV %**	**COV %**	**COV %**	**COV %**	**COV %**
tNAA	8.49	6.23	5.19	5.05	13.04	9.86
tCr	9.68	8.50	6.61	6.32	14.00	13.53
tCho	8.76	8.75	7.38	7.47	10.81	11.29
Glx	17.21	14.32	16.86	20.23	24.66	25.85
Ins	27.28	18.29	11.65	12.86	49.84	51.19

Table 2 Mean metabolite Coefficients of Variance for TE=35ms, 80ms and 144ms for region2 level with the Basal Ganglia, comparing Si.BL and Ex.BL analysis schemes.

	TE=35ms		TE=80ms		TE=144ms	
	Si.BL	Ex.BL	Si.BL	Ex.BL	Si.BL	Ex.BL
Metabolite	**COV %**	**COV %**	**COV %**	**COV %**	**COV %**	**COV %**
tNAA	39.32	17.15	8.32	5.59	4.80	3.83
tCr	16.73	14.81	9.54	8.34	5.10	4.89
tCho	28.29	23.42	12.06	11.78	6.09	6.28
Glx	33.05	29.60	34.84	32.34	21.70	22.52
Ins	61.55	56.62	27.89	27.72	27.29	31.98

Conclusion

An echo time of 80ms was found to yield the most reproducible metabolite estimates. However, the combined use of a short echo time sequence and fitting with an experimentally acquired baseline may be preferred as a compromise between good accuracy and reduced T2 bias on metabolite estimates.

References

[1]Schaller B et al. NMR Biomed. 2013;26:593–599.
[2]Gottschalk M et al. NMR Biomed. 2008;21:507–517.