A comparison between simulated and experimental basis sets for the analysis of short-echo in-vivo MRS data at 1.5T

M. Wilson[1,2], N. P. Davies[1,2], Y. Sun[2,3], K. Natarajan[2], T. N. Arvanitis[2,3], and A. C. Peet[1,2]

[1]Cancer Sciences, University of Birmingham, Birmingham, West Midlands, United Kingdom, [2]Oncology, Birmingham Childrens Hospital Foundation Trust, Birmingham, West Midlands, United Kingdom, [3]School of Electronic, Electrical and Computer Engineering, University of Birmingham, Birmingham, West Midlands, United Kingdom

Introduction

1H MRS is a non-invasive technique capable of extracting metabolic profiles from regions of the brain. These profiles can be used to characterise a number of brain pathologies and have been shown to be particularly useful for the investigation of paediatric brain tumours[1,2]. Since the spectroscopic data acquired is often complex, advanced signal analysis tools are crucial to extract accurate information on the underlying metabolite signals. One such tool, LCModel[3], has been in use since 1993 and has proven itself as a robust and accurate method for the measurement of metabolite signals at 1.5T.

The LCModel algorithm uses a linear combination of experimentally acquired metabolite signals to form a basis set. These signals are then adjusted during the algorithm to match the raw spectroscopic data allowing the metabolite quantities to be determined. However, the use of an experimental basis set has a number of drawbacks. Firstly, the preparation and acquisition of the metabolite basis is a time consuming process, which requires many hours of scanning time. Secondly, performing quality assessment across multiple scanners can be difficult as an experimental basis set is likely to have some dependence on the scanner from which it was acquired. Thirdly, a minor change in an experimental protocol such as a different echo-time or an increase in field strength requires the re-acquisition of a completely new basis.

More recently, the use of a quantum mechanically simulated basis has been proposed which can potentially eliminate the drawbacks outlined above[4]. The purpose of this study is to asses the differences between using a simulated and experimental basis for the analysis of short echo MRS data performed at 1.5T.

Method

871 spectra were recorded on Siemens and GE scanners at the Birmingham Children's Hospital from patients with a suspected brain tumour or metabolic disorder. Spectroscopy was performed using a 30ms PRESS sequence at a field strength of 1.5T. Metabolite basis signals were simulated, using the density matrix formulation, to match the experimental conditions with in house software and imported into LCModel. Simulation parameters were used as published by Govinderaju et at[5]. Paired LCModel analysis was then performed on each spectrum using a simulated basis and the short echo experimental basis supplied with the LCModel package (acquired on a GE scanner). Results were imported into the R statistical package and a correlation coefficient was calculated for each metabolite.

Results

Figure 1 shows a good correlation between the experimentally acquired and simulated basis sets for the majority of metabolites. Myo-inositol has the best agreement between the two methods, whereas glutamate has the worst. These two metabolites are plotted in figures 2 and 3 and both show a convincing y=x relationship; this feature was also observed for all the metabolite quantities estimated. A number of outliers are clearly present in figures 2 and 3 and a closer inspection of these data revealed that these points originated from poor quality spectra.

Discussion

From figure 1, NAAG shows a poor correlation, which may be explained by its low value and interference with NAA. Overlapping signals are also likely to be the reason why the combined signal GPC+PC is more strongly correlated than the other metabolites. Interestingly, the addition of glutamate and glutamine does not improve their correlation as these signals are known to overlap heavily. It is possible that poor signal-to-noise or interference with baseline and broad macromolecular signals may be the cause of poor correlation for these signals. Despite having the worst correlation between basis sets, glutamate still shows a convincing y=x dependence in figure 3 implying that using a simulated basis set does not introduce bias in the estimation of this metabolite.

Conclusion

The use of a simulated basis for the analysis of 1H MRS data does not appear to introduce bias in the estimation of metabolite concentrations. This finding validates the use of simulated basis sets, potentially improving the consistency of metabolite quantities across field strengths and experimental parameters.

Acknowledgements

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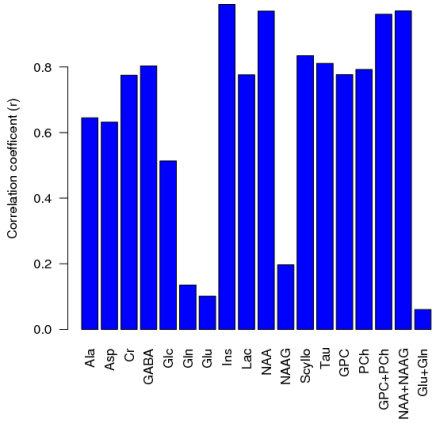

Figure 1 Correlation coefficients for each metabolite.

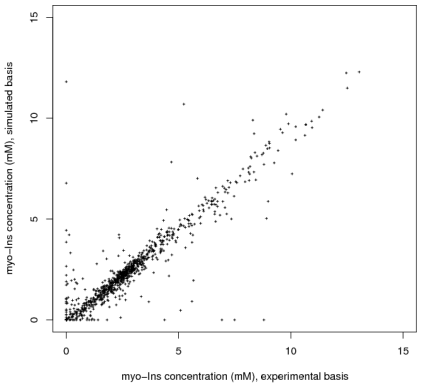

Figure 2 Myo-inositol scatter plot.

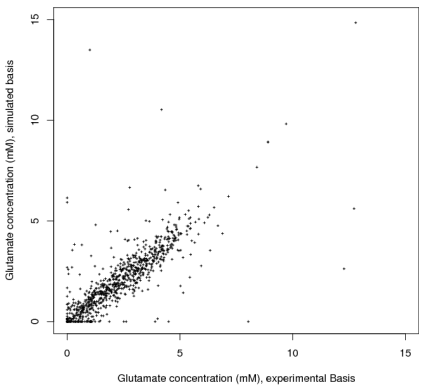

Figure 3 Glutamate scatter plot.

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