A Dynamic Susceptibility Contrast MRI Simulator for Determining Biomarker Accuracy

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Introduction

Dynamic Susceptibility Contrast (DSC-) MRI uses a gadolinium based contrast agent to assess perfusion within the brain[1]. There is variability in the quality of data acquired from different centres due to scanner and protocol differences, which makes obtaining robust biomarkers challenging. DSC-MRI is also susceptible to a range of artefacts such as patient motion and partial volume effects. Understanding how these factors affect the biomarkers calculated from DSC-MRI data is an important step in developing methods to improve biomarker accuracy.

Methods

DSC-MRI time courses were simulated in Matlab (version 9.4), using an adaptation of a model presented previously by Bjornerud et al[2], which accounts for DSC parameters, such as TR, TE, flip angle and temporal resolution. A range of artefacts, including noise, contrast agent leakage, motion and partial volume effects (PVE), have been simulated to allow assessment of data quality. SNR thresholds were determined from expert qualitative review of real DSC-MRI data. A selection of time courses from 10 different patient data sets were rated as good or poor quality. They were then ordered by SNR, which produced two threshold values of 5.5 (below which all patient data failed) and 7.6 (above which all patient data passed). These thresholds were then tested by the simulator. 6x6 grids of purely GM or WM were simulated. Noise was added to replicate the thresholds and % error in rCBV was calculated. rCBV was obtained by trapezoidal integration of a gamma variate fit to the first pass of the concentration time curve[3]. A full brain model, containing a mixture of GM, WM and CSF, was simulated. Motion artefacts and PVE were added.

Results and Discussion

Table 1 shows the median percentage error in rCBV for WM and GM at the two SNR thresholds. The percentage error in rCBV is greater in WM, due to it being less perfused than GM so that noise has a greater effect on the time course. Several time courses produced a larger change in rCBV than expected due to the time course being too noisy to fit a gamma variate to. Figure 1 shows the whole brain model simulating PVE.

Tissue	Median SNR	Median % Error in rCBV
Grey Matter	5.8	9.9%
	7.6	7.3%
White Matter	5.8	20.0%
	7.3	9.5%

Table 1: Effect of SNR on rCBV in GM and WM.

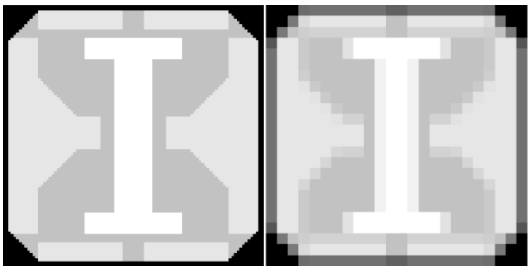

Figure 1: (L) Whole brain model. (R) PVE.

Conclusion

A DSC-MRI simulator, capable of simulating multiple artefacts found in DSC-MRI data, has been developed and used to validate threshold values for SNR, determined from previous work. Future work will involve incorporation of more artefacts, such as susceptibility artefacts, and generating test data sets for machine learning applications.

References [1] P. B. Barker et al, Clinical perfusion MRI: techniques and applications, Cambridge University Press, 2013. [2] A. Bjornerud et al., Journal of Cerebral Blood Flow & Metabolism, 2011, 31, 2041-2053. [3] M. S. Shiroishi, et al., *Journal of Magnetic Resonance Imaging*, 2015, 41, 296-313

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