Assessing the impact of excluding a subset of the diffusion acquisition on the resultant fractional anisotropy values in the preterm brain

Antonios Makropoulos[1], Gareth Ball[2], Joseph V. Hajnal[2], A. David Edwards[2], Daniel Rueckert[3], and Serena J. Counsell[2]
[1]*Centre for the Developing Brain, Imperial College London, London, London, United Kingdom,* [2]*Centre for the Developing Brain, King's College London, London, London, United Kingdom,* [3]*Biomedical Image Analysis Group, Department of Computing, Imperial College London, London, London, United Kingdom*

Introduction

Diffusion tensor imaging (DTI) provides a valuable tool to assess white matter development and injury in the developing brain. However, acquiring diffusion data in uncooperative infants is challenging, particularly due to image artefacts resulting from infant motion. A potential strategy to deal with infant motion in DTI data is to remove the individual diffusion acquisitions that are corrupt. Such strategies have been explored in the adult brain[1,2] .The aim of this study was to assess the impact of removing a subset of the diffusion acquisition on the resultant FA values in preterm infants.

Subjects

We studied DTI data acquired in 6 premature infants born at a median gestational age 26^{+5} (25^{+3}-30^{+4}) weeks and imaged at 31^{+1} (29-33) weeks. Single-shot echo planar DTI was acquired in 32 non-collinear directions with a b value of 750 s/mm^2.There was no evidence of motion artefact in any of the DTI data used in this study.

Methods

For each of the subjects' DTI data, a number of diffusion gradient directions, up to a maximum of 8, were randomly selected and excluded from subsequent analysis. The process was repeated with different combinations to form sets of images S_1, .., S_8 with 1, .., 8 directions removed for each subject. Analysing all the possible combinations is extremely computationally intensive even for a single subject. We acquired a number $N\{S_d\}$=100 of images at each set (apart from S_1, where $N\{S_1\}$=32 with all the possible combinations) for every subject. The FA map of each of the sample images is then calculated individually. The proposed pipeline is presented in Fig.1.

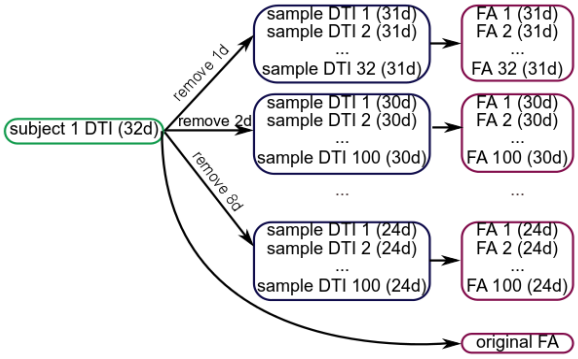

Fig.1: Direction removal pipeline

Results

An initial pairwise analysis quantified the difference between each sample FA map and the original FA_{all} maps obtained using all of the diffusion data. Cross-correlation is decreased with increasing number of omitted directions. Fig. 2 presents the average absolute difference of the FA maps when 7 directions are omitted, across the subjects' samples. The majority of the voxels with larger difference from the FA_{all} map are observed in the csf and csf-gray matter boundary. 6% of the sample images' voxels have absolute relative difference > 20% when 7 directions are removed.

Permutation testing was further performed to assess the exchangeability of the FA_{all} map with the different sets S_1, .. , S_8. The significance of difference among the FA_{all} images and the different sets S_1, .. , S_8 was assessed by performing an unpaired t-test of the FAall map against each data set with excluded diffusion data. When 8 directions are removed the resultant FA values are significantly different ($p < 0.05$) from FA_{all}. Table 1 demonstrates the results of the data analysis.

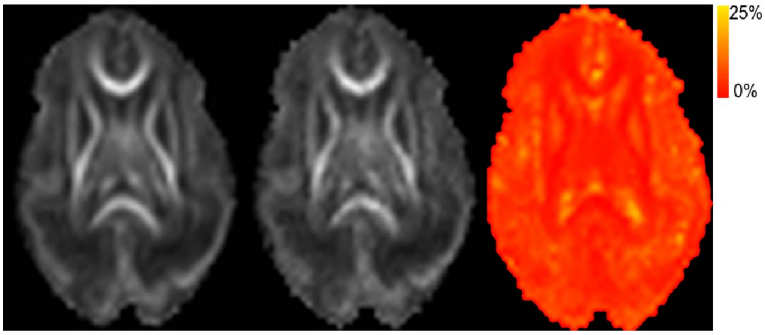

Fig. 2: Average FA map of the subjects with all the directions(a), with 7 directions removed (b) and the average absolute relative difference between the two maps

Number of directions removed (number of images)	Average crosscorrelation (standard deviation)	Percentage of voxels with absolute relative difference > 20%	Minimum p-value of difference with permutation testing
1 (192)	0.946 (0.064)	0.00375	0.152
2 (600)	0.921 (0.073)	0.00947	0.109
3 (600)	0.899 (0.082)	0.01795	0.129
4 (600)	0.873 (0.100)	0.02584	0.099
5 (600)	0.851 (0.113)	0.03720	0.109
6 (600)	0.829 (0.124)	0.04847	0.089
7 (600)	0.818 (0.124)	0.06106	0.069
8 (600)	0.799 (0.132)	0.07508	0.040

Table 1. Analysis results with increasing number of directions removed

Conclusion

Removing up to 7 out of the 32 diffusion acquisitions per dataset has little impact on the resultant FA in major white matter tracts compared to the original FA generated from all of the acquired data. Largest differences of the sample maps were observed in the areas of csf and csf-gm boundary. Future work will be focused on stability effects on a larger cohort of subjects, however these data suggest that, if a limited subsample of the diffusion data is corrupt, it is possible to discard these data from a neonatal DTI sample without impacting on calculated FA values.

References

1. Chang LC et al, RESTORE: robust estimation of tensors by outlier rejection, 2005, *Magnetic Resonance in Medicine*.
2. Hans-Peter Müller et al, Stability effects on results of diffusion tensor imaging analysis by reduction of the number of gradient directions due to motion artifacts: an application to presymptomatic Huntington's disease , 2011, PLoS currents