Impact of Outliers in DTI and Q-Ball Imaging - Clinical Implications and Correction Strategies

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Background

Corrupted images are often found to occur in diffusion-weighted magnetic resonance imaging (DW-MRI) using ultra fast sequences such as Echo Planar Imaging (EPI). These artifacts may originate from patient motion [1], physiological-related fluctuations [2], electrostatic discharge (spiking artifact) [3] and magnetic gradients causing patient table vibrations in specific directions [4]. Among the artifacts are those characterized by large, unpredictable signal variations within one or several slices of a DW volume (Figure 1a). As a result, diffusion tensor imaging (DTI) and q-ball imaging (QBI) data may be biased in an uncontrolled manner, leading to an impact on clinically-relevant metrics such as fractional anisotropy (FA), generalized FA (gFA) [7] and principal directions extracted from DTI and QBI. The purpose of this study was to measure the impact of outliers arising within DW-MRI data and to propose a robust method to correct for them. While other groups have previously investigated data corruption and correction in DW-MRI [5,6], the effect of outliers in standard clinical analysis remains unaddressed, as does their impact in more advanced reconstruction methods, like QBI.

Methods

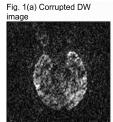
Monte Carlo simulations were first performed to evaluate the effects of outliers on DTI and QBI reconstruction [8] in a single voxel for both single fibre (Figure 2a,b) and crossing fibre (Figure 2c,d) scenarios. Second, a method to detect and correct these outliers in real data was implemented and validated in healthy subjects. This method included a quantitative comparison between the complete removal of corrupted volumes and the interpolation of those volumes in q-space for several different numbers of diffusion directions (12. 16. 32. 64). For QBI, the diffusion orientation distribution function (ODF) was computed using a spherical harmonics basis of order 6 and regularization lambda = 0.006 [8]. The impact of outliers was assessed by comparing the metrics FA (DTI), generalized FA (QBI) and principal eigenvector (PEV) dispersion (DTI/QBI) along the pyramidal tract, for cases with and without corruption. The effectiveness of the g-space interpolation method was verified by manually corrupting a series of previously uncorrupted DW data sets and comparing the resulting metrics with their original values before and after correction. The use of uncorrupted data as a baseline assured confidence in the derived metrics. All data were acquired as part of European Union (EU) Framework Programme (FP) 6 - GENEPARK: Genomic Biomarkers for Parkinson's Disease.

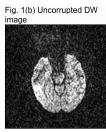
Results

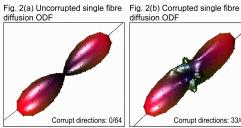
Outlier detection and q-space interpolation methods were successful in identifying corrupted voxels and restoring them to values consistent with those of uncorrupted images (Figure 1b). Those data sets containing a larger number of gradient directions (eg. 32, 64) were found to be less sensitive (< 10% change in FA/gFA/PEV values) to the removal of outliers than smaller data sets, and hence also less likely to benefit from correction by q-space interpolation. For smaller sets (eg. 12, 16), outlier removal was either impossible due to the limited number of volumes available for diffusion tensor/QBI reconstruction, or resulted in unreasonably large changes in DTI/QBI metrics (>10% change in FA/gFA/PEV values), making q-space interpolation a worthwhile alternative to complete volume removal.

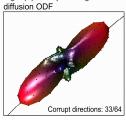
Summary/Conclusion

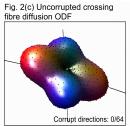
From the results obtained in this study, data processing strategies are proposed with which a robust assessment of corruption may be made (based on the number of gradient directions acquired and the extent of corruption in terms of volumes/slices detected within a data set), and from which an appropriate correction strategy may be selected and applied in a clinical setting.

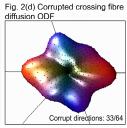












[1] Aksoy M, Liu C, Moseley ME, Bammer R. MRM, 2007; 59(5):1138-1150. [2] Kharbanda HS, Alsop DC, Anderson AW, Filardo G, Hackney DB. MRM, 2006; 56: 334-339. [3] Chavez S, Storey P, Graham SJ. MRM 2009; 62(2): 510-519. [4] Gallichan G, Scholz J, Bartsch A, Behrens, TE, Robson MD, Miller KL. HBM 2009. [5] Neithammer M, Bouix S, Aja-Fernandez S et al. MICCAI 2007; Part I, LNCS 4791:161-168. [6] Chang L, Jones DK, Pierpaoli C. MRM, 2005; 53: 1088-1095. [7] Tuch DS. MRM, 2004; 52(6):1358-72. [8] Descoteaux M, Angelino E, Fitzgibbons S, Deriche R. MRM, 2007; 58(3): 497-510.