

Automated Image Quality assessment for Diffusion Tensor Data

J. Meakin¹, S. Counsell², E. Hughes³, J. V. Hajnal³, and D. J. Larkman³

¹Physics Department, Imperial College London, London, United Kingdom, ²Imaging Sciences Department, Clinical Sciences Centre MRC, London, United Kingdom, ³Imaging Sciences Department, Imperial College London, London, United Kingdom

Introduction: DTI studies can generate large numbers of images which are combined to calculate diffusion properties (typically between 1500 and 9000 images per examination). Whilst single shot EPI is fast enough to "freeze out" most motion, individual diffusion weighted images can still be damaged if

motion occurs on the timescale of a single shot. The increased motion sensitivity generated by the diffusion gradients increases the likelihood of this. Motion between acquisitions can be corrected by image registration approaches but individually damaged images are generally uncorrectable (figure 1). DTI data is almost always oversampled, the diffusion tensor can be estimated from a minimum of 6 diffusion weighted images but typically 32-128 measurements are obtained to improve the robustness of the estimated tensor [1]. If a small subset of this data is then rejected the full tensor can still be estimated. Hence the challenge is to accurately and automatically identify such images from the large number of source images and reject them from the data set. Problems associated with motion are particularly prevalent when scanning babies (but can also be significant in some adult subjects). This work outlines an algorithm

designed to automatically identify damaged images in diffusion data. The program performs a standard pipeline of processing typical for DTI data prior to analysis. Registration, brain extraction followed by motion detection and data rejection. The novelty of this work

Figure 1 DTI image damaged by motion

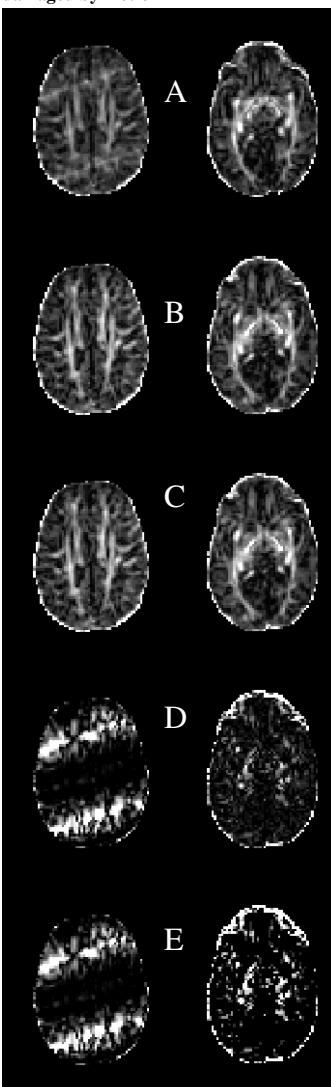


Figure 1 DTI image damaged by motion

lies in the data rejection step which calculates an estimate of the diffusion data using a data driven forward model and then compares this prediction to the acquired data using 2D image correlation to identify outlier images. This is performed entirely as a pre-processing step making the approach compatible with all existing DTI analysis software unlike the voxelwise outlier rejection approach proposed by Chang et al [2]. The method has been tested on 9 preterm infant data sets and 9 adult data sets. These data sets were also manually inspected for damaged data and the results compared.

Methods: **Data Acquisition:** On the assumption that motion occurs in short spasms (generally true with babies) we acquired 64 direction DTI data in 4 sections of 16 directions. Each 16 direction block consists of 16 unique diffusion weighting directions equally spaced on the surface of a sphere. The sphere is rotated between each block such that the combined 64 direction block has all directions also equally spaced on the surface of a sphere. This scheme ensures that if there is an extended period of motion then this does not result in a large number of nearby diffusion gradient directions missing, which would result in significant bias. **Data processing:** The 4 block data is read and assembled into blocks of data associated with individual slices (65 images per slice; 4 b=0 and 64 DT directions). These images were registered using an affine registration [3] and then stripped of the skull information using BET [4]. The target registration space was the first b=0 image acquired, due to the absence of diffusion weighting the b=0 image is extremely robust to motion (not damaged in the 18 data sets we investigated). The registered data is then used in its entirety to calculate the full diffusion tensor (which includes information from damaged slices) the combination of the mean b=0 image and the diffusion tensor is then used to estimate what the diffusion weighted images should look like given this tensor. In this way we create a prediction of the individual diffusion weighted images. The next step is to compare the measured diffusion data to this new prediction. We use a 2D correlation metric r (equation shown, where A and B represent pixel values in the pair of images and m and n are the 2D indices of the pixels): this generates a single number per image where 1 indicates an identical image. An automatically generated threshold is applied for each slice and any pair with a lower correlation is rejected. A second iteration of the process can then be started with a new estimate of the tensor to identify further outliers. The output data can then be read into any standard DTI analysis software package for subsequent analysis. The user is also presented with plots which show the registration parameters and locations of rejected images as a function of time as well as information regarding the number, location and b-value of rejected data. From this a rapid qualitative assessment can be made by the user as to the overall validity of the data. Automated warnings are generated to alert the user to any significant potential bias due to a sparse region of diffusion space or a large amount of rejected data.

$$r = \frac{\sum_{m} \sum_{n} (A_{mn} - \bar{A})(B_{mn} - \bar{B})}{\sqrt{\left(\sum_{m} \sum_{n} (A_{mn} - \bar{A})^2 \right) \left(\sum_{m} \sum_{n} (B_{mn} - \bar{B})^2 \right)}}$$

Results: 6 baby datasets were manually inspected and automatically analysed [see table 1]. The automated algorithm identified all the images which had been labelled as damaged by manual inspection. In many cases it also identified further images which on a second visual review were also seen to be damaged but not picked up in the first inspection. Examples of FA maps are shown from two subjects figure 2.

Table 1. 6 neonatal subjects (I-VI) Col A - number of images identified as corrupt by visual inspection. B number identified by algorithm. C those identified manually but not by algorithm. Each data set contained 3136 images in total

Conclusions: The impact of the damaged data on the initial estimate of the diffusion tensor is diluted because of the over sampling inherent in the acquisition and so tends to be reasonable. The estimate is refined in the manner described enforcing consistency between the forward model prediction and the measured data. Images near the very top and very bottom of the brain were excluded due to an intrinsically low image correlation which artificially biased any threshold determination step. This is a weakness of the method but we also found that manual detection also performs erratically in these regions. The time saving inherent in an automated selection is huge (up to 40 mins per subject to review subjects where significant motion is present) and we believe this alone, given the evidence of accuracy presented, gives the approach merit.

Acknowledgements: Nuffield foundation for grant funding. **References:** [1] Jones DK, MRM 51:807 (2004)[2] Chang et al MRM 53:1088-1095 (2005) [3] Jenkinson M, Medical Image Analysis, 5:143 (2001). [4] Smith SM, Human Brain Mapping, 17:143 (2002).

Data Set	A	B	C
I.	2	4	0
II.	31	33	0
III.	45	57	0
IV.	11	11	0
V.	125	146	0
VI.	46	48	0

Figure 2 Preterm infant data: The FA map calculated without any data rejection (A) with manual rejection (B) and automated (C). It can be seen that the automatic and manual detection results are identical for subject 1 (LHS, 1 image rejected) and slightly improved by automatic processing in subject 2, (RHS, 1 image rejected manually, 2 automatically) . D and E show A-B and A-C respectively.