Registration of high b value diffusion images

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Introduction:

High b value diffusion imaging has been suggested to provide an enhanced contrast toward different cellular components. Combined with an appropriate model, the analysis of low and high b value diffusion images may provide a comprehensive tissue characterization. Q-space imaging (*1*), DSI (*2*), hybrid imaging (*3*) and the composite hindered and restricted model of diffusion (CHARMED) (*4*) are alternative models to DTI that utilize high b value diffusion imaging. Despite the great advantages of high b value diffusion images, they suffer from low signal to noise ratio. In b values higher than 3000-4000 s/mm^2 only small portions of white matter (those exhibiting restricted diffusion along the encoding gradient) are visible. This feature of high b value diffusion images precludes the ability to perform motion/distortion correction of these images by registering to the non-diffusion-weighted data, and hence the credibility of the calculated results using such an approach decreases dramatically. In this work we suggest a framework based on both experimental data (DTI) and simulations (using the CHARMED framework) to register the high b value diffusion images.

Methods

Subject and image acquisition: The study consisted of 14 healthy young subjects (20-40 years) scanned on a 3T (GE) MRI system. The MRI protocol included whole brain DTI and CHARMED acquisitions. DTI was sampled along 19 gradient directions with a b value of 1000 s/mm^2 and additional b=0 images. CHARMED was acquired in a multi b-shell acquisition with increasing number of gradient directions with the increase in b value. The maximal b value was 6,000 s/mm^2 and number of directions was varied between 34 and 200.

DTI image analysis: The images were corrected for motion using SPM2 with appropriate reorientation of gradient vectors. DTI analysis was performed to generate diffusion tensor and FA maps.

High b value DWI template simulation: Direction and b value specific templates for each subject were generated using the CHARMED framework. CHARMED analyzes high b-value images and decomposes the diffusion signal into hindered (modeled by a diffusion tensor) and restricted (modeled by diffusion within impermeable cylinders) diffusion components. The CHARMED framework includes several parameters: the volume fraction of the restricted component (f_r), the diffusivity and orientation of the restricted component (D_r, ϕ and θ) and the diffusion tensor of the hindered component (D_h).
In the following work, we **inversely** used the CHARMED model to simulate high b value diffusion image templates, using the diffusion tensor data to provide an estimate of D_h, while D_r was estimated at 1μm^2/ms. F_r was predicted from FA data as these two parameters were found to be linearly correlated (Fig. 1). This procedure yielded template images that simulated the contrast seen in diffusion weighted images acquired at different b values and gradient directions in the native image space of each subject.

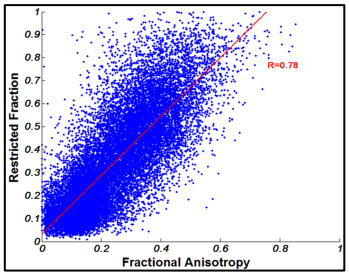

Figure 1: The correlation between FA of DTI and f_r of CHARMED.

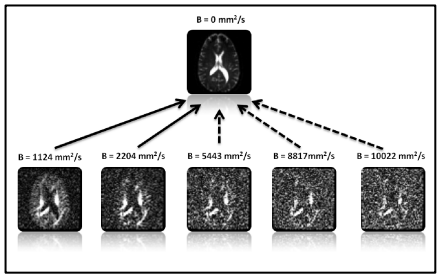

Figure 2: High b value data at different b values showing the issue of contrast change when acquiring DWIs with b>3000 s/mm^2.

Image registration: Each acquired high b value image was then registered to the matching high b value template (generated from the DTI images and the CHARMED simulation) using SPM2 with a 6 parameter affine transformation.

Data Analysis: To demonstrate the utility of the new motion/distortion correction procedure, the corrected high b value diffusion images were analyzed using the CHARMED framework described previously (*5*).

Results & Discussion:

Figure 2 shows a typical high b value diffusion data set acquired along the same gradient direction but for different b values. It is evident that the image contrast is not comparable between the different b values and that conventional registration routines (that rely on matching the image contrast to that of the non-diffusion-weighted images) will fail. Fig. 3 shows an example for the high b value registration procedure with a high b value template image (b=6000 s/mm^2) compared with the original acquisition at the same gradient direction and the corrected image following registration. CHARMED analysis indicated that following motion correction much better optimization was achieved (Fig. 4). By integrating the suggested pipeline with a model-based eddy-current distortion correction, further improvements in chi-squared can be observed [6].

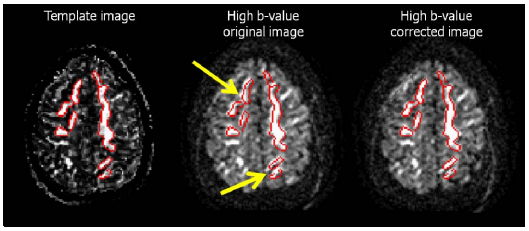

Figure 3: Example of high b value motion correction. (left) subject, direction and b value specific template, (mid) the acquired DWI and (right) the corrected volume. Yellow arrows indicated regions of motion artifact.

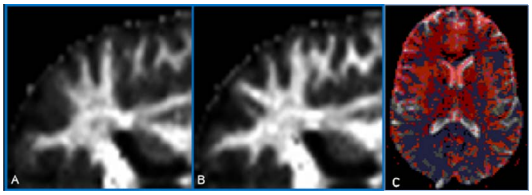

Figure 4: F_r images calculated from non-corrected (A) and corrected (B) dataset. (C) Chi-square analysis of images before and after motion correction showing reduction in the fitting residuals at the red regions.

Conclusion:

This new approach addresses a long-standing problem with high b-value diffusion imaging and makes correction of motion and distortion feasible for the first time. This will open an opportunity to explore and compare the abilities of the different high b value approaches in tissue characterization and disease diagnosis.

1. Y. Assaf *et al.*, *Magn Reson Med* **47**, 115 (Jan, 2002).; 2. D. S. Tuch, T. G. Reese, M. R. Wiegell, V. J. Wedeen, *Neuron* **40**, 885 (Dec 4, 2003). 3. Y. C. Wu, A. L. Alexander, *Neuroimage* **36**, 617 (Jul 1, 2007).; 4.Y. Assaf, P. J. Basser, *Neuroimage* **27**, 48 (Aug 1, 2005).; 5. Y. Assaf, R. Z. Freidlin, G. K. Rohde, P. J. Basser, *Magn. Reson. Med*, (2004). 6. S. De-Santis, Proc. ISMRM, submitted.