Motion and eddy-current correction in high b-value diffusion MRI: Systematic registration errors and how to avoid them

Markus Nilsson[1], Filip Szczepankiewicz[2], Danielle van Westen[3], and Oskar Hansson[4]

[1]*Lund University Bioimaging Center, Lund University, Lund, Sweden,* [2]*Dept. of Medical Radiation Physics, Lund University, Sweden,* [3]*Dept. of Diagnostic Radiology, Lund University, Sweden,* [4]*Clinical Memory Research Unit, Dept. of Clinical Sciences Malmö, Lund University, Sweden*

Introduction: Due to subject motion and the eddy-current induced image distortions occuring during the acquisition of high angular diffusion imaging (HARDI) data, the first step of a post-processing pipeline is to perform motion-correction of the data. The simplest approach for this purpose, here referred to as conventional motion correction, is to register each of the diffusion-weighted volumes to a volume acquired with $b = 0$ s/mm^2. However, registration of high b-value ($b > 2500$ s/mm^2) volumes to the non-diffusion encoded reference suffers from poor accuracy [1]. When tractography is performed based on high b-value data, and parameter maps such as the fractional anisotropy (FA) and mean diffusivity (MD) are inferred from low b-value data ($b \leq 1000$ s/mm^2), inaccurate registrations could produce substantial quantification errors. The purpose of the present work is to first, demonstrate the influence of systematic registration errors between low and high b-value data in tractography based on high b-value diffusion MRI. Second, we suggest a method that can eliminate this registration error by using low b-value data to extrapolate reference volumes for the high b-value data.

Method: Multi-shell diffusion MRI data were acquired in 43 elderly volunteers (65.2±8.5 years), using five shells with b = 0, 250, 500, 1000, and 2750 s/mm^2 that were distributed over 6, 6, 20, and 64 directions, respectively. Other imaging parameters were TR = 8100 ms, TE = 103 ms, voxel size of 2.3×2.3×2.3 mm^3. The data was motion corrected using two different methods, yielding two separate data sets. The first set employed conventional motion correction (C-MC), using affine registration to the first $b = 0$ s/mm^2 volume (ElastiX, [2]). The second set was registered using extrapolated references (extrapolation-based MC, EB-MC). The extrapolation was based on diffusion tensors calculated from the low b-value data after conventional motion correction. Two corrections were applied to the extrapolation procedure, in order to increase the similarity of the extrapolated and acquired volumes. The first correction separated the initial tensor $\mathbf{D}_{\text{init}}$ into the tissue component $\mathbf{D}_{\text{tissue}}$ and the cerebrospinal fluid component D_{CSF} $\mathbf{I}$, where $\mathbf{I}$ is the identity matrix, by assuming $\mathbf{D}_{\text{init}} = (1 - f_{\text{CSF}})\,\mathbf{D}_{\text{tissue}} + f_{\text{CSF}}\,D_{\text{CSF}}\,\mathbf{I}$. The calculation of $\mathbf{D}_{\text{tissue}}$ proceeded by first calculating f_{CSF} under two assumptions: $\text{Tr}(\mathbf{D}_{\text{init}})/3 = 0.8$ µm^2/ms and $D_{\text{CSF}} = 2.3$ µm^2/ms (set lower than the expected value of 3 µm^2/ms in order to stabilize the calculations). The second correction limited the signal attenuation of the tissue tensor by using the stretched-exponential model for the extrapolation, instead of the monoexponential model assumed in DTI, with α set to 0.80 [3]. Registration accuracy was evaluated by performing affine registration of FA-volumes calculated from the high b-value part (b = 0 and 2750 s/mm^2) of the data to those calculated from the low b-value part ($b \leq 1000$ s/mm^2). The FA was selected for this purpose because its contrast is nearly independent of the b-value. The effect on tractography was evaluated by analysing the two data sets using constrained spherical deconvolution (CSD), as implemented in MRtrix [4], with a maximum harmonic order of 8. CSD-based deterministic fiber-tracking (step-size 0.5 mm, FA > 0.1) was performed to extract a segment of the cingulum, from which the FA, calculated from the low b-value shells, was determined.

Results: At high b-values, we observed a shift in the border between image signal and background, especially in volunteers with mild to severe age-related atrophy that results in a rim of subarachnoid cerebrospinal fluid (CSF) surrounding the brain. While this rim is present in all of the low b-value data ($b \leq 1000$ s/mm^2), it is fully attenuated in the high b-value data ($b \geq 2500$ s/mm^2). Consequently, the conventional motion correction tend to match the border between the brain parenchyma and the background of the high b-value data to the border between CSF and background in the reference volume acquired with b = 0 s/mm^2 (Figure 1). This results in poor registration accuracy, which becomes apparent when comparing FA volumes from low and high b-value data for the C-MC set (Fig. 2). Quantified in terms of translation and scaling between these FA volumes, the registration error in the C-MC set amounted to 0.53±0.03 mm and 1.07±0.09%, 1.16±0.07 mm and 2.77±0.10%, and 0.40±0.05 mm and 2.18±0.15% in the x, y, and z-directions, respectively. For EB-MC, the corresponding average translations were all below 0.13 mm and scalings below 0.7%. When performing tractography, based on CSD-analysis of the high b-value shell, the poor registration accuracy of C-MC resulted in tracts shifted in position compared to DTI-results from low b-value shells (Fig. 3A). For the EB-MC set, the tractography of the cingulum was improved and resulted in high morphological agreement with the colour-FA map (Fig 3B). Comparing the FA in this segment of the cingulum, we first note that the FA values are generally higher with EB-MC, and second that EB-MC reduce the FA variability (Fig. 4). Mean and standard deviations of FA in the cingulum segment were 0.44±0.11 and 0.53±0.07 for C-MC and EB-MC, respectively.

Discussion: Our results shows that extrapolation-based motion correction substantially improves the outcome of tractography based on high b-value HARDI acquisitions. The concept of using the diffusion tensor to extrapolate a reference for motion correction of high b-value acquisitions has been employed previously [1], although without separating the diffusion tensor into two components representing tissue and CSF signals. This separation was instrumental to avoid registration errors between low and high b-value volumes. We also expect EC-MC to be advantageous for diffusional kurtosis imaging (DKI), in agreement with preliminary data (not shown).

Conclusions: Motion and eddy-current correction of high b-value dMRI data using non-diffusion encoded volumes can introduce substantial registration errors, potentially deteriorating the statistical power of group comparisons. Extrapolation-based registration alleviates this problem, and should be incorporated in the post-processing of high b-value diffusion MRI data.

References: [1] Ben-Amitay S, Jones DK, Assaf Y (2011) *Magn Reson Med* 67:1694–1702. [2] S. Klein, et al. (2010) IEEE Trans Med Imag 29:196–205 [3] Bennett KM et al. (2003) *Magn Reson Med* 50:727–734. [4] Tournier JD, et al (2012) *Int J Imaging Syst Technol* 22:53–66.

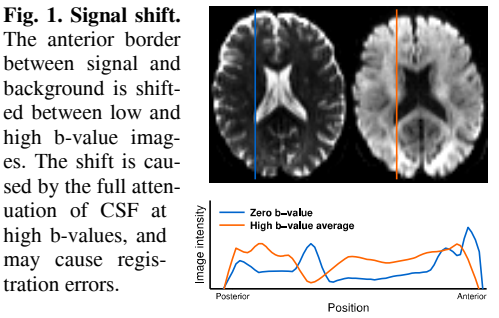

Fig. 1. Signal shift. The anterior border between signal and background is shifted between low and high b-value images. The shift is caused by the full attenuation of CSF at high b-values, and may cause registration errors.

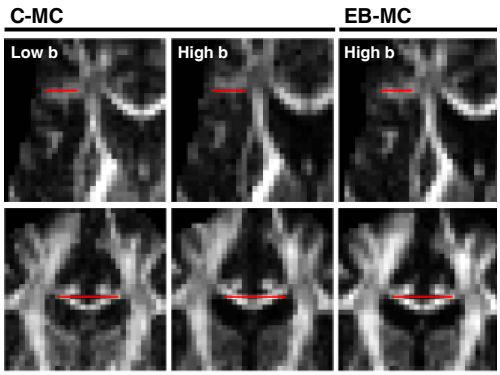

Fig. 2. Registration accuracy. With C-MC, the FA volume calculated from high b-value data is shifted in the anterior and superior directions (red line is positioned in a fixed position). This error is non-existent for EB-MC.

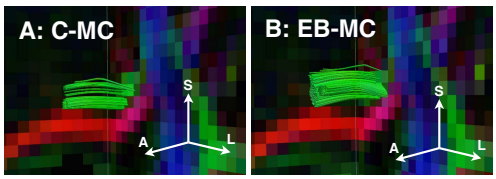

Fig. 3. Influence of choice of MC method on cingulum tractography. Using C-MC (A), the bundle is thin and shifted inferiorly compared to what is expected from the color-FA map. For EB-MC (B), the bundle is thick and its position is in agreement with the parameter map.

Fig. 4. Correlation between FA for the two MC methods. With EB-MC, FA values were generally higher, and exhibited a 38% lower standard deviation compared to C-MC. Line of unity shown in thick black.