Potential Misinterpretation of Diffusion Tensor Imaging Data due to Head Motion

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Introduction: Diffusion Tensor Imaging (DTI) has become increasingly important in the assessment of many neurological diseases and in studying and gaining further understanding of healthy human brain development and aging. DTI provides many quantitative parameters, in particular, fractional anisotropy (FA), being one of the most used indices derived from DTI acquisitions [1], which reflects white matter integrity. Changes in FA values due to brain abnormality have been reported. Previously, we introduced volumetric navigators [2] to perform prospective motion correction in (DTI). The purpose of this study is to highlight misinterpretation of FA that may result due to subject head motion as well as to compare the performance of retrospective motion correction to prospective motion correction with reacquisition of motion corrupted diffusion volumes.

Methods: A twice-refocused two-dimensional diffusion pulse sequence was previously modified to acquire a 3D-EPI navigator (526 ms) following the acquisition of each diffusion volume. The volumetric navigator contains 3D anatomical information for direct computation of motion parameters in which the accuracy of co-registration and motion estimates are not affected by the diffusion gradients even at high b-values. The diffusion sequence has been further modified to reacquire motion corrupted diffusion volumes during which the motion exceeded a pre-defined threshold. The maximum number of reacquisitions is specified by the user at the start of the scan, depending on the amount of extra time that can be tolerated.

Six healthy adult subjects (age 24-30 years) were scanned on a Siemens Allegra 3 T (Siemens Healthcare, Erlangen, Germany) scanner. Each subject was first scanned with the structural MPRAGE imaging sequence. This was followed by different diffusion acquisitions: an *at rest* baseline scan acquired with the standard diffusion sequence (**NoMo_basic**); a scan during which the subject moved acquired with the standard sequence (**Mo_basic**); and a scan during which the subject moved acquired using the navigated diffusion sequence with prospective motion correction and reacquisition (**Mo_vNav_all**). For the scans with motion, the subjects were instructed to change their head position upon verbal instruction five to six times during the scan. The subjects were asked to repeat the same movements for all the scans with motion. The diffusion data from the **Mo_basic** scan were analysed after retrospective motion correction **(Mo_basic_retro**).

The navigator parameters were the same for all navigated diffusion scans. The acquisition parameters for the navigator were: TR = 14 ms, TE = 6.6 ms, voxel size = 8 x 8 x 8 mm^3, acquisition matrix size = 32 x 32 x 28, FOV 256 x 256 x 224 mm^3, the bandwidth in the readout direction = 3906 Hz/pixel, flip angle = 2 degrees, and total scan time = 406 ms. The acquisition parameters for the diffusion sequence were: TR = 9500 ms without the navigator (basic sequence), TR = 10026 ms with the navigator (vNav sequence), TE = 86 ms, 72 slices, matrix size = 112 x 112, single channel birdcage head coil, slice thickness = 2 mm, 30 non-collinear diffusion gradient directions, b-values 0 and 1000 s mm^{-2}, four low b-value scans, and reacquisition was enabled with five reacquisitions.

The T1 weighted images for each subject was automatically segmented into cortical and sub-cortical regions using FreeSurfer (http://surfer.nmr.mgh.harvard.edu/) software library. From the atlas, the whole-brain white matter (WM) was determined. The diffusion data of the six subjects were quantified using the Diffusion Toolkit (http://trackvis.org/dtk/) software library, which generates all the diffusion maps. The FA maps were registered to T1 space using FMRIB's linear registration tool (FLIRT) and followed by a non-linear registration using FMRIB's non-linear image registration tool (FNIRT). Retrospective motion correction was only performed on the **Mo_basic** scan using FMRIB's linear registration tool (FLIRT). The FA histogram parameters of the WM were computed for the different scans for all six subjects. The WM histogram for each scan was compared with those of the *at rest* baseline (**NoMo_basic**) scan using a paired student's t-test. P-values less than 0.01 were considered statistically significant.

Results: Table 1 gives the mean FA histogram parameters for the WM for all six subjects, for the different acquisitions, as well as the values obtained after applying retrospective motion correction. The histograms of the six subjects for each scan were averaged and normalized to the number of pixels (Fig. 1).

It is clear from Table 1 that motion causes a significant reduction in the mean FA of the whole WM. It is also evident that retrospective motion correction causes further significant reduction. The FA histogram parameters changed significantly with motion and retrospective motion correction: both kurtosis (the curve becomes more peaked) as well as skewness (the curve becomes more asymmetric) increases and there is a significant leftward shift in the FA histogram peak location (Fig. 1). Interestingly, a study of traumatic brain injury (TBI) using diffusion tensor imaging was performed by Benson et al [3]. This group looked only at the global white matter histograms and it was reported that patients' FA histograms were globally decreased compared with control histograms. The shape of the TBI histograms also differed from controls, being more peaked and skewed with a leftward shift in the FA histogram peak location. Another study that was carried out by Cercignani et al [4] analysed the whole brain histogram FA and MD in patients with multiple sclerosis. It was found that patients with multiple sclerosis have significantly lower histogram average fractional anisotropy and peak location, and significantly higher peak height.

Conclusion: Subject motion can cause significant changes in DTI parameters. Retrospective motion correction does not recover the data but rather causes further changes. Prospective motion correction using the 3D-EPI navigator with reacquisition of severely motion corrupted volumes improves the diffusion data remarkably, almost fully recovering baseline values. The additional scan time for the navigator is 526 ms for each diffusion TR, which was 9500 ms in the current protocol. Each reacquisition (5 in the current protocol) requires one additional TR of 10026 ms.

Figure 1. Normalized whole-brain white matter histogram FA averaged for the six subjects compared for the different scans.

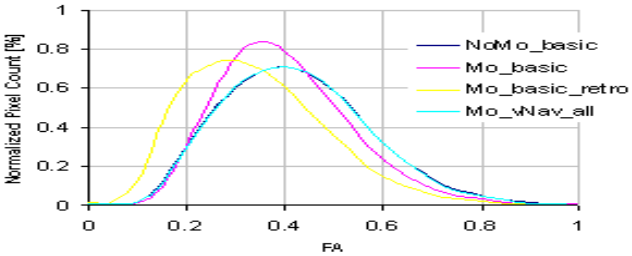

Table 1. Comparison of the whole-brain white matter FA histogram parameters averaged for the six subjects for the different scans.

WMH- FA Parameters	NoMo_ basic	Mo_ basic	Mo_basic _retro	Mo_vNav_ all
Mean FA	0.43	0.40*	0.36*	0.42
Peak Location	0.39	0.35*	0.3*	0.39
Skewness	0.53	0.81*	0.64*	0.55
Kurtosis	1.7	2.1*	1.8*	1.7

* $p<0.01$ paired student's t-test.

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