Mapping residuals along tracts: An effective quality control approach for tract specific measurements

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Target audience: Neuroimaging researchers and investigators involved in diffusion weighted imaging (DWI) studies.

Background and Purpose: Diffusion tractography is a well-established neuroimaging technique for the investigation of white matter (WM) connections. Using tractography, neuroscientists have been able to use individual tracts as customized regions of interests that adapt to each subject anatomy. This has made the use of "tract specific" measurements a very powerful tool to investigate the living human brain in normal and pathological conditions. However, Diffusion-weighted (DW) signals are also prone to artifacts due to head movement, physiological noises or scanner related issues. Mapping the fitting residual either from the diffusion tensor (DT) or spherical harmonics (SH) decomposition of the acquired signal has been suggested as one way to identify artifacts and possibly correct them[1,2,3]. In this work we propose to extend the use of residual maps as auxiliary measure to be taken into account during tract specific analysis. By measuring the residual along tracts it could be possible to assess the quality of tracts measurement and identify outliers derived by artifacts not corrected during previous processing.

Methods: A dataset of 11 healthy subjects, mean age 32 ± 5 years, was selected from a pre-existing diffusion imaging study with two subjects presenting signal loss artifacts in the superior occipital/parietal regions of the brain. Data was acquired using a 3T GE HDx system (General Electric, Milwaukee, WI, USA) with the following parameters: voxel size 2.4x2.4x2.4 mm, slices 60, b-value 3000 s/mm2, 60 diffusion-weighted directions and 7 non-diffusion weighted volumes. DTI processing was performed using ExploreDTI, SH decomposition up to order 6 (SH6) was obtained using custom written Matlab code. An Euler-like tractography algorithm was used for streamline propagation with a fractional anisotropy (FA) threshold of 0.2, angle threshold of 45 degrees and step-size 1 mm. Manual dissection of the left and right anterior segment, left long segment, left and right posterior segment, genu, body and right inferior fronto-occipital fasciculus were performed using Trackvis. The residual defined as difference between the fitted and the measured signals was computed for the DT and the SH models. The maximum residual value was computed for each voxel, obtaining maximum residual maps. Finally, the fractional anisotropy (FA), mean diffusivity (MD), DT and SH6 maximum residual maps were mapped along tracts and the average values of FA and MD and maximum values of DT and SH6 residuals were extracted. If a tract had a maximum residual two standard deviations higher than the mean across the subjects it was considered as an outlier.

Results: For the tracts listed above we identified those subjects (if any) which maximum residual value exceeded the defined threshold. Figure 1 displays the results of two tracts for SH6 residuals: Fig. 1a) refers to the right posterior segment, highlighting an outlier in the subject 11. The same subject, though, was not an outlier for the right anterior segment (Fig. 1b) suggesting that the tract was not intersecting a region with artifacts. Similarly subject 5 was an outlier for the second tract but not for the first one. The identification of outliers was not possible neither with the computation of the standard diffusion metrics (i.e. FA or MD) nor with the use of DT residuals. Overall, due to the high b-value acquisition, the DT residual map exhibited higher values mostly in regions of crossing fibers making difficult to identify outliers in the data. This confirms that residuals based on SH decomposition can be more sensitive to actual artifacts and less affected by the presence of complex microstructural organization of the tissue[1] (Fig. 2).

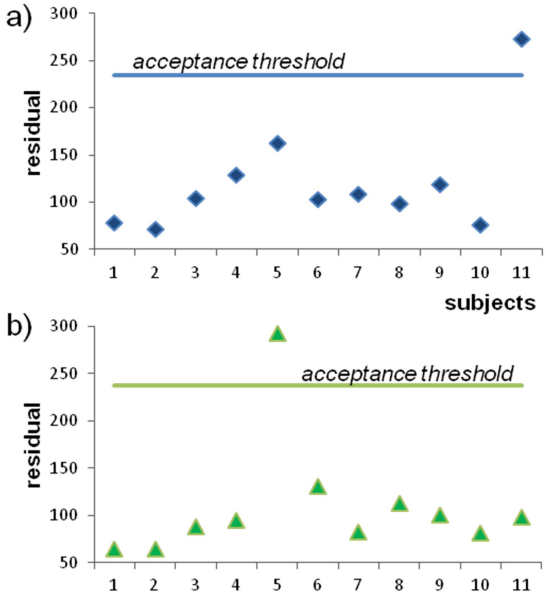

Fig 1. Examples of tract specific residual analysis obtained from SH6 fit. a) residual values of right posterior segment; b) residual value of right anterior segment. Acceptance threshold was defined as Mean+2*Standard Deviation across subjects for each tract.

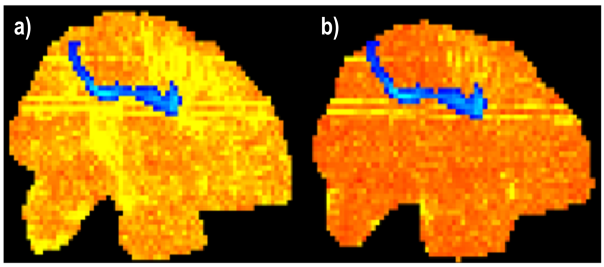

Fig 2. a) Density map of right anterior segment superimposed onto DT residual map. b) Density map of right anterior segment superimposed onto SH6 residual map.

Discussion and Conclusions: The proposed analysis allows a fast and effective quality control assessment of "tract specific" measurements by simply exploiting the value of fitting residuals. Depending on the considered tract, a subject could be included or rejected whether it is found to be or not an outlier for each specific tract. In this way, datasets considered completely unusable might be partially recovered for further analysis or datasets that may pass global quality control can be rejected more easily when looking at individual tracts. In conclusion**,** we propose this approach as a new way to perform data quality control for tract specific measurements.

References:

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