Microstructure-Informed Slow Diffusion Tractography in Humans Enhances Visualisation of Fibre Pathways

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Target Audience

This work evaluates the potential benefits of combining model-based, microstructural information with advanced fibre tracking and is of interest to scientists investigating the human connectome in relation with non-Gaussian diffusion models.

Purpose

Diffusion-based tractography exploits anisotropy of water molecular propagation due to macroscopic orientational ordering of axonal fibres. Usually, no microstructural information is required with fibre tracking algorithms. At high *b*-values, the signal is known to deviate from the mono-exponential function giving rise to the slow attenuation component. Several non-Gaussian diffusion models proposed to describe these deviations have been reported to provide deeper insights into microstructural tissue properties. However, such models were rarely combined with connectome estimations[1] and the potential of the combined approaches remains insufficiently explored. Our purpose was to elucidate the feasibility and potential benefits of the advanced "**m**icrostructure-**i**nformed" **s**low-**dif**fusion **f**ibre **t**racking (MI-SDIFT) method based on the biexponential analysis[2] of the diffusion-weighted signal in humans at 3T. In the frame of the established models, such as CHARMED proposed by Assaf and Basser (2005), MI-SDIFT refers to water fraction restricted in axons (in contrast to water in the intercellular space "sensed" in the range of low *b*-values). The results are compared with conventional DTI and constrained spherical deconvolution (CSD) reconstructions.

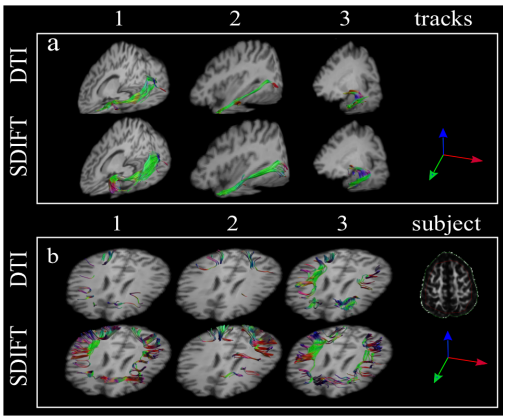

Figure 1. (a) inferior fronto-occipital (1), inferior longitudinal (2) and uncinate (3) fasciculi; (b) short association fibres for 3 subjects. The data is shown for termination criteria FA=0.2.

Materials and Methods

In vivo diffusion experiments were carried out with a whole-body 3T Siemens MAGNETOM Tim-Trio scanner using a double spin-echo EPI (2×2×2 mm^3; TE/TR, 113/1000 ms; number of slices, 72) in the range of $b \leq 6000$ s mm^{-2} for 6 and 30 gradient directions. Fibre tracking via the slow diffusion tensor was performed using the ExploreDTI streamline tracking routine[3] for three subjects to check on the stability of the results. The regions with crossing fibres were resolved using the constrained spherical deconvolution (CSD) algorithm introduced by Tournier et al. (2007).

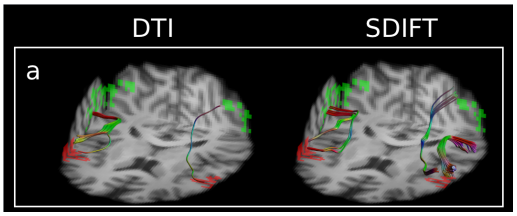

Figure 2. Fibres connecting Brodmann areas 44-45 and 39-40.

Results and discussion

The benefits of MI-SDIFT were analysed using several fibre tracking examples. Fig. 1 provides an overview of long (a) and short (b) association fibres. In particular, MI-SDIFT allowed us to reconstruct a significantly larger number (by factor 2 to 4) of fibre pathways constituting long association fibres than DTI; consider also an improved ("thicker") visual appearance of the fibres. MI-SDIFT enabled us to establish enhanced connectivity in the pre-cortical regions (this feature was stable for various fractional anisotropy (FA) thresholds terminating fibre tracks), Fig.1b. These benefits are due to significantly higher FA of the slow diffusion component that increases the reliability of estimated tensor orientations, especially, at the interfaces between white and grey matter tissues. One further example, Fig. 2a, demonstrates the fibres connecting the Brodmann areas 44-45 (Broca's region), red, with the Brodmann areas 39 - 40, green. These areas are involved, for instance, in language processing (Friederici, 2012) and might be important for understanding related deficits. Striking connectivity asymmetry is observed in DTI, whereas MI-SDIFT shows a more symmetric connectivity pattern. Finally, in the regions with complex white matter microstructure, MI-SDIFT has enabled us to visualise fibre "crossing" configurations with enhanced reliability, compare zoomed regions in Fig. 3.

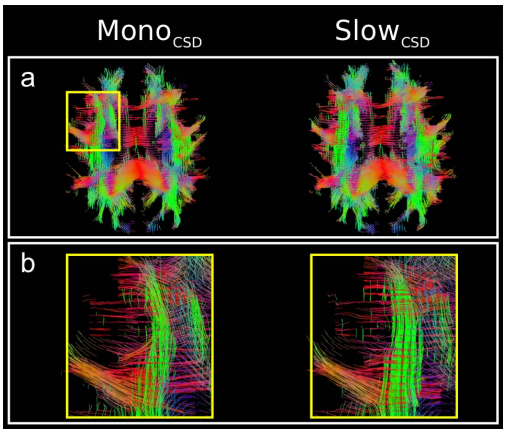

Figure 3. In both reconstructions ("mono" and "slow") using the CSD algorithm one can easily indentify the parts of fibres belonging to corpus callosum, corticospinal tract, superior longitudinal and fronto-occipital fascicule, as well as crossing regions.

Conclusions

In conclusion, advanced MI-SDIFT is a valuable complementary method that allows one to increase reliability of the evaluated fibre pathways and visualise more fibres, especially in pre-cortical areas where uncertainty of diffusion directionality in conventional methods tends to increase. Potential benefits can be expected in assessment of the residual axonal integrity in pathological tissues and in combined studies of functional and structural connectivity.

References

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