# A method for evaluating the similarity of HARDI-based fiber tracking methods

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**TARGET AUDIENCE** Researchers who are interested in brain Probabilistic Tractography

**PURPOSE** To develop a methodology for statistical tests of tractography. Tractography can be sensitive to a number of parameters. However, there are few methods for quantifying such sensitivity. We demonstrate a means for quantitative comparison of pathways by comparison with an ensemble of tracks. We apply the method to compare the results of two probabilistic tractography methods: a computationally intensive Monte Carlo (MC) approach[1] and fast partial differential equations (PDE) that is designed to rapidly replicate the results of the MC approach[2].

**METHODS** Six subjects (3 controls and 3 MS patients) were scanned under an IRB-approved protocol on a 3 tesla TIM-Trio with a standard 12-channel head coil (Siemens Medical Solutions, Erlangen) with high angular resolution diffusion imaging (2mm isotropic, 71 diffusion-weighting gradients with b=1000sec/mm² and 8 b=0 volumes, NEX=4). The transcallosal motor pathway was mapped in each subject by MC tractography using multi-voxel seed and target regions corresponding to hand motor regions, resulting in a track density map[1]. A center track was generated to characterize the track density map as a single curve in space[3]. A track density map and corresponding center track was then generated by PDE tractography between the same multi-voxel seed and target region in each subject. A *test ensemble* of center tracks was then generated by repeating the PDE tractography between pairs of single voxels in each seed and target region. MC and PDE tractography between the multi-voxel seed and target regions were then compared against the test ensemble by calculating the Hausdorff distance, a scalar measure of the similarity between curves.

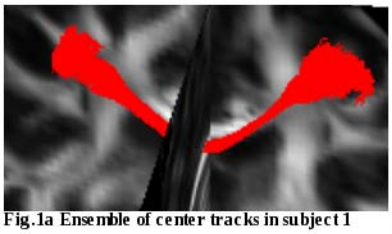


Fig.1a Ensemble of center tracks in subject 1

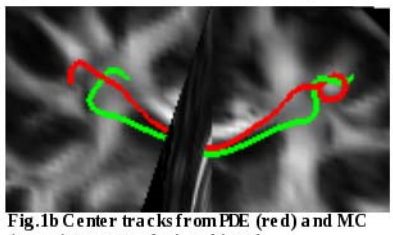
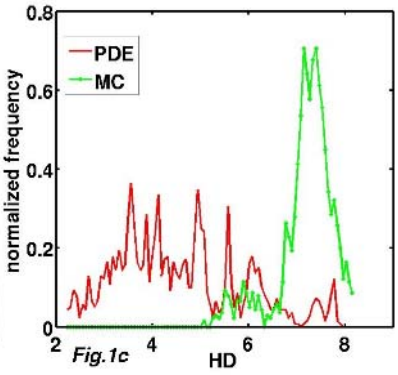


Fig.1b Center tracks from PDE (red) and MC (green) tractgraphy in subject 1



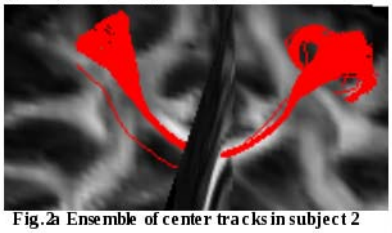



Fig.2a Ensemble of center tracks in subject 2

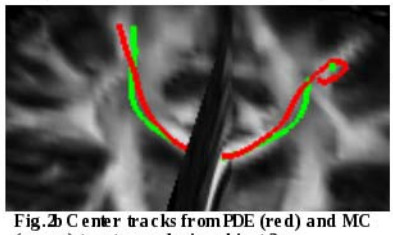
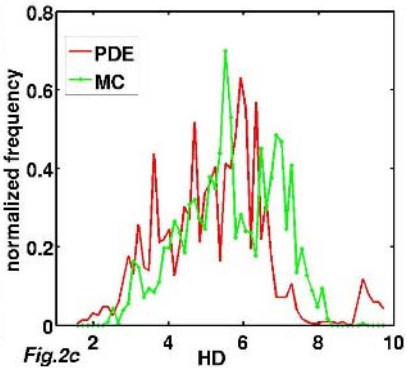


Fig.2b Center tracks from PDE (red) and MC (green) tractography in subject 2




**RESULTS** Fig. 1a shows the test ensemble generated from PDE tractography between pairs of single voxels in the seed and target regions. Fig. 1b shows the center tracks generated by the MC (green) and PDE (red) methods using multi-voxel seed and target regions. The distribution of Hausdorff distances between each of the tracks in fig. 1b and the ensemble in fig. 1a is shown in fig. 1c.Results from a second subject are shown in fig. 2.

**DISCUSSION** The lack of overlap in fig 1c suggests quantifiable differences between the MC and PDE methods in one subject while the overlap in fig 2c suggests similarity between pathways. In principle, a comparison such as a t-test could be used to quantify the degree of overlap. However, the pathways in each test ensemble are highly correlated, leading to a multiple-comparisons problem. Future work will examine corrections for multiple comparisons. Although the methods were applied to compare different tractography methods, they may be equally useful for between-subjects comparisons.

**CONCLUSION**

A general problem in tractography is a lack of quantitative tests. Typically, pathways are assessed by qualitative comparison against prior knowledge of anatomy. Here we lay the groundwork for quantitative comparison of track density maps generated by probabilistic tractography.

**REFERENCE**

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3. Mark J Lowe, Ken E Sakaie, Jian Lin, Lael Stone, and Micheal D Phillips, A Parametric Approach to Evaluating the Statistical Significance of Pathway Dependent Diffusion Measures. 20th Annual International Society for Magnetic Resonance in Medicine Meeting. Melbourne, Australia, (May 5-11, 2012).