The effect of computation strategy on fiber tractography metrics: A focus on fractional anisotropy and corpus callosum

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Introduction

The analysis of diffusion MRI metrics along pathways reconstructed with fiber tractography[1] (FT) (tractometry[2]) is becoming increasingly popular and reaching clinical application[3]. This kind of analysis requires, however, several computational steps and user choices, whose effect on the analysis step remains unknown.

In this work, we showcase the effect of two interpolation approaches and of three ways of assigning metrics to the points along a pathway on the reconstruction and quantitative analysis of the corpus callosum (CC) (Fig. 1a).

Subjects/Methods

Thirty subjects from the Human Connectome Project[4] were used for the analysis consisting of 18 volumes at b=0s/mm^2 and 90 volumes at b=1000s/mm^2.

Deterministic whole-brain DT-based FT was performed with a range of FA thresholds {0.1, 0.15, 0.2, 0.25, 0.3}, 1mm step size, 45° angle threshold, then the CC was delineated[5]. For each setting, FT was performed twice, calculating the FA at each point with DT- and FA-based interpolation. The FA was computed by averaging the FA values of each of pathways' points (denoted as "*plain"*), and by calculating the average and the weighted average FA on a voxel-basis. In the latter case, the weights were defined as the numbers of the unique pathways visiting each voxel, and the voxel assignment was performed both directly and using a Bresenham-like discretization algorithm[6] ("*Bresenham map*", Fig. 1b). Statistical testing was performed using the two-tailed Wilcoxon test with confidence level α=0.05.

Results/Discussion

From the FA profiles (Fig. 2a) it can be seen that different approaches to averaging FA values as well as using a different interpolation strategy (DT vs FA) provide different results. Fig. 2b shows that DT-interpolated FA values significantly differ from FA-interpolated FA values in most cases. The correlation between all the approaches is high (Fig. 2c), which is in line with the observed similarity in shape for the FA profiles (despite the offset). When zero-centering each bundle FA set, we did not observe significant differences between any pair of bundle FA sets, independently from the choice of the averaging and interpolation approaches (Tab. 1).

Our results suggest that FA values computed with different interpolation methods have near-identical sensitivity to physiological changes along the reconstructed pathways. However, the presence of an offset between the methods hampers the comparability of the results obtained with different settings, and suggests the need to report the chosen interpolation method along with other user-defined settings of FT.

Acknowledgements

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References

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Figure 1

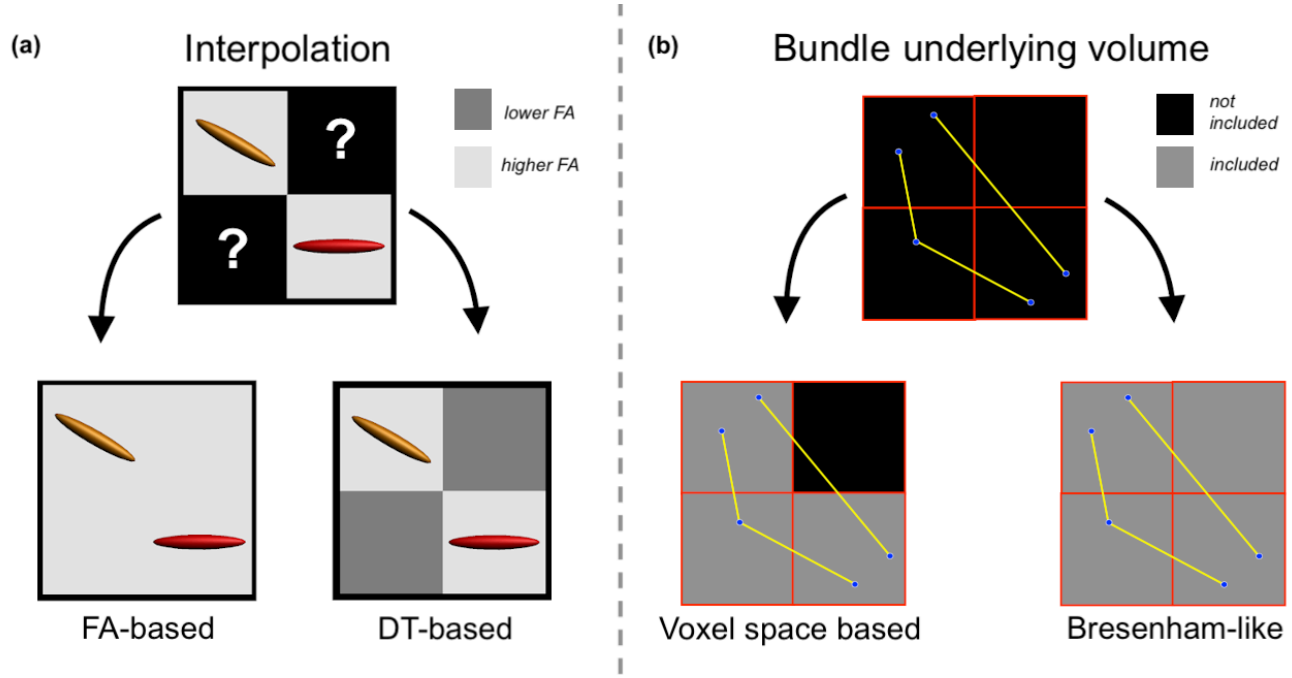
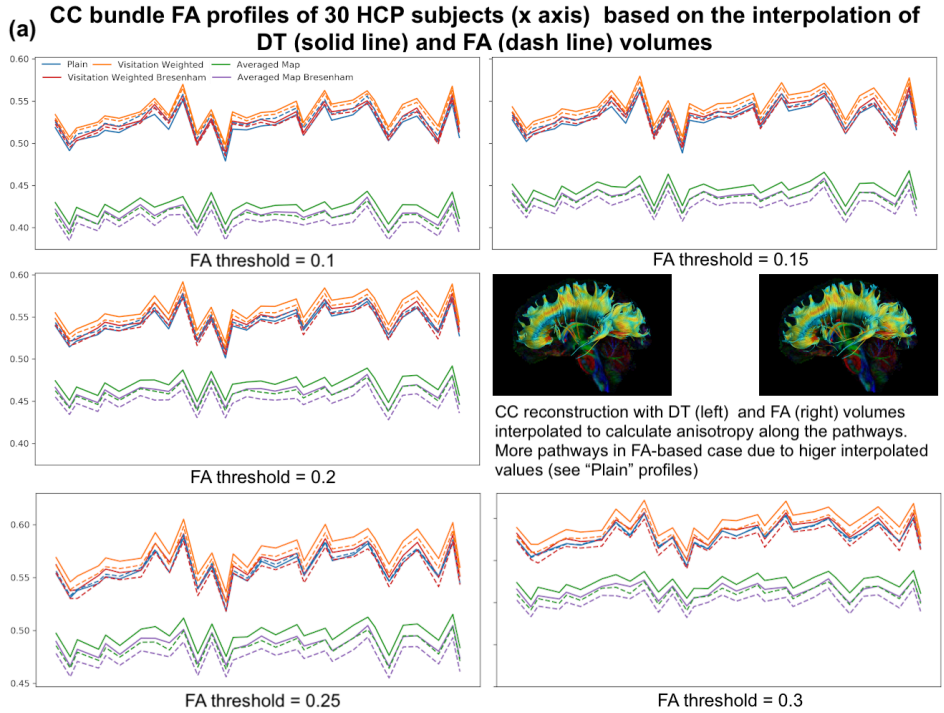


Figure 1 (a) Using either FA or DT volume for FA calculation along the pathway might lead to different results. (b) Using Bresenham-like approach voxels passed by pathways but not containing their points are included into the bundle-wise computations.

Figure 2



(b) P-values from the two-tailed Wilcoxon test (confidence level 0.05)

Bundle	**CC**				
FA Threshold	**0.1**	**0.15**	**0.2**	**0.25**	**0.3**
[DT]Plain Average vs [FA]Plain Average	0.000002	0.000002	0.000002	0.000002	0.021823
[DT]Plain Average vs [FA]Visitation Weighted Average	0.000002	0.000002	0.000002	0.000002	0.000002
[DT]Plain Average vs [FA]Average Map	0.000002	0.000002	0.000002	0.000002	0.000002
[DT]Plain Average vs [FA]Visitation Weighted Bresenham Map	0.000359	0.029235	0.484350	0.000345	0.000002
[DT]Plain Average vs [FA]Averaged Bresenham Map	0.000002	0.000002	0.000002	0.000002	0.000002

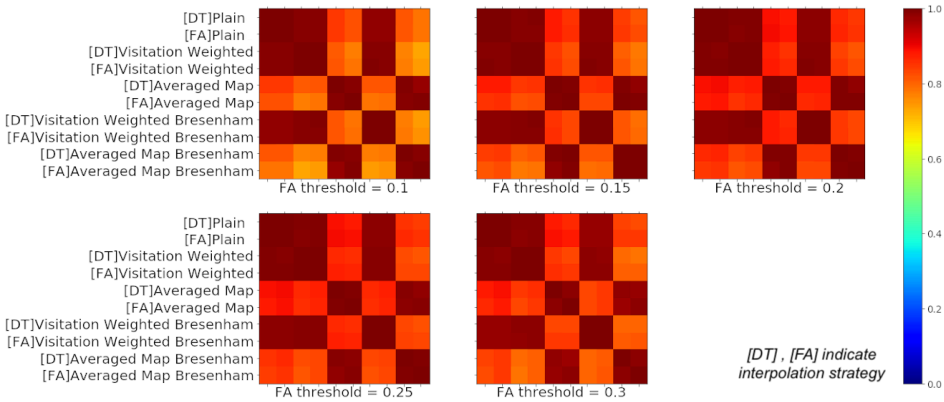


Figure 2 Despite similar shapes of the bundle FA profiles(a) mainly significant difference was reported by the Wilcoxon test(b). However, the bundle FA correlation is high(c) which is in conformity with the profiles' shapes.

Table 1

Table 1 Two-tailed Wilcoxon test results (p-values) on centered bundle averages of a subset of compared pairs of bundles where one is tracked with FA values inferred from DT and FA ([DT]-, [FA]-marked) volumes, showing insignificant differences ($\alpha = 0.05$).

FA Threshold	0.1	0.15	0.2	0.25	0.3
[DT] Plain Average vs [FA] Visitation Weighted Averaged Map	0.9181	0.8693	0.9672	0.8050	0.9344
[DT] Plain Average vs [FA] Averaged Map	0.8855	0.9836	1.0000	0.9836	0.9181
[DT] Plain Average vs [FA] Visitation Weighted Bresenham Map	1.0000	0.9672	0.9018	0.7892	0.5372
[DT] Plain Average vs [FA] Averaged Bresenham Map	0.9508	1.0000	0.9836	0.8855	0.9018
[DT] Visitation Weighted Averaged Map vs [FA] Averaged Map	0.9181	0.9836	0.9508	0.9508	1.0000
[DT] Visitation Weighted vs [FA] Visitation Weighted Bresenham Map	0.8855	0.8531	0.6658	0.9672	0.9508
[DT] Visitation Weighted Averaged Map vs [FA] Averaged Bresenham Map	0.9836	0.9672	0.9672	0.9836	0.9344
[DT] Averaged Map vs [FA] Visitation Weighted Bresenham Map	0.9836	0.9836	0.8693	1.0000	0.9836
[DT] Averaged Map vs [FA] Averaged Bresenham Map	0.9344	0.9508	1.0000	0.8531	0.9018
[DT] Visitation Weighted Bresenham Map vs [FA] Averaged Bresenham Map	0.9836	1.0000	0.8531	0.8693	0.9672