PROBABILISTIC FIBER TRACKING USING THE RESIDUAL BOOTSTRAP WITH CONSTRAINED SPHERICAL DECONVOLUTION MRI

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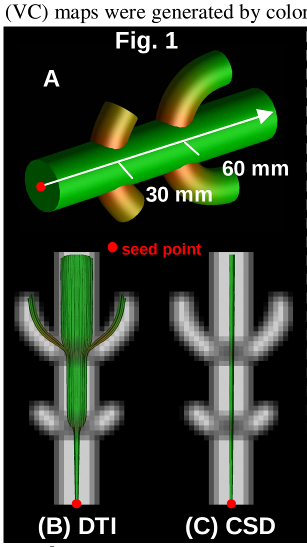
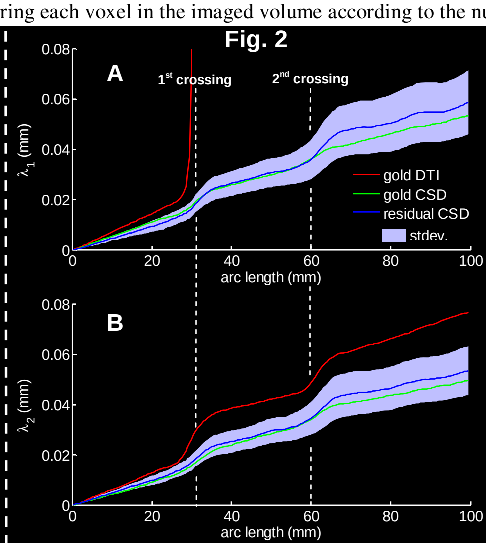
Introduction

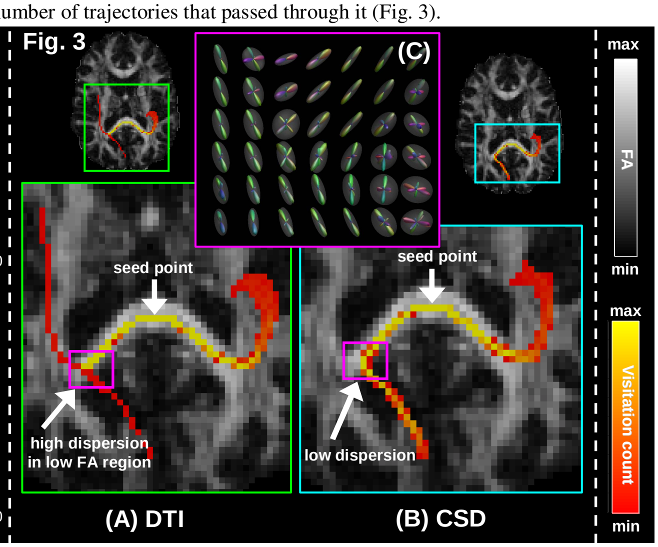
Diffusion tensor imaging (DTI) is widely used to extract white matter fiber orientations from diffusion-weighted (DW) MR data of the brain. However, since DW images are inherently noisy, the estimated fiber orientations and resulting trajectories are subject to uncertainty. Model based bootstrapping methods have been shown to accurately estimate this uncertainty from a single DTI acquisition [1, 2] and have recently been introduced for probabilistic DTI tractography [3]. In regions of fiber crossings, however, DTI has been shown to be inadequate. In this context, constrained spherical deconvolution (CSD) [4] has been proposed to address this issue of multiple fiber orientations. In a previous study [5], it was shown that the residual bootstrap allows for accurate estimation of CSD fiber orientation uncertainty at a voxel level. In this work, we present a new probabilistic CSD tractography algorithm based on the residual bootstrap. We used simulations to show that the residual bootstrap can be used to accurately generate CSD trajectories. We also compared the probabilistic CSD and DTI tractography techniques, using both simulated and real DW data.

Methods

Tractography: Standard DTI streamline tractography was adapted to work for CSD. The resulting algorithm can be summarized as follows: 1) start at seed point; 2) obtain the DW signal at its current position using linear interpolation; 3) estimate the fiber orientation distribution function (FOD) using CSD (harmonic order 8); 4) extract FOD peak closest to previous stepping direction using Newton optimization; 5) advance the trajectory by a fixed step size (1 mm) along the obtained direction. Tracking is ended when FOD peak intensities are beneath a fixed threshold (0.1), a maximum angle is exceeded (30°) or the tract leaves a specified brain mask. Gold standard: A noiseless DW dataset was simulated using the framework described in [6]. Fractional anisotropy (FA) of a single fiber population was set to 0.8 and mean diffusivity to 9×10^{-4} mm²/s. Imaging parameters were: voxel size: 2×2×2 mm^3; 60 gradient directions; b-value: 3000 s/mm². The simulated data set contained three fiber bundles with an arrangement as shown in Fig. 1, A. Rician noise was added to this dataset to give SNR (in the b=0 images) of 30. This procedure was repeated 1000 times, yielding 1000 noisy DW datasets. For each dataset, CSD tractography was started from a fixed seed point, resulting in 1000 gold standard probabilistic tracts (Fig. 1, C). For reference, we also did 1000 DTI tractography runs (Fig. 1, B). Residual bootstrap: Starting from a single noisy simulated dataset, 1000 realizations were constructed by repeating the following procedure. First the DW signal was fitted to a real and symmetric spherical harmonic (SH) model (order 8). Then, bootstrapping was performed on the model's residuals, i.e. residuals were randomly sampled with replacement. Finally, the resampled residuals were added back to the SH fit to result in a new realization of the dataset. Each realization was then processed independently using our tractography algorithm, resulting in 1000 bootstrap trajectories. The entire procedure was repeated 50 times. Quantitative comparison: Fiber dispersion of gold standard CSD, gold standard DTI and residual bootstrap CSD were compared using the tract dispersion measures as described in [7]. This method takes regular steps along the true noiseless trajectory and computes planes that are perpendicular to the tangent vector. The spatial locations of the intersection of each trajectory with the plane are determined and the distribution of these locations characterized using PCA. This yields two dispersion measures, λ_1 and λ_2, indicating the amount of fiber spread along the principal axes in this transverse plane. Real data: We applied our probabilistic CSD approach to a real DW dataset of the brain and compared the results with the probabilistic DTI tractography method [3]. Acquisition: 3 Tesla scanner, voxel size: 2×2×2 mm^3; 60 gradient directions, 6 B0 images; b-value: 3000 s/mm²). Seed point was selected in the splenium of the corpus callosum. Visitation count (VC) maps were generated by coloring each voxel in the imaged volume according to the number of trajectories that passed through it (Fig. 3).







Results

Fig.1, B shows 1000 gold standard DTI fiber tracts emanating from the same seed point (red dot), superimposed on an FA map. When the tracts enter regions of crossing fibers (low FA), there is considerable increase in tract dispersion due to the partial voluming effect. At the second fiber crossing, these tracts even disperse into the bifurcation. Fig.1, C shows the corresponding CSD tracts, having no bifurcations and much smaller tract dispersion. Fig. 2 plots tract dispersion as a function of arc length along the trajectory for gold standard DTI (red), gold standard CSD (green) and residual bootstrap CSD (blue). Both λ_1 (Fig. 2, A) and λ_2 (Fig. 2, B) show a considerably higher dispersion for DTI in the event of crossing fibers (arc lengths 30 and 60 mm) compared to CSD dispersion, which is much less affected by crossing fibers. Fig. 2 also shows that the bootstrap estimates of CSD fiber dispersion (both λ_1 and λ_2) are very close to the gold standard. However, note the error accumulation as a function of arc length. Fig. 3 shows VC maps of the probabilistic bootstrap DTI tractography (A) and our proposed algorithm (B), applied on real data. In the splenium (high FA, no crossing fibers), VC's of CSD and DTI tractography agree as expected. When the tracts enter a region of multiple fiber orientations (low FA), the probabilistic DTI pathways split into two distinct pathways. Probabilistic CSD tractography, however, follows one pathway with high certainty. This behavior is consistent with the plot of the FOD's overlaid on the diffusion tensors in Fig.3, C.

Conclusion

Our simulations show that the residual bootstrap is an accurate method to characterize CSD fiber trajectory uncertainty. This enables probabilistic CSD tractography using only a single DW acquisition, making it clinically feasible. By performing simulations and presenting a real data example, we have also clearly demonstrated the advantage of CSD based over DTI based probabilistic tractography: CSD is much less prone to fiber dispersion than DTI in regions of multiple fiber orientations.

References [1] Whitcher B et al, Hum Brain Mapp 29, 2008; [2] Chung S et al, NeuroImage 33, 2006; [3] Jones DK, IEEE TMI 27, 2008; [4] Tournier JD et al, NeuroImage 35, 2007; [5] Jeurissen B et al, OHBM 14th meeting proceedings, 2008; [6] Leemans A et al, MRM 53, 2005; [7] Lazar M et al, NeuroImage 24, 2005.