Resolution-Dependent Differences in Fiber Tracking and Quantification

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Abstract: Visualizing and measuring the uncertainty of DTI-based techniques is an important new challenge in the area of neuroimaging. In this paper, we demonstrate how fiber tracking and quantification of DTI parameters depend on the resolution of the underlying DTI data. For measuring the resulting differences, we propose a novel algorithm that allows for an automatic quantification of MR DTI parameters along arbitrarily oriented fiber bundles as well as an approach for quickly measuring the volume of the sheath enclosing a bundle. Our measurements show that the degree of uncertainty does not depend only on the chosen image resolution but also on the kind of fiber bundle.

Introduction: Over the last few years, diffusion tensor imaging (DTI) received raising attention within the neurosurgical and neurological community. Fiber tracking [1] as well as quantification algorithms [2] have been proposed with the motivation to identify major white matter tracts afflicted by an individual pathology or tracts at risk for a given surgical approach. However, the resulting parameters or fiber tracts can differ from the truth due to several reasons. One important factor, which is examined in this paper, is the resolution of the DTI images. Other errors, e.g., noise, distortions, registration errors, image blur, or ''incorrect'' parameter settings in the FT algorithm also limit the precision of the results. Although a quantitative assessment of the differences is essential in clinical applications, only little work has been done in this area. Experimental noise, e.g., by using the bootstrap method [3,4], may induce errors in the measured fiber directions, which will reduce the accuracy of the estimated white matter trajectories. The resulting uncertainties can be visualized along the streamlines using cones of uncertainty [3] or can be used to generate probabilistic connectivity maps [4]. This paper, however, addresses uncertainties due to different resolutions which cannot be simulated by experimental noise.

Methods: DTI data sets were acquired in 12 gradient directions from a healthy volunteer on a 3T Siemens head-scanner. Four different image resolutions were chosen; see Tab. 1 for resolution and acquisition times. In contrast to the approach of Basser et al. [5], neither the acquired DTI data nor the tensor field were smoothed, as we ultimately aimed to determine the differences in fiber tracking and quantification. Using a deflection-based fiber tracking algorithm, we reconstructed parts of the cingulum (Fig. 1 ii) as well as parts of the pyramidal tract (Fig. 1 iii) for all four DTI data sets (Fig. 1 i illustrates all tracked fibers).
We propose a method that allows for an automatic quantification of MR DTI parameters along arbitrarily oriented fiber bundles for measuring the average FA along the precomputed bundles. More precisely, each fiber is resampled so that all fibers consist of n equidistantly distributed fiber points. Using the resampled fibers, an average center line is computed which is used to determine n reference planes depending on the local curvature of the center line (such a reference plane is illustrated in Fig. 1 ii). Afterwards, a reference plane is used to determine an average FA value at a certain position of the bundle by taking into account one FA value per fiber with nearest distance to that plane.
Moreover, we propose to measure the volume of the sheath that encloses the single fiber tracts (see Fig. 1 iv). For computing the sheath, we propose a neighboring cells algorithm which is based on the well-known marching cubes algorithm where a volume (image) is scanned by discretizing it into cells. The necessary input volume is determined by voxelizing the 3D fiber tracts (line segments).

Results: Tab. 1 summarizes some of our experiments. It can be seen that parameters like average FA, the volume of the sheath, or the number of fibers depend on the resolution, but the amount of change also depends on the kind of fiber bundle. While the average FA value increases remarkably for the cingulum when increasing the resolution (see also Fig. 2), the FA value for the pyramidal tract only slightly increases. This can be explained by the fact that the single FA values at a certain position of the cingulum are much more inhomogeneous compared to the pyramidal tract as the cingulum is located very closely to a differently oriented fiber structure, namely the corpus callosum. This statement can be confirmed by a color-coding of all FA values contributing to a single average FA value. The volume of the sheath, however, differs more for the pyramidal tract. This may be explained by partial volume effects where bundles in isotropic surroundings are assessed too large whereas fibers in inhomogeneous areas are not tracked at borders.

Conclusion: Our initial experiments have shown that resolution-dependent differences in fiber tracking and quantification are differently pronounced in distinct areas of the brain. Thus, it should be examined whether our technique could be used to model the uncertainty depending on a certain image resolution and on the surrounding tissue of the fiber bundle. Moreover, our new technique may support the decision which resolution should be used when acquiring MR-DTI images.

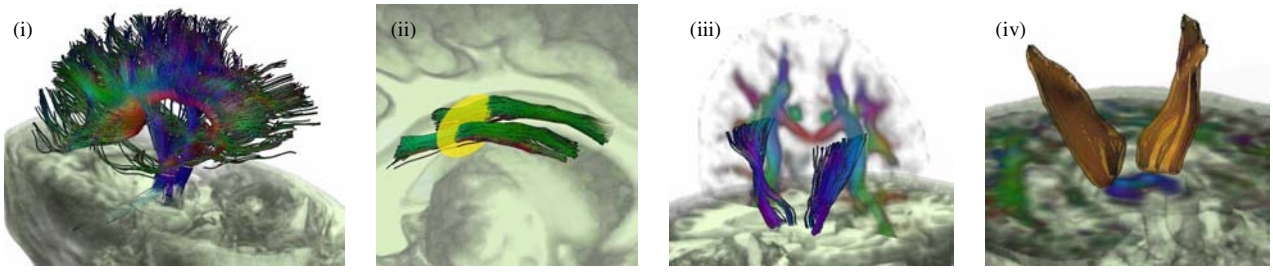

Fig. 1: *For measuring resolution-dependent differences in quantification and fiber tracking (e.g., expressed by parameters like average fractional anisotropy (FA), or the volume of the sheath enclosing all fibers (iv)), we tracked parts of the cingulum (ii) as well as parts of the pyramidal tract (iii, iv). For computing the average FA at a certain position of the bundle, a reference plane is computed depending on the local curvature (ii). This plane is used to determine contributing single FA values.*

Resolution (mm^3)	Volume per voxel (mm^3)	Acquisition Time (min.)	# Fibers (cg/pyt)	Average FA (cg/pyt)	Volume of sheath (cg/pyt)
1.6×1.6×1.6	4.096	16	484 / 442	0.600 / 0.602	5680 / 16,840
2×2×2	8	12	472 / 442	0.576 / 0.600	5680 / 19,376
2.5×2.5×2.5	15.625	10	454 / 384	0.503 / 0.588	5248 / 16,416
3×3×3	27	8	392 / 546	0.498 / 0.588	5064 / 21,648

Tab. 1: *Number of fibers, average FA, and volume of the sheath are shown depending on different resolutions of the DTI data for the cingulum (cg) and the pyramidal tract (pyt).*

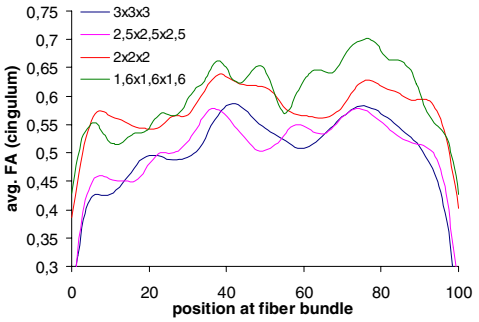

Fig. 2: *FA along the cingulum at different resolutions.*

References:
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