

## **Estimation of Fiber Bundle Sections for Interactive Neural Fiber Analysis**

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### **Purpose**

During the last decade the area of Diffusion Weighted MRI analysis has gained significant scientific attention and many techniques have been introduced for analyzing the diffusivity patterns in neural tissues and visualizing the neural fiber tracts. However, the majority of these methods have not been adopted for clinical use due to various reasons, including the computational demands that more often than not require long execution time as well as the large complexity of the analyzed neural fiber tracking information. In this paper we present an interactive algorithm for fiber bundle analysis that computes in real time statistics on the variation of the structure, size, and curvature along a fiber bundle. The proposed fiber metrics can be used as markers for diagnosing and monitoring atrophy for epilepsy, schizophrenia, depression, hypoxia-ischemia, trauma, Alzheimer's disease and other dementias

### **Methods**

In our method we introduce the idea of perpendicular fiber tracking and we present a novel method that implements it using dynamic programming. The proposed method reconstructs the perpendicular sections along a fiber bundle, which are surfaces consisted of points whose normal vectors are parallel to the direction of the local water diffusion. The statistical variation of the geometrical structure, area, and curvature of fiber sections along a fiber bundle can be efficiently analyzed, visually presented, and used as a novel tool for various clinical uses including diagnosis, monitoring, and surgical planning.

To the best of our knowledge there is no prior report in literature on perpendicular fiber tracking. Our proposed method is summarized in the following steps:

Input: A seed point defined by the user.

Step 1: A fiber is traced using the single seed point. Any deterministic fiber tracking method can be used in this step.

Step 2: The fiber is segmented into N fiber segments of equal length.

Step 3: For each fiber segment a surface is reconstructed, which is a perpendicular section of the fiber bundle. The sections are computed using a 3d cost map, which is generated by dynamic programming that is driven by a cost function that combines two terms: a) a geometric cost, and b) a fiber cost. The geometric cost drives the process of reconstructing a smooth and connected surface/section of the fiber bundle. The fiber cost makes sure that the reconstructed section is perpendicular to the local dominant fiber orientation at every point on the surface.

Step 4: For every perpendicular fiber section we compute various properties such as the area of the surface as well as the average curvature of the surface. These properties vary along the fiber bundle, and the variation pattern can be used as a biomedical marker for diagnosis.

## Results

We demonstrate the proposed method using a real DW-MRI dataset from a rat hippocampus. We present several ways of visualizing the results from the perpendicular fiber tracking and analysis in 3D as well as 2D plots. The acquisition protocol included acquisition of 22 images using a pulsed gradient spin echo pulse sequence with repetition time (TR) =1.5s, echo time (TE) =28.3 ms, bandwidth =35 kHz, field-of-view FOV =4.5 x 4.5 mm, matrix =90 x 90 with 20–30 continuous 200-  $\mu$ m-thick axial slices. After the first image set was collected without diffusion weighting ( $b \sim 0$  s/mm<sup>2</sup>), 21 diffusion-weighted image sets with gradient strength (G) = 415 mT/m, gradient duration  $\Delta t = 2.4$  ms, gradient separation  $\Delta s = 17.8$  ms, and diffusion time  $T_{diff} = 17$  ms were collected. Each of these image sets used different diffusion gradients (with approximate values of 1250 s/mm<sup>2</sup>) whose orientations were determined from the second-order tessellation of an icosahedron projected onto the surface of a unit hemisphere. The image without diffusion weighting had 36 signal averages (time =81 min), and each diffusion-weighted image had 12 averages (time = 27 min per diffusion gradient orientation).

Figure 1 shows the Fractional Anisotropy of an image in the dataset, as well as a colored FA. The red, green, blue colors represent underlying fiber orientations along the vertical axis, the horizontal axis, and perpendicular to the plane respectively.

Figure 2 and 3 show two examples of the output obtained from our proposed method, by placing the seed within stratum lacunosum-moleculare, and stratum oriens respectively. The plates in these two figures show: The reconstructed perpendicular fiber sections, the actual fiber bundle traced from the estimated surfaces/sections, the plot of the area of each surface and the plot of the curvature of these surfaces. From our observation, the calculated area and curvature match with the shapes of the reconstructed perpendicular fiber sections.

Furthermore we have validated the proposed technique using synthetic dataset with known fiber geometry. A DW-MRI dataset was synthesized simulating a single fiber bundle with straight fibers, and linearly increasing perpendicular area of the bundle. Since the fibers are straight the ground truth curvature of the perpendicular sections is zero. Figure 4, conclusively demonstrates the accuracy of the proposed algorithm. The area of the estimated fiber slices increases linearly, which agrees with the ground truth (dashed blacked line). Finally the curvature of the estimated fiber slices is zero, which also perfectly agrees with the ground truth.

All of our results were generated interactively (processing time <2 sec).

## Conclusions

The results from a real DW-MRI dataset of a rat hippocampus demonstrate the use of our method. Furthermore, the results obtained from the synthetic test conclusively demonstrate the efficiency and accuracy of our technique. The proposed method produces interactively comprehensive statistics on the variations of the perpendicular sections along a fiber bundle for real-time clinical use. We intend to use the proposed technique in our future research for generating novel markers for diagnosing cancer cell migration and surgical planning.

**fig.1**

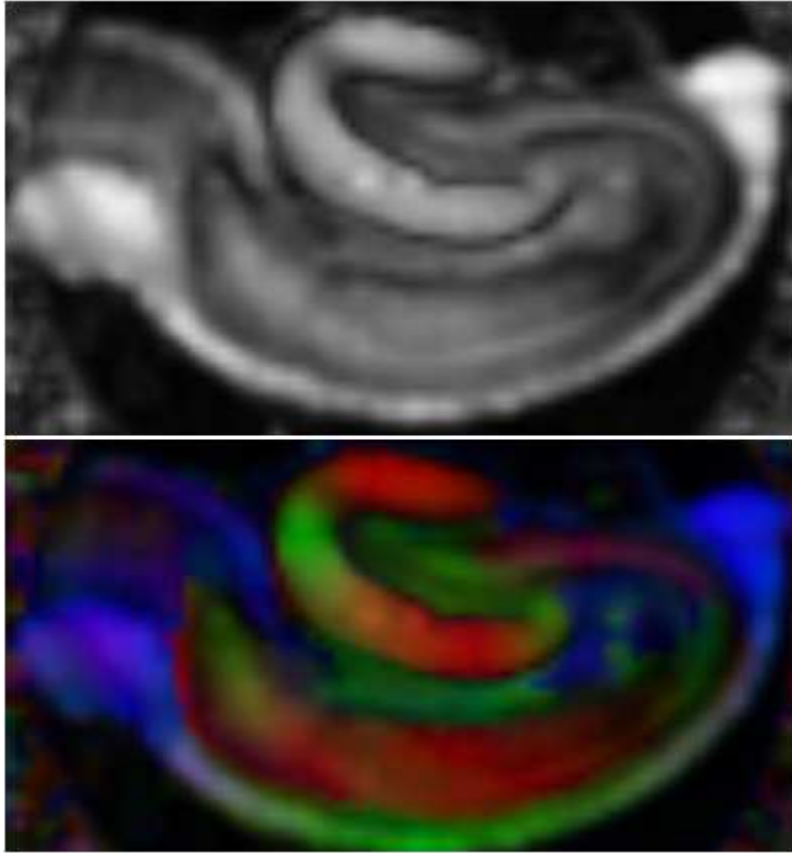


fig.2

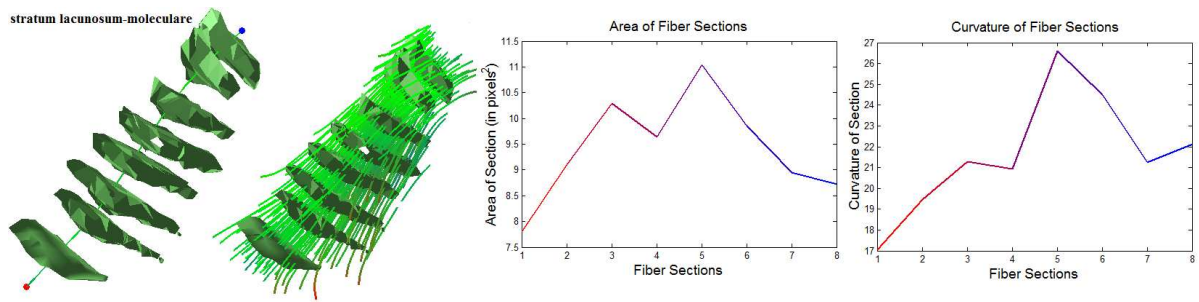


fig. 3

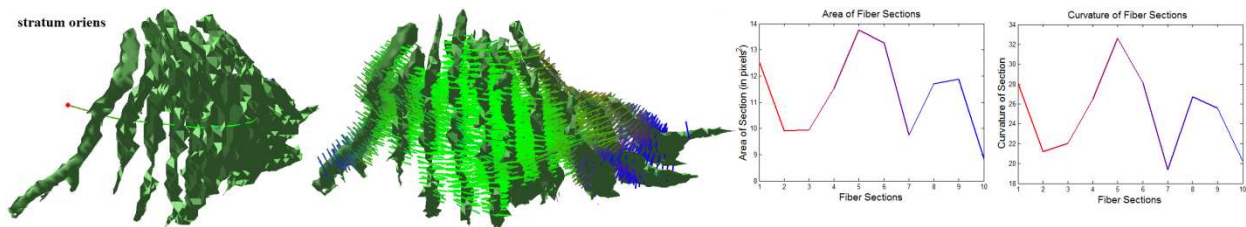


fig. 4

