Visualizing Differences of DTI Fiber Models Using 2D Normalized Embeddings

Guizhen Wang
Zhejiang University

Haidong Chen
Zhejiang University

Xiaoyong Yang
Mississippi State University

Shuang Ye
Zhejiang University

Guangyu Chen
Zhejiang University

Wei Chen
Zhejiang University

Song Zhang
Mississippi State University

Figure 1: Pairwise comparison for two brain datasets (top: 1248 fibers, bottom: 1622 fibers). From left to right: (a) the 3D fiber models; (b) 2D embedded points from multi-dimensional scaling projection of the fibers; (c) 2D embedded points from our approach; (d) the kernel density estimation maps based on (c) with Rainbow schemes; (e) the contoured KDE maps (12 levels) based on (d) with the color map from http://www.colorbrewer2.org. Circles in red and white indicate the significantly different patterns in similar locations of the two subjects.

1 INTRODUCTION

DTI fiber models vary due to several sources, like the MRI scan configuration and the parameter sensitive tractography. Statistical or topological features are used for comparison, e.g., Wild Bootstrap for quantifying uncertainties from DTI model parameters [1]. Comparison among two or more DTI models can help us identify the difference and understand the uncertainty of the DTI model. Projection techniques have been widely used to produce a low-dimensional view of high-dimensional datasets in a way that the projected layout preserves the variability mode in the original space. But these approaches do not share a common projection space for multiple datasets (see Figure 1 (b)). Our cluster-and-project approach can quickly cluster fibers based on fibers’ geodesic distance, and embed every fiber model into a common space to obtain an intuitive signature, a scatterplot associated with a KDE map and a contoured KDE map. The scatterplots show fiber models’ projection patterns, preserving the local and global space structure, and the KDE maps help observe the slight difference of fiber densities. Our method is effective for model characterization, pairwise comparison and group analysis.

2 APPROACH

Before a unique signature is designed for each fiber model in the fiber database \( L \), a preprocessing step is used to register all subjects of the same species to a common space such as the Talairach...
space for the brain datasets. Then, we reshape all fibers by fiber parameterization and fiber re-orientation. Every fiber is regarded as a high-dimensional point in the fiber space. For fiber parameterization, we perform an arc-length parameterization for each fiber, and equally subdivide the fiber into a fixed number of segments, so that fiber points have the same dimensions. Typically the number ranges from 50 to 70 in our experiments. For fiber re-orientation, we keep or inverse the fiber vertex sequences to guarantee that they have the same principal space direction. Three main stages are designed to compute a signature, as illustrated in Figure 2.

First, we employ a cluster algorithm that is the training part of self-organizing map (SOM) algorithm [2] to obtain a series of clusters from the entire fiber database (Figure 2(a)). The fiber geodesic distance is the minimum distance to measure the fiber proximity for clustering. Note that we do not use the mapping part of SOM, because the kohonen map layout is too regular to recognize in aesthetics. Second, the cluster centers C are obtained as the representative samples of the fiber database and projected into a 2D space to build a reference coordinate system, C_p (Figure 2(b)), with the Iso-map algorithm [4]. The last stage computes a 2D normalized scatterplot (Figure 2(c)) for each fiber model and constructs two associated maps, as shown in Figure 2(d) and Figure 2(e). Every fiber is projected into the embedding space C_p with the distance-preserving projection algorithm introduced in [5], ensuring that the distances between the fiber and the cluster centers in the 2D space are the same in 3D L. As such, the embedding space preserves both the local and global proximity structure of the fiber space. Figure 2(c) illustrates the generated embedding results. Further, the KDE map to describe the distribution density of points in the scatterplot is yielded by a nearest neighbor kernel density estimation (KDE) technique with the Gaussian kernel [3]. Each pixel of the KDE map records a density, of which the largest value is in red, as shown in Figure 2(d). By dividing the range of the computed density into multiple intervals, and coloring the elements within each interval, the contour-like map (Figure 2(e)) is generated.

3 RESULT AND CONCLUSION

We did two tests to verify our approach. Our human brain datasets were scanned with 64 gradient directions with b value 1000 on a Siemens 3T MRI scanner. If not specifically described, each DTI fiber model was generated under the same condition. Figure 1 compares two brain datasets from two subjects. Standard multi-dimensional scaling techniques can produce visual distinguishable results (see Figure 1(b)), but the bottom pattern is slightly rotated compared with the top pattern. Two patterns can not be compared because they are not aligned in a common embedding space. From Figure 1(c-d), in the common embedding space, two patterns have the similar point distributions, but different densities due to different subjects. For example, the layout of the region circled in red of the bottom model is different from that of the circle region in red of the top one. Likewise, the region circled in white of the bottom model contains more fibers than the white circle region of the top one. This inspection can be further verified by Figure 1(e).

For the parameter sensitivity analysis of fiber models, we generate six fiber models with varied parameter configurations from one DTI tensor volume dataset: all seeds are randomly located; the step sizes for fiber tracking are 0.75, 0.75, 0.58, 0.58, 0.58, and 0.58. From Figure 3, we find that the first two signatures are quite different from the other four, meaning that the step size could effect the fiber model’s fiber distribution.

In conclusion, our approach is proved to be effective to visualize the differences between fiber models in a common projection space. Users could easily observe the signature differences, and compare fiber models with interactive linked 2D and 3D views. In the future, we will try more clustering algorithms, other than SOM, and explicitly estimate elements that influence the accuracy, such as the dimensionality and structure complexity of the fiber space, as well as the embedding algorithm.

ACKNOWLEDGEMENT

This work is supported by 973 program of China (2010CB732504), NSF of China (No.60873123), and partially supported by 973 program of China (2010CB732504), NSF of China (No.60873123), NSF of Zhejiang (No.1080618).

REFERENCES