# Automated Hierarchical Clustering of DTI White Matter Fiber Tracts

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## Introduction

DTI has developed since its introduction in the 1980s because of its promising prospect in both research and clinical applications for its ability in characterizing the brain connectivity in white matter and its ability of predicting potential tissue damage. Currently, research in the DTI field is undergoing a rapid expansion to depict white matter connectivity and microstructural features of human brain tissues that weave these sites together into a system with spatially interacting neural elements. Recently, the tract-based analysis of white matter fibers has raised interests from the neurology and clinical neuroscience community since this methodology provides quantitative analysis of the properties of the specific fiber bundles, which provide a useful abstraction of the white matter structures and a clear identification of neural fibers. In order to benefit from the tract-based analysis, many clustering algorithms of the fiber tracts have been proposed. However, most approaches require a user initialization, and only a few works [1-3] succeed in the task of semi-automated classification of the whole ensemble of white matter fibers with atlas-based algorithms. In this paper, we propose a novel cluster method to automatically group brain white matter fibers into biologically meaningful neural tracts.

## Material and method

This project presents a framework for automated and unsupervised segmentation of white matter fiber tracts (Fig.1). The hybrid approach implements the following two procedures: (i) a three parts atlas (Corpus Callosum, Cortico-Spinal Tract and others) of fiber tracts was invoked to include the brief anatomical knowledge in the fiber bundles of entire brain, and (ii) segment the white matter fiber tracts with full features in each atlas part, using a hierarchical cluster tree with the inner squared distance. The applicability of the clustering framework has been demonstrated on human DTI data. MR images were collected with a GE 3.0 Tesla MR scanner system at New York State Psychiatry Institute. Before fiber clustering, there are several steps of data preprocessing in order to get meaningful fibers, including eddy current distortion correction, ensuring each tensor is positive defined and mapping MNI atlas to the brain, yielding a map of labeled white matter and grey matter structures in DTI space. Tensor fields were re-sampled to get isotropic voxels with resolution of $1\times1\times1mm^3$. We put seeding points on every voxels with FA>0.5 for fiber tracking. Fibers were generated by tracking the principal eigenvector of diffusion in both directions with $4^{th}$ order Runge-Kutta algorithm.

## Results and Discussion

Diffusion Tensor Imaging (DTI) provides in vivo information about the underlying tissue structure of brain white matter, including both the geometry of fiber bundles as well as quantitative information about tissue properties. The tract-based white matter fiber analysis has been recognized as an effective framework to study the DTI data of human brain, and there has been a growing demand for clustering white matter fibers into automatically meaningful bundles in clinical studies. Our experimental results (Fig.2) show that the proposed method has the potential to benefit from the atlas by incorporating it as prior information, and achieves reasonably good performance in detecting meaningful fiber bundles than the commonly used normalized cut and fuzzy c-mean algorithms (Fig 3). Furthermore, the use of PCA in conjunction with hierarchical clustering reduces the computational cost relative to the use of comparison methods. The proposed approach allows visualization with colored fiber bundles, revealing structures that look promising for future explorative studies of DTI data both in a single subject and over a population as a robust and automated tool.
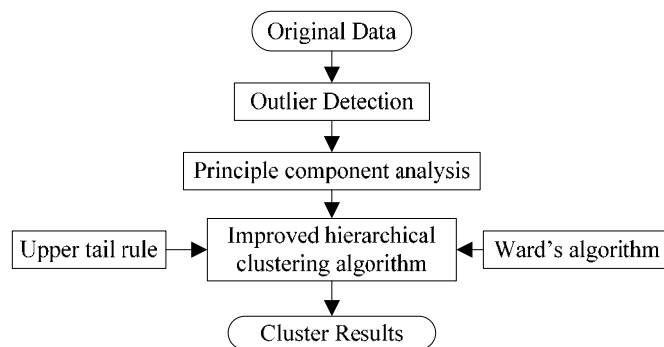


Figure 1. Flowchart of our proposed method.



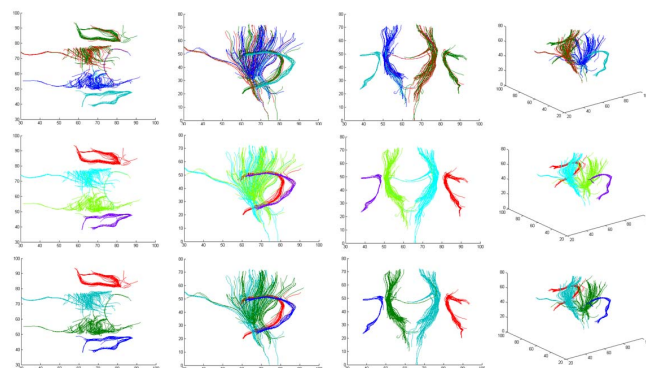Figure 2. Cortico-Spinal Tract and Corpus Callosum segmentation results.



Figure 3. Fiber cluster results using our method (Row 3), normalized cut (Row 2) and fuzzy c-mean (Row 1) algorithms on a specific brain fiber bundle

## References

[1] H. Li, NeuroImage, 2010; 49:1249–1258. [2] M. Maddah, MIA, 2008; 12:191-202. [3] D. Wasserman, NeuroImage. 2011; 57:918-927.