

INTRODUCTION

Diffusion Tensor Magnetic Resonance Imaging (DTI) provides a promising way of estimating the neural fiber pathways in the human brain non-invasively via white matter tractography. However, it is currently difficult to visualize and analyze these millions of resulting tracts quantitatively. Automated clustering these tracts would be particularly useful for the neuroscience community, such as for accurate neurosurgical planning, tract-based analysis, white matter atlas creation, etc. The present study aims at clustering these white matter tracts automatically. The pair-wise similarity of fibers is first calculated using adapted dynamical time warping and then a density-based clustering algorithm which is outlier-robust is applied.

OBJECTIVES

Currently, although some algorithms are already proposed for clustering these trajectories into meaningful bundles, the following problems are vital to be addressed :

Efficient Similarity Measurement: A more effective and efficient similarity measure for fiber pair-wise comparison is needed. It should not rely on specific assumptions, such as the same length.

Outlier-robustness: Due to experimental limitations, the resulting traces inherently include many imperfect fibers (outliers) after tractography. These noisy fibers should not be clustered into any fiber bundle and need to be excluded from further processing such as group tract-based analysis.

METHODOLOGY

1. Fiber Pair-wise Similarity: Adapted dynamical time warping (DTW) is used to measure the similarity between 3D fibers, which is defined as the average optional warping path. See Fig. 1.

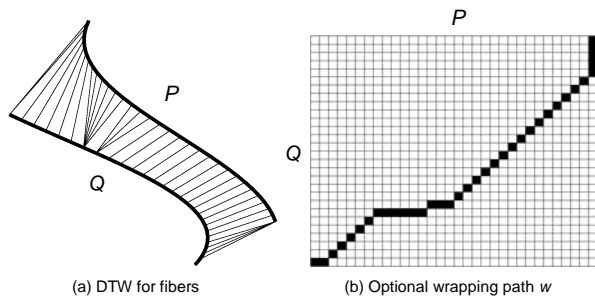


Fig.1 Fiber Similarity Measurement

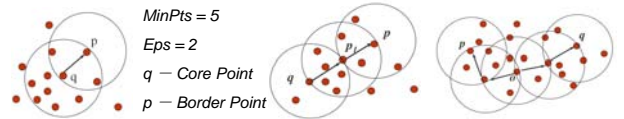
Similarity Distance

$$SimDist(P, Q) = \frac{\min\{\sum_{k=1}^K d(w(p_i, q_j))\}}{K}$$

where K is the length of wrapping path. $d(w(p_i, q_j))$ is the distance with the wrapping path connecting p_i and q_j .

Due to its complexity, calculating DTW is $O(mn)$. Therefore a lower bounding method is used to speed up the computation.

2. Density-based Clustering: After calculation of the fiber similarity, each fiber is viewed as a point in metric space. Then an outlier density-based clustering algorithm DBSCAN is used to group these points (Fig. 2). A cluster is defined as a maximal set of density-connected points.



(a) Directly Density-Reachable (b) Density-Reachable (c) Density-Connected

Fig.2 Density-based Clustering

EXPERIMENTAL RESULT AND ANALYSIS

We evaluate the effectiveness and efficiency of our method on synthetic data (Fig. 3) as well as on real data (Fig. 4).

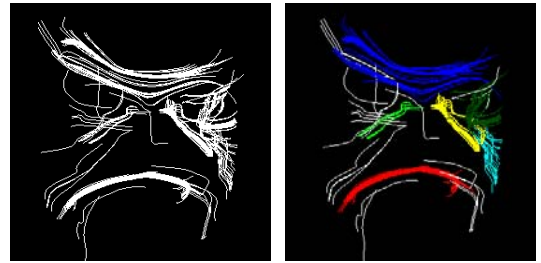


Fig.3 Synthetic data (Left: dataset, Right: results, 6 clusters, fibers with white color indicate noise)



Fig.4 Corpus Callosum (axial view) Left: 3 clusters (Eps= 5.6, MinPts = 4); Right: 7 clusters (Eps = 5, MinPts = 4)

CONCLUSION

We have shown that our novel method is a good way to automatically cluster fiber tracts. The adapted dynamical time warping distance is an effective and efficient measure for fiber comparison. The imperfect fibers can be excluded effectively during DBSCAN clustering.

Reference

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