A new approach to fully automated fiber tract clustering using affinity propagation

A. Leemans[1], and D. K. Jones[1]

[1]CUBRIC, School of Psychology, Cardiff University, Cardiff, Wales, United Kingdom

Introduction

Fiber tractography (FT) is increasingly being used to investigate the 3D organization and microstructural properties of white matter (WM) fiber bundles as an alternate approach to the more conventional labor-intensive region-of-interest (ROI) based analyses to reduce subjective biases when extracting diffusion parameters [1-3]. Although atlas-based approaches have been introduced to minimize operator dependency of seed and selection ROIs for these tract-based analyses [4-7], they rely on coregistration accuracy, definition of anatomical atlas labels, and inter-subject consistency. To improve the reliability of reconstructing WM fibers of interest, several automated fiber tract bundling methods have been proposed, based on *k*-means, hierarchical, spectral, expectation-maximization, and shape-based clustering algorithms [8-12]. In this work, we present a novel approach to fiber tract clustering approach on the recently introduced concept of 'affinity propagation' (AP) [13]. In contrast to other clustering methods, AP clustering allows one to (i) produce tract exemplars; (ii) incorporate asymmetric tract distance measures (e.g., Hausdorff metric); and – importantly – (iii) determine the number of clusters automatically. Here, we demonstrate 1) the superior performance of AP over spectral and hierarchical clustering methods and 2) how the AP method improves atlas-based tract segmentations.

Methods

Data acquisition & post-processing: Five cardiac-gated DT-MRI data sets (2.4 mm isotropic resolution) were collected (one per week for 5 weeks) from a healthy volunteer on a GE 3 Tesla MR system using a gradient sampling scheme of 6 non-diffusion-weighted (DW) images and 60 DW images (b=1200 s/mm^2) in which the gradients were uniformly distributed over the sphere [14]. The tensor was fitted using non-linear regression and deterministic streamline tractography was used to reconstruct WM fiber pathways [15, 16].

AP clustering of tracts: In summary, AP is a new, completely unsupervised clustering algorithm that can be viewed as the max-product algorithm in a graphical model describing the mixture model [13]. It takes as input a distance similarity ('affinity') between pairs of tract pathways and simultaneously considers all data points as potential exemplars. Real-valued messages are iteratively exchanged between these data points ('propagation') until a high-quality set of exemplars and corresponding clusters gradually emerges (a detailed/technical description of this method can be found in ref. [13]). As shown in [10], the symmetrical mean distance between pairs of closest points is a robust metric to calculate the distance between each pair of fiber pathways and is therefore also used here for both the AP, spectral (as described in [10]), and hierarchical (single-linkage, agglomerative as described in [11]) clustering approach.

1) Reproducibility: as an example, for each data set (S_n , n = 1,…,5), the right uncinate fasciculus (UNC) was reconstructed, based on the protocol described in [17] (and shown in Fig.1, A). Subsequently, clustering of the UNC was performed to differentiate the medial and lateral components of the UNC (Fig.1, B-D).

2) AP clustering in an atlas-based framework: WM fiber tracts were reconstructed automatically by first seeding the whole brain and then defining the MNI labels 'frontal lobe' and 'occipital lobe' as two 'AND' gates and the right cerebrum as a 'NOT' gate for the 'whole brain' tractography results (Fig. 2, A-D) [3]. The resulting tracts were clustered in 4 fiber bundles as determined by the AP algorithm.

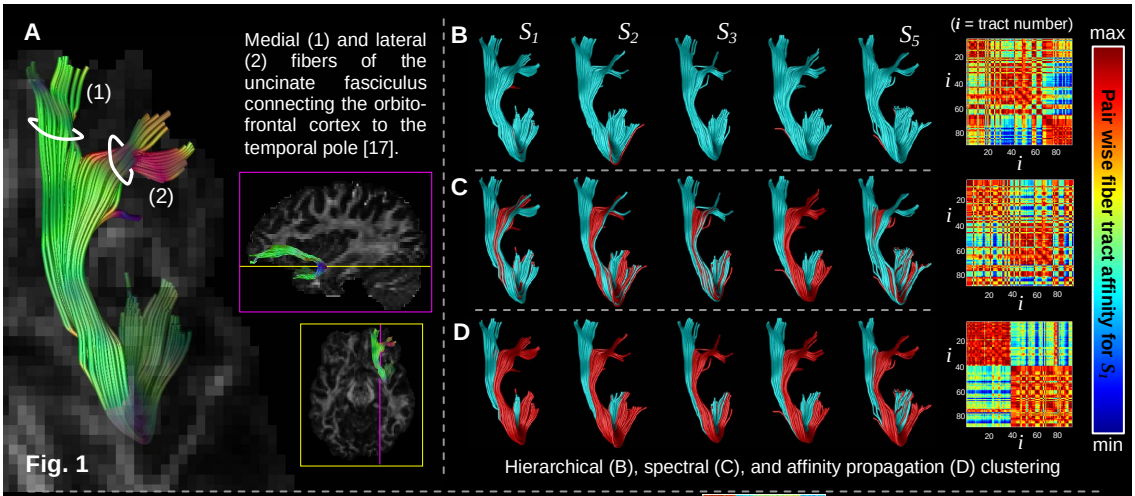

Fig. 1

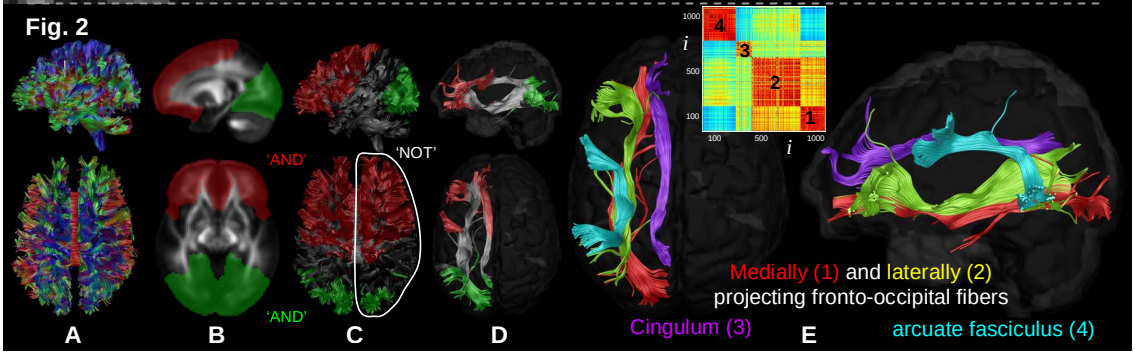

Fig. 2

Results

Visual assessment of the pair wise tract affinity matrix (reordered after clustering) in Fig. 1 (B-D) clearly demonstrates that AP clustering provides the most reproducible results. Note that the hierarchical clustering suffers from 'tract outliers' in the data. After performing full brain fiber tractography (Fig. 2, A) and defining the 'AND' and 'NOT' regions in the fiber tract selection procedure (Fig. 2, B-C), AP clustering of the resulting fiber bundles (Fig. 2,D) provided 4 anatomically plausible fiber bundles (Fig. 2, E). Note that from the corresponding reordered affinity matrix, these 4 clusters can be easily distinguished.

Discussion and conclusion

Previously, it has been shown that AP clustering can obtain better solutions than expectation-maximization, k-means, spectral, and hierarchical clustering in applications, such as image segmentation and studying gene expression models [13]. In this work, we used the AP algorithm for fiber tract clustering and demonstrated results that appear to be more robust than obtained from previously described methods. Although fiber tractography-based analyses may benefit from automated clustering methods to improve objectivity/reliability of the manual – and often labor-intensive – tract selections, user-induced variability is being replaced by parameter settings of the applied cluster method. By introducing the AP algorithm for fiber clustering, however, we have solved one of the major issues related to these parameters: *with AP there is no need to predefine the number of clusters a priori.*

References

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