Evaluation of White Matter Fiber Clustering Methods for Diffusion Tensor Imaging

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Introduction

Fiber tracking is a standard approach for the visualization of the results of Diffusion Tensor Imaging (DTI). Individual fibers are reconstructed from the tensor information by tracing streamlines. Usually fibers are defined by manually setting seed points. In this case, the result is biased by the user and therefore not easily reproducible. Some methods propose to seed through the whole volume to avoid manual seeding. However, white matter is a complex structure and the image gets easily cluttered. This makes it difficult to see meaningful structures. Fibers form anatomically entities called bundles. Several authors have proposed to use clustering techniques for fibers, such that the enormous amount of individual fibers is reduced to a limited number of logical fiber clusters that are more manageable and understandable. Clustering might also be used to explore and obtain quantitative comparisons by unbiased measurements in anatomically structures.

Different clustering algorithms and different options within a clustering algorithm (e.g., similarity measure between fibers) can be chosen. Furthermore, clustering algorithms have parameters to tune such as the amount of clusters to obtain. It is not clear which method or distance measure produces the best results. Many combinations exist and therefore it is also not viable that physicians evaluate all possible combinations.

We present the results of the evaluation of different similarity measures and clustering techniques using the framework presented by Moberts et al [1].

Materials en Methods

Three data sets from three different healthy volunteers were scanned in a Philips Gyroscan 1.0T with a singleshot EPI sequence, 3 b-values were used: 0, 400 and 800 s/mm2, Pulsed Field Gradients in 6 directions, voxel size 1.8x1.8x3mm, no slice gap. The fiber tracking technique described at Vilanova et al. [2] was used to generate fibers in the whole brain linear anisotropy at Cl = 0.2 was used as stopping criterium. The generated fibers were then classified manually using regions of interest. Two physicians classified six bundles: fornix, cingulate gyrus (left and right), corpus callosum, and corona radiata (left and right). This classification was used as ground truth. Four similarity measures between fibers were evaluated: closest point distance [3], mean of closest points distance [3], Hausdorff distance [3], and end points distance [4]. As clustering algorithms we used hierarchical clustering using single link (HSL), complete link (HCL) and weighted average (HWA). We also compared to the shared nearest neighbor (SNN) clustering algorithm, which has not been used before for clustering white matter fibers.

For the quantitative evaluation of the methods, we used as measure the Weighted Normalized Adjusted Rand (WNAR) with alpha value at 0.75, which was validated and calibrated by Moberts et al. [1]. Using WNAR, we compared each of the clustering results with the ground truth. The results of the clusterings were evaluated for all combinations of clustering algorithms and similarity measures, and the optimal results for each combination have been compared.

Results

In table 1, a summary of the value of the WNAR for each combination of clustering algorithm and similarity measure is shown. The values shown are the ones that correspond to the optimal parameter setting of each combination and each data set. The optimal parameter setting was determined by maximizing the WNAR via exploration of the parameter space (hierarchical 1D and SNN 2D) for each combination, figure 1.

Conclusions and disscusion

We found that the use of mean of closest points distance criterion gives the highest scores from the WNAR index. The HSL and SNN algorithms have a comparable performance in terms of quality. However, HSL is more stable for the parameter definition. All the results are based in the WNAR index who still needs a more complete validation.

References

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Similarity measure	HSL (WNAR) d1 d2 d3			HWA (WNAR) d1 d2 d3			HCL (WNAR) d1 d2 d3			SNN (WNAR) d1 d2 d3		
Mean of closest points	0.92	0.99	0.95	0.81	0.90	0.86	0.82	0.87	0.77	0.93	1.00	0.91
Closest point	0.46	0.50	0.50	0.79	0.82	0.76	0.77	0.79	0.69	0.82	0.83	0.86
Hausdorff	0.84	0.85	0.91	0.77	0.82	0.77	0.78	0.85	0.66	0.87	0.99	0.89
End points	0.87	0.88	0.93	0.87	0.82	0.72	0.67	0.77	0.74	0.92	0.97	0.92

Table 1: WNAR maximum value for each combination of clustering and similarity measure investigated
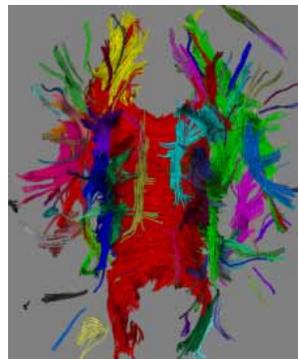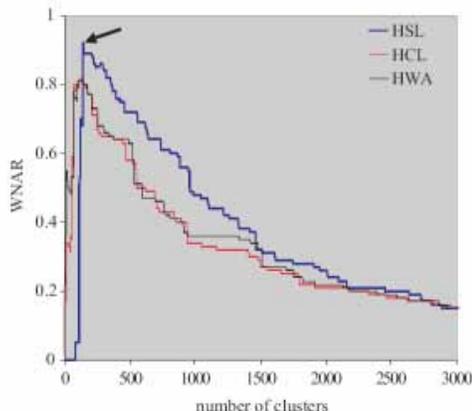
Figure 1 Left: Graphs showing the evaluation of the clustering methods using mean distance between fibers measure for one data set. The arrow indicates the parameter setting with the maximum WNAR value. Right: the resulting clustering that corresponds to the arrow.