A new combined distance measure for the clustering of fiber tracts in Diffusion Tensor Imaging (DTI)

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Introduction

In recent years various fiber tractography methods have been evolved. Although these resulting tractograms offers plenty of information, they are rarely used in clinical routine, due to the fact that processing is often time-consuming and an experienced operator is essential to obtain good results. Apart from that, tractograms can be very useful for surgeons who need to know where the main fiber bundles are located and if they infiltrated or relocated by a tumor. Furthermore, tractograms can also be employed by researchers for studying neurological diseases such as Schizophrenia or Obsessive Compulsive Disorder (OCD). For example, the connections or even the degree of connectivity between certain regions in the brain may contain important information about the disease itself and is maybe beneficial for an early diagnosis or a proper treatment. The analysis of tractograms is usually performed manually by experienced users, who select a Region Of Interest (ROI) to define the tracts of interest (those tracts that cross the ROI). This however, depends strongly on the user and his level of experience and is by no means an objective measure. Therefore it is not reproducible and prone to errors. To overcome this limitations cluster analysis can be employed to partition fiber tracts into clusters with the final intention to minimize the intra-cluster differences (the difference between the fiber tracts in the cluster) and to maximize the inter-cluster variability (the difference between the clusters). Thereby, the similarity between individual tracts is determined through comparison of tract-specific features or similarity measures. In recent studies several similarity measures such as the Hausdorff distance, the corresponding segment ratio [1] or the Euclidean distance have been observed, but no optimal measure was found yet. All methods have deficiencies and the combination of appropriate and distinguishable similarity measures is recommended to improve the results [2]. Therefore, the aim of this study was to develop a new combined similarity measure that incorporates various features.

Materials and Methods

The fiber tracts were calculated from afore acquired DTI dataset of a healthy volunteer. The data was measured on a clinical 3 T whole body MR-Scanner (Magnetom Tim Trio, Siemens Healthcare, Erlangen, Germany), using a conventional twice refocused Echo Planar Imaging (EPI) sequence with four bipolar diffusion gradients to compensate for eddy currents [3]. Fat suppression was achieved by applying a SPectral Attenuated Inversion Recovery (SPAIR) pulse. A 12 channel phased array matrix head coil was employed and the following parameters were used: a matrix of 128×128, 55 slices with a thickness of 2.5 mm resulting in a voxel size of $2.5 \times 2.5 \times 2.5$ mm³. Five b0 images without diffusion weighting (b = 0 s/mm²) as well as 30 diffusion weighted images sampled with different gradient directions at b = 1000 s/mm² were acquired. Fiber tracts were generated using the Diffusion Toolkit [4] for the whole. Then our combined distance measure was calculated for all tracts, exceeding a length of 70 mm.

The basis of our cluster method is a shape analysis method published by Attalla in 2005 [5]. In theory this algorithm works by defining several points P_i equally distributed on a polyline I (compare the black line in Fig. 1, which is in our case - the fiber tract). The centroid C_i of the polyline is then calculated and the segments S_i are defined. Based on these segments the angle of the triangle $C_iP_iP_{i+1}$, the distances r_i, r_{i+1} from the centroid C_i to the points P_i and P_{i+1} are calculated as well as a smoothness factor $m_i=v_i/t_i$. This is done for every segment of each polyline. For the comparison of two polylines the similarity of two polylines I and J is then given as the minimal difference between the corresponding segments of I and J. Due to the fact that the tracts usually differ in the number of tract points a partial tract matching was performed so that the number of segments for I and J is equals. To further distinguish between two tracts, we used the Euclidean distance between the centroids C_i and C_j as well as the angular difference between the mean orientation of tract I and tract J as additional feature. Everything was normalized to a maximum value 1 and accumulated to obtain the final similarity measure. The clustering of the data was then performed with a hierarchical clustering approach and Ward's method for the generation of the hierarchical cluster tree [6].

Figure 1: The similarity of two polylines I and J is assessed by determining the minimal difference between the corresponding segments of I and J.

Results

In Figure 2 first initial results of our combined distance measure are shown. Eight of 15 Clusters are visualized with different colors. The whole dataset consists of 5000 fiber tracts.

Discussion & Conclusion

In this study we have introduced a new combined distance measure that combines a shape based distance measure with other distance measures. To match fiber tracts with different length and an unequal number of tract points, we distributed points equally on the tract and a partial tract matching. Then the similarity between the tracts was assessed by using a shape matching and similarity algorithm. Additionally, the distance between the tract- centroid, as well as the orientation of the tracts was used in this distance measure. The first initial result were very promising und good group of cluster were obtained. However, a deeper analysis of this new measure is necessary to further improve the clustering results.

Acknowledgements

Figure 2: Initial results of our clustering. Every cluster is colored with a different color.

References

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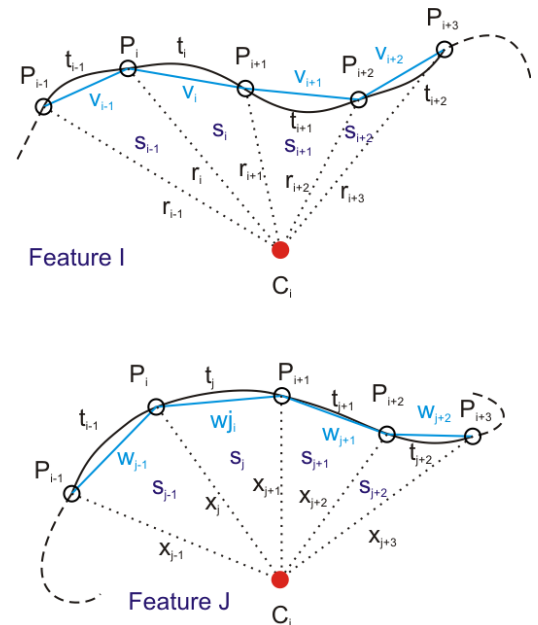[6] Xu R et al., Wiley IEEE Press, 2008