Atlas-guided cluster analysis of fiber tracts

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Target audience – Scientists who want to extract fiber bundles from fiber tracking data sets for a population of subjects in a consistent and reliable way.

Introduction – Analysis of Diffusion Tensor Imaging (DTI) data in multi-subject imaging studies is usually performed by analyzing quantitative diffusivity measures (e.g. Apparent Diffusion Coefficient (ADC), Fractional Anisotropy (FA), etc.). In recent years, various new techniques for quantitative tractography-based analysis of white matter fiber bundles have evolved [1, 2]. For this kind of analyses, fiber tracts have to be reconstructed in advance. Quantitative analysis is then performed for selected fiber bundles of interest. Hence, the correct delineation of fiber bundles across subjects is eminently important for tractography-based group analysis. As manual extraction of fiber bundles for multiple subjects is highly time consuming and prone to errors, automatic extraction methods are preferable. However, even with automated, unsupervised methods such as cluster analysis, reproducible and consistent results for multiple subjects are hard to obtain as these methods lack any anatomical reference to the course of the fiber bundles. With this contribution we present a new hybrid approach that incorporates anatomic information of a probabilistic white matter fiber bundle atlas into the cluster analysis. The previously presented high performance cluster analysis technique [3] has been extended to enable both conventional and atlas-guided clustering. The new technique enables not only the extraction of the fiber bundles from the atlas, it also has the advantage to identify bundles in the data set that are not present in the atlas.

Integration of the anatomical information of the atlas into the cluster analysis – In order to integrate anatomical information into the cluster analysis, we utilize a probabilistic atlas that contains various white matter bundles (also called classes). For each fiber bundle, the atlas describes how reliable a voxel can be associated with that bundle. An example for the probabilities of one bundle (forceps minor) is shown in Fig. 1. Blue indicates low and red high probability for a voxel. In Fig. 2, the color-coded probabilities for all fiber bundles are shown for one exemplary slice. Different fiber bundles are visualized with different colors. The reliability in each voxel is indicated by the color intensity.

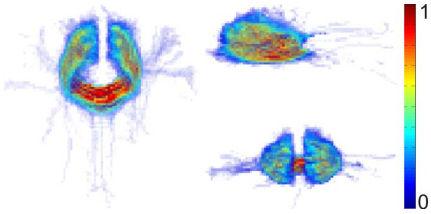

Fig. 1 – 3D representation of the forceps minor in the probabilistic atlas. Blue indicates reduced and red high reliability for a voxel.

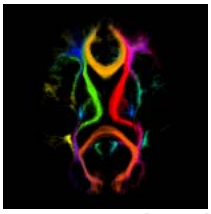

Fig. 2 – Color-coded reliability map for all fiber bundles (one exemplary slice is shown).

Cluster analysis is an iterative process in which the similarity or distance between fiber tracts is assessed and clusters are formed in each successive step, by merging the most similar clusters. This is repeated until a predefined number of clusters are obtained or a stopping criterion is fulfilled. An effective way to influence the clustering is, to perform an additional weighting that modulates the distance $d(C_1, C_2)$ for the clusters C_1 and C_2: $d_{corr}(C_1, C_2) = d(C_1, C_2) \times w(C_1, C_2)$. As those clusters with the shortest distance are merged, the weighting factor $w(C_1, C_2)$ has a direct impact upon the clustering. While values of $w(C_1, C_2) > 1$ will increase the distances and lead to a repulsion for C_1 - C_2, a weighting $w(C_1, C_2) < 1$ will result in an attraction effect for C_1 - C_2. In order to incorporate the anatomical information we exploit this effect and determine a weighting with respect to atlas-class membership of the clusters. We identify the two classes P_1 and P_2 of the atlas that have the highest probability p_1, p_2 to belong to the clusters C_1 and C_2. Then, we can distinguish between four cases, while each case modulates the weighting in a different way. In case 1, cluster C_1 and C_2 have no corresponding class in the atlas and P_1 and P_2 are both empty – we set $w(C_1, C_2) = 1$ and perform no weighting. In case 2, one cluster – either C_1 or C_2 – belongs to an atlas-class while the other cluster correspond to no class (P_1 or P_2 is empty). The weighting is then given by $w(C_1, C_2) = 1 \div p$, where p is the cluster-to-class probability of the cluster with the non-empty class P. *The weighting* $w(C_1, C_2)$ will be > 1. In case 3, both clusters belong to the same class ($P_1 = P_2$). The weighting is given by $w(C_1, C_2) = sqrt(((1-p_1)^2 + (1-p_2)^2) \div 2)$. It will be < 1. In case 4, both clusters belong to the different classes ($P_1 \neq P_2$). The weighting is given by $w(C_1, C_2) = 1 \div sqrt(((1-p_1)^2 + (1-p_2)^2) \div 2)$ and will be $>> 1$.

Materials and Methods – In order to demonstrate the feasibility of the proposed technique, DTI data sets of 46 healthy volunteers were acquired 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 [4]. A 12 channel phased array matrix head coil was employed and the following parameters were used: T_E=91 ms, T_R=6800 ms, α = 90°, iPAT=2, matrix of 96×96, 55 slices with a thickness of 2.5 mm, resulting in a voxel size of 2.5×2.5×2.5 mm^3. Five b_0 images without diffusion weighting as well as 70 diffusion weighted images sampled with different gradient directions at b=1000 s/mm^2 were acquired. In-plane interpolation was performed on the MR-scanner, resulting in a voxel size of 1.25×1.25×2.5 mm^3. The Diffusion Toolkit [5] was used to perform whole brain fiber tractography. Tracts having a length less than 30 mm were subsequently removed from the data set. For all data sets, non-linear registration was performed with the ANTs framework [6] in order to transfer the data into the space of the atlas. The probabilistic atlas was constructed with a semi-automatic technique and consisted of 18 fiber bundles [7]. Atlas-guided cluster analysis was then performed for all data sets using this atlas.

Results – The cluster analysis was successfully performed for all 46 datasets and the fiber bundles that correspond to classes in the atlas were reliably extracted. In addition, other clusters that belong to certain other white matter structures were identified by the algorithm. A selection of extracted fiber bundles is presented in Fig. 3. Compared to conventional clustering we observed an increase in computation time of ~10% for the atlas-guided clustering.

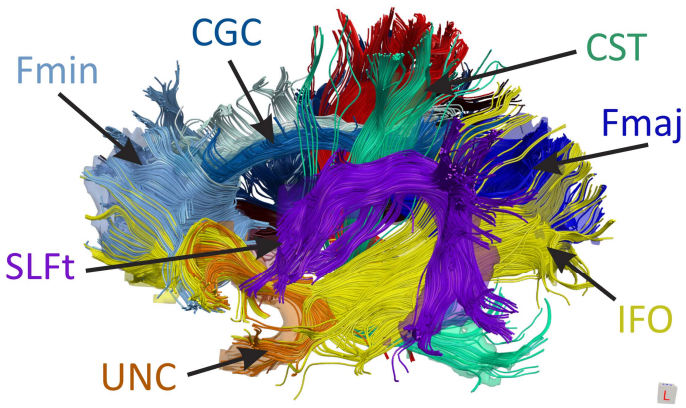

Fig. 3 – Selection of fiber bundles that were extracted with the atlas-based clustering approach: Forceps minor (Fmin), forceps major (Fmaj), cortico-spinal tract (CST), inferior fronto-occipital fasciculus (IFO), uncinate fasciculus (UNC), temporal part of the superior longitudinal fasciculus (SLFt), cingulum bundle (CGC).

Discussion & Conclusion – We present a new method for the fully automatic extraction of fiber bundles by using a new atlas-guided clustering approach. The anatomical information of a probabilistic white matter atlas was incorporated by determining individual weighting factors based on the atlas-class memberships of the tracts. For all subjects we were able to cluster the data and to extract the fiber bundles that belong to the classes in the atlas. As a hybrid approach, the technique combines the benefits of classification and clustering. It facilitates not only the extraction of the bundles that correspond to the classes of the atlas; it also enables the identification of bundles that are not present in the atlas. We further believe that this approach might be suitable for the efficient generation of white matter atlases by successively integrating automatically clustered bundles into the atlas.

Acknowledgements – This study was supported by the German Federal Ministry of Education and Research (BMBF), project number: 01GW0740. We like to thank Siemens Healthcare, Erlangen, Germany for their support.

References – [1] Berman et al, 2005, Neuroimage 27, 862–871 [2] Ros et al, 2012, Biomed Tech 57, 530-533 [3] Ros, 2011, Proc Intl Soc Mag Reson Med 18, #3965 [4] Heid, 2000, Proc Intl Soc Mag Reson Med, 8 [5] Wang et al, 2007, Proc Intl Soc Mag Reson Med 15, #3720 [6] Klein et al, 2009, Neuroimage 46, 786-802 [7] Ros et al, 2012, Proc Intl Soc Mag Reson Med 20, #3611