Recognition of bundles in healthy and severely diseased brains

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Target Audience This work is addressed to all researchers who are interested in extracting anatomically relevant bundles from dMRI tractography.

Purpose Extracting anatomically relevant bundles from tractography datasets is usually a time consuming task as these datasets are large and noisy and a great amount of manual work is requested from expert neuroanatomists to acquire these bundles of interest. We propose here a new automatic method which given a single model bundle from a single subject or from a bundle-specific atlas will recognize the same bundle in other subjects. We do this with precision and efficiency using a new algorithm based on streamline-based clustering[1] and streamline-based registration[2,3].

Methods This algorithm assumes that both the model bundle (MB) and the subject's streamlines (S) are in the same space registered using an initial linear registration. Then: a) we first use Quickbundles[1] to remove clusters which are far from MB to create a local set of streamlines (S-local), b) use streamline-based linear registration (SLR) to register S-local to MB, c) remove the streamlines that are not similar with MB using MDF and MAM distances[1]. The method is validated using IFOFs and UNC bundles from 60 subjects manually segmented by expert neuroanatomists with DTI streamlines with FACT. Additionally, we examined the detections of the corticospinal tract (CST) from HARDI streamlines on patients with a high grade tumor.

Results Our proposed method was able to clearly detect all IFOFs and UNC bundles from the 60 subjects without including parts from other bundles. Furthermore, 60-70% of the streamlines in the automatically recognised bundles were exactly the same with what the experts had manually segmented. In Fig. A, we show results for the automatic extraction of UNC in 4 subjects (S_1-S_4) in comparison to the expert segmentation. In Fig. B, we see the automatic recognition of the CST in a brain with a massive tumor. This is an example where an expert neuroanatomist had to use extra information from an fMRI finger tapping experiment to make sure that his segmentation was accurate. However, our new method picks it up automatically using a bundle segmented from another healthy subject S_1.

Discussion/Conclusion We introduced a novel algorithm for bundle recognition. This method is different from other automatic extraction techniques[5,6] as it introduces this new concept of local streamline-based registration using SLR[2,3] which is remarkably robust to noisy, missing or disease-related datasets[2,3]. The proposed method is efficient needing less than a minute to run and will be soon available in DIPY[7] version 0.9.

References [1] Garyfallidis, QuickBundles, Frontiers in Neuroscience, (2012), **[2]** Garyfallidis, Direct bundle registration, ISMRM (2014), **[3]** Garyfallidis, Robust and efficient registration of white-matter fascicles, Neuroimage (2014) (under review), **[4]** Zimmer, The new science of the brain, National Geographic 36–57 (2014), **[5]** Guevara, Automatic fiber bundle segmentation, Neuroimage (2012), **[6]** Tunc, Automated tract extraction, Neuroimage (2014), **[7]** Garyfallidis, Dipy, a library for the analysis of diffusion MRI data, Frontiers in Neuroinformatics, (2014).

A. Recognized uncinate

B. Recognized CST with tumor using healthy CST

FA of subject S_2 showing the extent of the grade 3 glioma tumor