Identification of U-Bundles Based on Sulcus Morphology

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1 Introduction

It is a fact that the brain cortical folding pattern morphology is specific to each human being. Neuroanatomists think that the folding pattern is strongly related to brain connectivity [1]. As each folding variation implies a specific rearrangement of the different white matter bundles, it also impacts the position of functional regions. This particularity raises an issue for precise brain spatial normalization, as nobody knows how to align brains with different folding patterns. For this reason, in the field of brain segmentation, old fashion approaches relying on a single model, often generated from a single subject or a group's average, cannot overcome the folding variability. Therefore, modern strategies are often built from a multi-subject atlas, which has proven to be a very efficient solution to overcome this difficulty [2]. In order to design an analogous solution for brain mapping, it was recently proposed to restrict statistical analysis to groups of subjects with compatible folding pattern [3], which has been experimented to deal with the impact of the central sulcus morphology on fMRI-based activation maps [4]. Differences in the cortical folding have been proved to be associated with differences in the localization of functional areas. Therefore, we need to understand better how to relate to each other brains with different folding patterns. In this abstract, we propose a new step in this direction: we performed a first attempt to observe an effect of a simple morphological polymorphism related to central sulcus on the underlying U-fiber organization.

2 Method

We studied the impact of the left central sulcus on the neighboring short bundles. The central sulcus is one of the most stable and prominent of the human brain, which makes it can be identified without ambiguity, and it presents a precise structure-function landmark called the "hand knob" [4]. We used 71 healthy subjects from the ARCHI database (23.5 ± 5.2 years old of age; 44 males, 27 females; 68 right-handed and 3 left-handed) [5]. First, the isomap of the central sulcus is calculated with the method

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described in [4], obtaining an axis of variability that goes from a "single knob" configuration to a "double knob" configuration (Fig. 1). After affine spatial normalization, the tractograms (i.e. sets of streamlines) of all subjects were further aligned in order to register all central sulci toward the most neutral sulcus i.e. the one with the shape that minimizes the average distance to the rest. Subjects were then gathered in morphologically compatible groups by dividing the isomap axis into 6 intervals of the same length. Subjects of each group did not overlap between them. To each group we applied a slight variation of the method described in [6] in order to identify reproducible short white matter bundles among the subjects (Fig. 2). Briefly, accordingly to the Desikan-Killiany atlas [7], we selected the ROIs around the central sulcus (namely precentral (PrC), postcentral (PoC), caudal middle frontal (CMF), pars opercularis (Op), superior parietal (SP), supramarginal (SM) gyri) and extracted the fibers connecting each pair of them. Then to the extracted sub-tractograms we applied an intra-subject average-link hierarchical agglomerative clustering in order to identify actual fiber bundles (i.e. fibers with similar shape and position along the gyri). The fiber bundles were then matched across the subjects by means of an inter-subject hierarchical clustering, and at the same time bundles that were no present in at least half of the population were discarded. This results in 6 different "atlases", each one specific to its group. Then a matching across atlases is performed to assign a common label to similar bundles. In order to do that a mean centroid representing each bundle is calculated. First, a centroid from the first atlas (the most to the left in the isomap) is taken. A nearby centroid is sought from the second atlas, within a distance threshold. If found, a new centroid is calculated from these two, which is used to seek a nearby centroid from the third atlas and so on. If no centroid is found in a particular atlas, it is just skipped. Unlike the original method were only two preliminary atlases were matched to keep only reproducible bundles [6], in this case we sought to identify the presence of the bundles among the atlases, therefore those with no matches are kept but labeled with a single different label. Also, for each bundle, the correlation of fiber coordinates from 5 equidistant points (beginning, a quarter, middle, three quarters and ending) with the isomap values was computed.

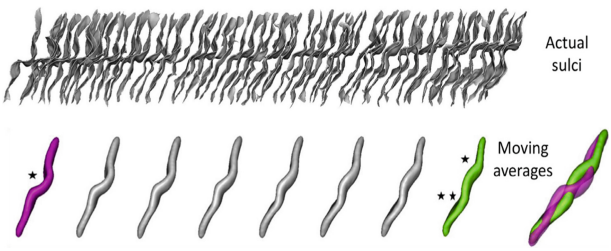


Fig. 1. Moving average of the central sulcus morphology.

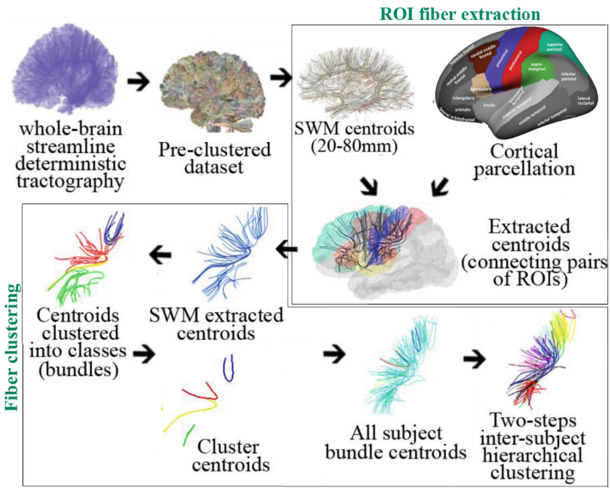


Fig. 2. Schematic of the U-fiber identification method.

3 Results

We computed bundles connecting pairs of 6 regions close to the central sulcus (Fig. 3). From the visual inspection, we identified 6 bundles showing regular changes either in position or shape, along the isomap axis (Fig. 4). Most of these differences correspond to fiber extremities moving up or down as the central sulcus shape shifts. Also, these bundles show a moderate correlation with the sulcus isomap values for at least one section of points, depending on their configuration.

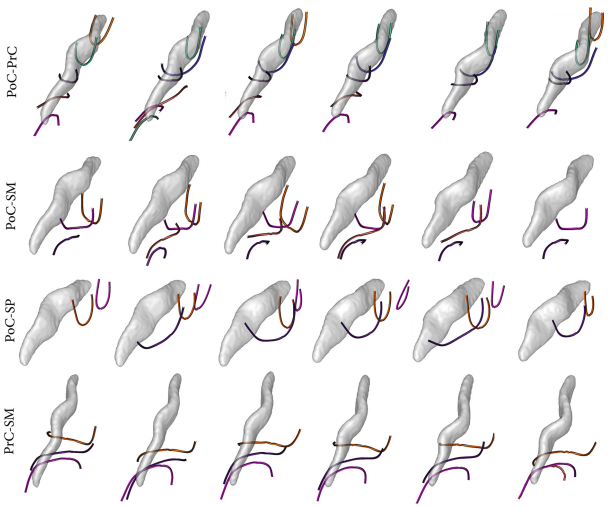
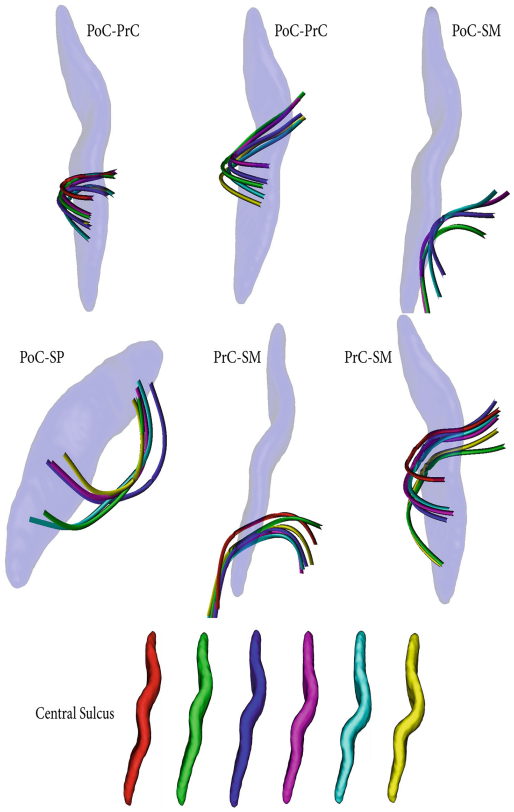


Fig. 3. Bundles obtained with the method.

We also applied the described method to a different database and selected a higher number of atlas. For a same bundle there seem to exist two different configurations among the groups (Fig. 5).



Bundle	r	p
PoC-PrC 1	0.175	<0.001
	0.165	<0.001
	0.128	0.001
	0.172	<0.001
	0.172	<0.001
PoC-PrC 2	0.237	<0.001
	0.217	<0.001
	-0.313	<0.001
	-0.032	0.519
	0.237	<0.001
PoC-SM	0.217	<0.001
	-0.188	<0.001
	0.233	<0.001
	-0.307	<0.001
	-0.395	<0.001
PoC-SP	0.21	0.011
	0.145	0.081
	0.057	0.494
	-0.05	0.546
	-0.025	0.767
PrC-SM 1	0.139	0.025
	0.184	0.03
	0.239	<0.001
	0.34	<0.001
	-0.261	<0.001
PrC-SM 2	0.145	0.02
	-0.232	<0.001
	0.083	0.186
	0.122	0.052
	-0.133	0.033

Fig. 4. Bundles showing differences along the isomap and their correlation for the five points.

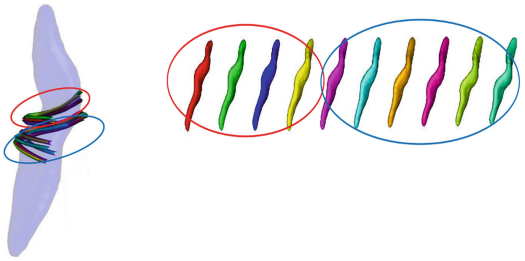


Fig. 5. Results from 10 atlas.

4 Conclusions

We presented preliminary results from the short bundle identification across groups with different central sulcus morphology. These results show that some bundles present different configurations which might drive or come from differences in the sulcus shape. Notice that sometimes, for groups in the extreme of the isomap axis some bundles are not present. Although these bundles might have been discarded during the filtering steps performed, it is interesting as it might be as well because of smaller or even nonexistent connections that impact the shape of the corresponding gyri. However, a better strategy needs to be found in order to ensure that bundles less reproducible within a group could survive until the matching step, as these bundles might present the transition between the two groups. Although these results are preliminary, it shows that there is a link between the brain wiring and the cortical folding pattern. Future work will be focused on testing these differences on a bigger dataset (HCP dataset [8]). This would also allow dealing with more groups which might lead to a smoother transition across the isomap axis.

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