Software pipeline for thickness profile based morphological analysis of the midsagittal section of the corpus callosum

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Target audience

Researchers involved in applications of MRI methods, paediatric researchers, clinicians.

Purpose

To present a fully automated software pipeline for thickness profile based morphological analysis of the midsagittal section of the corpus callosum (CC) using 3D structural T_1-weighted images. This pipeline facilitates efficient, robust and reproducible morphological analysis for large cohorts.

Methods

Background: The pipeline performs the following sequence of steps: midsagittal plane extraction, CC segmentation algorithm, graphical quality control tool, and thickness profile generation. Group-wise comparison studies are facilitated by statistical analysis routines and their results can be displayed with the included figure generator.

Pipeline component details: Mid-sagittal plane extraction involves firstly cropping the neck to improve robustness followed by either the model-based acpcdetect[1] or the registration-based FLIRT[2] tools. The centerpiece of the methods is the novel CC segmentation algorithm. This algorithm initializes using template probability maps constructed from the OASIS[3] dataset with alignment based on the real-time Lucas-Kanade Tracker[4]. Reinitialisation to a data-driven segmentation and refinement are performed with mathematical morphology operations. A postprocessing routine to remove posterior pericallosal veins/vessels is included. Thickness profiles are generated using a fully automated version of a previously published method[5]. Statistical analysis routines include the one-sample Student's and two-sample Welch's T tests with multiple comparison correction being performed by the permutation based step-down max$T$ p-value adjustment algorithm[6] and False Discovery Rate to control the Family Wise Error Rate and the False Discovery Rate, respectively. A 3D tube-based visualisation of an "ideal" callosal boundary is the basis of the results display routine. The colours of the tube represent p-values and the tube may be rotated to any view of the user's choosing.

Evaluation of the CC segmentation algorithm: The CC segmentation was executed on two publicly available datasets: OASIS[3] (316 images) and mindboggle101[7] (100 images). Both datasets contained manually defined CC segmentations along with thickness profiles which were used as ground truth. The Dice and Hausdorff metrics were computed for estimated versus ground truth segmentations to evaluate segmentation overlap and boundary discrepancies respectively. Thickness profile agreement was assessed with correlation coefficients computed between ground truth and estimated thickness profiles.

Results

Figure 1 shows the Dice (i) and Hausdorff (ii) metrics, average thickness profiles (iii) and thickness profile correlation coefficients (iv) after executing the CC segmentation algorithm on the mindboggle101 dataset; thickness profiles were generated with 100 nodes. Very similar plots were obtained for the OASIS dataset (data not shown). Figure 2 shows an example output of the results display routine for a fictional set of p-values.

Discussion and Conclusion

A software pipeline for morphological processing of the CC has been presented. The CC segmentation algorithm has been demonstrated to be accurate on the large publicly available dataset of mindboggle101 (100 images) with average Dice coefficients of 0.85 and average Hausdorff distances of 2mm. Similar results were obtained for the OASIS dataset.

Compared to ground truth, the estimated thickness profiles were consistently thinner. This effect was due to the difference between the choice of the boundary location with respect to the intensity ramp bordering the darker grey matter/cerebrospinal fluid tissue types. Given that the shapes of the thickness profiles were in high agreement, this underestimation acts effectively as a scaling factor and is therefore not a major issue for inter-subject comparisons based on the estimated segmentations versus the ground truth segmentations.

The pipeline is computationally efficient, producing a thickness profile from a 3D T_1-weighted MR image in 10 seconds on average. The processing pipeline along with the graphical quality control tool and group-wise statistical analysis routines, provides a comprehensive, efficient and robust environment for morphological analysis of the CC.

Figure 1: Summary results for mindboggle101 dataset. Quantitative evaluation of segmentation accuracy is given by the Dice coefficients (i) and Hausdorff distances (ii). Initial and final denote the initially generated segmentation and final denotes the final segmentation after all refinements. Mean estimated and ground truth thickness profiles and the correlation coefficients are shown in (iii) and (iv), respectively.
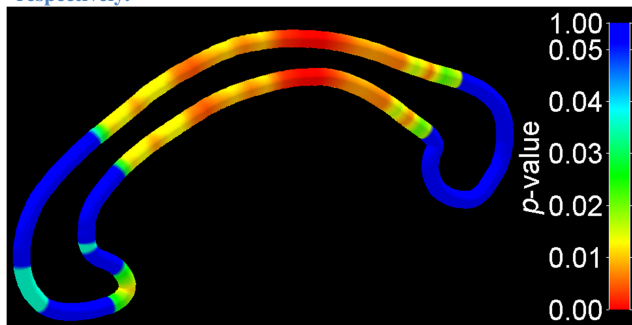
Figure 2: Example output of statistical results display script for fictional collection of p-values.

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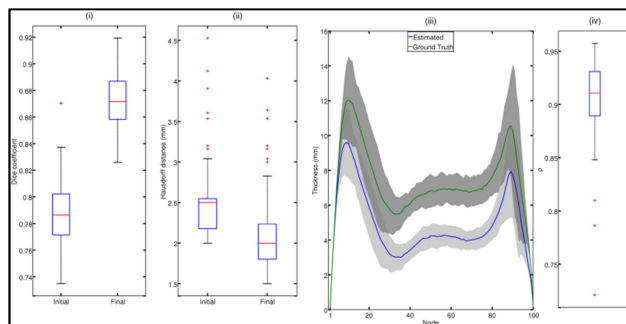7. Klein A, Tourville J. 101 labeled brain images and a consistent human cortical labeling protocol. *Frontiers in Neuroscience*. 2012;6(171).