

Multi-Atlas Corpus Callosum Segmentation with Adaptive Atlas Selection

Babak A. Ardekani^{1,2}, Toshikazu Ikuta^{3,4}, Alvin Bachman¹, and Philip R. Szeszko^{3,4}

¹Center for Advanced Brain Imaging, Nathan Kline Institute for Psychiatric Research, Orangeburg, NY, United States, ²Department of Psychiatry, New York University School of Medicine, New York, NY, United States, ³Feinstein Institute for Medical Research, Manhasset, NY, United States, ⁴Psychiatry Research, The Zucker Hillside Hospital, Glen Oaks, NY, United States

Introduction

Atlas-based brain image segmentation in MRI was introduced in mid 1990's. The idea is to nonlinearly deform (register) a brain image (the atlas), in which the location of a given structure is known, to a brain image (the test image) on which we would like to locate the same structure. The atlas information is then propagated onto the test image using the nonlinear mapping obtained by registration. A major advancement in this area, which became possible with advances in computer hardware and software technology, was the extension of the idea to using multiple atlases. Here, multiple atlases are used to provide independent segmentations of the test image. The final consensus segmentation is obtained by merging the individual predictions using multi-classifier fusion techniques. Several methods for consensus building have been proposed with simple majority *vote rule* being the most commonly used method to date. Further progress in this area has been the idea of atlas selection. In this approach, not all, but a subset of atlases that are most *similar* to the test image is used for multi-atlas segmentation. In this paper, we further extend this idea to *adaptive* atlas selection. In previous works, the subset of atlases were fixed beforehand and used in the classification of all pixels. In the new adaptive atlas selection, the subset of atlases used for classification varies from pixel to pixel. Here we use *local* similarity between atlas and test images to select the subset of atlases that would take part in the pixel classification. We have applied this technique to the problem of segmentation of the corpus callosum (CC) cross-sectional area on the mid-sagittal section of the brain in MRI.

Segmentation Algorithm

The algorithm first automatically locates the mid-sagittal plane (MSP) as the one that yields the maximum brain mirror symmetry. Then the locations of the anterior and posterior commissures (AC/PC) are located on the MSP using template matching, where the templates are obtained from a number of atlas scans with known AC/PC locations. Then a rectangular CC *search region* is defined on the MSP based on *a priori* information from the atlas dataset (Figure 1). Next, all available atlases are nonlinearly mapped to the test image using the ART non-linear registration software (<http://www.nitrc.org/projects/art>). ART displacement fields are only sought within the CC search region, substantially reducing the computation cost. For each atlas, a local cross-correlation (LCC) map is computed where pixel values represent LCC between the warped atlas and the test image. To classify a pixel within the search region, the subset of m atlases with the highest LCC's at the pixel under consideration are selected, and their corresponding classifications are merged using the vote rule. A novel element of our approach is that the subset of atlases varies by location, making the atlas selection process adaptive. The window size for LCC computation (w) and the size of the atlas subset (m) are fixed parameters that are obtained using leave-one-out cross validation (LOOCV) on the atlas set.

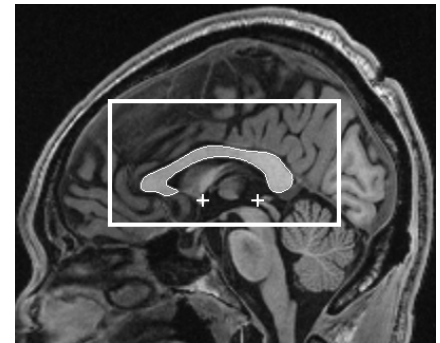


Figure 1: Automatically detected mid-sagittal slice, AC/PC landmarks, and rectangular CC search region.

Experiments and Results

We used a set of 76 high-resolution brain scans of normal subjects (42 male; 30 females; age: 35.0 ± 12.4 years) to evaluate our algorithm. T1-weighted 3D SPGR scans were acquired on a 3 Tesla GE Signa HDx scanner with the following parameters: TR/TE=7.8/3.0 ms; matrix size: 256×256 ; FOV: 240×240 mm²; number of slices: 216; slice thickness: 1.0 mm. The CC was manually delineated on all images on the automatically detected MSP by the same rater. Scans were

Table 1: Dice index summary statistics for intra- and inter-rater reproducibility and manual vs. automated segmentation.

	n	Avg.	S.D.	Min.	Max.
Intra-rater	10	.972	.010	.949	.986
Inter-rater	10	.961	.012	.935	.972
Manual vs. Automatic	38	.965	.012	.922	.984

randomly divided into two subsets of 38: an *atlas set* and a *test set*. Manual segmentations were repeated twice on a subset of 10 test set scans by the same rater and by a different rater. The Dice index was used to quantify the accuracy of the automated segmentations and intra- and inter-rater reproducibility. The optimal values of $w=7 \times 7$ mm² and $m=12$ were obtained using LOOCV on the atlas set. As an example, the automatically detected CC on a test scan is shown in Figure 1. The entire algorithm, implemented using the message passing interface (MPI) parallel programming library, takes approximately 15 seconds to run on a dual quad-core (8x2.4 GHz processors) computer with 38 atlases. Reproducibility and accuracy results are shown in Table 1. The average Dice index obtained between manual and automated segmentations in the test set was 0.965 which is close to averages obtained for intra- and inter-rater manual segmentations (0.972 and 0.962), demonstrating the accuracy of the algorithm.

Discussion and Conclusions

The CC is the largest white matter fiber bundle in the brain connecting the two hemispheres. There has been a large number of studies that analyze the size and shape of the CC in various groups and disorders, mostly employing manual segmentations of the CC, which are tedious to obtain. Availability of a fast and accurate CC segmentation method greatly facilitates such studies in the future by allowing analysis of larger cohorts. For example, we have applied this method to data from the ADNI and OASIS databases, where we have been successful in identifying a novel biomarker for diagnosis of Alzheimer's disease (abstract submitted separately).