

# Strucseg - A Pipeline for Segmenting Brain Structures using Open Source Tools

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**Abstract**—Structure segmentation is often the first step in the diagnosis and treatment of various diseases. Because of the variations in the various brain structures and overlapping structures, segmenting brain structures is a very crucial step. Though a lot of research had been done in this area, still it is a challenging field. Using prior knowledge about the spatial relationships among structures, called as atlases, the structures with dissimilarities can be segmented efficiently. Multiple atlases proves a better one when compared to single atlas, especially when there are dissimilarities in the structures. In this paper, we proposed a pipeline for segmenting brain structures using open source tools. We test our pipeline for segmenting brain structures in MRI of using the public data set provided by MIDAS

**Keywords**—Segmentation; brain structures; multiple atlases

## I. INTRODUCTION

Segmenting brain tissues/ structures is the primary step in diagnosis and treatment of various brain related disorders. The MRI scan gives clear and exhaustive images of soft tissue. Bones can't be visualize using MRI because bone tissue doesn't comprise much water. Due to this, MRI, fMRI are widely used in tissue and structure segmentation. Tissue segmentation can be done using intensity thresholding. But segmenting brain structures are complicated as a structure can be comprised of more than one tissue type. Various tools and techniques are available for segmenting brain structures. Out of all proposed techniques, segmenting structures using atlases gives good result. Since there are large anatomical variations in the structures, using multiple atlases rather than single atlas gives superior results. The accuracy of the result largely depends on the selection of atlases.

## II. MATERIALS AND METHODS

### A. Processing Pipeline

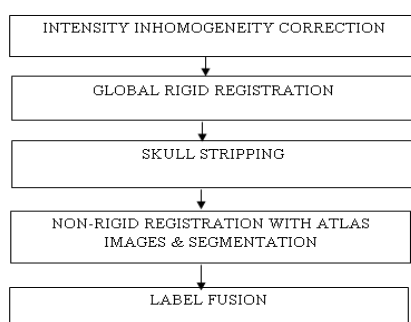


Fig. 1. Pipeline for segmenting brain structures

### B. Intensity Inhomogeneity Correction using ANTs's N4BiasFieldCorrection

The intensity inhomogeneity is caused mainly due to the RF coil imperfections. This artifact, results in the variations of intensities in the same tissues. These variations affect the segmentation results. Various methods are proposed for intensity inhomogeneity correction. N4 is a bias correction algorithm and is a variation of N3 algorithm described by Tustison et. al. [1]. Using N4BiasCorrection command [2], the intensity inhomogeneity of MRI scan can be corrected.

```
*N4BiasFieldCorrection -i inputfile.nii.gz -o outputfile.nii.gz
```

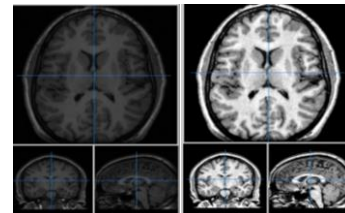


Fig. 2a. Before bias correction Fig. 2b. After bias correction

### C. Global Rigid Registration With MNI template space using 3DSlicer's BRAINS

Registration is an important preprocessing step in the analysis of images. It is a process of finding geometric transformation so that two images are perfectly aligned. Depending on the nature of transformation, the registration can be classified into rigid, affine, projective, curved and non-rigid[3].

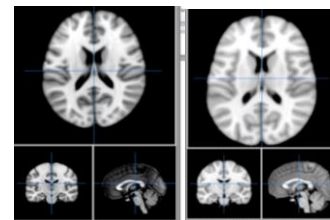


Fig. 3a MNI Template image (T1) - fixed Fig. 3b. Output image after global rigid registration

### D. Skull Stripping using the tool ROBEX

Skull Stripping removes non-brain tissue in MR brain images. Many Skull Stripping methods have been proposed[4-9]. Skull stripping improves the performance of the registration and segmenting process. We use the ROBEX tool proposed by [9] and downloaded from [10].

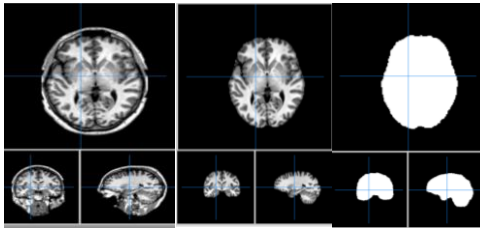


Fig. 4a. Input image Fig. 4b. After Masking Fig. 4c. Image mask

**E. Non-Rigid Registration of subject image with template image using ANTs 's ANT and WarpImageTransform tool**

There are enormous research in the segmentation of brain structures. Several studies have shown that applying prior knowledge in the process of segmentation gives a better performance[11-13]. Especially using multiple atlases gives greater accuracy when there are large variations in the structures[14]. To transfer labels from the atlas images, target image should aligned [non-rigid] with all atlases and a deformation field should be calculated. Using this, labels from the atlas images are propagated to the target image.

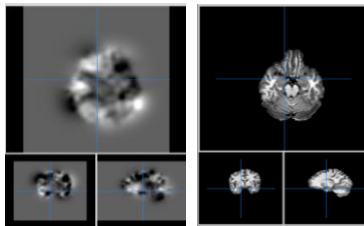


Fig 5a Warped image Fig. 5b Final Registered image

**F. Label Fusion Using Patch Differences**

For each voxel in the test image,  $TX_i$ , we have to select an optimal label from a label set  $(L_{i1}, L_{i2}, \dots, L_{im})$ .  $N$  refers number of atlases and  $M$  refers to the number of voxels. In our experiment, we select 10 atlas images. Mutual information between each atlas and test image pair is calculated and the top 10 atlas images are selected. As the intensity of a voxel dominated by its surrounding voxels, the label of a voxel is determined by the labels in the neighbouring voxels too. So, for each voxel in the test image,  $TX_i$ , we choose a  $3 \times 3$  neighbourhood patch. And for each patch in the test image, we select a patch that is closest to the patch in the test image from the patches from all the segmented images. We use Euclidean distance metrics to measure the distance between the patches. A patch with the smallest distance is selected for each voxel and the label from the selected patch is propagated to the test patch. Repeat this procedure for all the voxels in the test image.

**III. RESULTS AND DISCUSSION**

All the test and atlas images we used in our paper are downloaded from MIDAS digital archive system<sup>[15]</sup>. All data are already intensity homogeneity corrected. Preprocessing should be done to all subject and atlas scans. Intensity inhomogeneities were corrected using ANTs N4BiasFieldCorrection, then skull stripping were performed using ROBEX. The test image is registered with a set of atlas images using ANTs. Labels are propagated from the atlas

images using “warpimagemultitransform”. This step gives a set of segmented images for a test image. Finally the labels from these segmented images are fused together to gives a final segmentation. The bias field correction takes about 20 seconds for each image. The global registration takes 2 seconds for each image. For skull stripping, each image takes 12 seconds, non-rigid registration and label propagation takes about 40 minutes for each image atlas pair. Finally the label fusion takes 1 ½ hours. All these are done using shell scripting and the sample commands are given below:

```
>n4biasfieldcorrection -d 3 -i h:\data\training\1003_3.nii -o h:\newdata\bias_1003_3.nii.gz -s 4
>BRAINSfit --fixedVolume h:\newdata\bias_1003_3.nii.gz --movingVolume mnitemplate.nii.gz --outputTransform h:\newdata\rigid_1003_3.nii.gz --transformType Rigid --histogramMatch
>robex h:\newdata\rigid_1003_3.nii.gz h:\results\skullstrip\1003_3_robex.nii.gz h:\results\skullstrip\1003_3_robex_mask.nii.gz
>ants 3 -m PR[h:\results\skullstrip\1003_3_robex.nii.gz,h:\results\skullstrip\1007_3_robex.nii.gz,1,4] -i 50x50x0 -t Elast[1.0] -o h:\register\skull_pnew_seg37.nii.gz
>warpimagemultitransform 3 h:\results\skullstrip\1007_3_robex.nii.gz h:\register\skull_pnew_total37.nii.gz -R h:\results\skullstrip\1003_3_robex.nii.gz h:\register\skull_pnew_seg37warp.nii.gz h:\register\skull_pnew_seg37affine.txt --use-NN
>warpimagemultitransform 3 h:\data\training\1007_3_glm.nii h:\register\skull_pnew_glm37.nii.gz -R h:\results\skullstrip\1003_3_robex.nii.gz h:\register\skull_pnew_seg37warp.nii.gz h:\register\skull_pnew_seg37affine.txt --use-NN
```

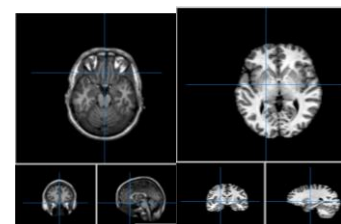


Fig. 6a. Test Image Fig. 6b. Test image after skull stripping

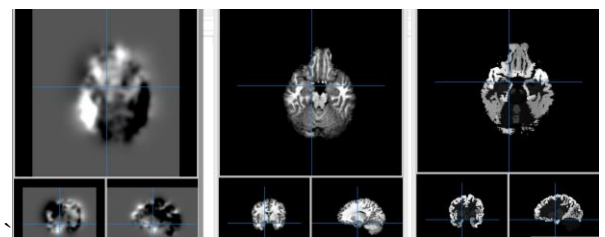


Fig 6 c –d : Registered Test image, its segmentation and its labeled image (for one set of atlas)

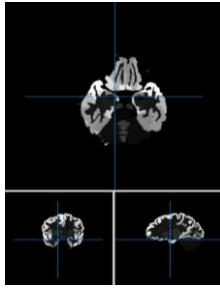


Fig 6e : Final segmentation of test image after fusion

To measure the efficiency of our pipeline, we use Dice coefficient, Jaccard co-efficient and kappa statistics. We compare the segmented image with the golden standard image. Our pipeline for the test image (Fig 5a) gives DICE= 0.954700, JACCARD= 0.913327 and KAPPA= 0.945266. Our experiment was conducted for 15 test images. The same test image gives DICE= 0.824501, JACCARD = 0.902120 and KAPPA= 0.932134 for simple majority voting method and gives DICE= 0.924500, JACCARD= 0.945255 and KAPPA= 0.89344 for weighted majority voting.

IV. CONCLUSION

We have presented a pipeline for segmenting brain structures using open source tools. We compare our pipeline with majority voting and weighted majority voting. For all the operations, only non-rigid registration and fusion steps consumes more time. For doing each set of registration, 30 to 40 minutes are needed. To do final fusion, the algorithm takes 1 1/2 hours. The time taken to compare our result with the golden standard is 49332 milliseconds. Fig 7a and Table I shows the performance of simple majority voting, weighted majority voting and our pipeline for a single test image. Fig 7b and Table II shows the segmentation performance of our pipeline for a various number of atlases and for the same test image. For 10 atlases, it gives a maximum accuracy. When compare to majority voting and weighted majority voting methods, our pipeline gives better accuracy.

TABLE I. PERFORMANCE COMPARISON OF VARIOUS ALGORITHMS

MEASURES	STRUCSEG	MV	WMV
DICE	0.9547	0.824501	0.9245
JACCARD	0.913327	0.90212	0.945255
KAPPA	0.945266	0.932134	0.89344

TABLE II: COMPARISON OF OUR SEGMENTATION PIPELINE FOR DIFFERENT NUMBER OF ATLASES.

Atlases	Total	Jaccard	Dice	False negative	False positive
10	0.895681	0.822509	0.902612	0.104319	0.09035
7	0.880107	0.802049	0.890152	0.119893	0.099571
5	0.85359	0.772619	0.871726	0.14641	0.10935
4	0.817069	0.729576	0.843647	0.182931	0.127988

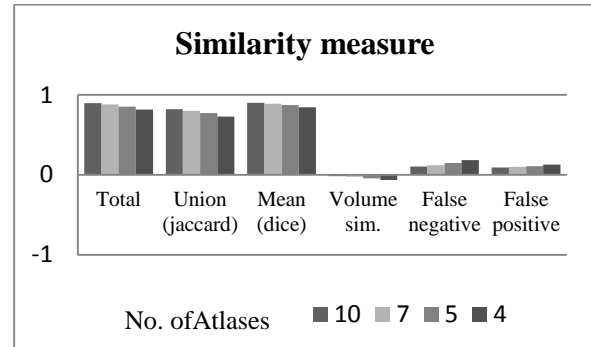


Fig. 7a : comparison for number of atlases

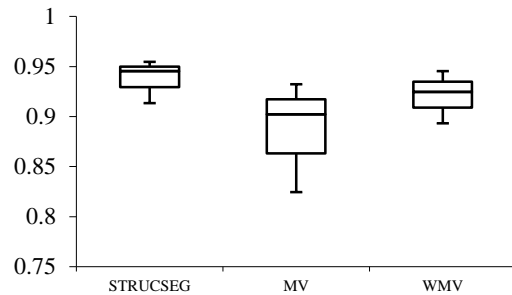


Fig. 7b: Comparison of Strucseg with MV & WMV

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