

Probabilistic Atlas for Brain Tissue Segmentation using Elastix and Transformix

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1 Overview

Automatic brain tissue segmentation into grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF) from magnetic resonance images (MRI) has helped diagnosing various types of neuro-disorders, such as multiple sclerosis, Alzheimer's, etc [1]. Various challenges exists with automatic brain tissue segmentation from MR images such as image artifacts or different anatomical structures sharing same tissue contrast, thus the presence of prior knowledge is important [2]. Atlases has been commonly used in the literature for automatic segmentation of brain structure and tissues as reviewed in [2]. Atlas-based segmentation methods aim to segment different targets, such as, for instance, brain structures, brain tissues, or lesions [2]. This laboratory session aims to develop an atlas using common registration and label propagation tools such as elastix and transformix for the purpose of brain tissue segmentation.

2 Objectives

The objectives of this laboratory sessions are to:

- (a) Research about probabilistic atlas.
- (b) To understand and use elastix for performing single registration of two 3D volumes as well as label propagation using transformix.
- (c) To write an algorithm that builds a probabilistic atlas and to discuss the assumptions and approaches taken.
- (d) To show 3-4 slices of the final probabilistic atlas (intensities and label probabilities) and the tissue models for each tissue class (histogram distribution).

3 Tools & Methods

3.1 Automating Elastix and Transformix

For a Windows operating system, both elastix and transformix were used using the command prompt. In order to register as many experiments as needed using different parameters files, this process has been automated in the submitted notebook, where a function called *execute_cmd* has been developed to take any command and execute it inside the notebook. This way, the process of registering and propagating the labels had became much quicker and easier, specially for the next section of selecting reference frame 3.3 as discussed.

Another automation was made to modify the transformation file generated from elastix for the purpose of obtaining a correct label volume was made in a function called *replace_text_in_file*. This function modifies certain values that was observed to alter the label propagation task, mainly the interpolator values, and thus to automate and quick the process, this function was used to alter the values. More explanation will be discussed in the following section 3.5.

3.2 Registration Parameters

Various parameters files has been experimented. From Model Zoo Elastix website, parameter files of *Par0010* has been used in this laboratory for the registration purpose. It consists of two files, both affine and B-spline that was used and developed on human brains using 3D MR volumes.

3.3 Selecting Reference Frame

As an initial step of building a probabilistic atlas for each label, a reference frame had to be

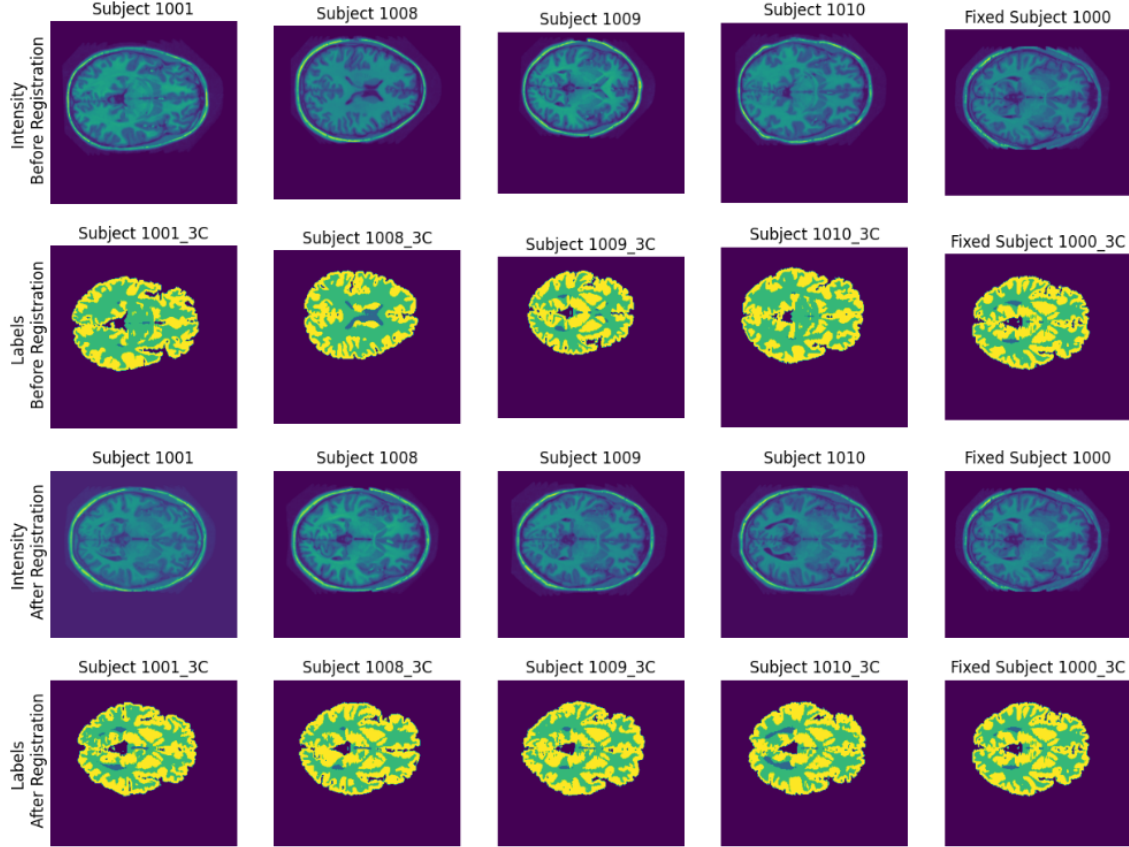


Figure 1: Registration and label propagation results using elastix and transformix.

selected to be used as the fixed image in the registration process. This step is very crucial to insure that all all volumes are in the same reference space. The ideal way of selecting the reference space is to find the most similar volume among all the training set by comparing it with all other volumes. This most similar volume, theoretically, should produce the best registration result with the highest similarity evaluation.

Choosing the most similar volume was done by registering each of the training images to all of the rest of the training images, and measuring both the mutual information (MI) and the normalised cross-correlation (NCC) between each fixed training image and the remaining 14 moving images. At the end, each fixed was registered with 14 moving images, and not with it's self. The average of the mutual information and normalised cross-correlation was computed. Finally, the fixed with the highest average mutual information was selected as the reference frame. Table 1 summarises the results obtained for registering each training image as a fixed, to the other possible combinations of moving images. It can be seen clearly that fixed image 1000 had the highest average mutual information, while 1001 had the highest averaged normalised cross-correlation. In this lab, image 1000 was selected

as the reference frame considering the averaged mutual information of all registration results for this fixed as the best metric to decide from. Using the selected parameter files of *Par0010*, some combinations failed in the registration and were eliminated from being selected as reference frame, such as 1002, 1006, 1015, 1036 volumes.

3.4 Registration using Elastix

After selecting a reference frame volume to be used as the fixed image in the registration process, the registration was made to the rest of the training volumes as the moving images, with the *execute_cmd* function and parameters discussed in sections 3.1, 3.2 respectively. An example of a command for registering a moving image to the fixed image is `elastix -f "1000.nii.gz" -m "1001.nii.gz" -p "Par0010affine.txt" -p "Par0010bspline.txt" -out "output/images"`.

As a result, all of the training volumes are in the same reference space of the fixed volume, making it possible to process them as in the next sections. Figure 1 shows a comparison between transformed and fixed images.

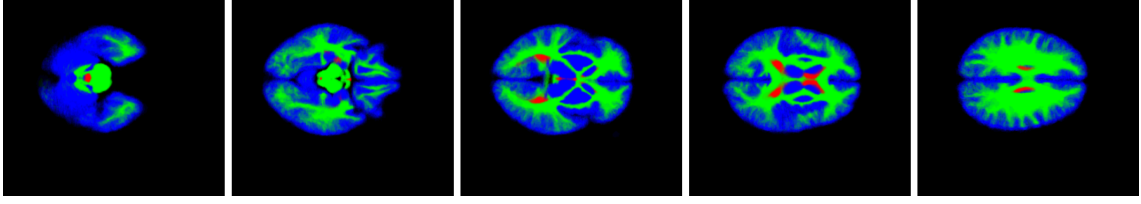


Figure 2: Combined averaged volumes of the three brain tissues.

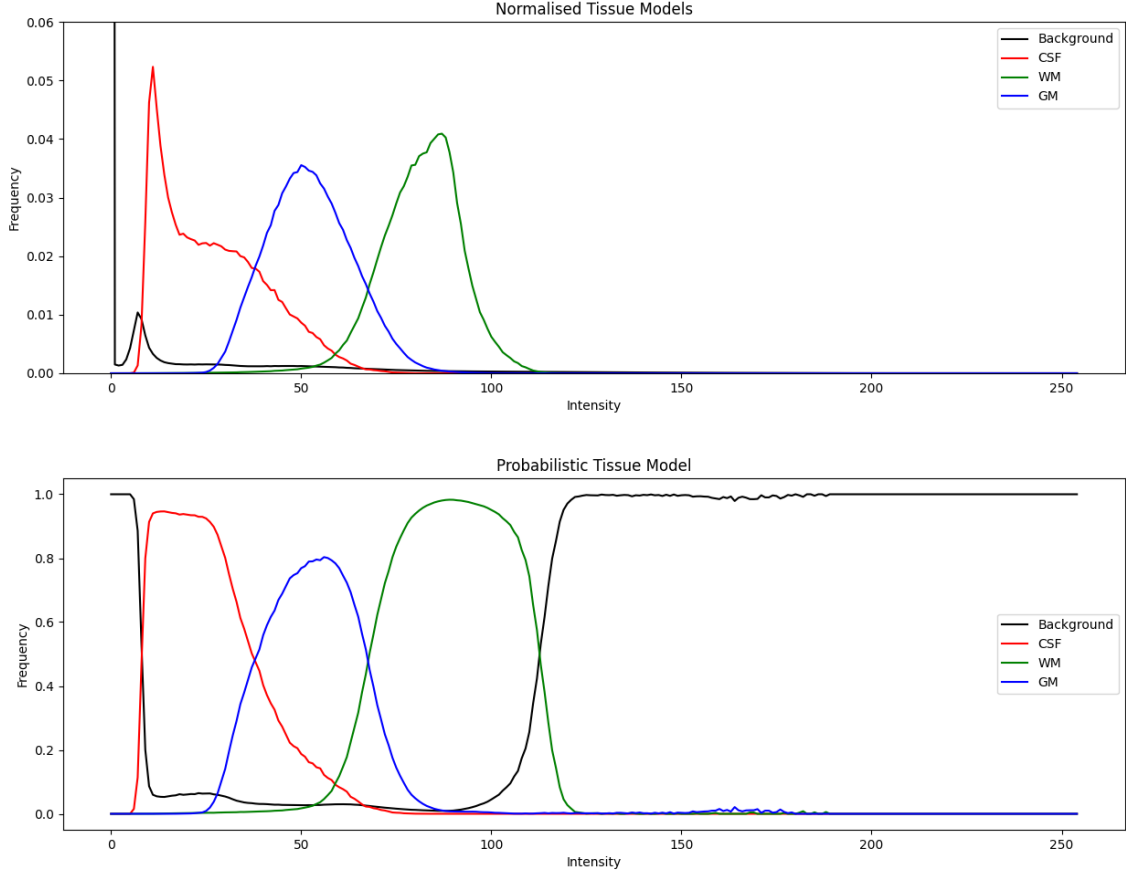


Figure 3: Tissue models using the training images and their respective labels.

3.5 Label propagation using Transformix

The next step after registering the intensity images with elastix is to propagate the labels to have the same registration in the same reference space using the transformations generated by elastix. This is done using transformix tool and the transformation parameters of each registered moving image.

To make the final propagated label volume has integer and not floating values, the interpolator value inside the transformation parameters files had to be modified. This is done using `replace_text_in_file` function that modifies the value of (`FinalBSplineInterpolationOrder` 3) to

(`FinalBSplineInterpolationOrder` 0). Then, the commands were passed to `excute_cmd` function as in 3.4 section to perform label propagation. An example of transformix command is `transformix -in "1001.nii.gz" -tp "1001/TransformParameters.1.txt" -out "output/labels"`.

3.6 Average Shape Atlas

After the label propagation, all of the labels now are in the same reference frame of their respective registered volumes, making it possible to build the atlas. A probability map was built by averaging all of the transformed labels masks for each of the classes, where all the masks are in the reference space. This averaging provides

Table 1: Comparative results of elastix registration result using *Par0010* on all possible fixed image combinations.

Fixed Image	Average Mutual Information (MI)	Average Normalized Cross-Correlation (NCC)
1000	0.544003	0.924832
1017	0.506419	0.916047
1001	0.506243	0.935060
1010	0.497656	0.932794
1008	0.491070	0.933131
1011	0.487106	0.932651
1013	0.443361	0.925239
1009	0.441582	0.931403
1012	0.434398	0.927540
1014	0.416701	0.929175

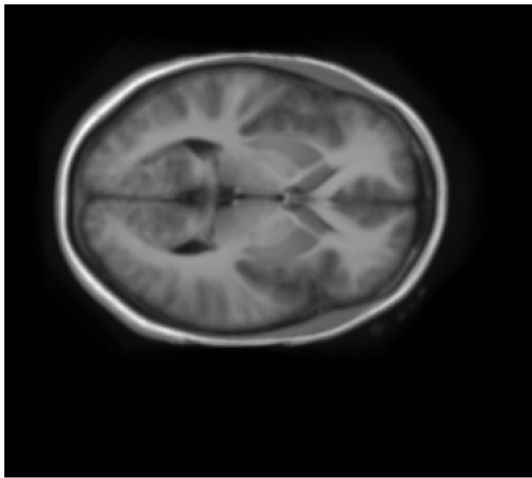


Figure 4: Averaged intensity atlas volume.

a probabilistic map that indicates the presence of the region of interest in certain area. For our case, 3 probabilistic maps were developed, one for each tissue. The atlas results for the averaged volumes of the three tissues are displayed in Figure 5. Figure 2 also displays those atlases in color map for different slices.

3.7 Average Intensity Image

Same approach was made for the intensity images, where the registered training images in the reference space were averaged to create an average intensity image that will be used to register any new test image, acting as a reference space. The averaged intensity map atlas is displayed in Figure 4.

3.8 Tissue Models

Tissue models were generated using the original dataset of training images and labels for each of the brain tissues. Firstly, the intensity images and their labels volumes were loaded. Then,

they were normalised using min-max normalisation where the max was set to 255 as 8-bit image type. After normalisation, the histograms were obtained using a built-in numpy function that returns the histogram, where a histogram was created for each of the brain tissues by segmenting the tissue using the labels volume. As there are many training images, the histograms were added to form a single histogram that represent the tissue in all of the dataset.

To create the normalised histogram as in Figure 3, the final combined histograms were normalised by dividing each of them by the sum of the elements inside. The probabilistic tissue model was made in a similar approach by dividing each of the normalised histograms by the sum of the values from each bin from all tissue models, creating probabilities between 0 and 1.

Conclusions

In conclusion, all the lab objectives had been achieved. The built atlases shows a descent probabilistic map for each tissue and will be used further in another lab for brain tissue segmentation.

References

- [1] Pulkit Kumar, Pravin Nagar, Chetan Arora, and Anubha Gupta. U-segnet: Fully convolutional neural network based automated brain tissue segmentation tool. In *2018 25th IEEE International Conference on Image Processing (ICIP)*, pages 3503–3507, 2018.
- [2] Mariano Cabezas, Arnau Oliver, Xavier Lladó, Jordi Freixenet, and Meritxell Bach Cuadra. A review of atlas-based segmentation for magnetic resonance brain images. *Computer Methods and Programs in Biomedicine*, 104(3):e158–e177, 2011.

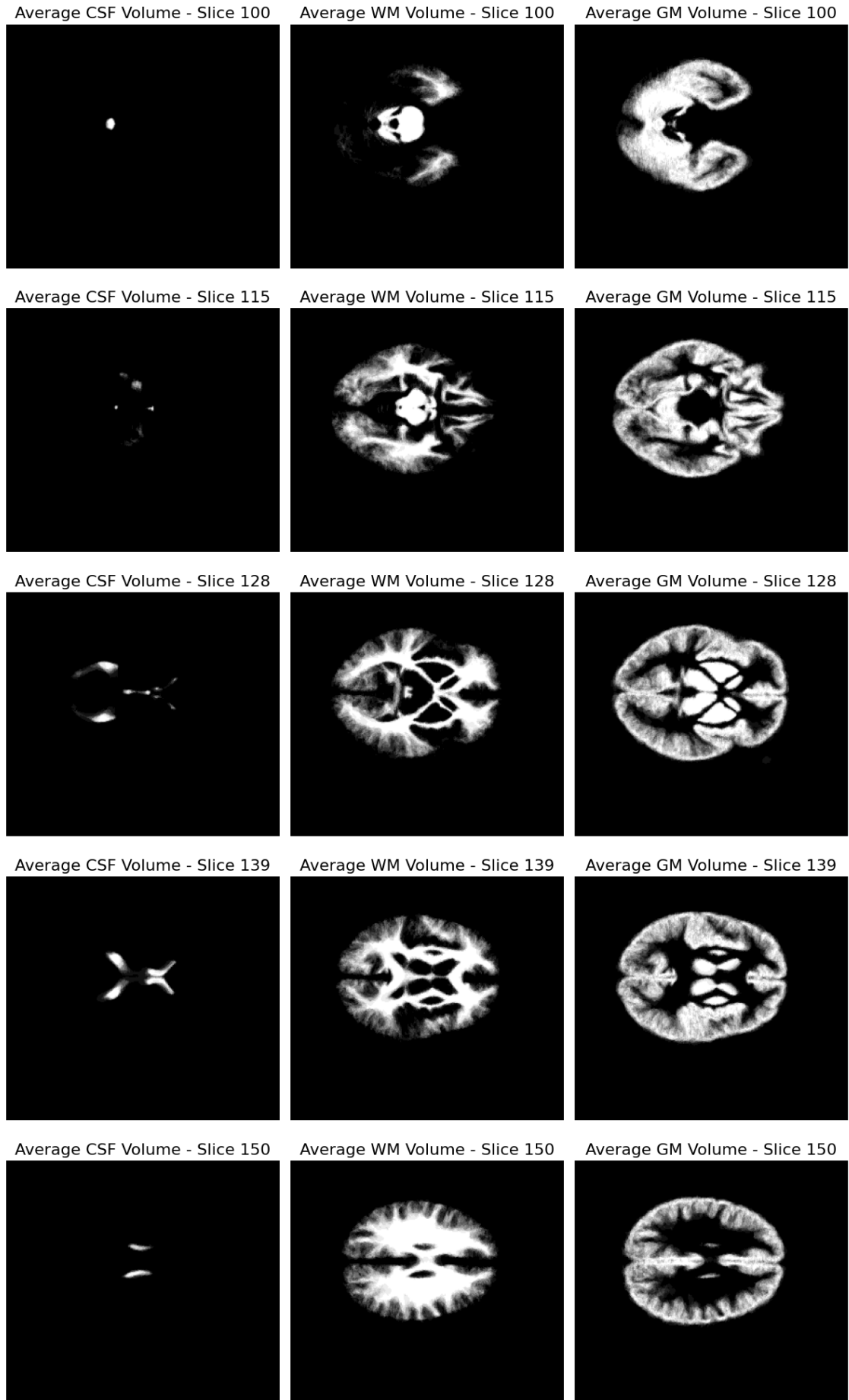


Figure 5: Probabilistic volumes for the averaged labels for the three tissues at different slices.