University of Girona
Medical Imaging and Applications (MAIA)

Medical Image Registration and Applications
And
Medical Image Segmentation and Application
Lab Practice 3 Report: Atlas + EM Algorithm

Submitted By :

Tewele Weletnsea Tareke,

Aroj Hada

Submitted To:

Dr. Sandra González-Villà

Prof. Marti Marly Robert

Prof. Llado Bardera Xavier

1. Introduction & Problem Statement

Segmentation tasks may be very difficult to approach when there is presence of shifting or deformation on anatomic structures. These problems linked to segmentation are often due to low contrast, fuzzy contours or too similar intensities with adjacent objects. In such cases, Atlas segmentation can prove to be very robust. Atlas segmentation exploits the knowledge from previously labeled training images or a reference system or volume image that has been selected as a reference image of objects to segment the target image. This spatial information permits to save a lot of processing time in the localization of the objects to extract and it allows distinguishing the objects of interest from other objects with similar features. This information allows detecting the object contour in the area of interest. Finally, the atlas can point out the features of adjacent objects.

The main goal of this lab is the segmentation of the brain into three different regions, White Matter (WM), Cerebrospinal Fluid (CSF), and Gray Matter (GM), using Atlas-based segmentation, Tissue Model, EM and combination of them. The algorithm will be evaluated with the provided data (coming from a MICCAI 2012 Challenge), reporting also a quantitative analysis using the Dice Similarity Coefficient (DSC) measure. In this report, we present the research directions that aim at overcoming current segmentation limitations using atlas-based segmentation approaches based on registration.

2. Algorithm analysis

Part A : The most known atlas-based segmentation approach consists of reducing the segmentation problem to an image registration problem. The main task here is to build a probabilistic atlas from a set of brain volumes with the available labels of three classes (WM, GM and CSF). First, one image was selected from the dataset as a reference image and then, the rest of the images were individually registered into the reference image. Then, all the scans were averaged voxel-by-voxel and the probabilistic maps for the brain tissue were created (for all the CSF, GM and WM).

As mentioned above, the main goal is building a probabilistic Atlas from the provided training set. All training images are registered into a fixed reference image through non-rigid registration (affine + Bspline parameters) and moving labels are registered into fixed labels using transformation parameters obtained from the previous registration iteratively. Then finding the mean of the train set volumes results in an intensity volume used for registering new unsegmented volumes and the average of the labelled volumes after separation into tissue specific volumes results in a probabilistic label volume (containing tissue probabilities at each

voxel). The final result should be a probabilistic atlas with intensity volume and a probabilistic volume for each tissue present.

Part B : The next part of the lab is to segment the provided test images using multiple algorithms :

1. Using the Atlas that we have built using the train images and the train labels
2. Using the MNI Atlas
3. Using the MNI Atlas + the EM (Expectation- Maximization) algorithm
4. Using the built Atlas + the EM (Expectation- Maximization) algorithm

To achieve the said segmentation, we first register the training reference volume to the test set volumes and then transform the training probabilistic Atlas to the Testing Labels. Similarly, we also register the MNI Template volume to the testing volumes and transform the MNI Atlas to the provided testing labels. Then we segment the testing volumes also integrating the EM algorithm along with the built Atlas as well as the MNI Atlas.

To perform a quantitative comparison between the different algorithms/pipelines, we compute DSC values with the provided mask for the test images.

3. Design and implementation of the proposed solution

3.1 Registration

All registration tasks were performed using the software Elastix, a free to use software consisting of a collection of algorithms that are commonly used to solve medical image registration problems.

The registration of the training brain images dataset was divided in two main parts: The first part was to apply an affine transformation (rigid registration) in order to align the moving image as the fixed one, changing thus the translation, rotation, scale, shearing and tearing of the moving images. The second step was to apply BSpline non-rigid registration to move the pixels in a local level and thus, improve the registration details.

Once the registration of the train images is done, it is also necessary to register the train labels of the moving images into the fixed one, by applying transformix function under the same Elastix software . Transformix applies a transform on an input image with parameters obtained through the previous registration through elastix.

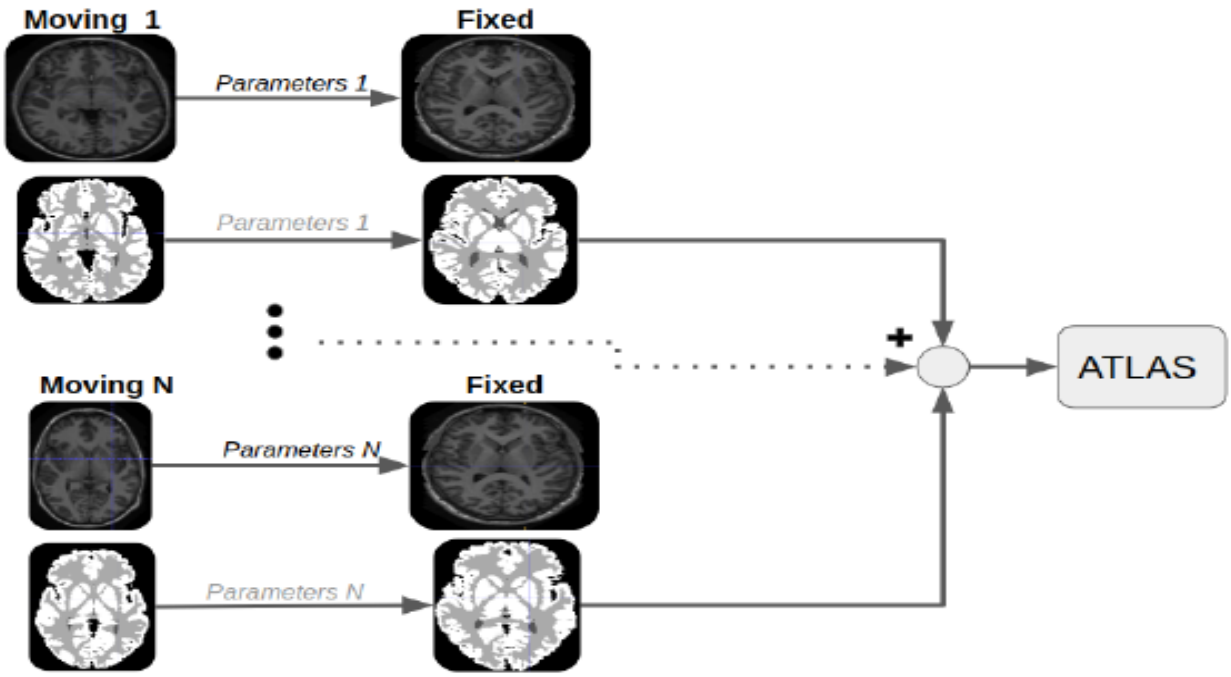


Fig. 1: Flow diagram of Atlas

3.1.1 Parameters Selection for Registration

Using Atlas for segmentation turns the segmentation task into a Registration task, because the segmentation result will depend on how good the registration is. Therefore, choosing the best parameters for registration is a crucial step. The chosen parameters were the ones recommended by the Elastix Manual [1]

- **Metric**: Elastix has different choices for the similarity measure as a Normalized Correlation Coefficient (NCC), Mean Squared Difference (MSD), Normalized Mutual Information (NMI, Mutual Information (MI), and Kappa Statistic (KS). The choice for the metric was MI due to the fact that it takes into account the relation between the probability distributions of the intensities of the fixed and moving image.
- **Image Sampler:** a registration over all the pixels of the fixed image is not needed. So, Elastix offers us different ways to select the subsets. We have chosen a Random Coordinate that randomly selects a user-specified number of coordinates.
- **Interpolator:** During the optimization, the intensity interpolation is needed, when the evaluation is in non-voxel positions. Elastix provides different types of interpolation as nearest neighbor, Linear Interpolation or N^{th} order B-spline.
- **Optimizer:** Elastix has different optimizers, in our case, the Adaptive Stochastic Gradient Descent was selected, because it is a more advanced version of the Standard Gradient Descent, requires less parameters to be set and tends to be more robust.

- **Multi-resolution:** Start the registration process using images that have lower complexity, increase the chance of success in registration. If the images are not only smoothed, but also downsampled, the data is not only less complex, but the amount of data is actually reduced, so it saves a lot of time in the first resolution levels due to the image containing much fewer voxels.
- **Transformation label**: In this registration task the transformation selected was BSplineTransform which is defined by a uniform grid of control points. The grid is determined by the spacing between the grid nodes, which defines how dense the grid is. An important parameter in the transformation parameter files is the FinalBSplineInterpolationOrder. Usually it is set to 3, because produces the best quality result image after registration, but as we are using transformix to deform a label image, we should set this parameter to 0, in order to be sure that the deformed segmentation is still a label image

3.2. Reference Image Selection: Among the training volumes provided, we decided to fix the first brain volume, 1000.nii as the reference fixed image. After registration, we computed the mean image of all registered images including the fixed image 1000.nii to get the intensity volume of the probabilistic atlas.

3.3. Tissue Model: We need to compute the probability of intensities given each class, based on prior information of the training image and analyze the intensity of CSF, WM and GM. We need these per class computed probabilities to segment the testing images later.
In order to create a tissue model for each class, first we preprocess the training images. The preprocessing is done using edge-preserving noise removal algorithms. Using the given labels of all training images, we computed the histogram of intensities for each class. We used one bin for each intensity value as a result the histogram has 1000 bins.

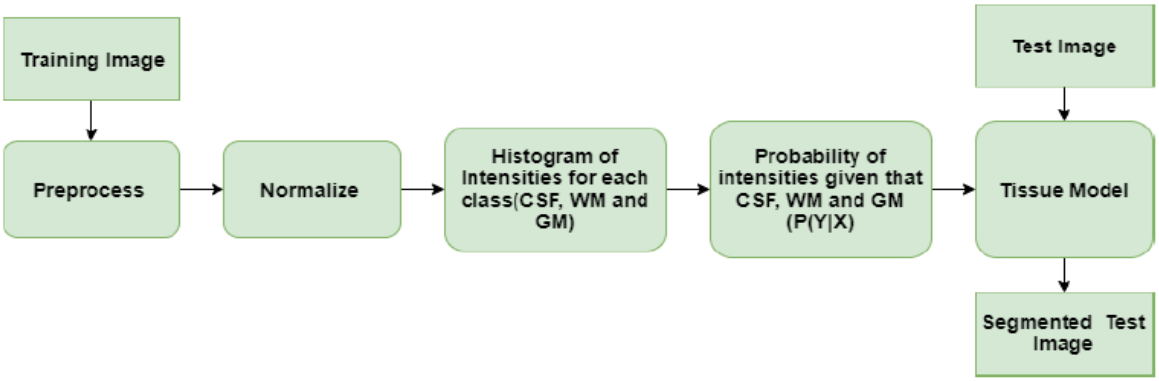


Fig 2: Flowchart for Atlas based segmentation

3.4. <u>Segmentation</u>: Segmentation is performed voxel wise by selecting the tissue with highest probability and approaches which are used in the segmentation are:

Tissue Models: Supervised segmentation approach based on intensity. As it was explained in the MIRA part, the training images were used to create the probability distribution of each intensity. The probability for each voxel on the testing image is defined as the probability of the tissues for this intensity.

Joint EM-Atlas: Well known unsupervised segmentation approach based on Expectation Maximization (EM) combined with Atlas to perform more robust segmentation.

Label Propagation: Supervised segmentation algorithm based on spatial information. Having an Atlas (the one previously made or MNI) we register the Atlas (moving image) into the testing images (fixed image) in order to calculate the transformation parameters. These parameters are used to transform the probabilistic Atlas for each tissue to the probabilistic prediction.

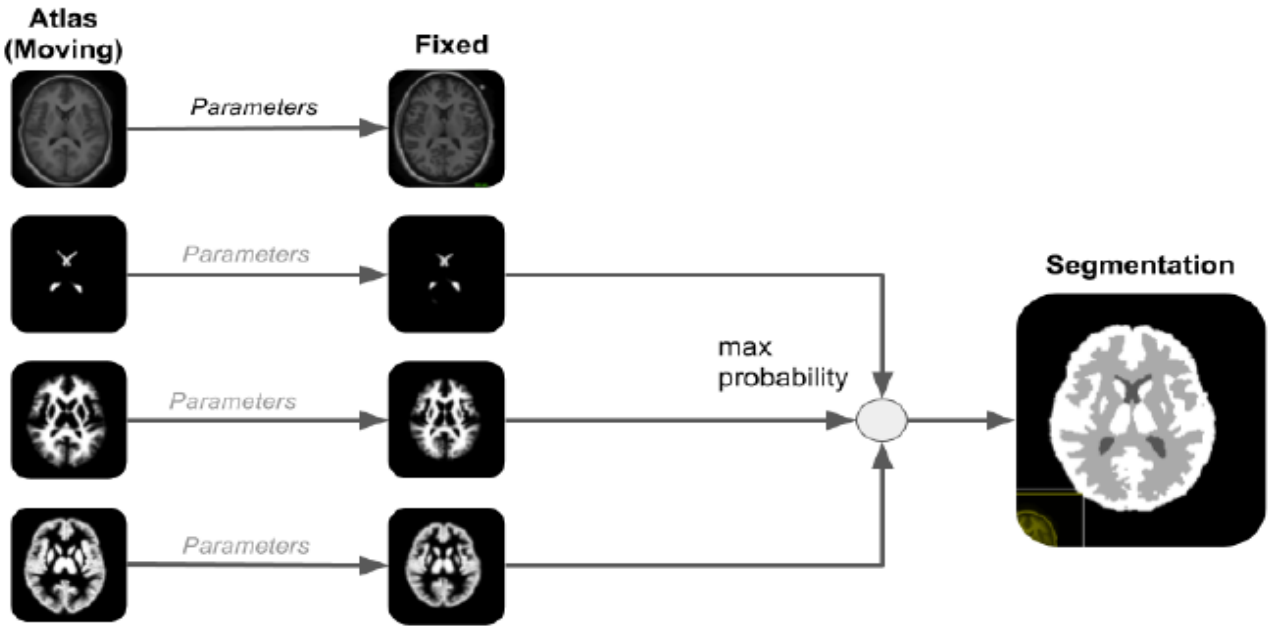


Fig 3: Label propagation diagram

4. Experimental section and results analysis

4.1 Analysis of the Built Atlas

In the following figure it is possible to see the results of the intensity volume obtained after averaging the results obtained from the registration of all the train images.

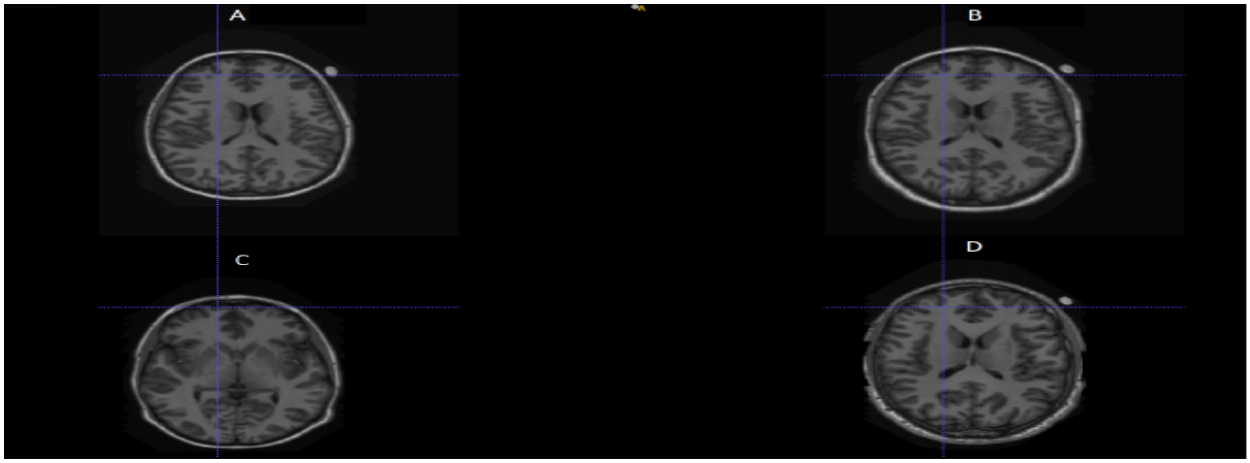
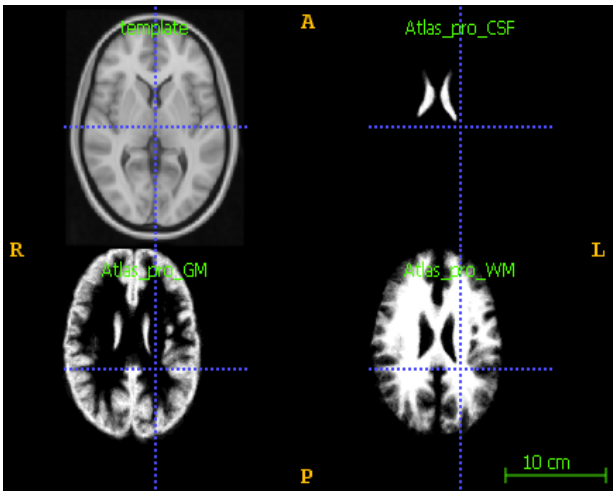
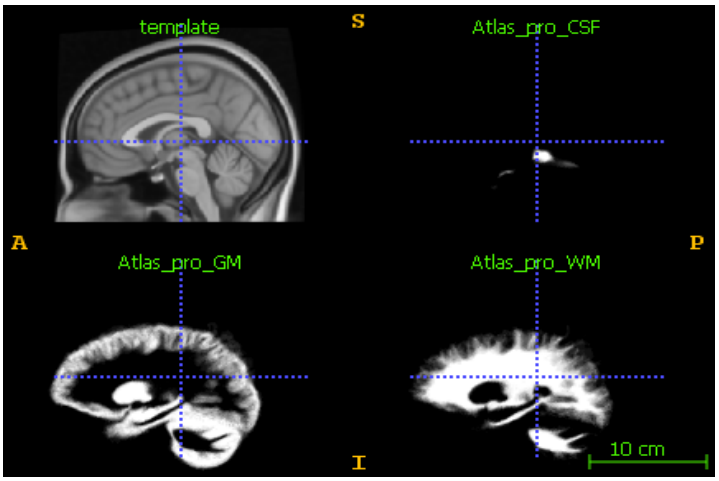


Fig 4: Qualitative Evaluation of Rigid and Non-rigid registration: A) Result after Rigid Registration B) Result after Non-Rigid Registration C) Moving Image D) Fixed Image

Figure 5 shows the Axial (left top), Sagittal (right top) and Coronal (bottom) views of the created probabilistic volume of the Atlas visualized using itk-Snap. The images include some final slices of the whole MRI volume. Each of the images correspond to the slices visualized from the probabilistic atlas for each tissue model.





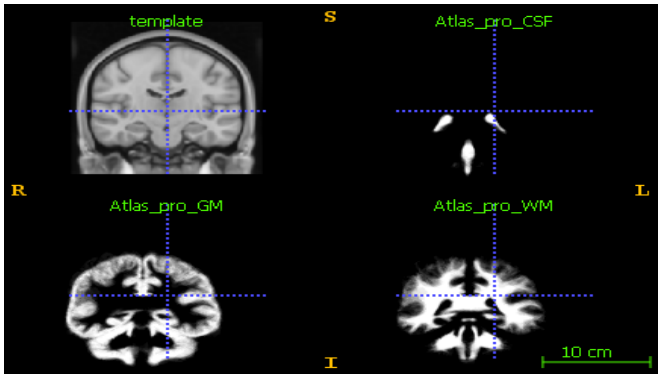


Fig-5: Axial (left top), Sagittal (right top) and Coronal (bottom) views of the created Atlas for different tissues

Qualitatively, the results from the registration look good and all the images from the train data seem to have been properly registered.

The following figure shows the histogram distribution for each class. From all training images, the distribution for WM is 39.32%, for GM is 59.32% and for CSF is 0.0134%. The sum of the probabilities for all the tissues in each pixel should be 1. However, we realized that in the borders of the brain the probabilities do not sum 1. This may be due to the fact that in some of the images, those particular pixels, are considered part of the background

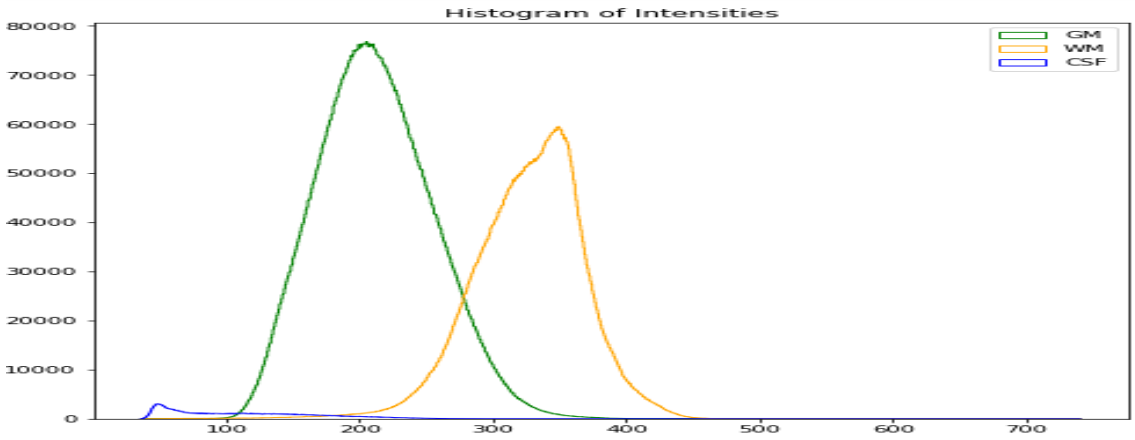


Fig 6: Histogram of intensities of training images for CSF, GM and WM

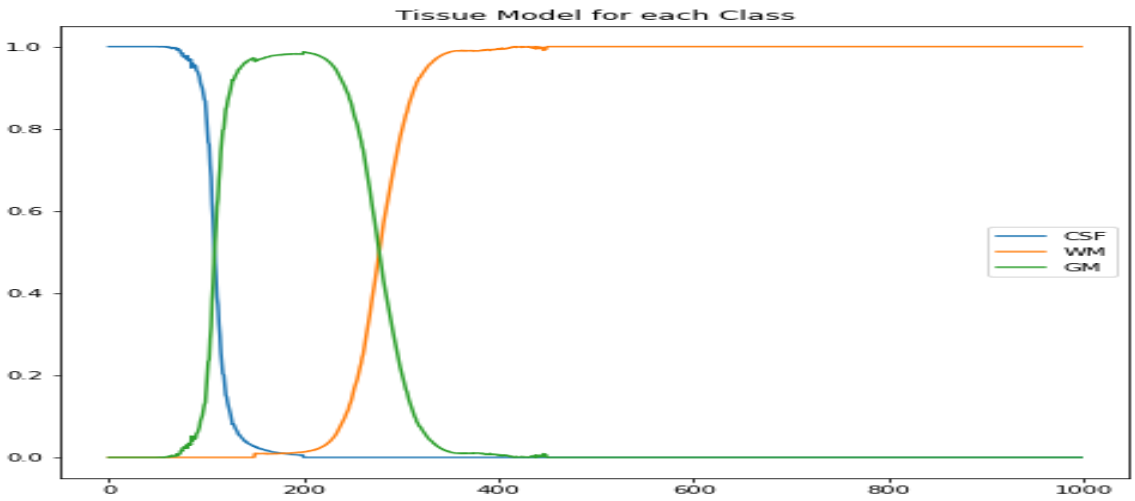


Fig 7: Tissue Model for each class

4.2. **Analysis of the Segmentation**

In the following figure, we can qualitatively see the differences between the probabilities in the case of tissue model and label propagation. For example, in the case of the tissue model, in the GM, the probabilities of a pixel depend only on the intensity, because in the WM part some of the pixels have been given a high probability.

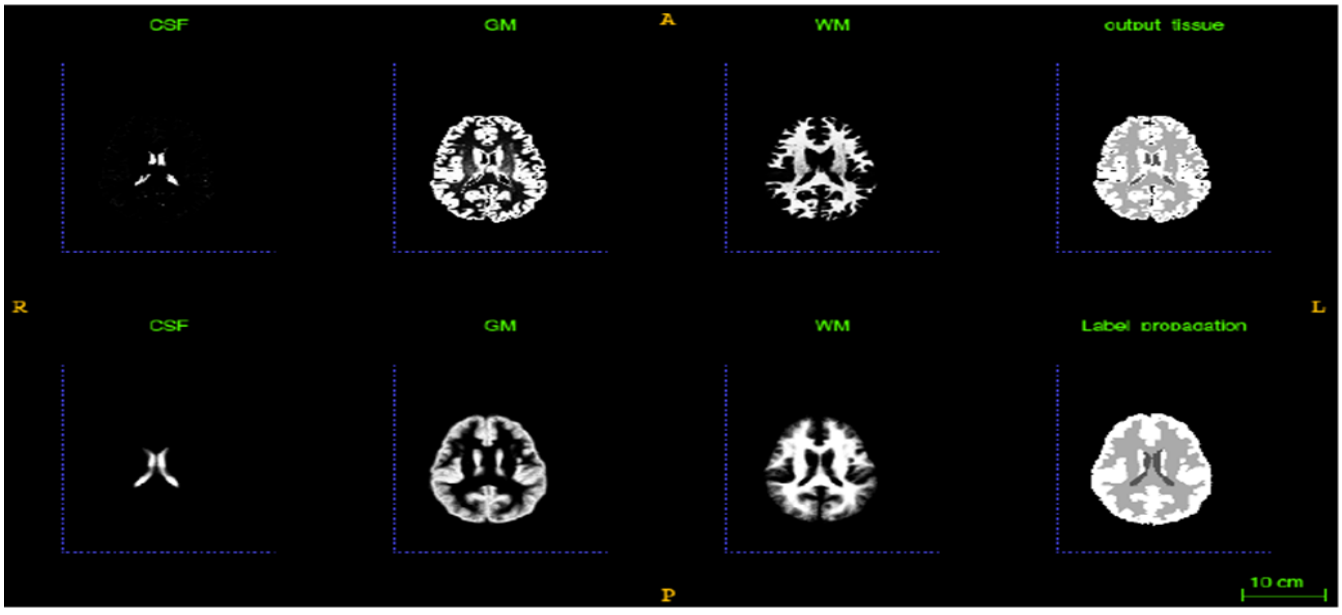


Fig 11: Probabilities for each tissue: CSF, GM and WM, and the segmented Image for Tissue Models (top), Label propagation (bottom) algorithms

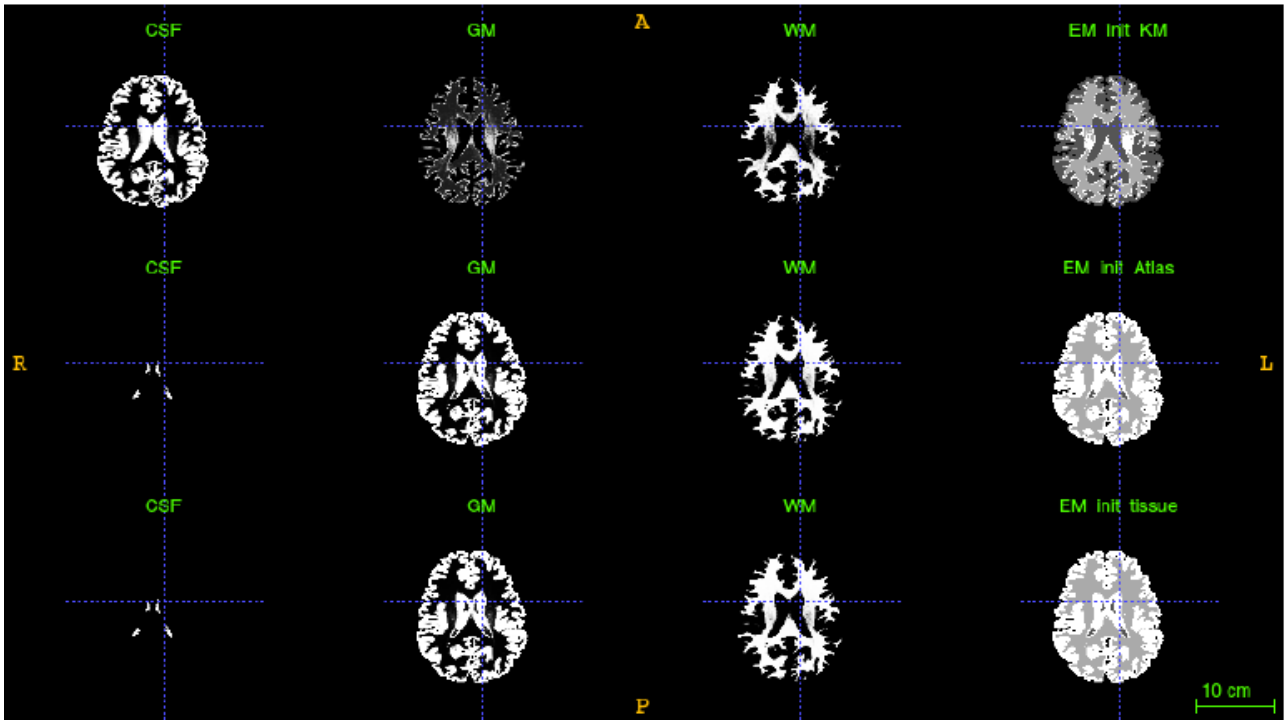


fig 12: Probabilities for each tissue: CSF, GM and WM, and the segmented image for EM initialized with k-Means (top), Label propagation algorithms(middle), Tissue models (bottom)

As we have seen in the section 4.2.1 "Simple Approach", probabilistic atlas is a very powerful segmentation approach. However, the segmentation results depend on the registration, where almost all information taken in account by the algorithm is spatial. Therefore, adding intensity information should boost the performance of the algorithm.

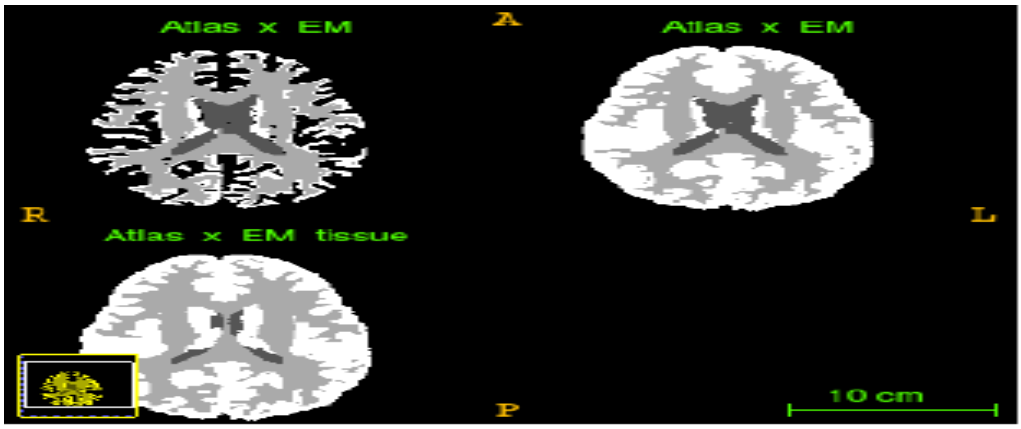


Fig 13: Segmentation based on EM initialization technique

4.2.1 **Quantitative comparison between the different segmentation approaches**

We calculated the average Dice Similarity Coefficient (DSC) measure for each of the cases present in the test set. The table below shows the average Dice scores on test images for each of the algorithms used for each label on both the MNI atlas and the atlas created from train data and labels provided.

As expected, the best average DSC value for both GM and WM tissues was obtained by the K-means initialized EM + Atlas based segmentation. However, the DSC values for the CSF segmentation were similar or higher for the Tissue model based segmentation and the K-means initialized EM + Atlas based segmentation. Using only Atlas yielded the lowest values of DSC among the compared pipelines.

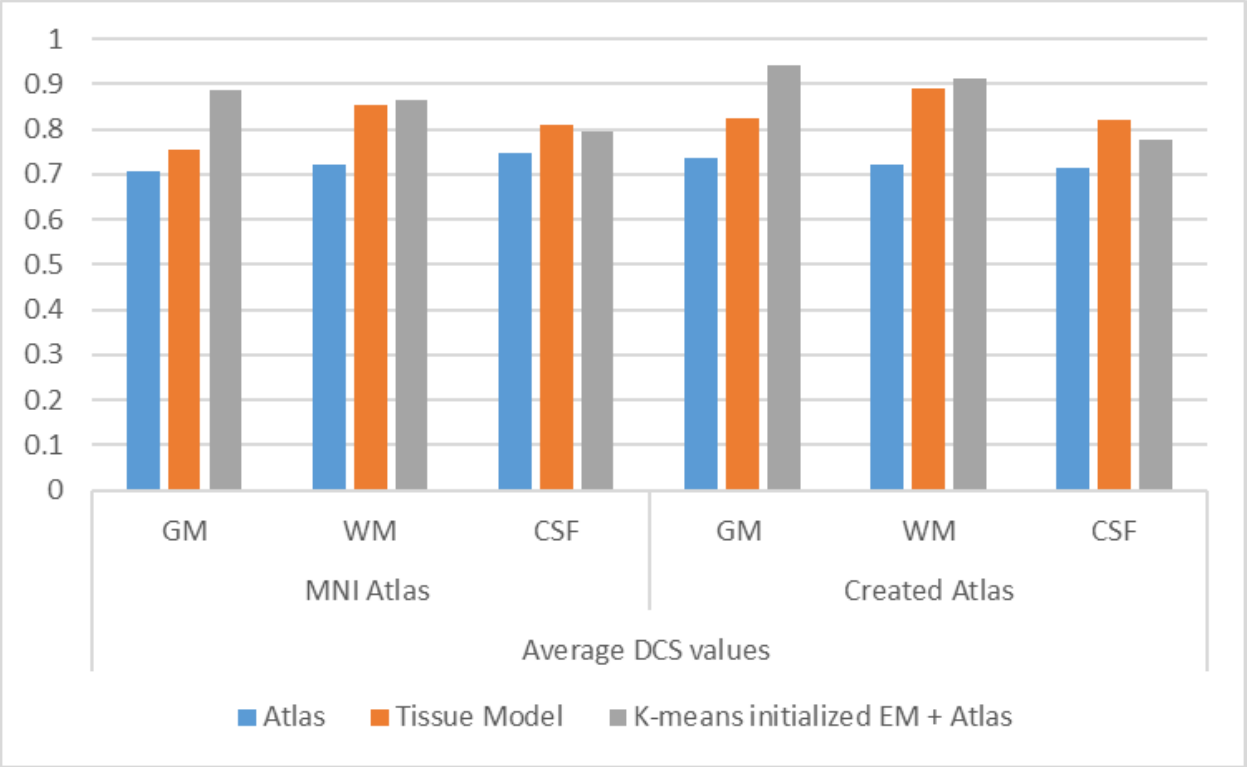
Comparing the MNI Atlas against the created atlas, we can clearly see that the average DSC values in each of the tissues for each of the pipelines was higher in the created Atlas and lower in the MNI standard Atlas. This may have happened as the atlas we built is a specific atlas that resembles the test dataset more than compared to the standard MNI Atlas.

Algorithm	**Average DCS values**					
	MNI Atlas			**Created Atlas**		
	GM	**WM**	**CSF**	**GM**	**WM**	**CSF**
Atlas	**0.705766**	**0.7223163**	**0.7470965**	**0.7349897**	**0.7226478**	**0.7154978**
Tissue Model	**0.755652**	**0.8533981**	**0.8079489**	**0.8231560**	**0.8904421**	**0.8190044**
K-means initialized EM + Atlas	**0.8874700**	**0.8658588**	**0.7962618**	**0.9408861**	**0.9123008**	**0.7767737**

Table 1 : Quantitative comparison between different algorithms for the MNI and Created Atlas for each tissue label using DCS metric

The bar-graph below shows a visualization of the dice metric presented in the above table comparing the different algorithms for each tissue type. It can be observed that dice values have increased in the order of EM + Atlas > Tissue models > Atlas only. Furthermore, it also clearly depicts the increase in accuracy of using a created atlas compared to using the MNI

atlas. The reason behind is that our Atlas has been built with a training dataset that has the same distribution as the testing dataset. However, the MNI Atlas has been built using a di erent dataset from a different distribution.



5. Organization and development of the coursework

To finish the laboratory within the given time frame, we created a schedule and implemented the lab accordingly. We divided the lab into different modules. Each group member was assigned a different task. There was a group discussion every four days. During group discussion, all the problems faced were raised and best solutions were chosen. The table below shows the division of the work into different modules as well as the schedules.

Task	Time	Assigned to	Comment
Preprocessing and Normalization	Week 2	All	Delayed
Selecting the best reference image	Week 2	Tewele Weletnsea	Very Good
Selecting best Parameter files	Week 2	Aroj Hada	//

Creating Atlas	Week 2	Aroj Hada	//
Tissue Model	Week 3	Tewele Weletnsea	//
EM K-means ,Atlas initialization	Week 3	Tewele Weletnsea	//
Atlas + EM segmentation	Week 3	All	//
MNI experiment	Week 4	Aroz Hada	//
Code Documentation	Week 4	All	//
Report Writing	Week 4	All	**Delayed**

Table 2. Project Schedule for MISA

6. Conclusion

The aim of this lab session was to design, analyse and implement an atlas based segmentation algorithm on the provided brain volumes. We first built the atlas from the training data and labels provided by performing a non-rigid registration through the elastix program and then using this atlas performed segmentation of the test volumes. We also performed segmentation of the test volumes with a standard MNI atlas. Furthermore, the EM algorithm designed in the previous lab was also combined with the atlas to perform segmentation. Thus, obtaining multiple pipelines for segmentation which were evaluated quantitatively using average dice scores for each region; Grey Matter (GM), White Matter (WM) and Cerebro-Spinal Fluid (CSF).

The best DICE scores were achieved by the Atlas + EM algorithm for GM and WM segmentation on the created Atlas and for the CSF segmentation, the highest DCS values were achieved by the Tissue models pipeline.

From the results, it can also clearly be seen that creating your own atlas, if you have the training data, yields better results and more accurate segmentations then using a standard Atlas such as the MNI atlas.

Hence, We can conclude that Atlas based segmentation is a powerful technique capable of classifying the brain tissues with high accuracy. Furthermore, when combined with an EM algorithm for brain tissue segmentation, the algorithm is capable of segmenting the tissue labels more accurately as evident from the DCS values obtained.

7. References

[1] Stefan Klein and Marius Staring: Elastix, the manual

[2] M. Bach Cuadra, V. Duay, and J.-Ph. Thiran: Atlas-based Segmentation

[3] Mariano Cabezas [a,c] , Arnau Oliver [a,*,] Xavier Lladó [a], Jordi Freixenet [a], Meritxell Bach Cuadra[b,c::] A review of atlas-based segmentation for magnetic resonance brain images