Medical Image Segmentation and Applications
Lab 3 Solution: Atlas based Segmentation

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1 Introduction and problem definition

Segmentation is one of the most important tasks in the field of Medical Imaging since it helps Computer-Aided Diagnosis (CAD hereinafter) systems to improve their performance by focusing on areas of interest depending on the medical application they have been built for. For instance, a CAD framework trained for classifying brain tumors would get more important and distinctive information in the region of the lesion (which requires segmentation), than from normal tissue areas. However, segmentation continues to be a challenging task since it is not yet possible to be done perfectly (which would be the ideal case), and there will always be an error due to several factors, e.g, noise and artifacts due to intrinsic uncertainty of the equipment used or errors during the image acquisition phase, etc. Nowadays, one of the most well-known methods for improving the results of segmentation in the medical imaging domain is by using prior information from the images through an atlas. As the name suggests, the atlas is a map that contains information of the anatomic structure of several individuals mapped into a single image space.
The main goal of this lab was to use the information from the probabilistic atlas built in the second MIRA lab in order to do the segmentation of brain images from 20 different patients in 3 different tissues: CSF, White Matter (WM), and Gray Matter (GM). The atlas information was used in the following scenarios: first, by using the tissue models (normalized atlas histograms) generated in the second MIRA lab, then using label propagation (registering the atlas to each of the patients, and then transforming the patient's labels accordingly), and finally combining those two methods. The second task consisted of using the EM algorithm implemented during the second MISA lab and initializing it with the following methods: k-means, tissue models, and label propagation. The third task consisted of including the atlas information into and after the EM algorithm for the best-performing initialization method of task 2 (k-means, tissue models or label propagation) and for the combination of both. Finally, the fourth task consisted of using the information from a given atlas (MNI atlas) in EM algorithm. The following sections explain the design and implementation of the tasks, as well as the algorithm analysis, results in analysis, and conclusions.

2 Algorithm Analysis

The algorithm involved during this lab was the Expectation Maximization algorithm (EM). It was already implemented in the previous MISA lab. However, some subtle changes are introduced in order to introduce the atlas information after and before the algorithm. In this section, a description of the changes done are described, and the flowchart diagrams of the new algorithm versions are presented.

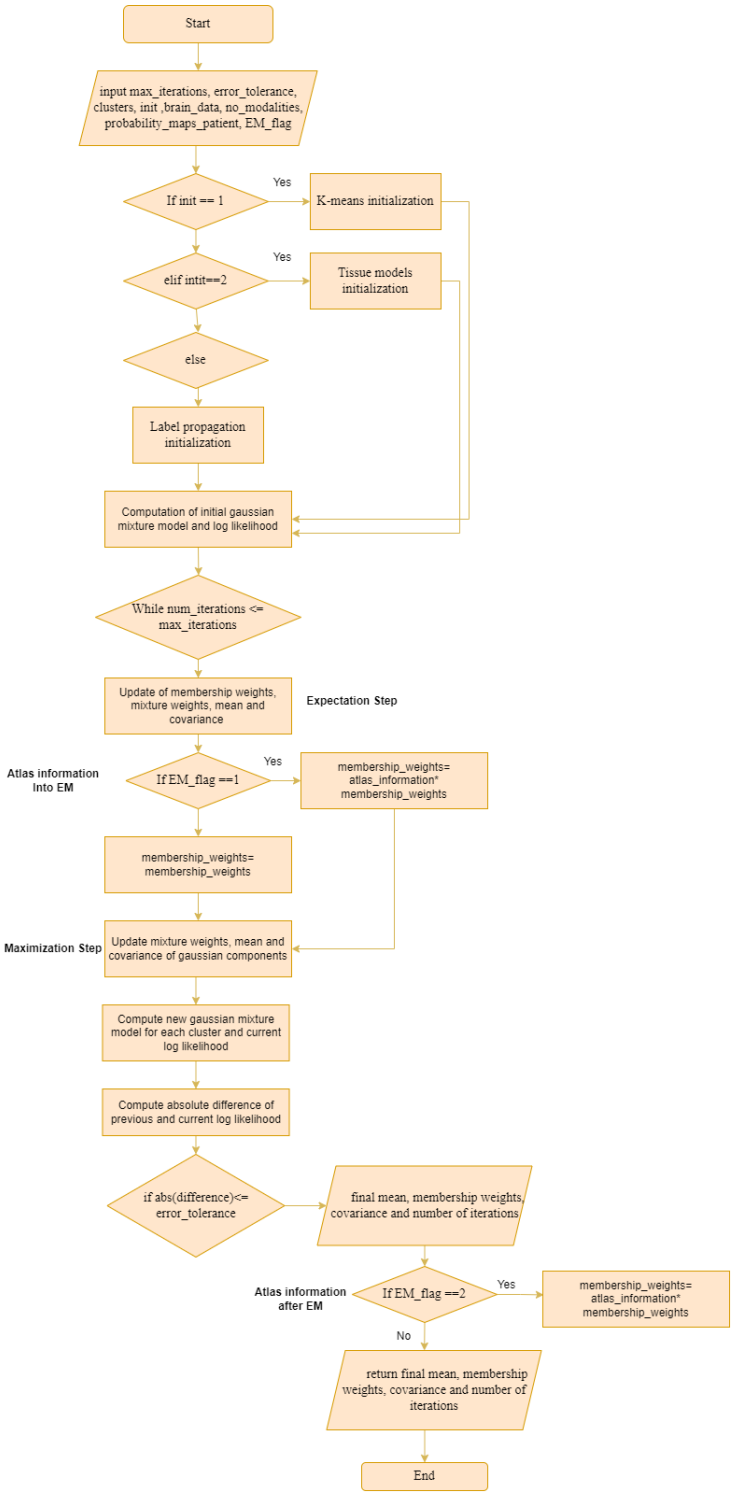

Fig. (1) EM algorithm with atlas information included into and after as well as new initialization methods.

2.1 Atlas into EM:

In order to include atlas information in EM algorithm, the membership weights computed after each expectation step are multiplied by the atlas information, which is a matrix of dimensions (N,3), being N the number of voxels inside the brain area. To achieve this, the probabilistic maps of each of the tissues are flattened, and then only the data points inside the brain and considered. Afterward, those three vectors are stacked vertically and then transposed to get the (N,3) matrix. Figure 1 shows the flowchart of the algorithm signaling where the changes were introduced.

2.2 Atlas after EM:

It is known that the EM algorithm returns the final membership weights for each of the voxels (their probability of belonging to each of the tissues). Therefore, after the last iteration of the algorithm, those weights are multiplied by the atlas information, which is a matrix of dimensions (N,3), as explained in the previous subsection. Figure 1 shows the flowchart of the algorithm signaling where the changes were introduced.

3 Design and implementation of the proposed solution

Various techniques have been used in this lab to segment brain tissues into three classes (CSF, WM, GM). The techniques were divided into three parts.

- Segmentation Without EM
- Segmentation Using EM
- Segmentation Using EM and Atlas

In the following sections, these techniques will be described briefly.

3.1 Segmentation Without EM

First, the segmentation was done without using the Expectation-Maximization(EM) algorithm generating the probabilities map belonging to each of the three tissue classes (CSF, WM, GM). To generate the probability maps, **tissue histogram model** and prior information from the **atlas** (computed in the previous lab) were used.

Tissue Models: The tissue models are normalized histogram distributions for each of the tissues, which means that for each of the intensity values present in the voxels of a given image, that voxel will have a probability value of belonging to each of the tissues. The tissue models (after smoothing with a digital filter) are presented in figure 2. After loading the tissue models, the procedure for generating the segmentation of the images of each patient was the following:

- Stacking the three tissue models vertically
- Generate a lookup table both for the generation of the segmentation. This means that the index + 1 (in order to have labels 1,2 and 3) of the maximum value (highest probability) among all tissues for a given voxel intensity was stored in a single vector. Therefore, the lookuptable consists of a 1D vector of 5392 values (all intensity values present in the test set), with the corresponding label the voxel corresponds to (1 : CSF, 2 : WM, 3 : GM).

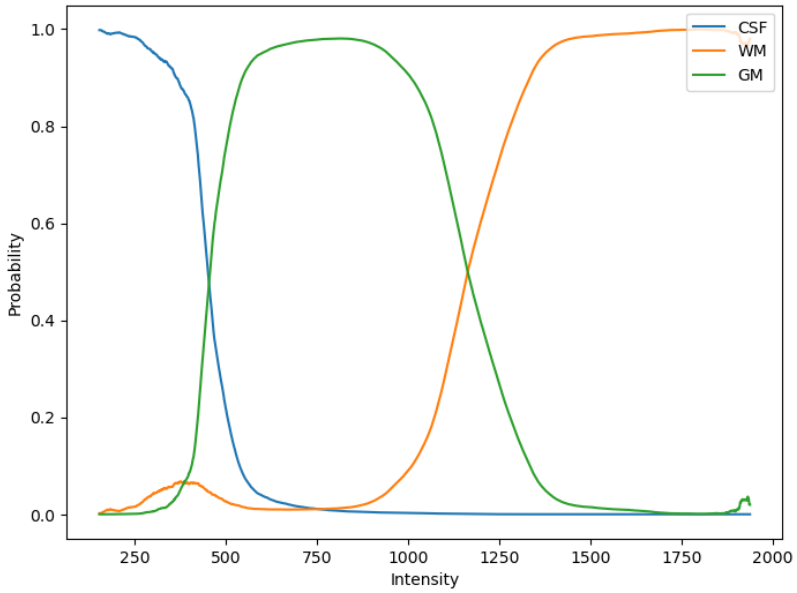

Fig. (2) Tissue models for CSF, WM and GM

- Once the lookup table is generated, it is mapped into the original image, so that for every intensity voxel of the test image a label can be assigned. The resulting image from this step is an image of the same shape as the test one, but with the labels 1,2,3.
- Before finishing this step, the tissue models are mapped into the original image in order to get the probability maps for this task which will be used when combining tissue models and label propagation.

Label Propagation: In the previous lab, using the training images, the intensity atlas and three probabilistic atlases for each of the three tissues were generated. Those atlases were used in this case to generate the segmentation of the test images.

For this task, the intensity atlas was registered with respect to each of the 20 given test images. A toolbox named ***Elastix*** was used for the registration of images. It is open-source software, based on the well-known Insight Segmentation and Registration Toolkit (ITK). The software consists of a collection of algorithms that are commonly used to solve (medical) image registration problems for which it was also chosen in this lab. Elastix offers many parameter files which can be applied for different types of registration. Out of all, **inter-patient** Brain 3D MRI Parameter file 0009 was chosen as it offers affine and B-Spline transformation using mutual information as a similarity metric. To do image registration with Elastix, The modular design of elastix allows the user to quickly configure, test, and compare different registration methods for a specific application. A command-line interface enables the automated processing of large numbers of data sets, by means of scripting. To do so, first, the executable file for windows was downloaded and then added to the directory of the desired drive. Then using command-line commands the images were registered with respect to one fixed image. The following command was used to register images using Elastix [1].

```
elastix -f fixedImage.ext -m movingImage.ext -out outputDirectory
```

```
-p parameterFile.txt
```

In this case, each of the test images was kept as a fixed image and the intensity atlas as a moving image. The whole process was wrapped up in a loop to generate the resulting intensity atlases and deformation fields for the test images. The next step is to use the deformation field generated at each step to transform the probabilistic atlases. For each of patient, there will be three probabilistic map atlases generated after transformation. As there were two transforms (affine and elastic) that were used sequentially, the last transformation matrix holds both transformations and can be used to transform the labels in the same way as the intensity images. For that, the following command with Transformix was used.

```
transformix -in inputImage.ext -out outputDirectory -tp
TransformParameters.txt
```

Here the input images will be each probabilistic atlases and the deformation field from each of the patient registration will be kept as the Transformation parameter. Finally, for each patient, three probability maps will be generated that will give the probability values belonging to each of the three tissue classes. After that, three probability maps were stacked together and the maximum probability along it was chosen for the label of that pixel. That's how the segmentation was done using prior information from the atlas generated in the previous lab.

The same procedures were repeated also for the well-known **MNI Atlas** template given and thus the probability maps were also generated using the MNI Atlas.

Tissue Models and Label Propagation: In the last step of the first part of the task, the probability maps generated from tissue histogram and label propagation were combined together by multiplication. After that, three probability maps generated after multiplication were stacked together and the maximum probability along it was chosen for the label of that pixel. That's how the segmentation was done by multiplying the tissue probability map and the prior probability information from the atlas generated in the previous lab.

3.2 Segmentation With EM

In this part, the segmentation was done using the Expectation-Maximization algorithm implemented in the previous MISA lab. But three different methods were used for the initialization step for EM which are the segmentation results of Kmeans, Tissue Models, and Label Propagation. In the "**KG-EM.ipynb**" notebook, **INIT** flag was used for initialization where 1 denotes using K-means, 2 for Tissue models, 3 for Label Propagation, and 4 for both combined tissue model and label propagation segmentation.

K-Means Initialization: K-means clustering can be one of the methods that can be used for initializing unknown parameters for the EM algorithm. The hard levels assigned to the data points by K-means can be used for computing the mean, covariance, and prior probabilities of each cluster. Firstly, K, the number of clusters is specified which is 3 in this case and the points are assigned to the clusters in an iterative process until the algorithm reaches convergence.Kmeans Clustering is used from sklearn.cluster.KMeans. The Inputs are n-clusters= Number of clusters, K-means++: initial cluster centers for k-mean clustering in a smart way to speed up convergence, and Random State: Determines random number generation for centroid initialization. The outputs are the centroids and the levels assigned by K-means. The flowchart for the K-means algorithm can be demonstrated in Figure 3.

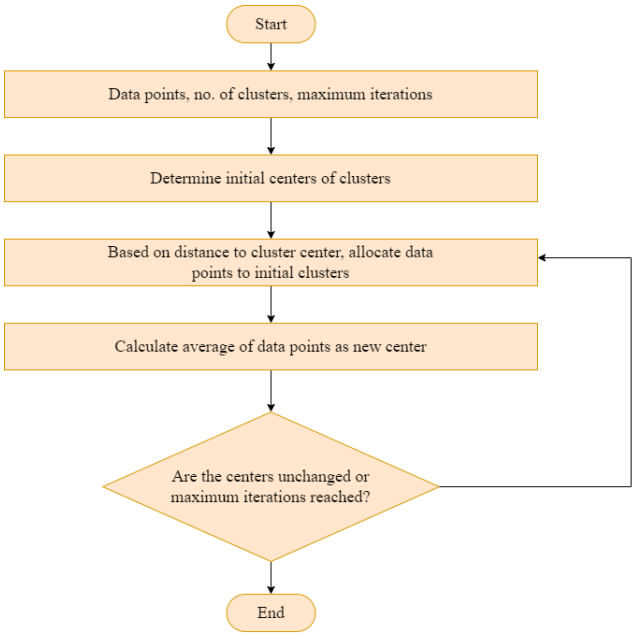

Fig. (3) Flowchart for K-means algorithm.

The problem with the initialization by K-means was that the assigning of the labels by K-means was implicit and the assignment was done randomly. But to maintain the same labels for each tissue class for each run,the mean intensities for each of the cluster centroids were sorted and the labels were assigned to each cluster in an ascending way of the mean as CSF(1), WM(2), and GM(3). In this way, the robust assignment of the labels is ensured.

Tissue Models Initialization: For the tissue models initialization, the following steps were followed:

- The test image is mapped with each of the voxels corresponding to each tissue using the segmented image (image of the same shape as the original image, but with labels 1,2 and 3) from the tissue models in the following way: test_image[segmented_image==1], test_image[segmented_image==2], test_image[segmented_image==3].
- After the voxels corresponding to each tissue are stored in three vectors, the mean, covariance and prior probabilities were sent to EM algorithm.

Label Propagation Initialization: In the previous section of Segmentation without EM, Label propagation was used from the intensity and three probabilistic atlases were used for generating segmented images for each patient. In this part, the segmentation results from each of the patients will be used for the initialization of the EM algorithm. For that, the probability maps generated from each of the three probabilistic atlases were stacked together in the order of CSF, WM, and GM. Then the index of the maximum probability was chosen as the label of each particular pixel. After that, for each tissue class, the region of the image assigned to that class was picked to compute the mean and variance of that tissue class. Also, the prior probabilities belonging to each three classes were computed

using the number of pixels assigned to that class divided by the total number of pixels in the image. Finally, the mean, covariance, and prior probabilities were sent to EM algorithm.

3.3 Segmentation with EM and MIRA Atlas

In this part of the lab, the atlas information was also used in EM algorithm to improve the segmentation results further. For initialization, the best initialization model obtained in the previous step which is by using tissue model histogram was used. Also, the combined tissue model and label propagation method were used for initialization. Two following techniques were used to add the atlas information as an initial segmentation are as follows:

- Atlas into EM
- Atlas after EM

EM-flag was used for choosing the technique where 1 denotes 'into' the EM and 2 denotes 'after' the EM.

Atlas into EM: To add the Atlas information into EM, a modified version of EM was used which can be seen in Figure 1. In this part, the probabilistic atlases for each tissue class for each patient were used. Later, they were flattened and stacked in a column-wise fashion where each column denoted each of the brain tissues. As the Expectation part of the EM algorithm generates the weight vector at each iteration, the idea was to multiply the stacked atlas information with the weight vector after EM to start the EM with an initial segmentation. Thus, not only intensity but also positional information was added as a part of initial segmentation which makes the EM more robust and powerful.

Atlas after EM: Another way of adding the atlas is after completing EM. To add the Atlas information after EM, a modified version of EM was used which can be seen in Figure 1. Here also, the probabilistic atlases for each tissue class for each patient were used. Later, they were flattened and stacked in a column-wise fashion where each column denoted each of the brain tissues. But instead of multiplying the weight vector with atlas information after each expectation step iteration, the multiplication was done once EM reached convergence and completed generating final weight vectors. In this case, the final weight vectors were only multiplied by the atlas information.

3.4 Segmentation with EM and MNI Atlas

In this part, the same steps of adding atlas information were repeated but instead of the transformed atlases of each patient by MIRA lab atlas, the transformed atlases of each patient using a well-known MNI template were used. A flag named **flag-atlas** was used to choose which atlas to use where 1 means MIRA atlas and 2 means MNI atlas. For initialization, the most feasible initialization method which was tissue model histograms was used. To aim of using the MNI atlas was to compare the performance of both atlases and check if one outperforms the other or not.

4 Experimental section and result analysis

For the experimental section, the following setup was followed:

- First, the segmentation is done using tissue models, label propagation and a combination of both.

Table (1) Dice Score results for task 1: Segmentation with different methods without EM

Patient ID	Segmentation Without EM with different methods								
	Tissue Model			Label Propagation			Both Combined		
	Dice CSF	Dice WM	Dice GM	Dice CSF	Dice WM	Dice GM	Dice CSF	Dice WM	Dice GM
1003.nii	0,339944	0,805005	0,823079	0,686426	0,806242	0,86417	0,669629	0,860415	0,88919
1004.nii	0,637735	0,923305	0,947578	0,806831	0,800403	0,849032	0,82876	0,931158	0,952977
1005.nii	0,872894	0,918988	0,945656	0,842167	0,775736	0,845861	0,915742	0,91736	0,948242
1018.nii	0,493721	0,884428	0,908726	0,792153	0,801984	0,856648	0,765178	0,906723	0,932077
1019.nii	0,442205	0,918225	0,949875	0,722219	0,787136	0,854633	0,747525	0,921773	0,952952
1023.nii	0,425563	0,873952	0,899305	0,699559	0,80169	0,862254	0,730252	0,908239	0,932994
1024.nii	0,590968	0,897605	0,929093	0,779345	0,794226	0,856547	0,797728	0,911626	0,941071
1025.nii	0,852048	0,912586	0,945727	0,833513	0,773078	0,851492	0,902111	0,913018	0,949758
1038.nii	0,492191	0,907679	0,92963	0,785456	0,803804	0,859861	0,744455	0,919341	0,943705
1039.nii	0,378267	0,912606	0,939209	0,674339	0,768164	0,837128	0,701483	0,913476	0,943174
1101.nii	0,704327	0,901452	0,927633	0,807758	0,793617	0,866575	0,813519	0,919076	0,946028
1104.nii	0,624444	0,856801	0,895257	0,728519	0,74971	0,806437	0,731266	0,85929	0,899135
1107.nii	0,091946	0,645967	0,695359	0,723298	0,815648	0,884954	0,396436	0,807105	0,852645
1110.nii	0,589386	0,877274	0,911301	0,744029	0,792672	0,856007	0,731196	0,893257	0,929189
1113.nii	0,327375	0,732185	0,72392	0,753465	0,815189	0,869911	0,59904	0,825063	0,847181
1116.nii	0,685907	0,914597	0,931289	0,739473	0,756293	0,835667	0,834816	0,905764	0,938831
1119.nii	0,812788	0,826155	0,844492	0,847303	0,795774	0,858772	0,879089	0,879102	0,906523
1122.nii	0,80429	0,808292	0,825764	0,685827	0,773865	0,835621	0,799972	0,860508	0,887897
1125.nii	0,866692	0,891665	0,913273	0,693111	0,796138	0,863689	0,785903	0,908129	0,933396
1128.nii	0,659492	0,804563	0,889026	0,619969	0,775193	0,849845	0,71884	0,879237	0,923829

Table (2) Dice Score results for task 2: EM with different initialization methods

Patient ID	Segmentation With EM with different initialization methods								
	K-means			Tissue Model			Label Propagation		
	Dice CSF	Dice WM	Dice GM	Dice CSF	Dice WM	Dice GM	Dice CSF	Dice WM	Dice GM
1003.nii	9,07E-05	0,75301	0,922041	0,111212	0,892275	0,935626	0,032574	0,818419	0,617115
1004.nii	1,47E-05	0,729298	0,940814	0,406417	0,895824	0,933514	0,406417	0,895824	0,933514
1005.nii	0,049704	0,867499	4,58E-06	0,748718	0,867499	0,921298	0,748718	0,867499	0,921298
1018.nii	2,21E-05	0,766936	0,941931	0,259674	0,894808	0,93365	0,073044	0,893346	0,932067
1019.nii	0,000411	0,796138	0,88282	0,097774	0,894135	0,940996	0,036134	0,835701	0,731047
1023.nii	0,000167	0,758918	0,934481	0,208716	0,890758	0,933384	0,024226	0,774785	0,113643
1024.nii	3,66E-05	0,752174	0,934098	0,353235	0,901599	0,941472	0,353235	0,901599	0,941472
1025.nii	0,050567	0,862026	8,79E-06	0,731521	0,862026	0,922221	0,731521	0,862026	0,922221
1038.nii	0,000155	0,778344	0,935806	0,269906	0,898872	0,933774	0,271731	0,898872	0,933786
1039.nii	0,000692	0,734784	0,918494	0,088761	0,888278	0,935543	0,032817	0,802738	0,621282
1101.nii	0,027209	0,869938	0,000156	0,549032	0,867127	0,922373	0,549032	0,867127	0,922373
1104.nii	9,20E-05	0,791365	0,921925	0,42678	0,880822	0,932317	0,42678	0,880822	0,932317
1107.nii	0,00384	0,792645	0,876792	0,04607	0,784372	0,168067	0,075077	0,823858	0,788432
1110.nii	0,002074	0,70896	0,936932	0,365357	0,911225	0,943005	0,365357	0,911225	0,943005
1113.nii	0,001012	0,711008	0,940629	0	0,793756	0,885097	0	0,793756	0,885097
1116.nii	0,01363	0,865948	0,345091	0,614712	0,865929	0,917848	0,614712	0,865929	0,917848
1119.nii	0,004961	0,778262	0,642414	0,684081	0,811879	0,88957	0,684081	0,811879	0,88957
1122.nii	0,006736	0,868874	0,585845	0,642201	0,872248	0,916315	0,642201	0,872248	0,916315
1125.nii	0,056082	0,835284	4,67E-05	0,75867	0,835284	0,89914	0,75867	0,835284	0,89914
1128.nii	0,006162	0,75582	0,572999	0,257827	0,702491	0,711195	0,259288	0,702491	0,712948

Table (3) Dice Score results for tasks 3 and 4 (Atlas information into EM)

Patient ID	**Segmentation With Atlas into EM**								
	MIRA Atlas						**MNI Atlas**		
	Tissue Model			**Combined Model**			**Tissue Model**		
	Dice CSF	**Dice WM**	**Dice GM**	**Dice CSF**	**Dice WM**	**Dice GM**	**Dice CSF**	**Dice WM**	**Dice GM**
1003.nii	0,224969	0,922562	0,949169	0,224969	0,922562	0,949169	0,077773	0,836135	0,912543
1004.nii	0,520612	0,925411	0,947005	0,520612	0,925411	0,947005	0,426102	0,867434	0,921137
1005.nii	0,778085	0,916223	0,941032	0,778085	0,916223	0,941032	0,754045	0,847211	0,914077
1018.nii	0,408542	0,922039	0,94592	0,408542	0,922039	0,94592	0,316878	0,862067	0,920295
1019.nii	0,197497	0,91824	0,949361	0,197497	0,91824	0,949361	0,101831	0,865601	0,930229
1023.nii	0,287309	0,915204	0,943936	0,287309	0,915204	0,943936	0,210639	0,85871	0,919811
1024.nii	0,465143	0,915673	0,945345	0,465143	0,915673	0,945345	0,380571	0,870111	0,929306
1025.nii	0,758382	0,910908	0,940598	0,758382	0,910908	0,940598	0,740932	0,84422	0,916455
1038.nii	0,399914	0,917144	0,941492	0,399914	0,917144	0,941492	0,311804	0,867669	0,92102
1039.nii	0,189057	0,918621	0,948502	0,189057	0,918621	0,948502	0	0,475653	0,823344
1101.nii	0,613909	0,89793	0,935497	0,613909	0,89793	0,935497	0,570011	0,850884	0,916412
1104.nii	0,551987	0,901288	0,935253	0,551987	0,901288	0,935253	0,497078	0,880139	0,932672
1107.nii	0,235528	0,886052	0,929726	0,235528	0,886052	0,929726	0,180973	0,800675	0,898131
1110.nii	0,475571	0,920308	0,944433	0,475571	0,920308	0,944433	0,412928	0,877355	0,930148
1113.nii	0,411596	0,906996	0,93484	0,411596	0,906996	0,93484	0,362857	0,802822	0,891038
1116.nii	0,647136	0,899315	0,931648	0,647136	0,899315	0,931648	0,634993	0,848007	0,911627
1119.nii	0,731132	0,890943	0,921569	0,731132	0,890943	0,921569	0,721096	0,791004	0,883828
1122.nii	0,680661	0,904523	0,929497	0,680661	0,904523	0,929497	0,661553	0,866979	0,914883
1125.nii	0,778175	0,887164	0,919863	0,778175	0,887164	0,919863	0,772425	0,8634	0,910497
1128.nii	0,616211	0,843002	0,900798	0,616211	0,843002	0,900798	0,605476	0,674608	0,605921

Table (4) Dice Score results for task 3 (EM with atlas information After)

Patient	**Segmentation with Atlas after EM**					
	MIRA Atlas					
	Tissue Model			**Combined Model**		
Patient ID	Dice CSF	Dice WM	Dice GM	Dice CSF	Dice WM	Dice GM
1003.nii	0,519192	0,920535	0,9528	0,008538	0,901512	0,002847
1004.nii	0,716567	0,929002	0,954079	0,716567	0,929002	0,954079
1005.nii	0,845807	0,90105	0,943117	0,845807	0,90105	0,943117
1018.nii	0,669545	0,924601	0,953344	0,669545	0,924601	0,953344
1019.nii	0,508721	0,924346	0,957812	0,732894	0,898476	0,947254
1023.nii	0,590525	0,923207	0,953187	0,007771	0,00088	0,023044
1024.nii	0,672619	0,932175	0,959742	0,672619	0,932175	0,959742
1025.nii	0,828244	0,89515	0,943119	0,828244	0,89515	0,943119
1038.nii	0,659082	0,925361	0,953188	0,659082	0,925361	0,953188
1039.nii	0,533837	0,909193	0,947515	0,703397	0,865059	0,928013
1101.nii	0,725198	0,90314	0,944322	0,725198	0,90314	0,944322
1104.nii	0,658287	0,896892	0,937184	0,658287	0,896892	0,937184
1107.nii	0,014714	0,002182	0,08516	0,013401	0,888967	0,007051
1110.nii	0,618098	0,927701	0,958065	0,618098	0,927701	0,958065
1113.nii	0,751644	0,864113	0,922013	0,751644	0,864113	0,922013
1116.nii	0,719742	0,884565	0,932497	0,719742	0,884575	0,932502
1119.nii	0,81344	0,867245	0,922198	0,81344	0,867245	0,922198
1122.nii	0,710934	0,893862	0,931969	0,710934	0,893862	0,931969
1125.nii	0,730742	0,884034	0,927607	0,730742	0,884034	0,927607
1128.nii	0,762053	0,850736	0,916176	0,762098	0,85118	0,916383

Table (5) Mean and standard deviation of DICE Scores for each task

Task	Mean			Standard Deviation		
	CSF	WM	GM	CSF	WM	GM
1_1_TM	0,584609	0,860667	0,88876	0,210626	0,072167	0,0723
1_2_LP	0,748238	0,788828	0,853255	0,062414	0,018397	0,016277
1_3_TMLP	0,754647	0,891983	0,92254	0,114542	0,033904	0,031898
2_1_KNN	0,011183	0,788861	0,661666	0,018815	0,054736	0,376666
2_2_TM	0,381033	0,86056	0,87582	0,252886	0,051748	0,174021
2_3_LP	0,354281	0,845771	0,823724	0,279316	0,051927	0,198144
3_1_After_TM_MIRA	0,65245	0,857955	0,899755	0,178374	0,202824	0,192198
3_1_Into_TM_MIRA	0,498571	0,905977	0,936774	0,200759	0,019107	0,012192
3_2_After_TMLP_MIRA	0,694452	0,894855	0,892022	0,171805	0,02444	0,20972
3_2_Into_TMLP_MIRA	0,498571	0,905977	0,936774	0,200759	0,019107	0,012192
4_1_Into_TM_MNI	0,436998	0,822534	0,895169	0,242145	0,093976	0,072199

- Second, the segmentation is done using EM algorithm with three initialization methods: kmeans, tissue models, label propagation.
- Third, the segmentation is done including information of the constructed atlas in MIRA lab 2 into and after the EM algorithm for best initialization of the second step, and for the combination of tissue models and label propagation.
- Fourth, the segmentation is done including the information of the atlas provided in the assignment (MNI atlas) into the EM algorithm by using the most feasible initialization (decided from the previous tasks).

The results obtained will be summarised in the following way:

4.1 Tabular results

- Table 1, presenting the dice score results for task 1.
- Table 2, presenting the dice score results for task 2.
- Table 3, presenting the dice score results for task 3 (atlas information into EM) and task 4.
- Table 4, presenting the dice score results for task 3 (atlas information after EM).
- Table 5, presenting the mean and standard deviation of the dice scores for each one of the tasks.

Tabular results analysis From table, it can be seen that segmentation of CSF tissue using tissue models is poor (below 0.5) for some cases such as patient 1038.nii, 1039.nii, 1107.nii,1113.nii, being the lowest dice score close to zero (0.091946) for patient 1107.nii. On the other hand, dice scores for white matter and gray matter are generally good. For most of the patients, the dice score obtained for grey matter is higher than that of white matter. In the case of label propagation, the dice segmentation scores for CSF tissue are noticeably higher than for tissue models, but this is not the case for WM and GM, since their dice scores decrease a little. When using a combination of both methods, the segmentation results are quantitatively better for most of the cases except for patient 1107.nii, 1110.nii, and 1113.nii for CSF, 1005.nii, 1116.nii for WM, 1005.nii,1107.nii,1113.nii for GM.

From table 2 it can be seen that in all three cases the dice score for CSF tissue is very poor since in many cases the dice score is close to 0 or even 0. However, for the other two tissues (WM and GM) results are generally good. The best results are obtained when initializing the EM algorithm with tissue models. Therefore, this is the preferred initialization method used for the next tasks.

From table 3 it can be noticed that when including the information of the atlases into EM (both the constructed atlas in the previous MIRA lab and the provided MNI atlas), the segmentation results are generally improved for most of the cases in the three tissues. However, when comparing from which atlas to add the information from EM, it is seen that when using the MIRA atlas the results are much higher, especially in CSF tissue.

From table 4 it can be analyzed that when using atlas information after EM, it is better to initialize it with tissue models instead of a combination of tissue models and label propagation since higher dice scores are obtained for most of the patients in all tissues when initializing EM with tissue models.

From table 5 it can be seen that for most of the experiments done, WM and GM have generally good average results in terms of the dice score. However, if the task was to compare which approach yields the best average results in terms of dice scores for all tissues, the approach of not using EM and using Tissue models and Label Propagation would be the best performing one, since it provides an average dice score of 0.754647, and this is normally the most problematic tissue.

4.2 Image results

- Image 4(a), presenting a box plot of the results of dice score for each of the tasks with CSF tissue.
- Image 4(b), presenting a box plot of the results of dice score for each of the tasks with WM tissue.
- Image 4(c), presenting a box plot of the results of dice score for each of the tasks with GM tissue.
- Image 4(e), presenting a comparative bar chart of the mean of dice scores for each task.
- Image 4(e), presenting a comparative bar chart of the standard deviation of dice scores for each task.

Image results analysis From image 4(a), the following information can be seen:

- For task 1.1 (segmentation without EM, using tissue models), 50% of the scores are within the range 0.45-0.75. There are a few points in the lower and upper quartiles, and there is no presence of outliers.
- For task 1.2 (segmentation without EM, using label propagation), 50% of the scores are within the range 0.7-0.8. There are a few points in the lower and upper quartiles, and there is no presence of outliers.
- For task 1.3 (segmentation without EM, using a combination of tissue models and label propagation), 50% of the scores are within the range (around 0.73-0.85). There are a few points in the lower and upper quartiles, and there is one outlier at around 0.4.
- For task 2.1 (segmentation with EM, k-means initialization), most of the scores are very close to zero and there is the presence of one outlier at around 0.05.
- For task 2.2 (segmentation with EM, tissue models initialization), the data points are more spread. 50% of the scores are within the range of 0.15-0.65. The data distribution is almost symmetric (the median is close to the middle of the box and the whiskers of the plot are equal in length), and there is no presence of outliers.
- For task 2.3 (segmentation with EM, label propagation initialization), the data points are even more spread, 50% of them between the range 0.05-0.65. There is no presence of outliers.
- For task 3.1 (segmentation with EM initialized with tissue models and including MIRA atlas information after the algorithm), 50% of the scores are distributed between the range 0.65-0.75, and there is the presence of one outlier with the score close to zero.
- For task 3.1 (segmentation with EM initialized with tissue models and including MIRA atlas information into the algorithm), 50% of the scores are distributed between the range 0.35-0.65. There is no presence of outliers and the distribution looks symmetric.

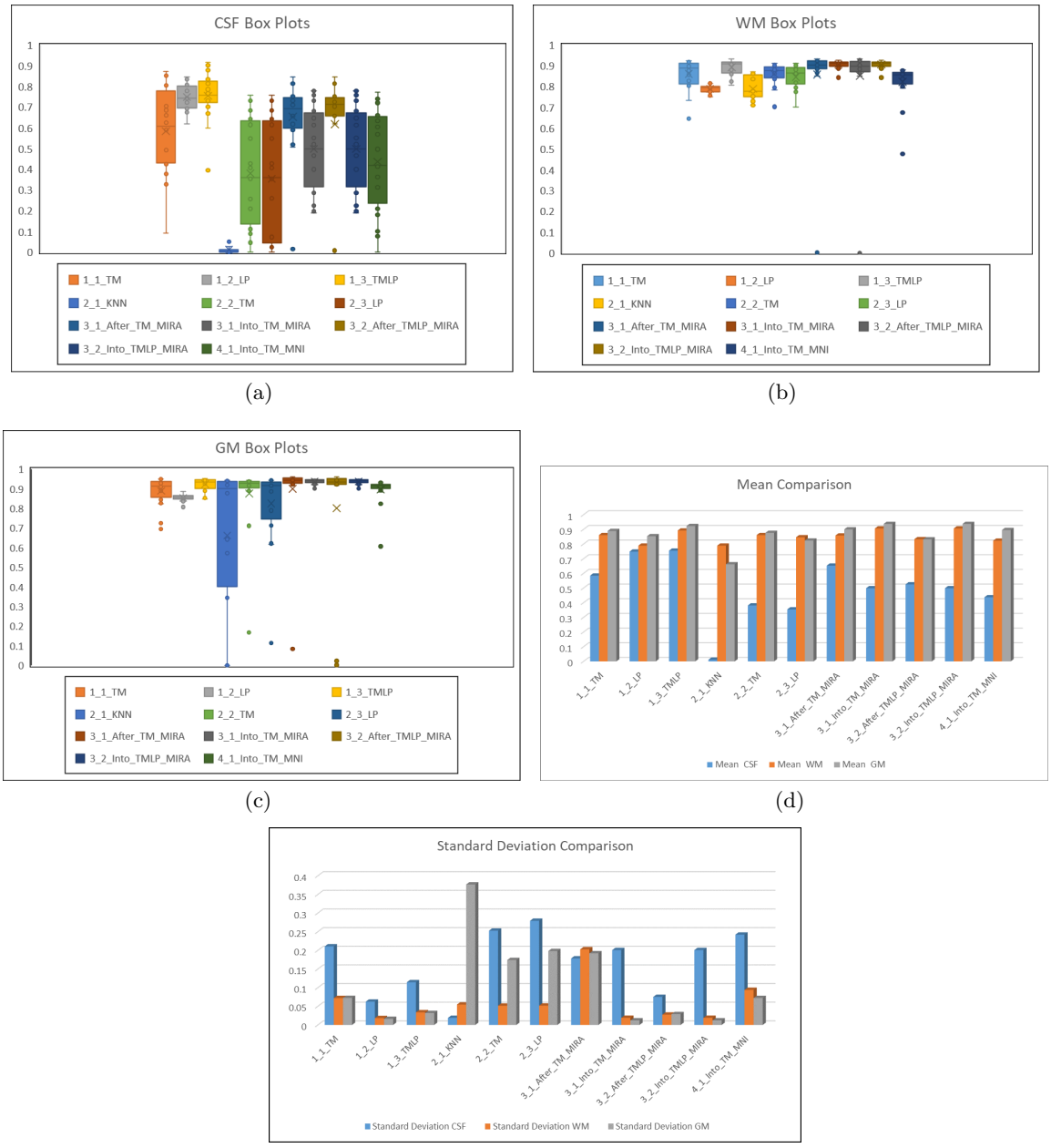

Fig. (4) A set of five subfigures: (a) Dice Scores Box Plots (CSF); (b) Dice Scores Box Plots (WM); (c) Dice Scores Box Plots (GM); (b) Mean Dice Scores; and, (e) Standard deviation of Dice Scores

– For task 3.2 (segmentation with EM initialized with a combination of tissue models and label propagation including MIRA atlas information after the algorithm), 50% of the data points are located within the range 0.67-0.75 and there is no presence of outliers.

- For task 3.2 (segmentation with EM initialized with a combination of tissue models and label propagation including MIRA atlas information into the algorithm), 50% of the data points are located within the range 0.35-0.65, there is no presence of outliers and the distribution looks symmetric.
- For task 4.1 (segmentation with EM initialized with tissue models including MNI atlas information into the algorithm), 50 % of the data points are located within the range 0.25-0.64. There is no presence of outliers and there are a few point located in both lower and upper quartiles.

From image 4(b), the following characteristics can be noted:

- The distribution of the dice scores obtained for each of the classes is generally over 0.7, which indicates that the segmentation results for white matter are good. However, for the case of tasks 1.1, 2.2, 3.2, and 4.1, there is the presence of outliers not so far away from the data distribution. In the case of tasks 3.1 and 3.2, there is one extreme outlier where the dice score obtained was 0.
- For task 1.1, most of the values (75%) are located over 0.8. In the case of task 1.2, the scores are distributed between 0.7 and 0.8. For task 1.3, the data points are distributed above 0.8. In the case of task 2.1, the scores are distributed between 0.7 and 0.85. For task 2.2, most of the dice scores are distributed between 0.8 and 0.9, with an exception of one outlier located a little bit below 0.7. For task 2.3, data points are located above 0.7 and below 0.9. For task 3.1 (MIRA atlas into EM, tissue models initialization), the scores are located between 0.8 and 0.9, with one extreme outlier with the value of 0. For task 3.1 (Mira Atlas into EM, tissue models initialization) , values are located between 0.85 and 0.9 with an outlier at 0.8 approximately. In the case of task 3.2 (MIRA atlas after EM with tissue models and label propagation initialization), the behavior is the same as in task 3.1. For task 2 (MIRA atlas into EM with tissue models and label propagation initialization), the behavior is the same as in task 3.1. Finally, for task 4.1 most of the values are distributed above 0.8 except for two outliers located at 0.7 and 0.45 approximately.

From image 4(c), the following characteristics can be noted:

- For most of the cases (tasks 1.2, 1.3,2.2,3.1 (MIRA atlas with tissue models initialization into and after EM), 3.2 (Mira atlas with combined initialization into and after EM), have dice scores values above 0.8, which is an indication that the segmentation of GM was good in most of the pipelines.
- For task 1.1, most of the values are located above 0.8, with an exception of two outliers located between 0.65 and 0.73, approximately. In the case of task 1.2, the scores are distributed between 0.8 and 0.9. For task 1.3, the data points are distributed above 0.8. In the case of task 2.1, the scores are much more distributed between 0.45 and 0.95. There is the presence of outliers (one around 0.37 and another one around 0, approximately). For task 2.2, most of the scores are distributed above 0.85 with an exception of one outlier close to 0.7 and another one close to 0.2. For task 2.3, most of the scores are distributed above 0.75 with an exception of some outliers present around 0.7, 0.6, and 0.15, approximately. For task 3.1 (MIRA atlas into EM, tissue models initialization), the scores are located well above 0.85. For task 3.1 (Mira Atlas into EM, tissue models initialization), scores are also located above 0.85. In the case of task 3.2 (MIRA atlas after EM with tissue models and label propagation initialization), the behavior is similar to task 3.1. However, there is a presence of two outliers close to zero. For task 3.2 (MIRA atlas into EM with tissue models and label propagation initialization), the behavior is the same as in task 3.1. Finally, for task 4.1 most of the values are distributed above 0.8 except for two outliers located at 0.8 and 0.6 approximately.

From image 4(e) it can be seen that the best performing pipeline is doing the brain segmentation without EM by combining both tissue models and label propagation, and this is also agrees with

image 4(e), where it can be seen that this is the pipeline with lowest standard deviation. Other than that, it can also be noticed that using tissue model initialization with EM performs best and that using MIRA atlas information with tissue model initialization for both after and into EM has better results than using MNI atlas information into EM.

4.3 Image Segmentation Results

In the appendix, a set of images with the segmentation results is presented. This corresponds to slice 150 of patient 1005 for each of the tasks and per each tissue.

5 Project Management and Details

The problems we faced during this lab are:

- Registration of the test images for generating probability maps. (Solved by changing **ResultImagePixel** from 'short' to 'float'.)
- When doing the segmentation using the tissue models it was noticed that the maximum intensity of the testing images was 5392 vs 3077 in the training set the atlas was built on. This problem was solved by enlarging the tissue model to have 5392 elements and for every voxel having an intensity value greater than 3077 the highest probability from the voxel 3077 was assigned (which corresponded to white matter voxel).
- A problem arose while using the label assignment of K-means which was not robust. (Solved by using 'label-trick' from the mean intensity of the clusters.)
- There was an issue regarding the use of covariance in the EM part which was throwing inf/nan error because of zero division. Later it was solved by adding a small number 10^{-10} to the covariance matrix in the diagonals.

Other than that, no problems were faced and the workload has been divided equally between the partners both for the coding and writing parts.

6 Conclusions

- During this lab, brain image segmentation with ten different pipelines was done. From the results obtained it can be concluded that the brain atlas actually helps improve the segmentation results for this particular task, since the best-performing pipeline was the one containing tissue models and label propagation, which is a combination of segmentation using both intensity and position information from the constructed atlas in the previous MIRA lab. This conclusion is supported by the fact that when comparing the results of a segmentation method that uses no atlas information (EM with KNN specialization), the segmentation results improved drastically (from almost 0 in CSF tissue to over 0.7). The results for other tissues also improved.
- It was found that using tissue models as an initialization method for EM provides better results than just using label propagation. Therefore, for this particular group of tasks, using intensity information had a higher impact on improving the results of the brain segmentation.
- From the last set of tasks, it was numerically found that including atlas information after the EM algorithm and using tissue models as initialization provides better results than using a combination of tissue models and label propagation (into and after EM) and it was also better than using information from the MNI atlas that was provided in the assignment data. Therefore, it can be

concluded that the MIRA atlas had a higher impact in improving the results of brain segmentation for this particular set of tasks. However, when seeing the results in general, it was numerically found that adding atlas information into EM does not provide better segmentation results than using pure atlas information without EM (best pipeline).

References

1. K. M. M. V. J. P. S. Klein, M. Staring, "elastix: a toolbox for intensity-based medical image registration," *IEEE Transactions on Medical Imaging*, vol. 29, no. 1, pp. 196–205, 2010.

7 Appendix

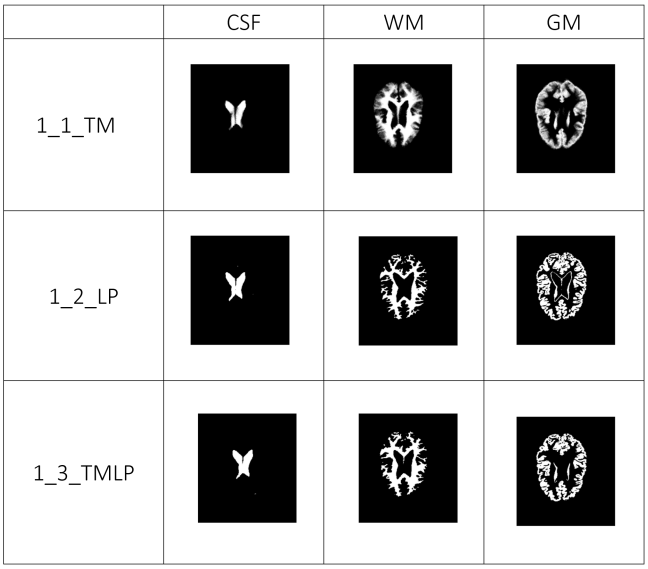

Fig. (5) Segmentation(Slice:150, Patient:1005) of task 1: Segmentation with different methods without EM.

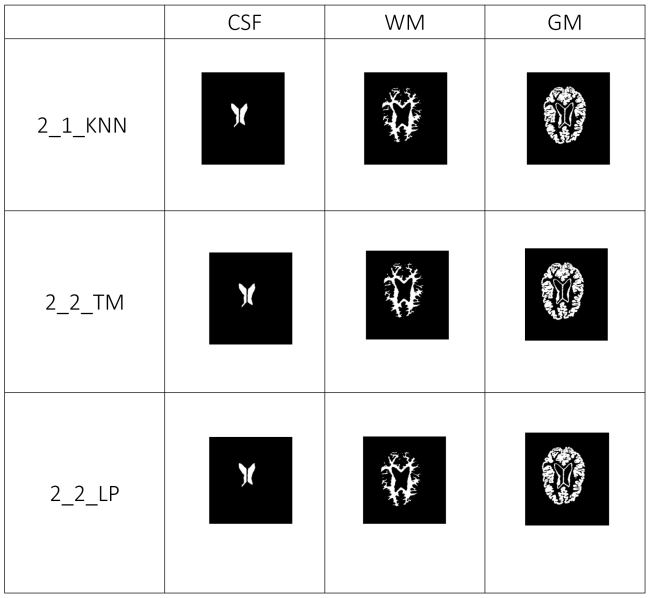

Fig. (6) Segmentation(Slice:150, Patient:1005) of task 2: EM with different initialization methods.

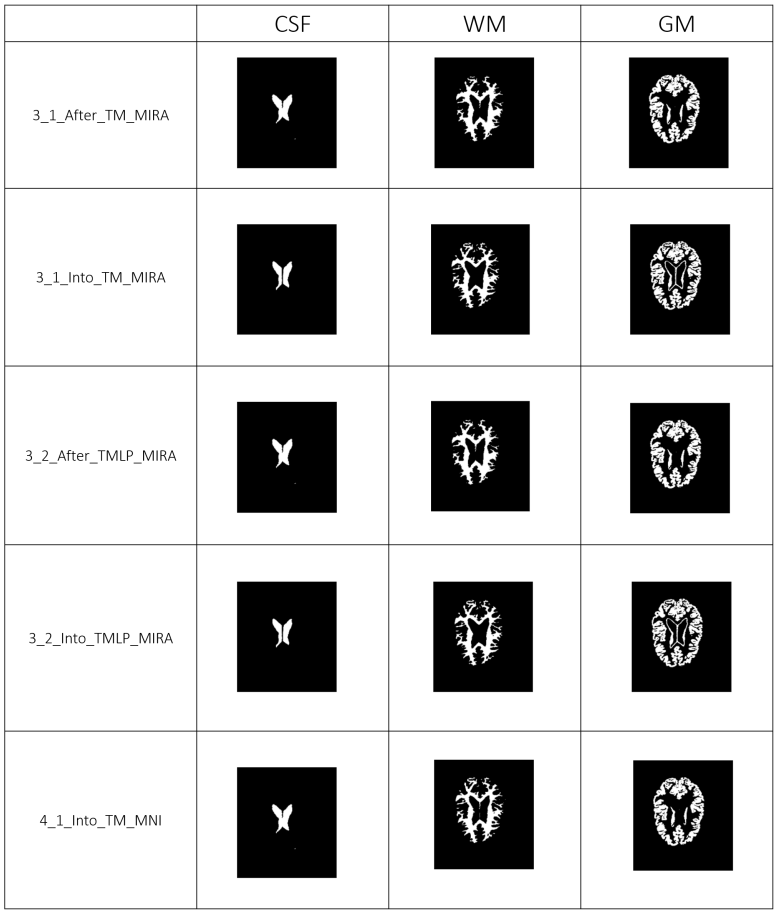

Fig. (7) Segmentation(Slice:150, Patient:1005) of tasks 3 and 4 (Em into/after Atlas).