Brain Tissue Segmentation Using Expectation Maximisation and Probabilistic Atlases

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November 20, 2023

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]. Atlases has been commonly used in the literature for automatic segmentation of brain structure and tissues as reviewed in [2]. As cited by [3], the GMM parameters are estimated using an Expectation-Maximization (EM) algorithm, where a Gaussian classifier is applied to obtain the class label of each voxel.
In this laboratory, we experimented using atlases in initializing the EM algorithm with intensity and position information obtained using atlases, comparing both MNITemplate atlas, and a probabilistic atlas that was developed in an earlier laboratory session. We also evaluated the segmentation results on various experiments with different initialization and final probabilistic configurations.

2 Objectives

The objectives of this laboratory sessions are to:

(a) Information search.

(b) To understand the segmentation algorithm when integrating atlas information. To design, analyse and implement the algorithm in python.

(c) To test the algorithm at least with the provided images (training images for building the atlas and testing for providing results). To study the problems and possible improvements. To evaluate the results using the ground truth provided and the DSC. Note that DSC values should be provided per class.

(d) Documentation.

3 Methodology

This section highlights all the steps taken to achieve the laboratory objectives.

3.1 Registration and Label Propagation to Patient Space

The fist step was to register all the atlases, both ours and the given MNITemplateAtlas to the patient space. This is made using elastix registration tool and the automated code developed in the previous laboratory. After registering, all atlases for all tissues (CSF, WM, and GM) were propagated to the same patient space using the generated transformation files. For this registration, parameter files of $Par0010$ has been used to perform affine + BSpline registrations. This results to a registered atlases version for each test subject, in that specific subject space. The code for registration and label propagation can be found in $1\_ProbabilisticAtlas\_EDA\_Registration$ and $1\_MNITemplateAtlas\_EDA\_Registration$ notebooks for our atlas and MNITemplateAtlas respectively. The main functions responsible for registration and label propagation can be found in $ElastixTransformix$ class inside *EM.py* submitted file. Some of the registration results can be seen in Figure 1 for the intensity volumes on different subjects.

3.2 Segmentation without Expectation Maximization (EM)

This step was mainly focused on utilizing the transformed atlases and the tissue models to segment test subjects without the use of EM algorithm. In other words, developing the functions that handle the registration independently of the EM algorithm. This task was split into 3 separate functions.

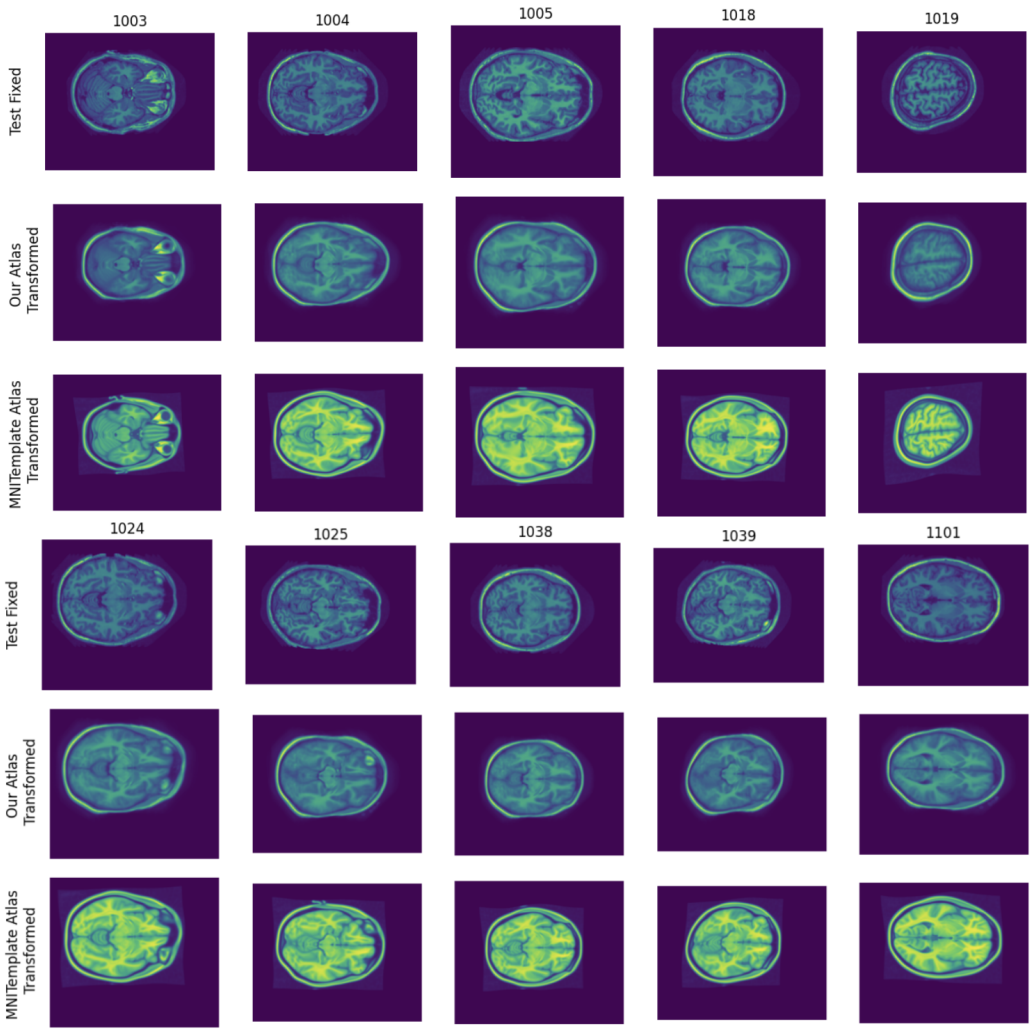

Figure 1: Registration results for both atlases on different test samples, slice 125.

All three functions can be found in *BrainAtlasManager* class inside the submitted *EM* python script file, and has been used in the submitted notebooks, *2_atlas_based_segmentation_experiments* and *2_EM_experiments* respectively. In addition, all segmentation results from the implemented functions can be seen in Figure 2, comparing it with the label and demonestrating the original and pre-processed images.

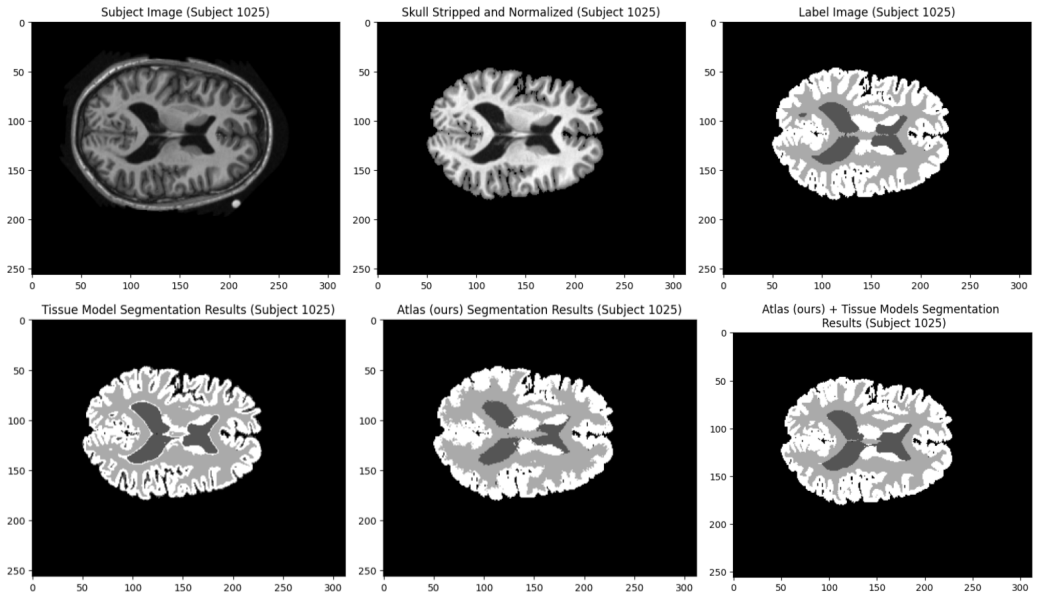

Figure 2: Segmentation results (without EM, only segmentation) using our implemented functions on subject 1025 using the three approaches, slice 148.

3.2.1 Segmentation using intensity information

Firstly, to segment only using the tissue models, *segment_using_tissue_models* function was developed to take a normalized [0, 255] and skull stripped input image, which is the test volume as shown in Figure 2. This will be used for segmentation. In addition, the tissue maps were used in the form of 3 columns, each column from the tissue maps file corresponds to a specific tissue type (class, also known as cluster).
The label volume for that input test volume is also used to work only on tissues of interest by binarizing it to create a mask, thus neglecting background voxels. As observed in the tissue map, pixels above intensity threshold of 100 are dominant to background, which we neglect in the tissue map for the three tissues, thus, any value of the tissue map that is above that given threshold is mapped to WM label. This way, we mapped all of the values from the input volume pixel values, to their respective probability from the tissue map. This resulted to 3 probabilities to each pixel, and the final shape of the probabilities of the pixels are $N \times K$, where N is the number of samples, and K is the number of clusters, for our case, 3 clusters. This function returns

the new segmentation label image, as well as the atlas probability for each pixel.

3.2.2 Segmentation using position information

Secondly, *segment_using_tissue_atlas* function that segments using the atlases. The function takes the same inputs as the previous function, both the standardized and label volumes. In addition, this function requires the 3 atlases that corresponds to the three tissues. It maps every pixel from the test volume to its 3 probabilities from the 3 atlases, where the cluster with highest probability is used as the label for the respective pixel. This function also returns the new segmentation label image, as well as the atlas probability for each pixel.

3.2.3 Segmentation using both intensity and position information

Finally, *segment_using_tissue_models_and_atlas* function that combines both approaches of tissue maps and atlases by multiplying their probabilities to find the final probability that is based on both intensity and position information. This final probability is used to map each pixel with its tissue cluster based on the highest probability. Likewise the previous two functions, this function returns both new segmentation label image, as well as the atlas probability for each pixel.

3.3 Segmentation with Expectation Maximization (EM) using Different Initialization Techniques.

The segmentation functions that were developed in the previous sub-section 3.2 has been integrated into the EM algorithm in two parts. This section will discuss about the integration into the algorithm model parameters initialization.

Considering the three new segmentation approaches, they required the images to be all normalized. We normalized the input volumes to the algorithm to facilitate this task using min-max normalization, where it falls in the range of [0, 255] 8-bit intensity values.

The three functions were integrated into *initialize_parameters* function, where the three of them returns the segmentation result that we used as the new labels, and the atlas probability depending on the approach, that

has a shape of $N \times K$. Using those results, we managed to compute the clusters means, clusters covariance matrices, and the mixture weights in the same way they were computed in the previous labs, as shown in the Equations below 1, 2. We experimented all possible initialization techniques as summarized in Table 1.

$$\mu_k{}^{\text{new}} = \frac{1}{N_k} \sum_{i=1}^{N} w_{ik} \cdot x_i \tag{1}$$

$$\sum_{k}^{new} = \frac{1}{N_k} \sum_{i=1}^{N} w_{ik} \cdot (x_i - \mu_k{}^{\text{new}})(x_i - \mu_k{}^{\text{new}})^T \tag{2}$$

3.4 Integrating atlases probabilities with EM using a posteriori approach.

All atlases probabilities, that were obtained as discussed in the previous section 3.2 from the initialization, were integrated using a posteriori approach to the EM algorithm posterior probabilities after converging or finishing the defined number of iterations. This was made by multiplying the output of the EM algorithm with the atlas probabilities of the same shape as shown in Algorithm 1. Both our atlases and MNITemplate atlases were integrated in the same way, where more will be explained in the experiments section 4 in detail.

Algorithm 1 Algorithm for integrating EM and atlas probabilities

```
procedure FIT
    Initial maximization step when we include the atlas probability.
    MAXIMIZATION(...)
    for i ← 1 to n_iterations do
        EM_prob = EXPECTATION(...)
        LOG_LIKELIHOOD_CONVERGENCE_VALIDATION(...)
        MAXIMIZATION(...)
    end for
     final_prob = EM_prob × atlas_prob
end procedure
```

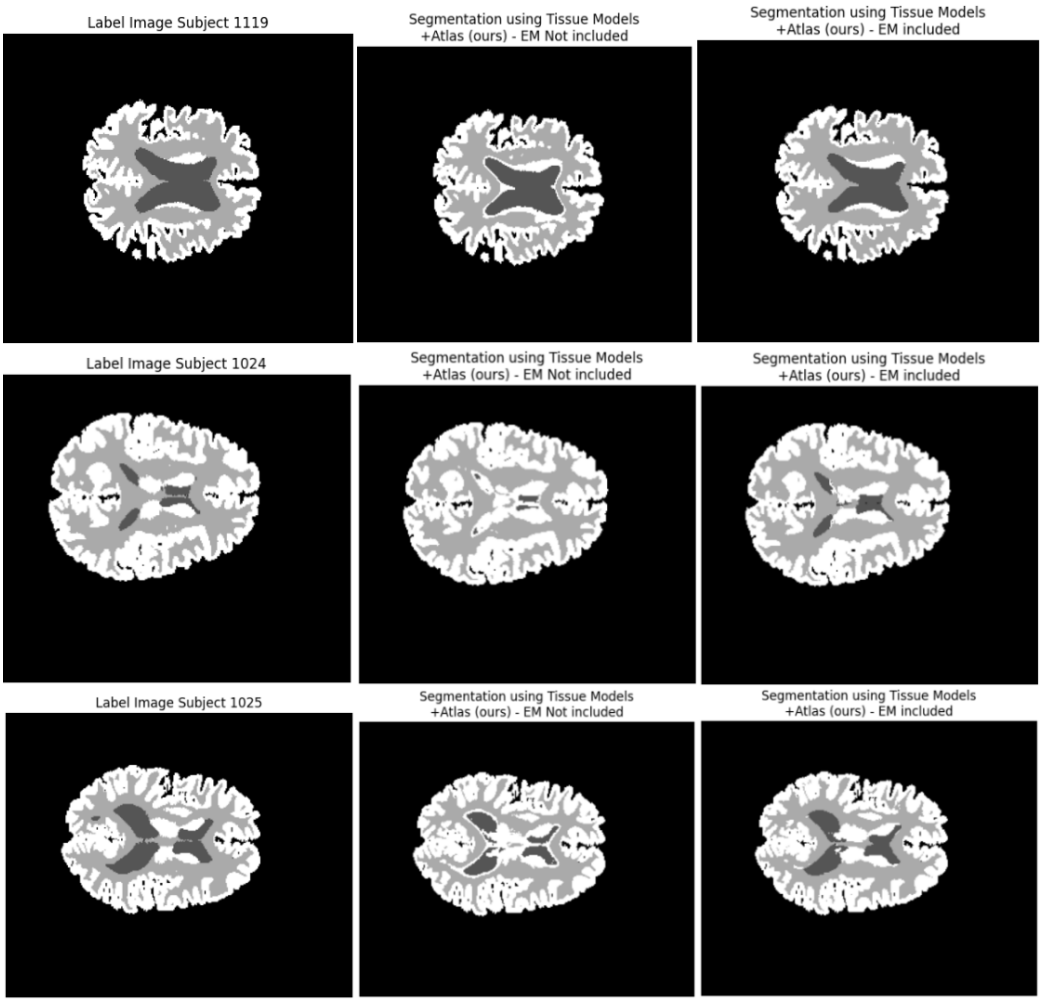

Figure 3: Comparing segmentation results using tissue models and altas (ours) for different subject with and without EM integration, slice 148.

4 Experiments

Different experiments were performed to find the best combination of configuration for brain tissue segmentation, by trying different initialization approaches and tissue maps, with different atlases. Table 1 summarizes all the experiments taken with their configurations that were performed during this laboratory and their evaluation results will be summarized in section 5.

Table 1: Experiments performed and their configurations.

Experiment Number	Initialization Type	Atlas Integrated into EM
1	KMeans	-
2	Tissue Models	-
3	Tissue Models	a posteriori
4	Atlas (ours)	-
5	Atlas (ours)	a posteriori
6	Atlas (ours) + Tissue Models	-
7	Atlas (ours) + Tissue Models	a posteriori
8	Atlas (MNITemplateAtlas)	-
9	Atlas (MNITemplateAtlas)	a posteriori
10	Atlas (MNITemplateAtlas) + Tissue Models	-
11	Atlas (MNITemplateAtlas) + Tissue Models	a posteriori

5 Results and Discussion

Atlases registration has been successfully performed using all test subjects and the atlases as demonstrated in Figure 1, where sample results are plotted. The parameter files $Par0010$ that performs affine + BSpline registrations successfully registered all atlases to all subjects using Elastix and Transformix version 4.2.

As for the segmentation using intensity and position information with EM, the three functions resulted in a significant result in segmenting the three tissues as shown in Figure 2. Comparing the three implementations, segmenting using both intensity and position information atlas probabilities resulted in the highest DICE scores for all three tissues.

Among all of the experiments performed, experiment 7 that combines both our atlas and tissue models into EM using a posteriori approach had the highest average dice score for the three tissues as shown in Table 2. The results without integrating the atlas probabilities (experiment 6) with the same configuration were high as well, however, integrating both intensity and position information boosted the dice scores significantly for all the three tissues, more specifically on the CSF scores. The best CSF average dice scores were obtained from the same experiment number 7, where the rest of experiments showed low scores for this specific tissue type. Table 3 shows the results for each test subject using the best experiment configurations.

Table 2: Experiments results using average dice score for each tissue.

Experiment Number	WM	GM	CSF
1	0.882733 ± 0.021103	0.630461 ± 0.145555	0.184494 ± 0.206078
2	0.89603 ± 0.025142	0.922521 ± 0.034503	0.449993 ± 0.285033
3	0.897307 ± 0.032948	0.886876 ± 0.046452	0.399878 ± 0.203793
4	0.897671 ± 0.02567	0.931921 ± 0.021117	0.418734 ± 0.311306
5	0.925919 ± 0.016916	0.9504 ± 0.015369	0.691848 ± 0.144316
6	0.895475 ± 0.027181	0.930286 ± 0.024205	0.419792 ± 0.296216
7	0.928687 ± 0.021643	0.950733 ± 0.01827	0.714166 ± 0.133116
8	0.890758 ± 0.023054	0.411738 ± 0.455594	0.270383 ± 0.335913
9	0.858455 ± 0.015252	0.879694 ± 0.014929	0.169122 ± 0.122397
10	0.895256 ± 0.024531	0.359989 ± 0.44138	0.282609 ± 0.322399
11	0.868236 ± 0.017017	0.881497 ± 0.018652	0.184314 ± 0.103206

To assess the scores visually, several box-plots figures are reported here for all the experiments that were performed, where as reported in Table 2, the best plot was for the same highest scored experiment number 7. All box-plots of all experiments can be seen in Figures 4, 5, 6.
In addition, Figure 3 demonstrates segmentation results using the best experiment 7 for segmenting tissues on 3 different subjects, where it is clear that integrating both intensity and position information from atlases probabilities with EM probabilities resulted in better visual segmentation assessment for the three tissues.

6 Conclusion

In conclusion, all the lab objectives had been achieved. Expectation-Maximization algorithm showed high DICE scores in segmenting the three brain tissues (WM, GM, CSF) when initialized with both intensity and position information obtained from a probabilistic atlas, when the atlas probabilities were combined with the EM probabilities using a posteriori approach. Our atlas that was obtained from a previous lab resulted in higher DICE scores, compared to MNITemplate atlas. Figures 7 and 8 shows the final segmentation results for all test subjects using both intensity and position information obtained from atlases, for EM initialization and integrating atlas probabilities

Table 3: Dice score for each test subject per class using the best experiment 7.

Subject	WM	GM	CSF
1003	0.947717	0.956709	0.358067
1004	0.942342	0.963529	0.792909
1005	0.931516	0.956739	0.825748
1018	0.949074	0.965473	0.714524
1019	0.941935	0.967264	0.72365
1023	0.943422	0.96271	0.625117
1024	0.944706	0.964662	0.718801
1025	0.918533	0.953594	0.809891
1038	0.94424	0.961547	0.734399
1039	0.946638	0.967059	0.685071
1101	0.935618	0.959501	0.740335
1104	0.910857	0.942243	0.722809
1107	0.929838	0.932783	0.364507
1110	0.940731	0.963487	0.745048
1113	0.934987	0.952638	0.672979
1116	0.920737	0.952512	0.87617
1119	0.911172	0.926244	0.708268
1122	0.897929	0.925518	0.771528
1125	0.925168	0.947461	0.840356
1128	0.85658	0.892992	0.853149

with EM results, as experiment 7.

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.

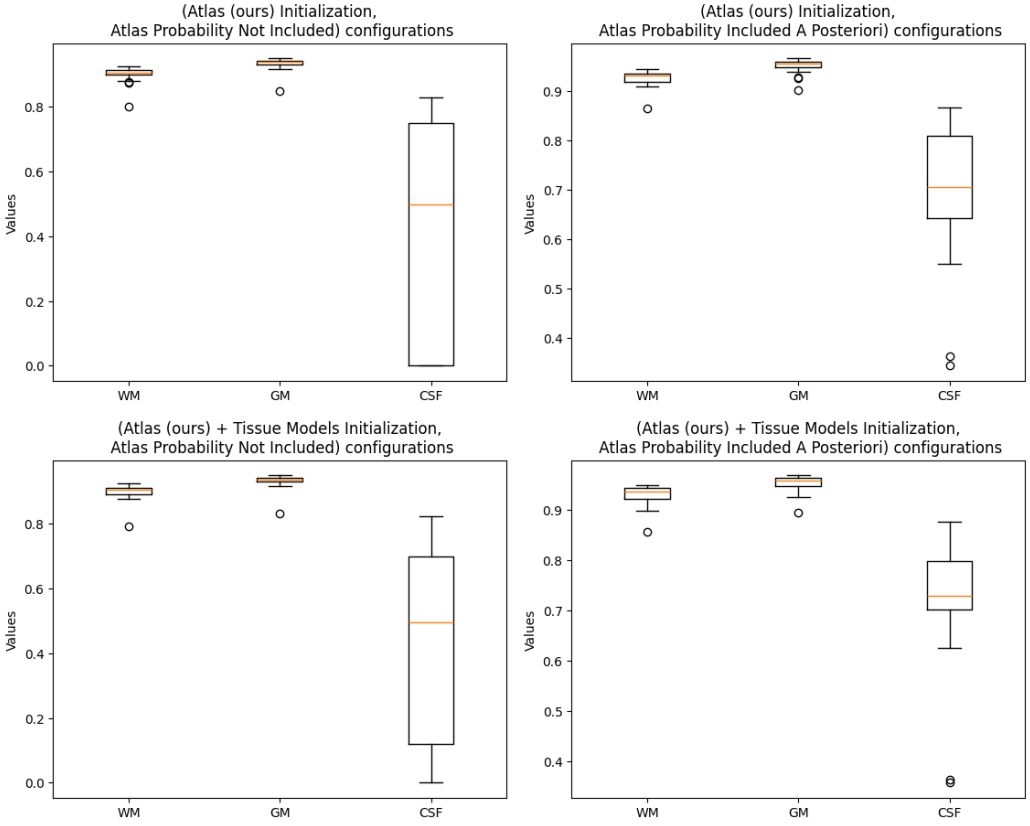

Figure 4: Box-plots for the atlases (ours) experiments performed for the average dice scores.

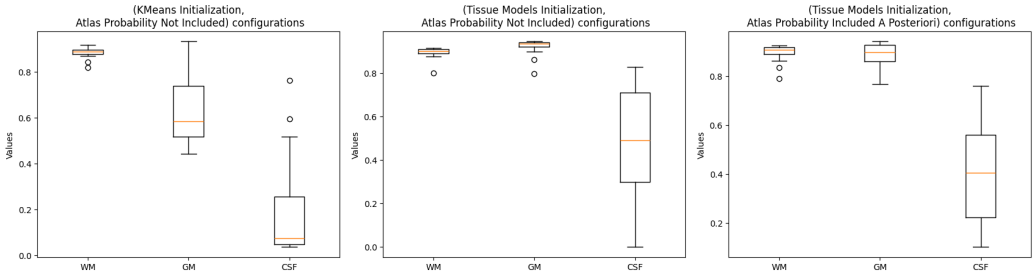

Figure 5: Box-plots for tissue models and KMeans experiments performed for the average dice scores.

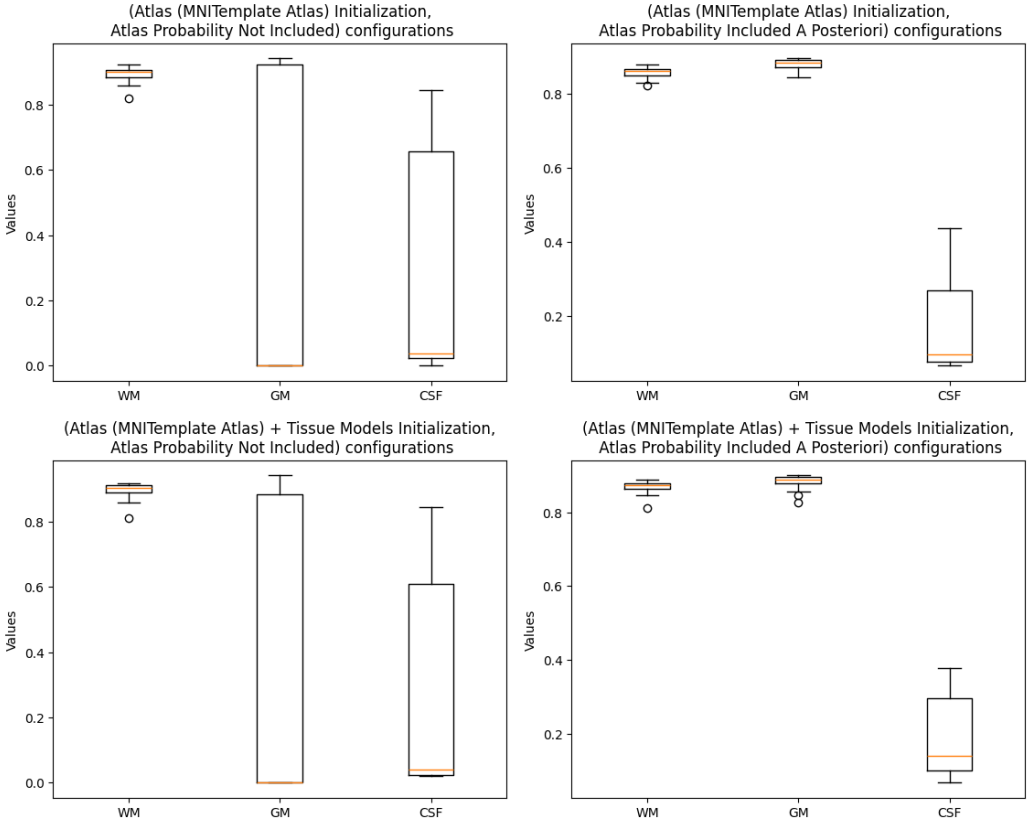

Figure 6: Box-plots for the atlases (MNITemplateAtlas) experiments performed for the average dice scores.

[3] Guangjian Tian, Yong Xia, Yanning Zhang, and Dagan Feng. Hybrid genetic and variational expectation-maximization algorithm for gaussian-mixture-model-based brain mr image segmentation. *IEEE Transactions on Information Technology in Biomedicine*, 15:373–380, 5 2011.

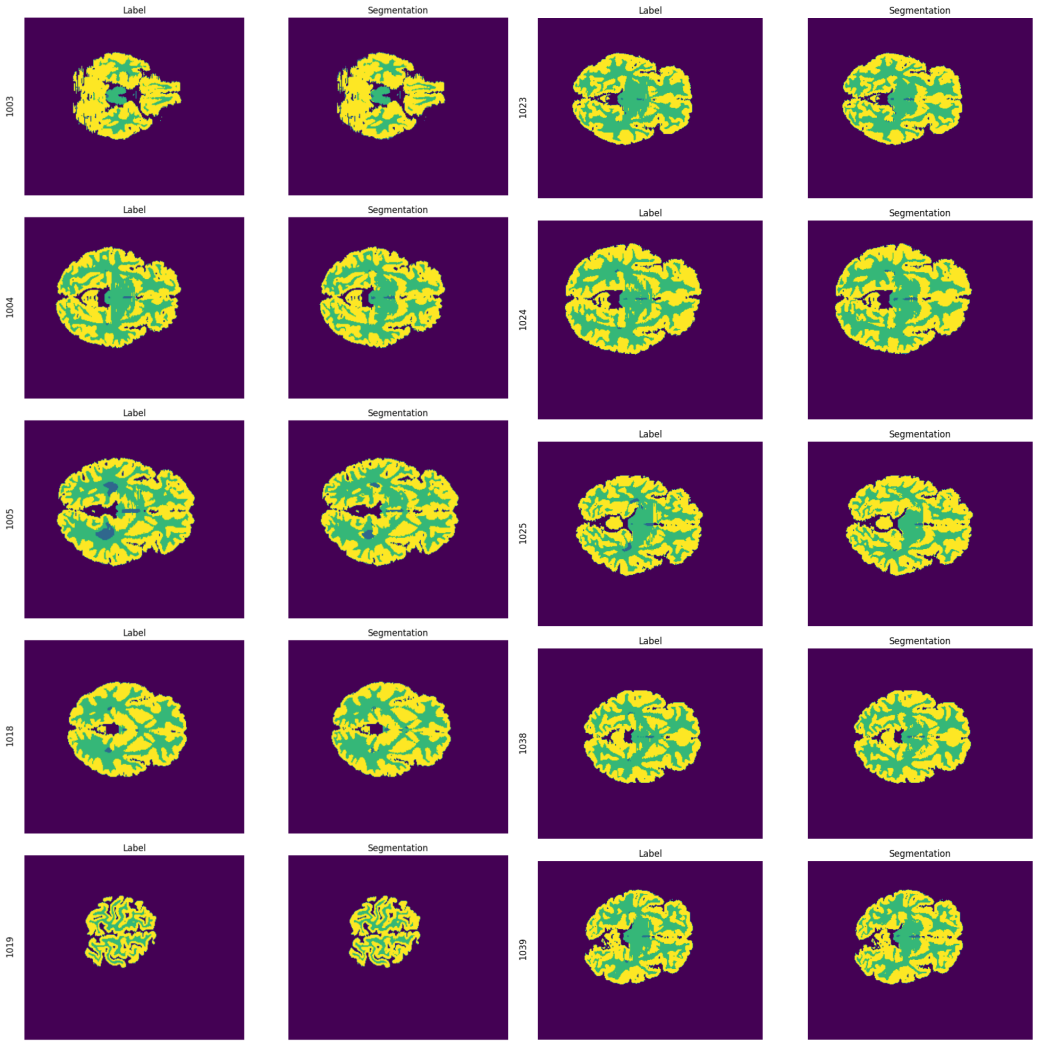

Figure 7: Final Segmentation result for test images using both intensity and position information with EM probabilities, experiment 7.

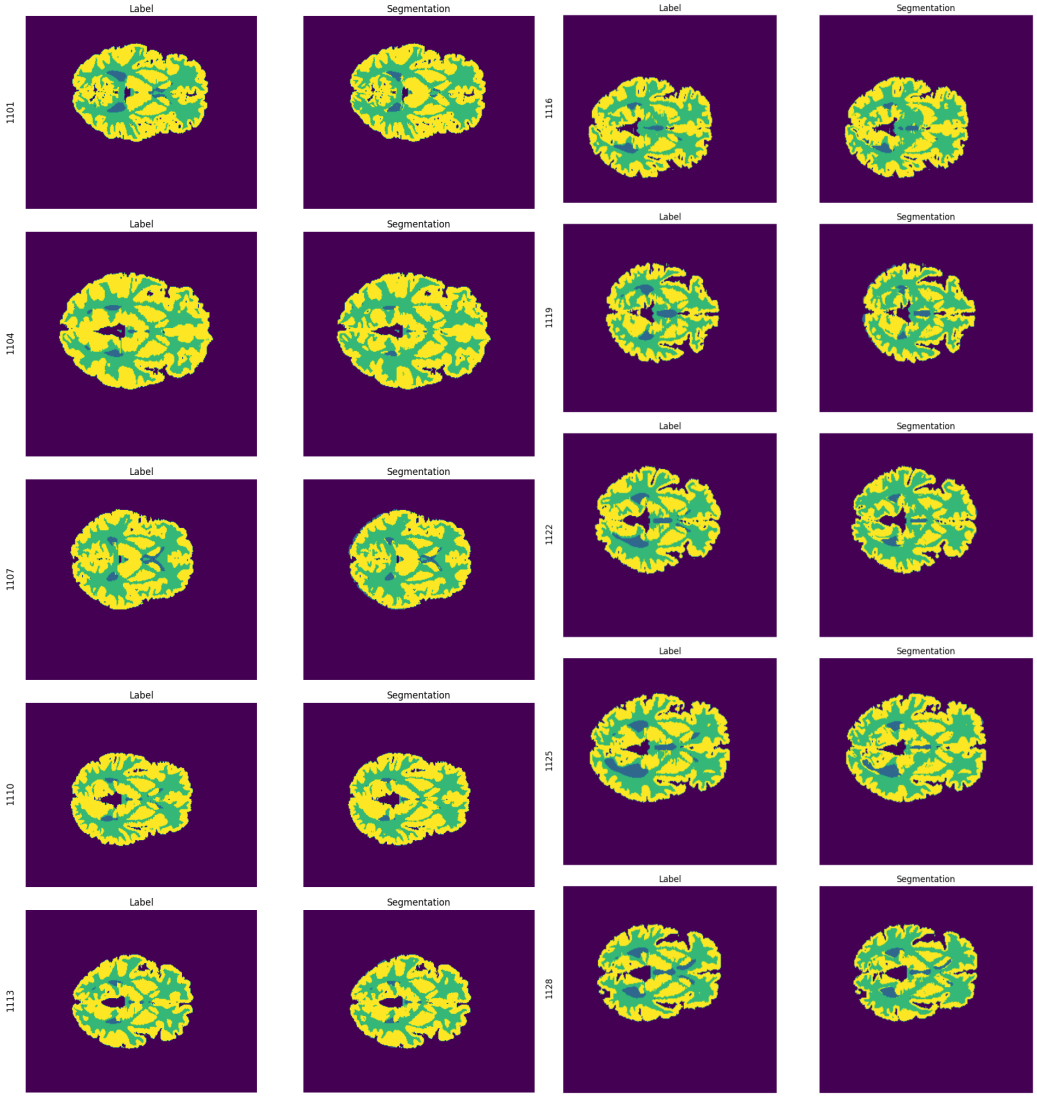

Figure 8: Final Segmentation result for test images using both intensity and position information with EM probabilities, experiment 7.