Universitat de Girona

Medical Image Segmentation & Application

Medical Image Registration & Application

Lab Report: 3

Atlas Based Segmentation

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1 Introduction

The main goal of this lab is to apply different segmentation approaches for brain MRI images to segment three types of brain tissues, which are CSF (CerebroSpinal Fluid), WM (White Matter) and GM (Gray Matter). This report is divided into two main sections. The first section we used rigid and non-rigid image registration techniques to generate Atlases and Tissue Models from the training set, and then registering the generated Atlases for the testing images, as shown in the block diagram in figure 1.

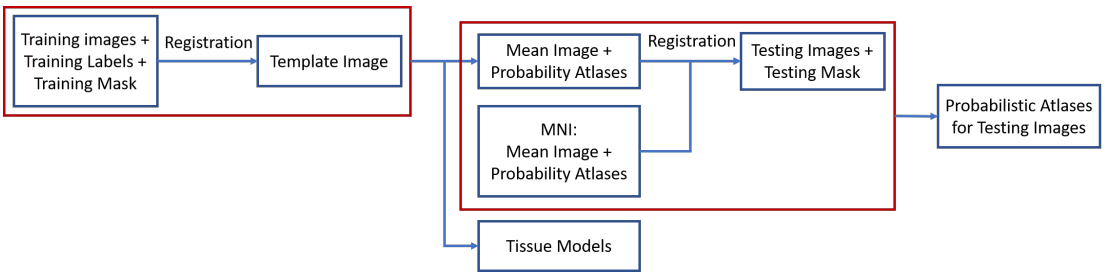

Figure 1: Image registration block diagram

In the second section of this report, we combined the Probabilistic Atlases with EM and Tissue Models to segment the brain tissues as shown in the block diagram in figure 2. Moreover, we applied three different parameters initialization for the EM algorithm, such as K-Means, Label Propagation and Tissue models. Then, we did a quantitative and qualitative studies for these segmentation approaches by calculating the dice similarity metric function between the segmented labels and the testing images labels, and visualizing the segmentation results.

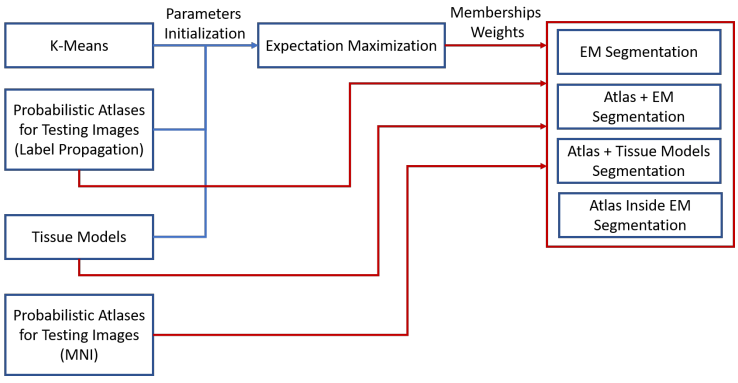

Figure 2: Image segmentation block diagram

2 Image Registration

In the image registration section, we used *Elastix* software to apply 3D registration of moving image on fixed image. In our case, we are applying registration for MRI brain images. Therefore, we downloaded and used the specific parameters files, which are *'Par0000affine'* for rigid registration and *'Par0000bspline'* for non-rigid registration. We used two different Atlases the first one we built it from a given brain MRI training set, while the other one is from Montreal Neurological Institute (MNI) which is standard atlas for brain. This MNI atlas was built by using a large series of MRI scans.

2.1 Building Atlas

In this section, we explain the steps to generate the mean image and building a probabilistic atlases for CSF, WM and GM from the given training set. Then we explained how to registered these probabilistic atlases on the testing set.

2.1.1 Training Image Registration

At first, all the training images have been registered by a reference image where is the first image *'1000.nii'* of the training data. Then we applied a non-rigid registration using b-spline for all of the training images on the selected reference image, as shown in figure 3. After registration, a b-spline transformation file is generated for each registered image. Then the generated transformation file is used to deform the associated labels for each training image on the reference image by using *transformix* command. In order to make sure that the deformed labels after registration are still a binary, we have to manually change the *'FinalBSplineInterpolationOrder'* in the transformation file to 0.

In the following step, the mean of all registered training images are computed to create a mean image. This image contains the general information for the registered pixels intensities which is later used as reference image to register the Atlases on the test images.

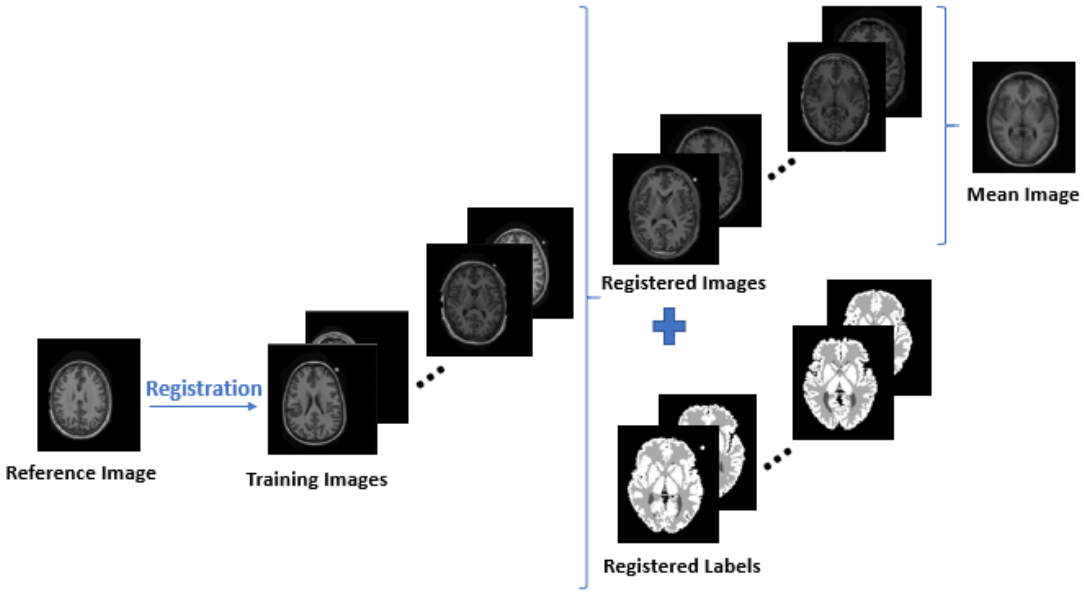

Figure 3: Registering Training images

2.1.2 Probabilistic Atlas Formation

Using the associated registered labels and registered images the probabilistic atlas of CSF, GM and WM have been computed which is shown in figure 4.

The probabilistic atlas term represents the particular atlas contains all the probabilities of all the pixels for all registered images which belong to that particular class of probabilistic atlas. That is how we get three different probabilistic atlases where for example CSF contains the probability of each pixel of all registered images to belong to CSF probabilistic atlas.

Figure 4: Probabilistic Atlases

2.1.3 Atlas Registration on Testing Images

There are two main approaches to apply registration for the Atlases with the testing set. The first approach is to register the testing set on the mean tissue image. In this condition, after segmentation process the output labels are required to be inverse transformed to the original testing image. The second approach is implemented in this lab is to make the testing images as a fixed images and registering the mean tissue image and the labels on it.

In this stage, generated mean atlas is registered on the testing images by using b-spline registration technique to generate a transformation file. Then the *transformix* command is used to deform the probabilistic atlas for CSF,GM and WM images on the testing set, as shown in figure 5. In the transformation file the *'FinalBSplineInterpolationOrder'* is set to 3, and the *'ResultImagePixelType'* is manually changed from "short" to "float" to obtain a higher resolution deformed image.

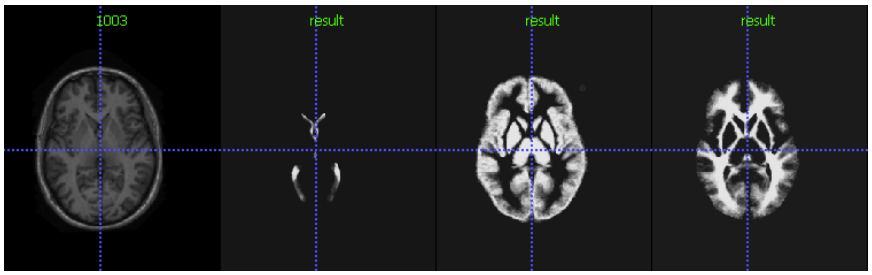

Figure 5: The generated Atlas after registration on the testing image '1003'

2.2 Using MNI Atlas

In the MNI atlas data files we have the 'template.nii' (as shown in figure 6) file which contains the mean images information, and the the 'atlas.nii'which contains 4 combined probabilistic Atlases with the background in one image. Since the MNI mean atlas is generated from different dataset with different header parameters, firstly we have to apply rigid transformation using affine then non-rigid transformation using b-spline. Some of the testing files requires to include the background mask during registration otherwise the *Elastix* program will crash. When we tried to register MNI atlas on all the testing images, it worked for all the images except the image '1039'.

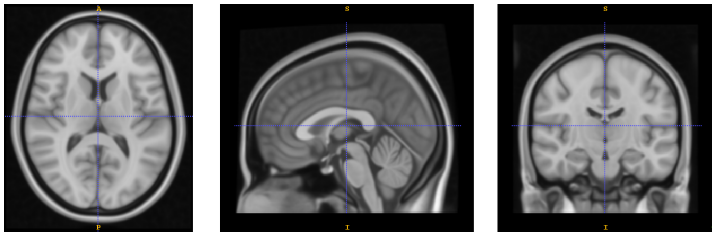

Figure 6: MNI template image

From the 4 combined probabilistic atlases, we split the CSF, WM and GM probabilistic atlases into three files, as shown in figure 7. Then the *transformix* command is used to deform the MNI probabilistic atlas for CSF,GM and WM images on the testing set using the generated transformation file from affine ans b-spline respectively, as shown in figure 8. In the both transformation files, the *'FinalBSplineInterpolationOrder'* is also set to 3, and the *'ResultImagePixelType'* is manually changed from "short" to "float". The template MNI image is poorly registered on some images of the testing set, consequently the MNI atlases are poorly deformed on these testing images.

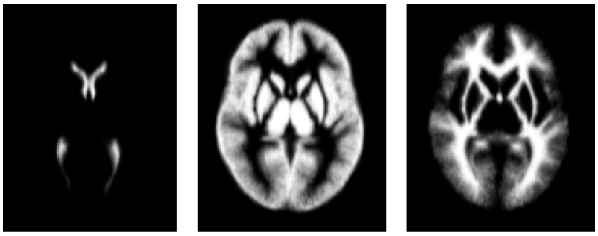

Figure 7: MNI Probabilistic Atlases

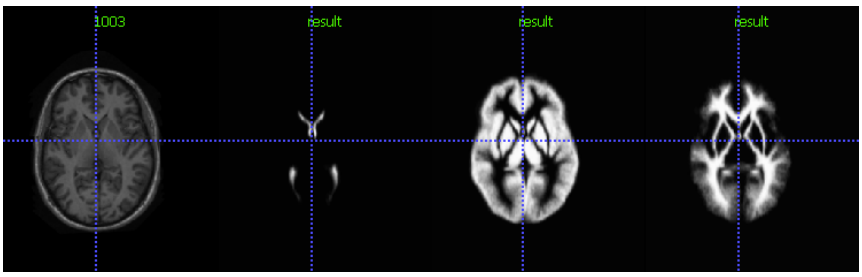

Figure 8: The MNI Atlas after registration on the testing image '1003'

2.3 Tissue Models

The tissue models of CSF, GM and WM have been computed from registered training images and their corresponding registered labels. Once we got our registered training images, we concatenated all the pixels intensities which fall under a particular region (for example CSF). So we build a three set of pixel dedicated for that particular class. In order to obtain the tissue models for each brain tissue, we calculated the histogram for each set of pixels individually, as shown in figure 9.

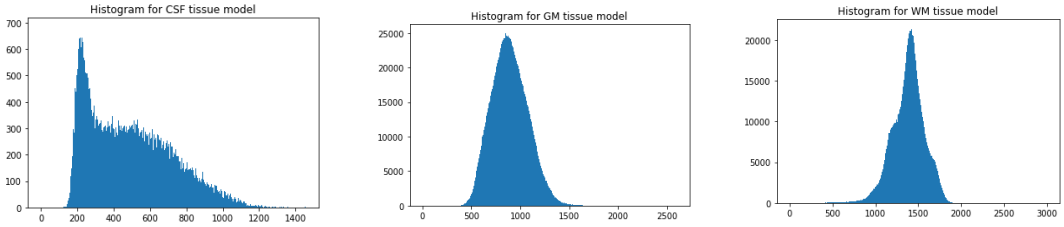

Figure 9: Tissue models histograms

Then all the histogram are normalized by dividing histogram value at each bin by the summation of all three histogram at the same bins. In this condition, the summation of all histogram probabilities at each bin will be equal to one, as shown in figure 10. Since we have training images from the same MRI scanner in our case, we don't have to apply intensity normalization before generating the tissue model.

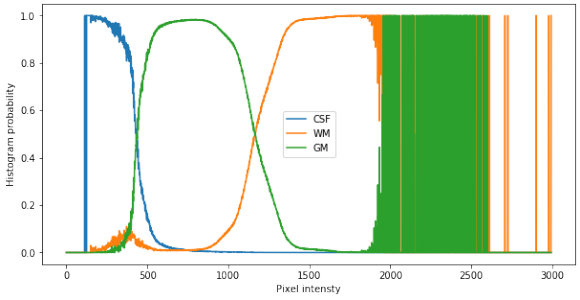

Figure 10: Normalized Tissue Models histograms

2.4 Conclusion

In conclusion, in this lab we used the *Elastix* as a software tool to apply 3D registration for Brain MRI images. We selected one of the training images as a

reference image to build Atlases and to generate mean tissue image and probabilistic Tissue Models. Then, we applied registration this mean tissue image on the testing images, and we used the generated transformation matrix to deform the the Atlases on these test images. In addition, we applied the same testing registration steps using MNI database. Then all off these generated model will be combine in the second section to segment the CSF, WM and GM of the testing set.

From the experimental works, we observed that the MNI has poor segmentation results and it crashes during registering it on some testing images, because it is generated from different MRI scanner with different intensity and number of slices. Therefore, some layers are interpolated during the registration process.

The generated Normalized Tissue Model, and the registered Atlases for the all images in the the testing set are merged together, or with the EM algorithm to segment CSF, WM and GM tissues. This part is explained in the second section of the report.

3 Image Segmentation

In the image segmentation section, the generated Atlases and the MNI Atlases probabilistic models for each testing image are combined with the Tissue Models probabilities and the EM membership weights in order to boost the segmentation performance for the CSF, WM and GM tissues.

3.1 Expectation Maximization(EM)

In the previous lab, we developed the EM algorithm using multivariate GMM to work with a 2D features vectors T1 and T2. In this lab, we used the same EM algorithm but with only 1D feature vector for the given T1 MRI testing images. Moreover, we applied different parameters initialization techniques for the EM, such as K-Means, Label Propagation and Tissue Models.

3.1.1 Pre-processing

The pre-processing is the first stage before applying image segmentation. In this stage, the 3D images of T1, the ground truth labels, and the mask are loaded. Then, the T1 image is multiplied by the mask to segment the brain region only and removing unwanted regions(skull, eyes..etc), as shown in figure 11. In the following step, 3D Region Of Interest(ROI) is flattened and reshaped into one vector which are considered as 1D feature vector.

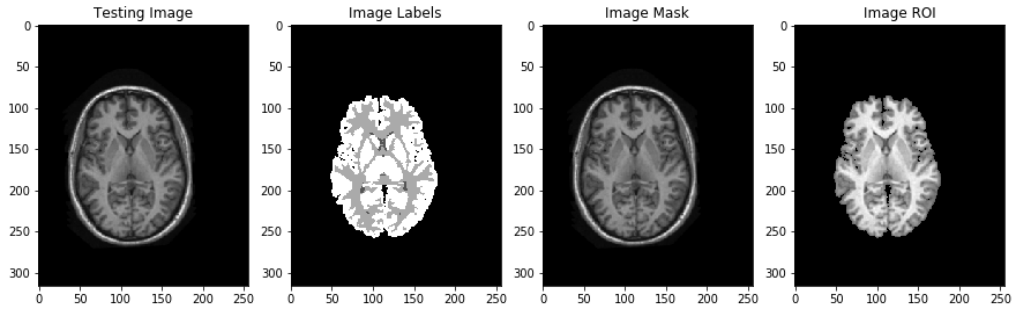

Figure 11: Pre-processing steps

3.1.2 Initialization Using K-Means

In this condition, we firstly applied K-Means segmentation for the flattened feature vector with k = 3, and with random initialization for the centroids. The feature vector is unsupervised segmented into three clusters. The centroids of theses clusters intensities are sorted according to the CSF, WM and GM

tissue intensities, and then they are used as initialization parameters for the EM algorithm:

- Firstly, the mean values of the Gaussian models $\underline{\mu}_k$ are initialized with the generated centroid clusters values from the K-means.
- Since we have 1D feature vector, we will have a variance Σ_k for each Gaussian model instead of covariance matrices, these variances are initialized according to the following equation, where N_k in the number of pixels for each class and the memberships w_{ik} are initialized with 1 for each corresponding class.

$$\Sigma_k^{new} = \left(\frac{1}{N_k}\right) \sum_{i=1}^{N} w_{ik} \cdot (\underline{x}_i - \underline{\mu}_k^{new})(\underline{x}_i - \underline{\mu}_k^{new})^t \quad 1 \leq k \leq K.$$

- The mixture weights parameters α_k are initialized with values $1/k$.

Quantitative Result

- **Dice Coefficient using K-Means algorithm:**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different test images using K-Means algorithm.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.0406	0.5881	0.9222
1004	0.0604	0.5783	0.9141
1005	0.3451	0.7885	0.9162
1018	0.0611	0.5962	0.9177
1019	0.0401	0.6172	0.9135
1023	0.0415	0.6020	0.9159
1024	0.0522	0.5850	0.9145
1025	0.3246	0.7823	0.9106
1038	0.0691	0.5911	0.9152
1039	0.0421	0.6062	0.9140
1101	0.1161	0.6551	0.9115
1104	0.0731	0.6098	0.9027
1107	0.0706	0.6220	0.9034
1110	0.0919	0.6342	0.9239
1113	0.0943	0.6237	0.9193
1116	0.2102	0.7270	0.9146
1119	0.2842	0.7078	0.9014
1122	0.2544	0.7232	0.9045
1125	0.4118	0.7820	0.9008
1128	0.2498	0.7177	0.8409
Mean	**0.14432**	**0.6521**	**0.9015**

- **Result of K-Means segmentation:**

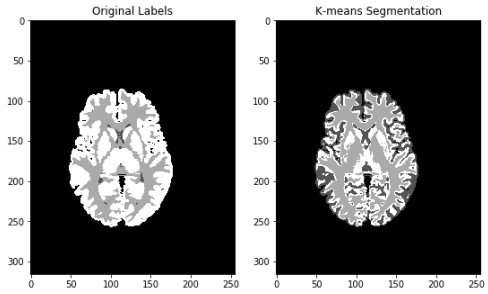

Figure 12: K-Means Segmentation output

- **Dice Coefficient of Expectation Maximization with KMeans:** Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using EM algorithm with K-Means initialization.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.0376	0.5348	0.9039
1004	0.0517	0.4755	0.8996
1005	0.6418	0.9156	0.9191
1018	0.0555	0.5344	0.9084
1019	0.0389	0.6007	0.9068
1023	0.0390	0.5667	0.9054
1024	0.0459	0.5059	0.9056
1025	0.5435	0.8995	0.9154
1038	0.0620	0.5199	0.9097
1039	0.0402	0.5773	0.9022
1101	0.2226	0.8777	0.9101
1104	0.1106	0.7702	0.9029
1107	0.0690	0.6084	0.8921
1110	0.1500	0.8407	0.9219
1113	0.0903	0.5902	0.8930
1116	0.2478	0.7861	0.912
1119	0.3301	0.7653	0.8975
1122	0.2900	0.7795	0.9094
1125	0.4838	0.8387	0.9046
1128	0.2698	0.7485	0.8429
Mean	**0.1874**	**0.6831**	**0.9097**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) of EM algorithm initialized by K-Means.

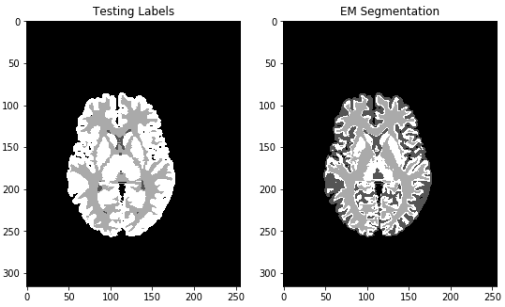

Figure 13: Segmentation result of EM initialized by K-Means

Observation

From above mentioned quantitative and qualitative result, we can see that the dice score in general increases using EM algorithm along with K-Means than that of using K-Means segmentation alone even thought the dice scores of CSF and WM is not that good.

The reason behind this poor dice score of CSF is the ground truth itself is biased so after applying K-Means initialization, the CSF region segments the region of CSF itself and part of WM as well (both inner boundary and outer boundary) which is not correct and eventually affects the dice score of WM.

3.1.3 Initialization Using Label Propagation

In the case of label propagation initialization, we firstly applied segmentation by calculating the maximum argument of the atlases probabilities for each corresponding tissue class. For instance, as shown in figure 14.

Then, we calculated the mean value of the pixels for each class, and we used them to initialize the mean values $\underline{\mu}_k$ for the EM algorithm. The variance Σ_k and mixture weights parameters α_k are initialized by following the same steps in the K-Means initialization.

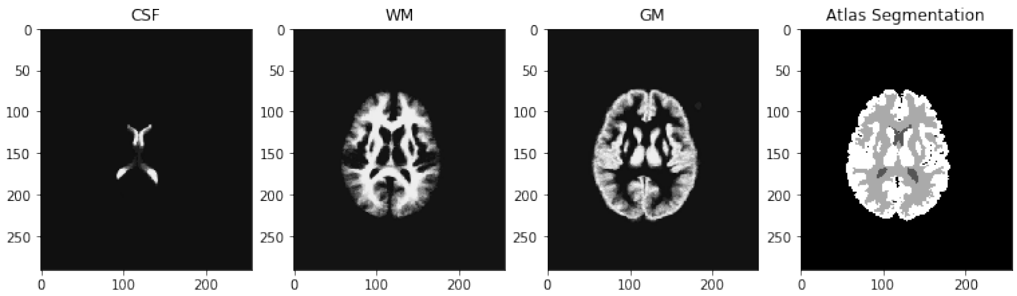

Figure 14: Segmentation using atlas for the testing image '1008'

Quantitative Analysis

- **Dice Coefficient of EM with label propagation initialization**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images of EM algorithm using label propagation initialization.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.0000	0.9500	0.9278
1004	0.5317	0.946	0.9231
1005	0.7756	0.9375	0.9165
1018	0.3480	0.9455	0.9222
1019	0.0000	0.9430	0.9154
1023	0.0000	0.9430	0.9154
1024	0.4384	0.9456	0.9157
1025	0.7559	0.9373	0.9125
1038	0.3770	0.9413	0.9177
1039	0.000	0.9478	0.9243
1101	0.6261	0.9395	0.9083
1104	0.5913	0.9290	0.8944
1107	0.000	0.9353	0.9059
1110	0.5436	0.9370	0.9099
1113	0.4074	0.9442	0.9286
1116	0.6516	0.9364	0.9128
1119	0.7186	0.9198	0.9024
1122	0.6847	0.9287	0.9090
1125	0.7512	0.9198	0.8912
1128	0.5938	0.8949	0.8418
Mean	**0.4321**	**0.9319**	**0.9524**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) of EM algorithm initialized by Label Propagation.

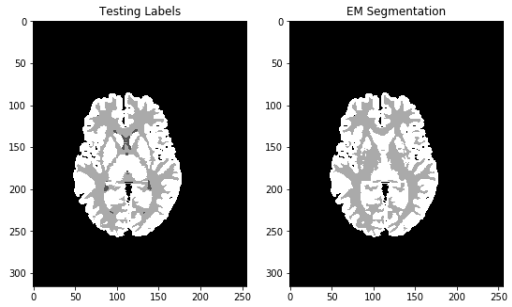

Figure 15: Segmentation result of EM initialized by Label Propagation

Observation

From the dice score table, we can see that the dice in general increases a lot when EM is initialized by label propagation than that of EM init K-Means as here in label propagation it contains information of the atlas itself so it can identify the WM than the CSF which has increased the value of WM from 68 percent to 93 percent and also other two regions' dices improved.

3.1.4 Initialization Using Tissue Models

In the tissue models initialization, firstly we remapped the tissue models probabilities for each tissue model in figure 10 with each pixel value of the testing image. Then, we also applied segmentation by calculating the maximum argument of the remapped probabilities images for each corresponding tissue class, as shown in figure 16. The the mean $\underline{\mu}_k$, variance Σ_k and mixture weights parameters α_k are initialized by following the same steps in the label propagation initialization.

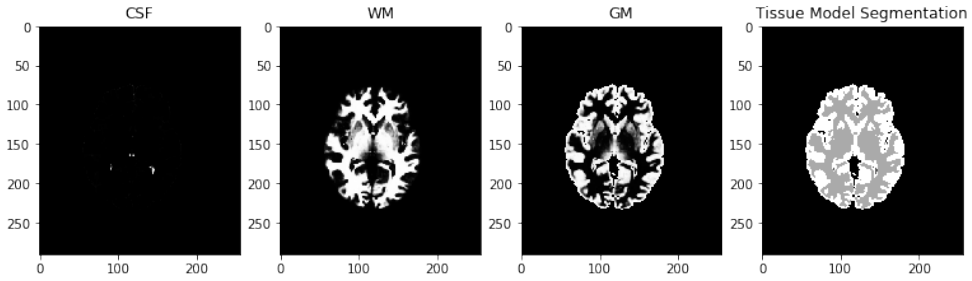

Figure 16: Segmentation using the generated Tissue Models maps for the testing image '1008'

Quantitative Analysis

- **Dice Coefficient using EM by tissue model initialization**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using EM algorithm by tissue model initialization.

Image	DSC of CSF	DSC of WM	DSC of GM
1003	0.2927	0.8944	0.8674
1004	0.4852	0.9431	0.9156
1005	0.7660	0.9386	0.9101
1018	0.4100	0.9421	0.9211
1019	0.2251	0.9492	0.9155
1023	0.3409	0.9353	0.9117
1024	0.4614	0.9436	0.9144
1025	0.7493	0.9363	0.8993
1038	0.3811	0.9408	0.9184
1039	0.2255	0.9500	0.9252
1101	0.6127	0.9404	0.9148
1104	0.5406	0.9225	0.8877
1107	0.0000	0.7803	0.7734
1110	0.4724	0.9328	0.9058
1113	0.5695	0.8277	0.8185
1116	0.8211	0.8679	0.7884
1119	0.7285	0.8694	0.8521
1122	0.6893	0.8668	0.8470
1125	0.7759	0.9236	0.9052
1128	0.7166	0.8947	0.8030
Mean	**0.5143**	**0.9224**	**0.8921**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using EM algorithm with tissue model initialization.

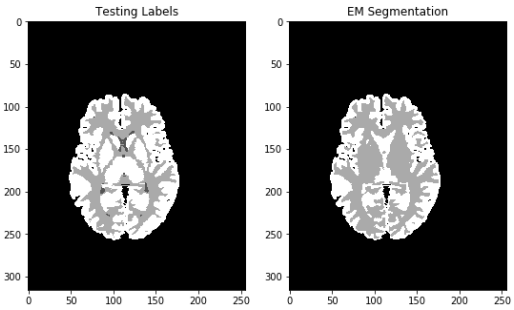

Figure 17: Segmentation result using EM with label propagation initialization

Observation

From the given dice score table and qualitative result, we can see that the

dice of CSF in general increases but the dices of WM and GM are not as good as EM with label propagation initialization but better than EM with K-Means initialization as tissue models also contains information of atlases (probabilistic atlases).

3.2 Combining Probabilities

The segmentation problem can expressed mathematically using Bayesian framework, where X represents final segmentation labels and Y represents the target image intensity values (testing image). Our target is to maximize the Maximum Posteriori Probability(MAP) by estimating X that best explain Y, $P(X|Y)$ according to the following equation:

$$P(X|Y) = \frac{P(Y|X)P(X)}{P(Y)} = P(Y|X)P(X)$$

3.2.1 Atlas Inside EM

From the MAP equation, $P(X)$ represents the probabilistic atlases for the three atlases, while $P(Y|X)$ represents membership weights for the EM. The EM is merged inside the EM iterations, by multiplying Membership Weights by Atlases for each brain tissue.

Quantitative Analysis

- **Dice Coefficient using our atlas inside EM (Label Propagation):** Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using our atlas inside EM with labek propagation initialization.

Image	DSC of CSF	DSC of WM	DSC of GM
1003	0.4741	0.9322	0.9066
1004	0.8415	0.9649	0.9479
1005	0.8729	0.9367	0.9067
1018	0.8170	0.9615	0.9422
1019	0.7591	0.9565	0.9285
1023	0.7394	0.9613	0.9394
1024	0.8311	0.9629	0.8110
1025	0.8433	0.9392	0.9062
1038	0.7933	0.9598	0.9405
1039	0.7454	0.9592	0.9358
1101	0.8591	0.9576	0.9315
1104	0.8110	0.9430	0.9117
1107	0.7332	0.9516	0.9210
1110	0.7521	0.9504	0.9222
1113	0.7636	0.9578	0.9405
1116	0.8512	0.9514	0.9259
1119	0.8446	0.9307	0.9013
1122	0.8810	0.9479	0.9240
1125	0.3807	0.9017	0.7835
1128	0.4448	0.8896	0.7685
Mean	**0.7516**	**0.9484**	**0.9015**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using our generated atlas inside EM.

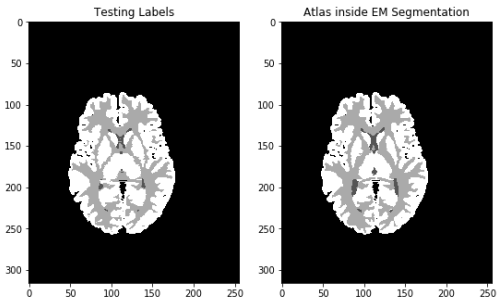

Figure 18: Segmentation result using our Atlas Inside EM

Observation

From the dice score table we can see that the dice scores are much higher

than all other combinations discussed earlier. Here for EM initialization label propagation has been used and also our generated atlas is incorporated inside EM which together performed a good segmentation as has lot of spatial information so it can segment three regions better.

3.2.2 Our Atlas with Tissue Model

In this approach, $p(X)$ represents the probabilistic atlases for the three atlases, while $P(Y|X)$ represents Tissue Models.
Quantitative Analysis

- **Dice Coefficient using our generated atlas with tissue model algorithm:**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using atlas with tissue model.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.6887	0.9102	0.8818
1004	0.8401	0.9561	0.9323
1005	0.9017	0.9466	0.9127
1018	0.7889	0.9500	0.9283
1019	0.0389	0.6007	0.9068
1023	0.745	0.9476	0.9253
1024	0.8213	0.9569	0.9324
1025	0.8840	0.9462	0.9042
1038	0.7680	0.9550	0.9334
1039	0.7424	0.9547	0.9283
1101	0.8225	0.9517	0.9255
1104	0.7798	0.9336	0.9001
1107	0.1870	0.8596	0.7505
1110	0.7450	0.9448	0.9138
1113	0.4737	0.8586	0.8208
1116	0.8684	0.9494	0.9191
1119	0.8460	0.9158	0.8875
1122	0.8573	0.9157	0.8893
1125	0.4323	0.9269	0.8637
1128	0.5427	0.9004	0.7958
Mean	**0.6815**	**0.9231**	**0.9026**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using our generated atlas with tissue model.

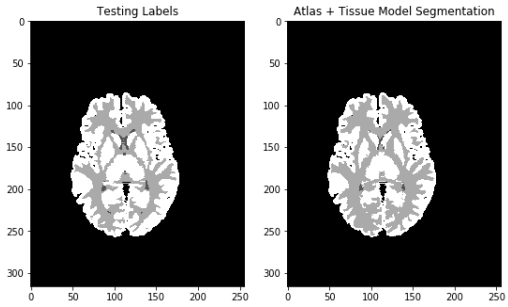

Figure 19: Segmentation result using our atlas with tissue model

Observation

From the dice score table, we can see that the dice score of CSF has increased than the scores of EM alone but not as good as when atlas is inside the EM.

3.2.3 MNI Atlas with Tissue Model

In this case, the pipeline is same as before what we did for our atlas with tissue model except here as atlas MNI atlases have been used.

Quantitative Analysis

- **Dice Coefficient using MNI atlas with tissue model algorithm:** Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using MNI atlas with tissue model.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.1426	0.8826	0.8477
1004	0.0686	0.8090	0.7330
1005	0.3224	0.8283	0.7181
1018	0.1067	0.8394	0.7821
1019	0.0196	0.6079	0.3293
1023	0.0187	0.7915	0.7371
1024	0.0327	0.7703	0.6761
1025	0.3645	0.8384	0.7245
1038	0.0898	0.8310	0.7594
1039	——	——	——
1101	0.0441	0.7602	0.6680
1104	0.0408	0.8193	0.7420
1107	0.0126	0.7095	0.5907
1110	0.7450	0.9448	0.9138
1113	0.0142	0.6510	0.5982
1116	0.0365	0.6819	0.5097
1119	0.2741	0.7868	0.7286
1122	0.1430	0.7771	0.7228
1125	0.1643	0.7921	0.7037
1128	0.1620	0.7703	0.5971
Mean	**0.1435**	**0.8234**	**0.6866**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using MNI atlas with tissue model.

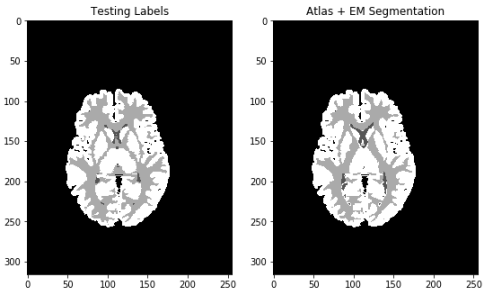

Figure 20: Segmentation result using MNI atlas with tissue model

Observation

From the dice score table and visualization, we can clearly see that the dice score is not that good at all as here we are using the MNI atlases come from different environment and moreover MNI mean atlas is generated from different dataset with different header parameters so it doesn't perform good in segmentation task and also the ground truth itself is biased so together this combination performed bad.

3.2.4 Our Atlas with EM using different initialization

In this condition, $P(X)$ represents the probabilistic atlases for the three atlases, while $P(Y|X)$ represents membership weights for the EM.

Quantitative Analysis

In the following the result has been shown for our generated atlas with EM where EM has been initialized using K-Means in one case and in other two cases with tissue model and label propagation.

- **Dice Coefficient using our atlas with EM (K-Means Initialization):**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using our atlas with EM.

Image	DSC of CSF	DSC of WM	DSC of GM
1003	0.6581	0.9576	0.9258
1004	0.7195	0.9581	0.9294
1005	0.9173	0.9582	0.9300
1018	0.7770	0.9627	0.9348
1019	0.6904	0.9635	0.9265
1023	0.6363	0.9574	0.9278
1024	0.7208	0.9649	0.9360
1025	0.9085	0.9576	0.9268
1038	0.8334	0.9620	0.9346
1039	0.6725	0.8796	0.8466
1101	0.8422	0.9596	0.9291
1104	0.7976	0.9568	0.9241
1107	0.8311	0.9484	0.9074
1110	0.8415	0.9628	0.9368
1113	0.8525	0.9531	0.92103
1116	0.8926	0.9564	0.9264
1119	0.8954	0.9428	0.9076
1122	0.8954	0.9542	0.9267
1125	0.6507	0.9232	0.8922
1128	0.6976	0.9206	0.8645
Mean	**0.7915**	**0.9524**	**0.9135**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using our generated atlas with EM algorithm using K-Means initialization.

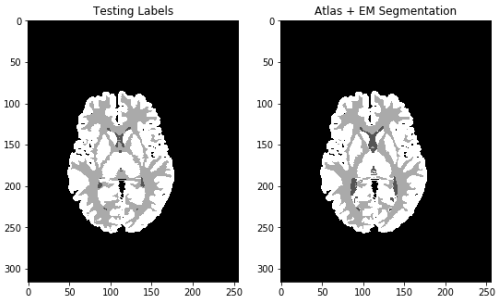

Figure 21: Segmentation result using our atlas with EM by K-Means initialization

Observation

In this particular case of our atlas with EM (K-Means initialization) algorithm, we can clearly see a high boost in dice scores overall. Specially, in the case of CSF and WM the dice scores are much more improved than the result of EM only with K-Means initialization (Without the presence of our atlas).
In the case of EM only with K-Means initialization, the CSF region was getting segmented too much taking the outer boundary and portion of WM as well but later when we have added our atlas it could identify properly which one is correct boundary of CSF and which one is for WM. So, it clearly indicates that the presence of our atlas played an important role improving the dice scores where the spatial information helped.

Dice Coefficient using our atlas with EM (Label Propagation Initialization):
Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using our atlas with EM where as EM initialization, label propagation is used.

Image	**DSC of CSF**	**DSC of WM**	**DSC of GM**
1003	0.5367	0.9636	0.9440
1004	0.8038	0.9648	0.8602
1005	0.8117	0.9485	0.9259
1018	0.7913	0.9651	0.9447
1019	0.5732	0.9597	0.9342
1023	0.5720	0.9590	0.9365
1024	0.7849	0.9660	0.9430
1025	0.7854	0.9480	0.9218
1038	0.7954	0.9621	0.9415
1039	0.5555	0.9615	0.9399
1101	0.7207	0.9528	0.9261
1104	0.7962	0.9469	0.9167
1107	0.5345	0.9485	0.9171
1110	0.7652	0.9552	0.9291
1113	0.7740	0.9609	0.9431
1116	0.7181	0.9492	0.9240
1119	0.7644	0.9343	0.9100
1122	0.7421	0.9453	0.9250
1125	0.5263	0.9160	0.8891
1128	0.6385	0.8955	0.8034
Mean	**0.6820**	**0.9502**	**0.9224**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using our generated atlas with EM algorithm using label propagation initialization.

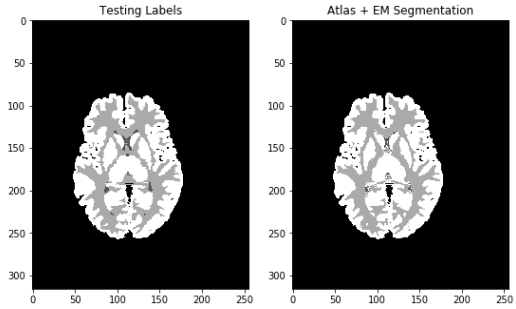

Figure 22: Segmentation result using our atlas with EM by tissue model initialization

Observation

Here, in case of our atlas with EM (label propagation initialization) algorithm, the dice scores got better compared to the result of EM with label propagation initialization only (without our atlas). In this case also, our atlas helped to improve the segmentation.

Here, the dice score of CSF improved almost 1.5 times compared to the dice score of EM algorithm initialized by tissue model initialization only even though the result of WM and GM didn't improve.

Dice Coefficient using our atlas with EM (Tissue Model Initialization):

Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using our atlas with EM with tissue model initialization

Image	DSC of CSF	DSC of WM	DSC of GM
1003	0.4741	0.9322	0.9066
1004	0.7022	0.9602	0.9407
1005	0.7635	0.84927	0.8103
1018	0.6739	0.9620	0.9450
1019	0.5168	0.9624	0.9366
1023	0.5676	0.9574	0.9384
1024	0.6659	0.9627	0.9418
1025	0.7848	0.9472	0.9159
1038	0.6503	0.9603	0.9420
1039	0.5165	0.9620	0.9400
1101	0.7016	0.9550	0.9320
1104	0.6721	0.9413	0.9114
1107	0.6267	0.9197	0.8881
1110	0.6178	0.9513	0.9250
1113	0.7642	0.8976	0.8747
1116	0.8571	0.9522	0.9237
1119	0.7648	0.9171	0.8915
1122	0.7358	0.9218	0.8982
1125	0.4187	0.8871	0.8535
1128	0.1108	0.8260	0.7815
Mean	**0.6416**	**0.9284**	**0.8815**

Qualitative Analysis

Following is the segmentation result of one of the test images (1003.nii) using our generated atlas with EM algorithm using tissue model initialization.

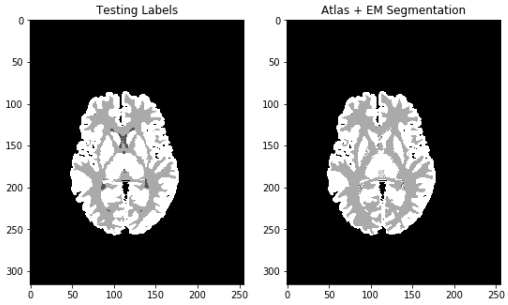

Figure 23: Segmentation result using our atlas with EM by tissue model initialization

Observation

In this case of our atlas with EM (tissue model initialization) algorithm, the

result is pretty similar with the result of the previous pipeline (our atlas + EM with label propagation initialization).
But if we compare this result with EM only (initialled by tissue model), the result of WM and GM are pretty similar even though the score of CSF got improved due the same reason (presence of our atlas).

Final Result of our atlas + EM (three different initialization)

Atlas	**EM initialization type**	**DSC of CSF**	**DSC of WM**	**DSC of GM**
Our	K-Means	**0.7915**	**0.9524**	**0.9135**
Our	Label Propagation	0.6820	0.9502	0.9244
Our	Tissue Model	0.3316	0.8934	0.8615

From above mentioned table, we can clearly see that our atlas performed best with the EM of K-Means initialization.
As our atlas with EM of K-Means initialization is the best combination so we have performed this combination with the MNI atlas as well which is shown in the next step.

3.3 MNI Atlas with EM (K-Means initialization)

Quantitative Analysis

- **Dice Coefficient using MNI atlas with EM (K-Means Initialization):**
  Following is the dice coefficient table for CSF, white matter and gray matter for twenty different images using MNI atlas with EM (K-Means initialization)

Image	DSC of CSF	DSC of WM	DSC of GM
1003	0.2361	0.9071	0.8455
1004	0.0793	0.8197	0.7529
1005	0.3873	0.8399	0.7852
1018	0.1188	0.8632	0.7947
1019	0.0192	0.6160	0.3589
1023	0.0394	0.8139	0.7433
1024	0.0462	0.7847	0.6829
1025	0.3588	0.8542	0.8016
1038	0.1033	0.8534	0.7856
1039	—	—	—
1101	0.0475	0.7822	0.7140
1104	0.0733	0.8284	0.7481
1107	0.0508	0.7809	0.6795
1110	0.0136	0.7216	0.6090
1113	0.0152	0.5871	0.2986
1116	0.0324	0.6858	0.5502
1119	0.3435	0.7958	0.7188
1122	0.1975	0.7923	0.7367
1125	0.1698	0.4917	0.1475
1128	0.2301	0.7852	0.6926
Mean	**0.1267**	**0.7636**	**0.6615**

Qualitative Analysis

Following is the segmentation result using MNI atlas with EM where EM has been initialized by K-Means.

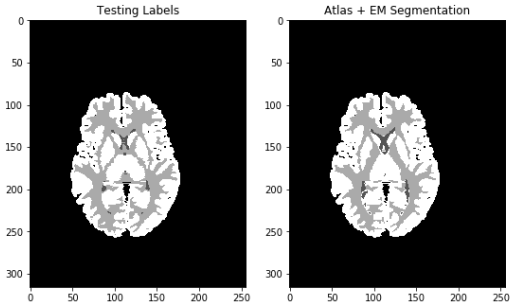

Figure 24: Segmentation result using MNI atlas with EM by K-Means initialization

Observation

Here, in the case of MNI atlas with EM (K-Means propagation initialization) algorithm, the dice scores are very poor and the reasons behind this poor segmentation are: The MNI atlases come from different environment and moreover MNI mean atlas is generated from different dataset with different header parameters so it doesn't perform good in segmentation task and also the ground truth itself is biased so together this combination performed bad.(Here, the 1039.nii image failed during registration so it fails in segmentation as well)

3.4 Final Result

Analysis of all experiments

First Case

Exp.	Pipeline	DSC of CSF	DSC of WM	DSC of GM
1	K-Means + EM	0.1874	0.6831	0.9097
2	Label Propagation + EM	0.4321	0.9319	0.9524
3	Tissue Model + EM	0.5143	0.9224	0.8921

Second Case

Exp.	Pipeline	DSC of CSF	DSC of WM	DSC of GM
4	Our atlas + Tissue Model	0.6815	0.9231	0.9026
5	MNI atlas + Tissue Model	0.1435	0.8234	0.6866

Third Case

Exp.	Pipeline	DSC of CSF	DSC of WM	DSC of GM
6	Our atlas inside EM	0.7516	0.9484	0.9015
7	**Our atlas + EM(K-Means initialization)**	**0.7915**	**0.9524**	**0.9135**
8	Our atlas + EM(Label Propagation initialization)	0.6820	0.9502	0.9224
9	Our atlas + EM(Tissue Model initialization)	0.6416	0.9284	0.8815
10	MNI atlas + EM(K-Means initialization)	0.1267	0.7636	0.6615

Segmentation results

First Case

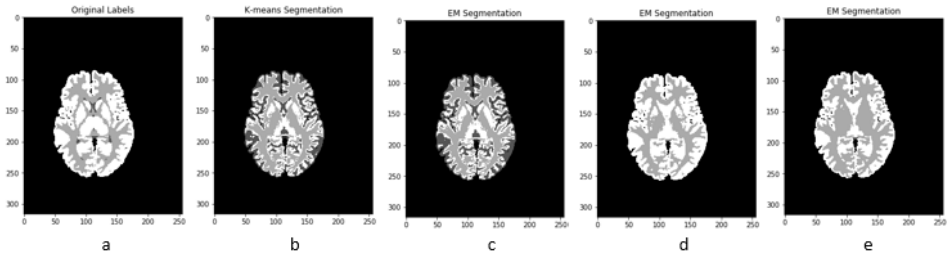

Figure 25: a) Original label, b) KMeans segmentation, c) EM with KMeans, d) EM with Label Propagation, e) EM with Tissue Model

Second Case

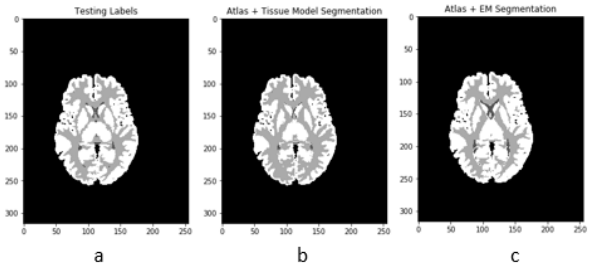

Figure 26: a) Original label, b) Our Atlas + Tissue Model, c) MNI Atlas + Tissue Model

Third Case

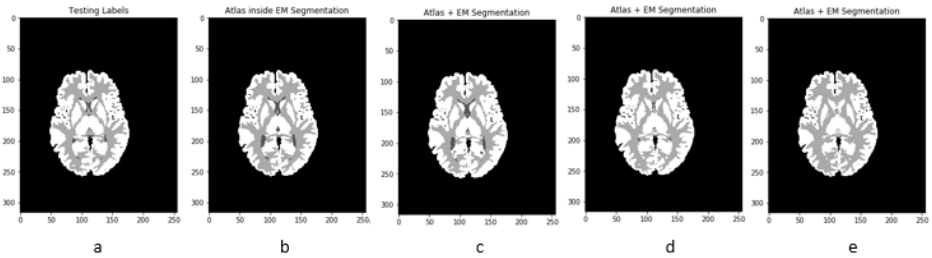

Figure 27: a) Original label, b) Our Atlas inside EM, c) Our Atlas + EM (KMeans initialization), d) Our Atlas + EM (Label Propagation initialization), e) Our Atlas + EM (Tissue Model)

Mean DSC bar-chart

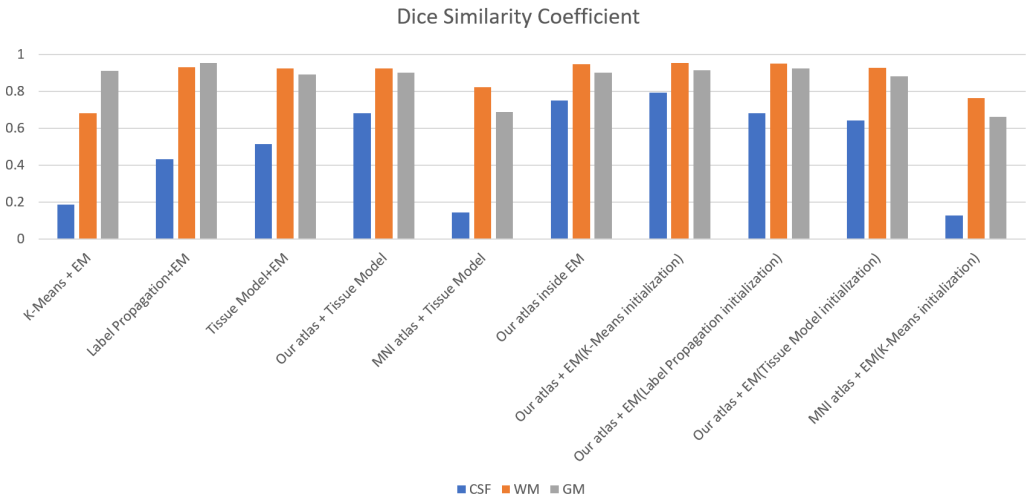

Figure 28: Mean DSC bar-chart for all segmentation approaches

3.5 Discussion and Conclusion

After performing different experiments for segmentation we can conclude that in our case the best segmentation algorithm is the combination of our generated atlas with EM where EM algorithm itself is initialized by KMeans even though EM alone with KMeans initialization is not good.

The reason why EM alone with KMeans didn't perform well is because the ground truth itself is biased and as KMeans is unsupervised method so it segments outer boundary and inner boundary for the CSF region and also it considers some portion of WM as CSF so eventually it performs poor in both CSF and WM and also in GM.

On the other hand, after having this EM with KMeans initialization when we merge this with our atlas it improves the segmentation as it contains spatial information so it can differentiate in between CSF and WM region what EM alone can't perform well.

Also, other experiments which performed better all of them are connected to our generated atlases so we can conclude that our generated atlas based segmentation is better than EM alone.

Even though our atlases played an important role to improve the segmentation but in the case of MNI atlases the scenario is not the same as MNI atlases come from different environments where the mean of them is generated from different dataset with different header parameters so it doesn't perform good in segmentation task and also the ground truth itself is biased so together this combination performed bad.

3.6 References

[1] 'Brain MRI Segmentation Using an Expectation-Maximization Algorithm' by Koen Van Leemput, Tutorial MICCAI 2003.

[2] Lecture of 'Atlas based segmentation' by Robert Martí.