UNIVERSITAT DE GIRONA

MEDICAL IMAGE SEGMENTATION AND APPLICATIONS - MISA

Final Project: Brain Tumor Segmentation IBSR18

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1 Introduction

Magnetic Image Resonance -MRI- is a widely used technique to take images of the brain. This non invasive technique allows the diagnosis of multiple diseases such a Alzheimer, brain tumor, Parkinson, among others. The automatics segmentation of the tissue types of the brain which include cerebrospinal fluid -CSF-, gray matter -GM- and white matter -WM-, using MRI images has played an important role in the diagnosis of diseases and in the neuroscience research.

In order to perform a good segmentation of the tissues, there are some considerations to take into account that impact the results. The first one is the variation of intensity across patients and scanners. In MRI images, the intensity of the pixels does not have a fixed meaning. Hence, setting values for the parameters in automatic methods becomes challenging and intensity normalization is required. The second one is associated to the atlas segmentation method, which will be the one used for the segmentation in this project. In order to build the atlas of each tissue type, the correspondence between the coordinates has to be correct. Therefore, a registration step is needed. Finally, the segmentation method. Currently, deep learning approaches has reached very good performance with high accuracy. However and despite of the time that takes to perform the preprocessing of the dataset, we want to use atlas segmentation and Expectation Maximization -EM- algorithm combined with atlas segmentation for the development of this project.

In this report we described the preprocessing and segmentation results obtained for the IBSR18 dataset. In section 2 we describe the methodology applied. Then, the details of the dataset and our implementation are described in the section 3. We dedicated section 4 to the project management and finally the conclusions are presented in section 5.

2 Methodology

2.1 Intensity normalization

The variation between the intensity of the images is one of the drawbacks of the MRI images. We consider two methods to normalize the intensity. The first one

is the standard intensity normalization described as:

$$I_{new} = \frac{I_{current} - mean}{Standard\ deviation} \tag{1}$$

where I is the intensity of the pixel.

The second method is the one proposed by [1] consisting in two steps. The first step called training consist in the learning of the histogram transformations from a set of images. The second step called transformation, the images are transformed with the parameters learned in the first step. The transformation is image dependant and needs to be done for each image.

2.2 Image Registration

Given a training set we want to build the atlas of each tissue type. In order to do it, we need to assure that a given coordinate correspond to an specific tissue type in each image. Hence, the registration of the images is required. There are multiple software to perform the registration. All of them include the components that define the registration: transformation, metric, interpolator and optimizer. In general, to obtain good results in the registration of the images is required to applied a rigid transformation followed by a nonrigid transformation. The rigid transformation will compensate the pose differences and the the nonrigid transformation will perform local deformations.

Another registration is required when the atlas of each tissue type is given. Having a validation dataset for the segmentation, once again we need to be sure about the correspondence of the coordinates between each validation image with respect to each atlas. Hence, a registration, also rigid follows by nonrigid registration must be perform. Otherwise, the validation image will be in a different spacial location than the atlases and the segmentation results can be null or very bad.

2.3 Atlas segmentation

To perform atlas segmentation, a probabilistic atlas is needed. The probabilistic atlas defines the probability of a pixel to be a determine tissue type. The first step is building a probabilistic atlas for each tissue type. The algorithm followed to

build the atlases is described in 1.

Algorithm 1: Probabilistic atlas.

```
Data: Registered label and intensity images of the training dataset
Result: Probabilistic atlas of each brain tissue type
initialization
for i ← 1 to numImg do
    load label image;
    load intensity image;
    Extract CSF, GM and WM pixels;
    Concatenate CSF, GM and WM pixels;
    Concatenate intensity images;
mean of CSF, GM and WM;
mean of intensity images;
save images;
```

Given the atlases, the atlas segmentation can be carry out. This method consist in assigning the label with the highest probability to a tested pixel.

2.4 Expectation maximization initialized with atlas segmentation results

The EM algorithm is a clustering method to perform segmentation based on probability estimation of the maximum likelihood. One of the most challenging issues of the EM algorithm is the initialization. A good initialization leads to find faster an optimal maxima and decrease the possibility to be in a wrong local maxima. Thus, considering that the atlas segmentation is simple but provide good segmentation results, the output can be used as initialization for the EM algorithm. The result of the EM algorithm can also be improved using the atlas of each tissue type. Having into account that the output of the Expectation Maximization loop are probabilities of a pixel to belong to a class, that in this case are the tissue types, this probability can be enhance if it is multiplied by the probabilities of the probabilistic atlas. Then, the resulting segmentation should be better than a simple atlas segmentation. A pseudo-code is shown in 2.

Algorithm 2: Atlas Segmentation + EM algorithm + Probabilistic atlas

Data: Segmentation resulting from atlas segmentation, intensity images, mask and labels
Result: Brain tissue segmentation
initialization
Load segmentation, intensity image and mask;
Reshape matrices to vectors;
Remove skull from probabilistic atlases and intensity image;
Compute covariance and mean of each label;
Initialize α;
Compute the weights and labels;
for $i \leftarrow 1$ **to** 7 **do**
    Expectation Maximization algorithm
load probabilistic atlases;
weights = weights * probabilistic atlases;
Compare probabilities: highest probability = label;
Load label image;
Compute similarity;
Save segmentated image;

3 Implementation and discussion

3.1 Materials

The project and proposed solution is evaluated on the Internet Brain Segmentation Repository -IBSR- dataset. It has a total of 18 images shown in figure 1.These are divided into 3 categories: 10 training images, 5 validation images and 3 testing images. Training and validation set have ground truth whereas testing set has not. The images are 1.5mm scans with skull-stripping.

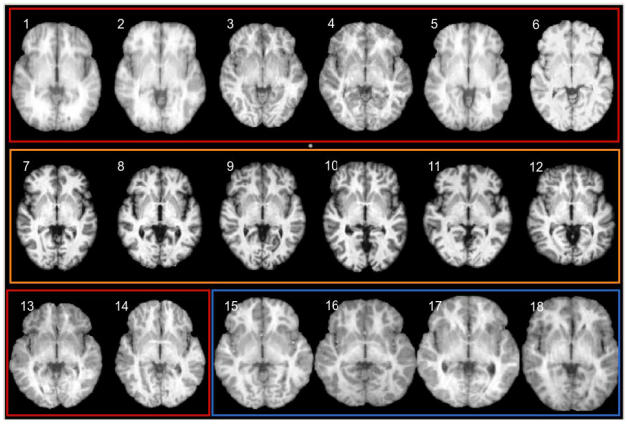


Figure 1: IBSR18 dataset. Red: training images, blue: validation images and yellow: testing images.

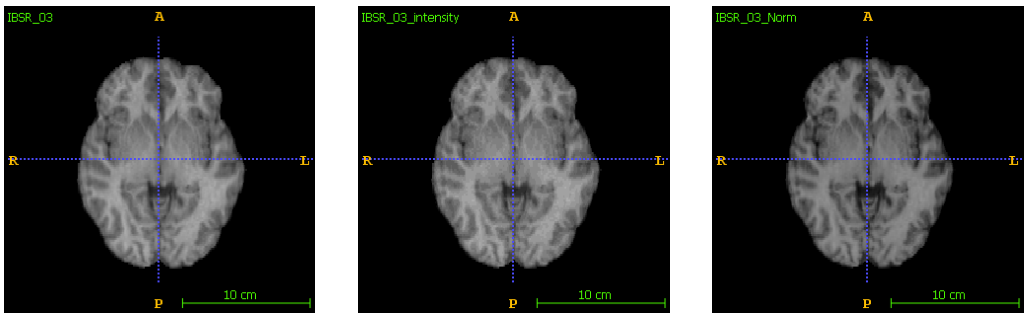
3.2 Intensity normalization

For the first normalization method, a simple implementation is required. The images are normalized in a range between 0 to 255. To normalize the intensity of the images using the second method, an implementation available in `https://github.com/sergivalverde/MRI_intensity_normalization` is used. Note that in the original method a set of standard histogram landmarks are learned from a set of MRI images. These landmarks are then used to equalize the histograms of the images being normalized. In both learning and transformation, the histograms are used to find the intensity landmarks. In this implementation, the landmarks are computed based on the total range of intensities instead of the histograms. All the images are normalized in a range between 0 to 255. In figure 2.

3.3 Segmentation

To evaluate the segmentation results the DICE score is used as similarity metric.

All the training images were intensity normalized using both methods. The two sets of normalized images where registered to the template image of the MNI template. They are registered to this image in order to have all the images with the standard spacing of 1x1x1 mm. Before the registration, the skull of the MNI template was remove. Then, we performed the registration using `elastix`. From the set of available parameters of this software we use `par0000`. The resulting transformation was then applied to the labels. We build the atlas and the template



(a) Original (b) Normalization 1 (c) Normalization 2

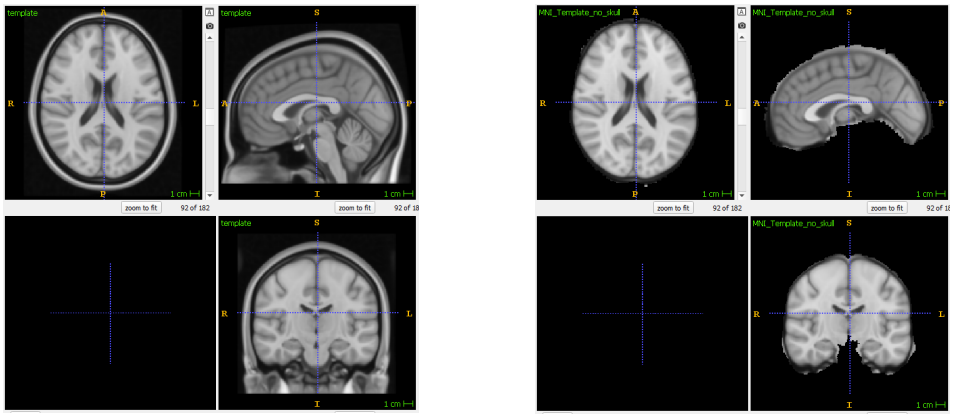
Figure 2: Intensity normalization of ISBR_03 image.

	Atlas Segmentation				**EM+Atlas segmentation+Atlas**			
	CSF	**GM**	**WM**	**Time (sec)**	**CSF**	**GM**	**WM**	**Time (sec)**
IBSR 11	0.4179	0.8076	0.7641	7.79	0.4860	0.8539	0.8563	24.39
IBSR 12	0.6245	0.8276	0.7995	8.23	0.7082	0.8554	0.8709	19.94
IBSR 13	0.5796	0.8341	0.7223	6.45	0.6623	0.8513	0.7825	20.58
IBSR 14	0.6222	0.8503	0.7887	7.38	0.7403	0.8853	0.8660	21.70
IBSR 17	0.6952	0.8538	0.7461	7.44	0.7622	0.8837	0.8294	27.57
Mean	0.5879	0.8347	0.7641	7.4580	0.6718	0.8659	0.8410	22.8361
Standard deviation	0.0430	0.0014	0.0039	1.7287	0.0488	0.0012	0.0053	39.6389

Table 1: Dice score using the second normalization method and registration to the training set to MNI template.

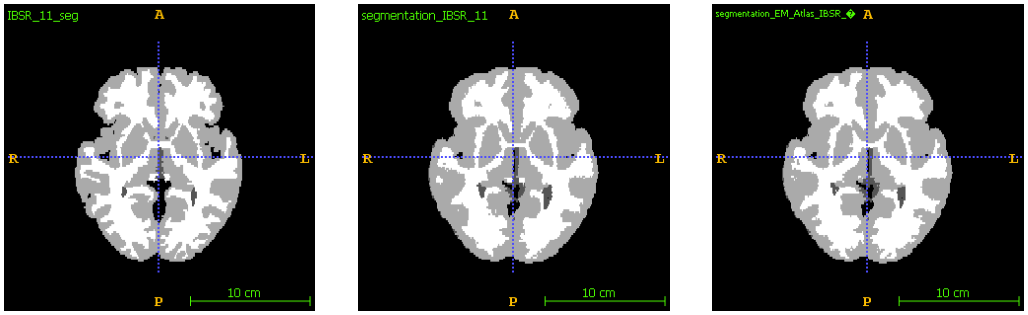
image of each normalized set. Later, the build template was register to each validation image. In this case, an affine transformation of the `par0000` were used and after the Bsplines transformation of the `par0009`.

With the first normalization method we obtained very poor results for CSF applying atlas segmentation. Therefore, we know that the results cannot be improved with the EM algorithm. We tested, but as expected, no changes were seeing in the DICE score. Hence we decided not to include the results in this document. The dice score results of the segmentation with the second normalization method are shown in table 1 and figure 5. The dice score for atlas segmentation and EM+atlas method are good, considering how simple they are. However, we can observe a poor segmentation result for the CSF and oversegmentation of the gray matter.



(a) MNI template (b) Skull-stripped template

Figure 3: MNI template image before and after skull-stripping



(a) Original (b) Atlas segmentation (c) EM+Atlas Segmentation

Figure 4: Segmentation results of ISBR_11.

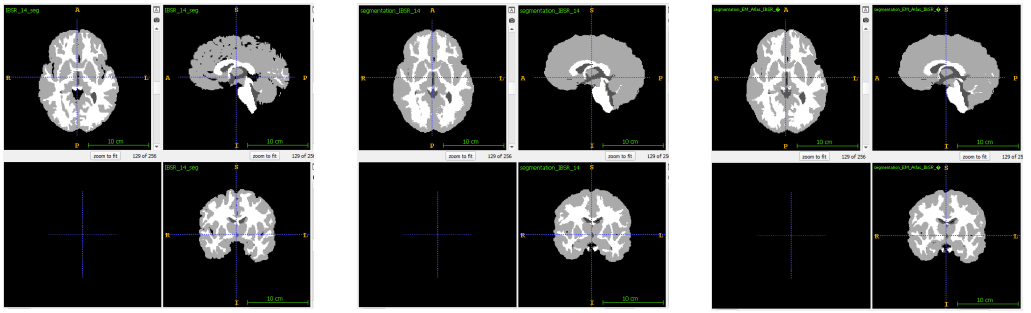
Trying to overcome the segmentation issues and considering the source of possible error in our method, we register the training set to the first image of the training set. The reasoning to try a different fixed image for the registration are two: one is that the MNI template is not skull-stripped. Hence, we did a simple skull-stripping taking a binary image provided in the atlas.nii structure of the MNI atlas dataset and defining the region of interest of the MNI template based on this image. The resulting skull-stripped template, figure 3, has an irregular border that affect the registration of the pixels coordinates than rely on this space. The second is the intensity of the image. We perform intensity-based registration where the

	Atlas Segmentation				EM+Atlas segmentation+Atlas			
	CSF	**GM**	**WM**	**Time (sec)**	**CSF**	**GM**	**WM**	**Time (sec)**
IBSR 11	0.4860	0.8539	0.8563	24.39	0.4959	0.8662	0.8700	23.59
IBSR 12	0.7082	0.8554	0.8709	19.94	0.7475	0.8818	0.9071	18.85
IBSR 13	0.6623	0.8513	0.7825	20.58	0.7365	0.8873	0.8500	20.45
IBSR 14	0.7403	0.8853	0.8660	21.70	0.7870	0.9119	0.9073	20.92
IBSR 17	0.7622	0.8837	0.8294	27.57	0.7533	0.9093	0.8772	27.73
Mean	0.6718	0.8659	0.8410	22.8361	0.7040	0.8913	0.8823	22.3064
Standard deviation	0.0488	0.0012	0.0053	39.6389	0.0556	0.0015	0.0025	48.4197

Table 2: DiCE score results for the validation set using atlas built registering the training set to the first training image.

similarity between the intensity of the pixels is searched. Since we did not apply intensity normalization in the MNI template, the intensities between the training set images and the template has a big difference. These leads to increase the error in the registration, and therefore in the segmentation. The dice scores are shown in table 2.

Compared with the results of the first method, the DICE score is higher in almost all the cases, but visually the images does not change much. In fact we still have an over segmentation of the GM. In the case of the CSF, when atlas segmentation is applied the results are better but in the case of EM+Atlas both methods are very similar. This suggest us that using our method there is no place for more improvement. Certainly, choosing an appropriate registration improve the results, but this does not solve the problems of the oversegmentation. The problem of our method is mainly in the border between the GM and WM. Our method is not able to define an adequate border between the two tissues.



(a) Original (b) Atlas segmentation (c) EM+Atlas Segmentation

Figure 5: Segmentation results of ISBR_14.

3.4 Testing new images

To test new images, it is necessary to follow the step showed in the figure 6. In order to have good results, it is compulsory to register the atlases to the input image. Otherwise, since the images may be in different spaces the segmentation will not be correct.

Figure 6: Pipeline to segment new images using the proposed method.

4 Project Management

Considering the time frame given for this project, we plan our activities considering an atlas segmentation approach following the diagram showed in figure 7. There are some additional activities that were carried our trying to improve our results that are shown as additional activities since in the original planning we did not consider different registration scenarios.

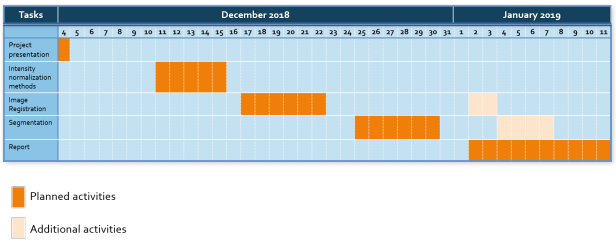


Figure 7: Gantt Diagram for the segmentation project

5 Conclusion

In this project, we applied the knowledge acquired during the medical image segmentation and application -MISA- course. This include have a better understanding of the atlas segmentation and the expectation maximization algorithm. We faced the problems that are present in real data and public datasets as IBSR18, as intensity differences and voxel spacing. About the proposed method, we could see that using simple approaches is possible to obtain good results. However, this kind of methods are time consuming in the registration stage. The major fail is in the borders between the the GM and WM, where our method does not define the border, instead label the pixels as GM in most of the cases. Regarding to the CSF segmentation, it is know from our previous experience that having better results than the ones obtained here using this kind of method is difficult.

References

[1] László G Nyúl, Jayaram K Udupa, and Xuan Zhang. New variants of a method of mri scale standardization. *IEEE transactions on medical imaging*, 19(2):143–150, 2000.