

Medical Image Segmentation and Applications

Lab 1 Solution

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1 Introduction and problem definition

Magnetic Resonance Imaging (MRI hereinafter) is a medical imaging technique used for the analysis of organs and anatomic structures of the human body (tissues, bones, etc). It is widely used for the examination of the brain, e.g, spot presence of tumors, aneurysms, inflammation, etc. It is important to assure that the image is as clear as possible in order to have a more accurate study. Therefore, in the computational analysis of MRI images a preprocessing stage is needed, in which artifacts and noisy elements of the images are removed. These artifacts might come from the machine itself or during the data acquisition stage. During this lab session two of the most common preprocessing steps in brain MRI imaging are studied: skull-stripping and bias field correction. There are a lot of different tools to do the processing of the images, but in this case SPM in Matlab was used. The problem consists on applying the preprocessing steps mentioned previously and also segmenting the brain tissues (specifically: grey matter, white matter and cerebrospinal fluid), for MRI images of 5 patients in two different image modalities: T1 and T2 FLAIR. The next sections present the algorithm analysis, the design and implementation of the solution, results, analysis and conclusions.

2 Design and implementation of the proposed solution

The solution of the lab problem consists of the following steps:

- Running the segmentation algorithm for the 10 images using SPM varying the following parameters: bias regularization, full width at half maximum (FWHM) cutoff and number of Gaussians. Some combinations of these parameters were tested in order to analyze its impact on the quantitative results.
- The segmentation results for each case are evaluated using dice score. Also, statistic metrics such as mean and standard deviation of the dice scores along all patients for a given tissue and modality are computed and these are used as an indicator of the impact of each given set of parameters.

The solution was implemented using SPM and a simple matlab code for the final segmentation of the tissues. Visualization was done through ITK-SNAP.

Skull stripping process consists of removing all other tissues that are not part of the brain. On the other hand, the Bias Field is known as an MRI artifact in which a non-uniformity of intensities in uniform tissues is observed. Therefore, the correction involves making these intensities more uniform within the tissue.

3 Algorithm Analysis

The segmentation was done through SPM. The configurations were done in order to obtain both the bias field and the bias field corrected version of the images, as well as the 6 different images priors that SPM returns (gray mater, white matter, csf, skull, soft tissue, air). After that, code snippet presented below was used and run iteratively for all the 10 images and for the different parameters combinations presented in the results section. Since SPM has six images priors for the segmentation of MRI brain images, these 6 priors were used. However, since only the segmentation required is only of the first 3 tissues the rest of them are labeled with 0s. The condition $cf = cf.*((c1+c2+c3) > 1)$ assesses whether the current voxel is within the brain or not. After that, the segmented image is exported and dice scores for each of the tissues of interest are calculated. In a final stage, the means and standard deviation of dice scores along all patients given an imaging modality and tissue are calculated and reported in the results section.

```
c1 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c1T1.nii");
c2 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c2T1.nii");
c3 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c3T1.nii");
c4 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c4T1.nii");
c5 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c5T1.nii");
c6 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\c6T1.nii");

[~, pmax] = max([c3(:), c1(:), c2(:), c4(:), c5(:), c6(:)], [], 2);
cf = reshape(pmax, size(c1));
cf(cf==4)=0;
cf(cf==5)=0;
cf(cf==6)=0;
cf = cf.*((c1+c2+c3)>1);

niftiwrite(cf,"F:\udG\MISA\Labs\Lab 1\P2_data\1\final_T1.nii");

gt1 = niftiread("F:\udG\MISA\Labs\Lab 1\P2_data\1\LabelsForTesting.nii");

dice_csf1=dice(cf==1,gt1==1);
dice_gm1=dice(cf==2,gt1==2);
dice_wm1=dice(cf==3,gt1==3);
```

4 Experimental section and result analysis

For the brain tissue segmentation with SPM, five different patients and two image modalities are used: T1 and T2-FLAIR. For each patient case, both T1 and T2-FLAIR images are provided with the ground truths. In SPM, segmentation of the brain volume in 3 tissue classes: CSF(Cerebrospinal Fluid), White matter, and grey matter is done using a modified Gaussian Mixture Model. By knowing the prior spatial probability of each voxel being grey matter, white matter, or cerebrospinal fluid, it is possible to obtain a more robust classification. In addition, a step for correcting bias field is also included in SPM, which makes the method more applicable to images corrupted by smooth intensity variations. After that, the posterior probabilities are obtained for each of the six tissue classes (grey matter, white matter, CSF, bone, soft tissue, and air/background). Different parameters are also

Table 1. Results Obtained with Default Parameter Set in SPM.

Patient	Image Modality	Tissue	Dice Score
1	T1	CSF	0,765068481
		Grey Matter	0,753788894
		White Matter	0,828044567
	T2 FLAIR	CSF	0,682193427
		Grey Matter	0,611124618
		White Matter	0,684509778
2	T1	CSF	0,700100755
		Grey Matter	0,706133586
		White Matter	0,760363575
	T2FLAIR	CSF	0,696447087
		Grey Matter	0,636344495
		White Matter	0,245866645
3	T1	CSF	0,700020869
		Grey Matter	0,732672016
		White Matter	0,82587749
	T2FLAIR	CSF	0,64258332
		Grey Matter	0,605713578
		White Matter	0,67764556
4	T1	CSF	0,762086556
		Grey Matter	0,763731141
		White Matter	0,815510963
	T2FLAIR	CSF	0,647021136
		Grey Matter	0,594920966
		White Matter	0,639930657
5	T1	CSF	0,756502527
		Grey Matter	0,787373568
		White Matter	0,843241537
	T2FLAIR	CSF	0,660603523
		Grey Matter	0,598339938
		White Matter	0,659153356

tuned for preprocessing to check how it affects the results and finally picked up the best parameter combination. To evaluate the segmentation for each tissue class, Dice Score is used and to evaluate the overall results for all the patients, the mean and standard deviation of the dice scores of the tissue classes are used.

Table 1 shows the results with the default parameter set provided by spm. Later different parameters such as Bias Regularization, Bias FWHM and the Number of Gaussians for each tissue class are tuned to find the best parameter combination. As MR images are usually corrupted by a smooth, spatially varying artifact that modulates the intensity of the image, it is important to distinguish the intensity variation due to MR scanning and those variations due to different tissue properties. Bias regularization can be a good measure to increase the effectiveness of the algorithm if we know beforehand about the uniformity information of the artifacts. Normally, a large regularization value is used for fewer non-uniformity parameters. In this case, the results were better when heavy regularization is used which shows there are fewer non-uniformity parameters in the data. Also, for non-uniform intensity, Bias FWHM or gaussian smoothness of bias should be high. As here, there was less non-uniformity, and 60 mm cutoff of gaussian smoothness of bias, provided

better results than of other values used. The effects of both parameters in the results can be shown in Table 2 with values in bold mean good results.

As the tissue probabilities may map to several clusters, one single gaussian distribution for each

Table 2. Effects of Bias Regularization and Bias FWHM on results.

Bias FWHM	Bias Regularization	Image Modality	Tissue	Mean	Standard Deviation
60 mm cutoff	0,001	T1	CSF	0,736755838	0,033638653
			Grey Matter	0,748739841	0,030887962
			White Matter	0,814607627	0,031901
		T2 FLAIR	CSF	0,665769699	0,023057792
			Grey Matter	0,609288719	0,016389595
			White Matter	0,581421199	0,188380523
60 mm cutoff	0,1	T1	CSF	0,738118466	0,034460729
			Grey Matter	0,747696138	0,031835081
			White Matter	0,814105663	0,031260783
		T2 FLAIR	CSF	0,667119325	0,026918997
			Grey Matter	0,614309055	0,017037677
			White Matter	0,586659802	0,179159589
60 mm cutoff	0,0001	T1	CSF	0,735843301	0,032987428
			Grey Matter	0,750011618	0,029358052
			White Matter	0,814623581	0,031653934
		T2 FLAIR	CSF	0,665418108	0,025580619
			Grey Matter	0,605424335	0,01504249
			White Matter	0,575412617	0,196202742
60 mm cutoff	1	T1	CSF	0,737668978	0,034952296
			Grey Matter	0,747178991	0,032234342
			White Matter	0,814024321	0,03138065
		T2 FLAIR	CSF	0,666840131	0,028762429
			Grey Matter	0,615683	0,018096253
			White Matter	0,586026028	0,175969938
90 mm cutoff	0,1	T1	CSF	0,737618489	0,034914457
			Grey Matter	0,747138704	0,032205459
			White Matter	0,814028601	0,031403613
		T2 FLAIR	CSF	0,666773374	0,02888121
			Grey Matter	0,615714481	0,018116754
			White Matter	0,586338107	0,175475627
30 mm cutoff	0,0001	T1	CSF	0,737928989	0,034545502
			Grey Matter	0,747450251	0,031809251
			White Matter	0,813650154	0,031241816
		T2 FLAIR	CSF	0,666905621	0,028534067
			Grey Matter	0,615796203	0,017588872
			White Matter	0,58542257	0,178469083

class might not provide good results. To consider this partial volume effect or pixel probabilities belonging to a number of tissues can be achieved by changing the number of gaussian distributions of the tissue classes. The values of gaussian distribution for WM, GM, and CSF can be 1 or 2 but better results are obtained using value 2 for all of them which can be shown in Table 3.

The final consideration was made to assign the pixels to each of the three-brain tissue classes using

Table 3. Effects of Gaussian Distribution Number on Results.

Bias FWHM	Bias Regularization	Image Modality	Tissue	No. Of Gaussian	Mean	Standard Deviation
60 mm cutoff	0,1	T1	CSF	2	0,738118466	0,034460729
			Grey Matter	1	0,747696138	0,031835081
			White Matter	1	0,814105663	0,031260783
		T2 FLAIR	CSF	2	0,667119325	0,026918997
			Grey Matter	1	0,614309055	0,017037677
			White Matter	1	0,586659802	0,179159589
60 mm cutoff	0,1	T1	CSF	2	0,738764915	0,027067631
			Grey Matter	2	0,751186063	0,026363166
			White Matter	1	0,814675796	0,031290193
		T2 FLAIR	CSF	2	0,665070525	0,030110272
			Grey Matter	2	0,617090686	0,016690405
			White Matter	1	0,582279571	0,183999511
60 mm cutoff	0,1	T1	CSF	2	0,741607041	0,024272901
			Grey Matter	2	0,74399258	0,025576391
			White Matter	2	0,811676052	0,030783695
		T2 FLAIR	CSF	2	0,670976965	0,023446789
			Grey Matter	2	0,617637393	0,046293363
			White Matter	2	0,63829312	0,08293973

the prior probabilities of either only three tissue classes or all six tissue classes. The latter provided better performance. Finally, Table 4 shows the mean and standard deviation of the dice scores and Table 5 show the dice scores of each tissue class of all the patients considering the best parameter set (Bias Regularization=**0.1**, Bias FWHM=**60 mm cutoff**, Number of Gaussian distribution per WM, GM and CSF=**2** using the prior probabilities of the **six** different tissue classes.).

Table 4. Mean and Std Obtained with Best Parameters Combination.

Image Modality	Tissue Name	Mean	Standard Deviation
T1	CSF	0,766799063	0,032036996
	Grey Matter	0,744340783	0,025274236
	White Matter	0,811927416	0,0307794
T2 FLAIR	CSF	0,711090511	0,015430316
	Grey Matter	0,61897292	0,046254209
	White Matter	0,638544548	0,083001527

At the end of the document, the resulting images obtained for each of the five patients are shown in the appendix. The order of the images is as follows: Original Image, Bias Field, Bias Corrected Image, Skull Mask, Segmentation result, and the ground truth. T1 images provided better segmentation results whereas the results obtained using T2-FLAIR are not that satisfactory. The results obtained for T1 images of Patient 1 and Patient 4 are the best that can be visualized from the images.

Table 5. Dice Scores obtained with Best Parameters Combination.

Patient	Image Modality	Tissue	Dice Score
1	T1	CSF	0,792142283
		Grey Matter	0,741771659
		White Matter	0,822980352
	T2 FLAIR	CSF	0,702141697
		Grey Matter	0,615848564
		White Matter	0,688056199
2	T1	CSF	0,764354288
		Grey Matter	0,718366254
		White Matter	0,762553683
	T2 FLAIR	CSF	0,734190864
		Grey Matter	0,696577247
		White Matter	0,493352201
3	T1	CSF	0,773103495
		Grey Matter	0,728053134
		White Matter	0,82874743
	T2 FLAIR	CSF	0,773103495
		Grey Matter	0,57301764
		White Matter	0,695327679
4	T1	CSF	0,790869776
		Grey Matter	0,749383163
		White Matter	0,803763552
	T2 FLAIR	CSF	0,702514362
		Grey Matter	0,749383163
		White Matter	0,653305122
5	T1	CSF	0,713525472
		Grey Matter	0,784129706
		White Matter	0,841592065
	T2 FLAIR	CSF	0,719473721
		Grey Matter	0,602853487
		White Matter	0,662681539

5 Conclusions

In this experiment, the main objective was to perform brain tissue segmentation into three classes (White matter, grey matter, and CSF) using SPM using different preprocessing parameters to check their effects on the final results. First, the prior probabilities of each tissue class were calculated and the pixels were assigned to each of the tissue classes taking the max probability of belonging to one particular class. In the preprocessing step, the brain skull was stripped and bias field was corrected. Also, different parameters were tuned to achieve the best segmentation result based on the mean and standard deviation of the dice score. So, The objective of this lab was successfully achieved which can be beneficial to understand future labs and performing more robust brain tissue segmentation.

A Appendix

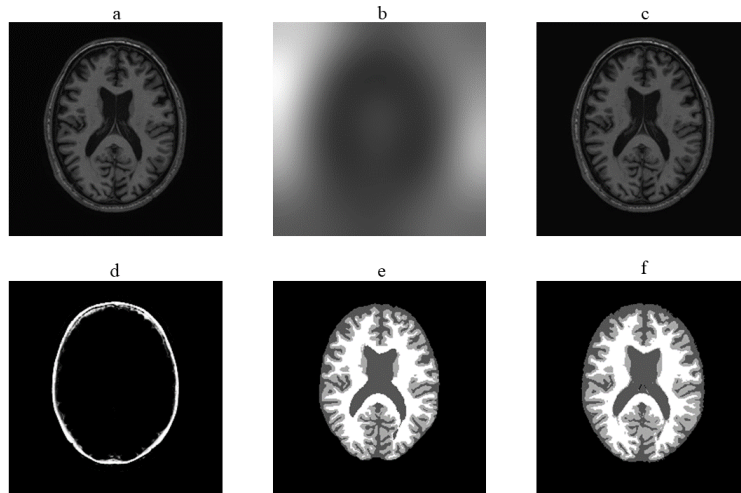


Fig. 1. Patient-1 (T1): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f) Ground Truth .

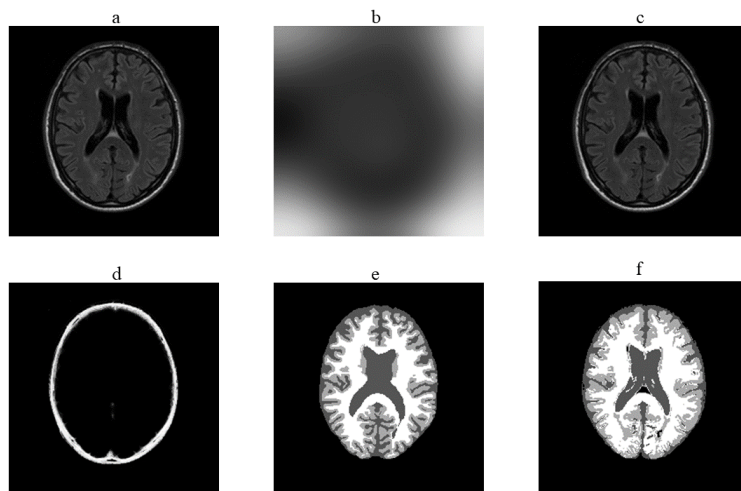


Fig. 2. Patient-1 (T2-FLAIR): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f) Ground Truth .

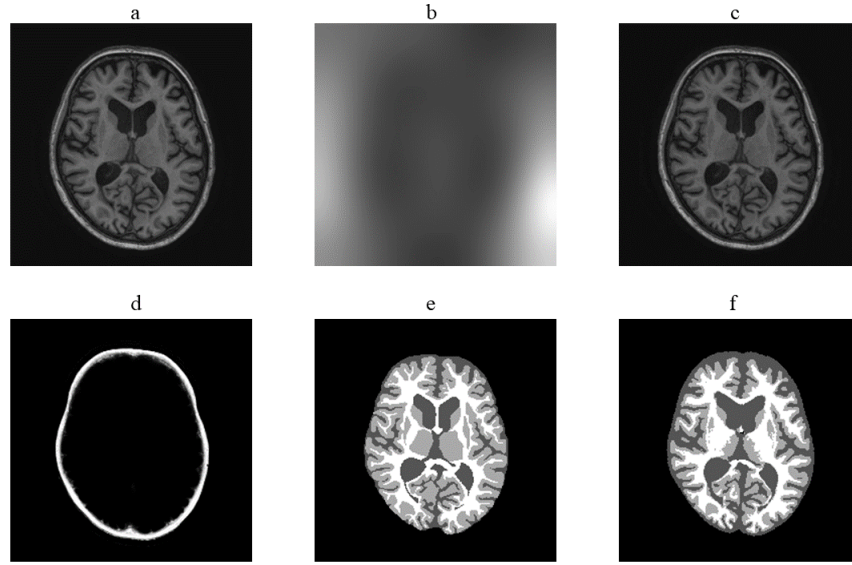


Fig. 3. Patient-2 (T1): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

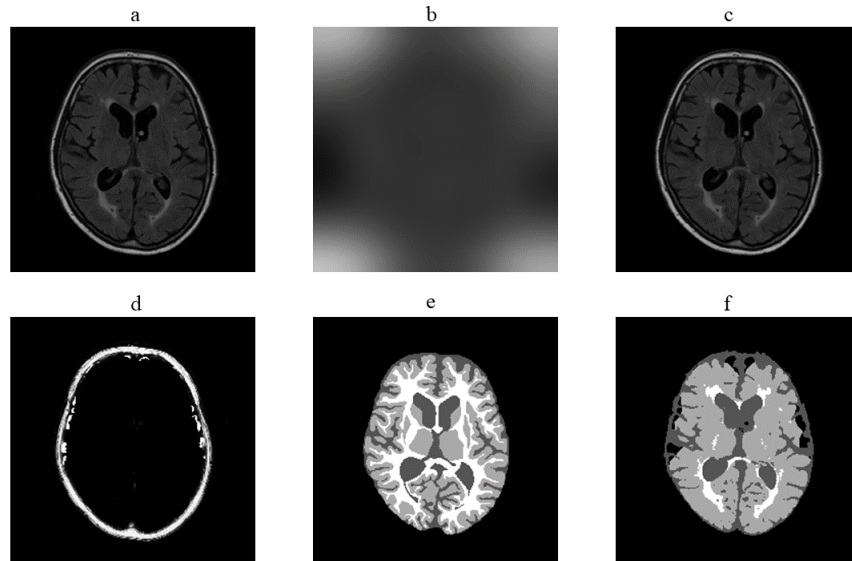


Fig. 4. Patient-2 (T2-FLAIR): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

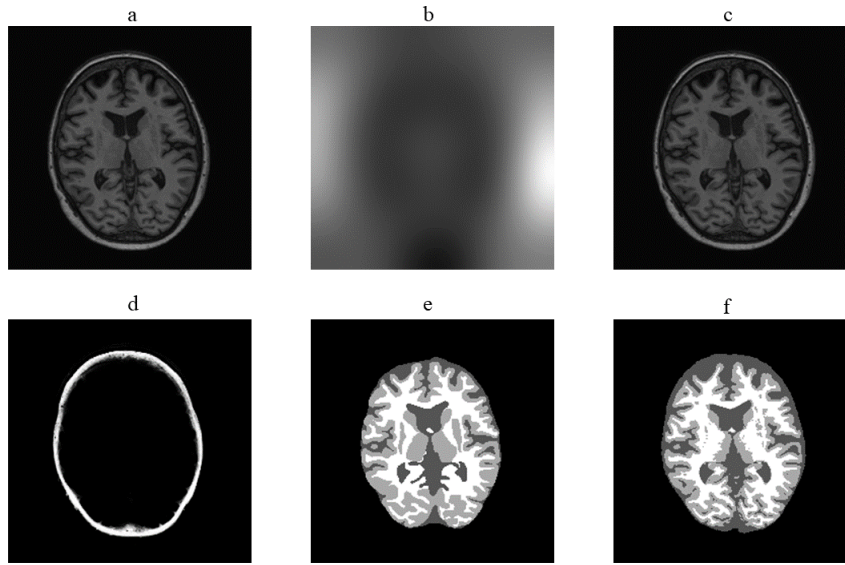


Fig. 5. Patient-3 (T1): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

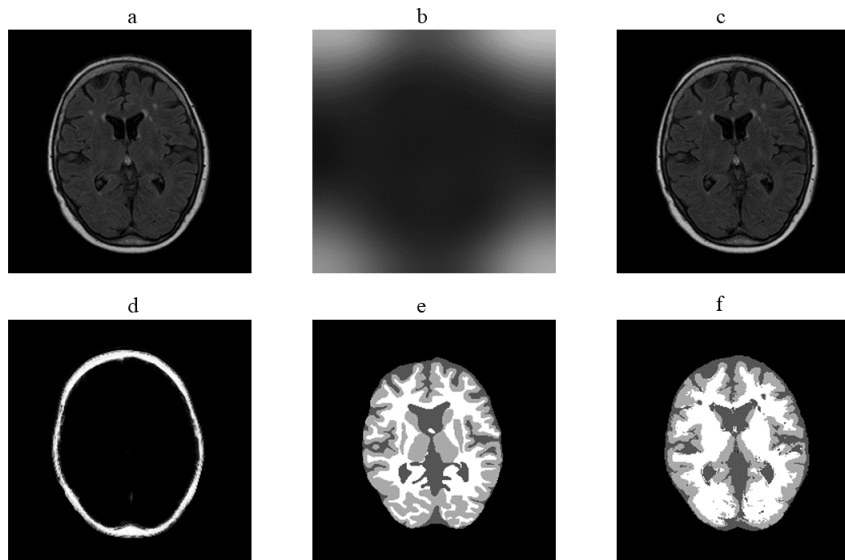


Fig. 6. Patient-3 (T2-FLAIR): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

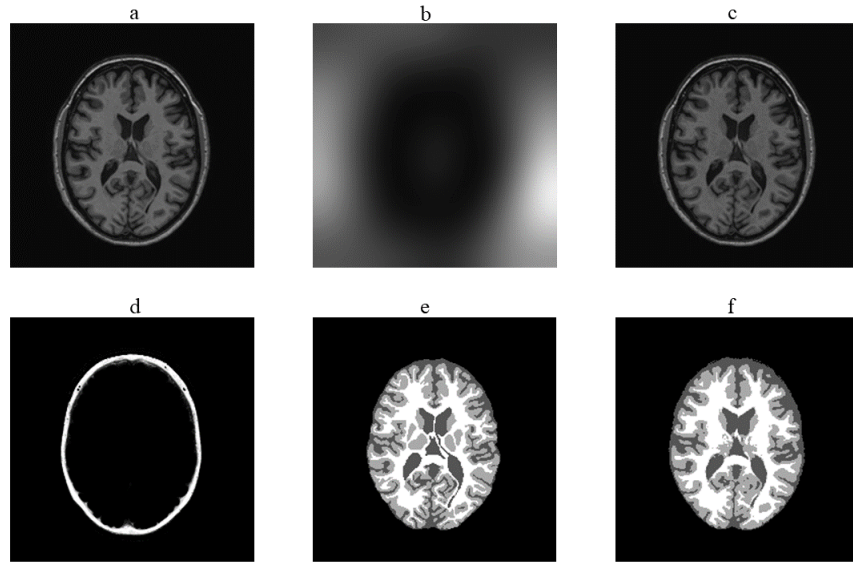


Fig. 7. Patient-4 (T1): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

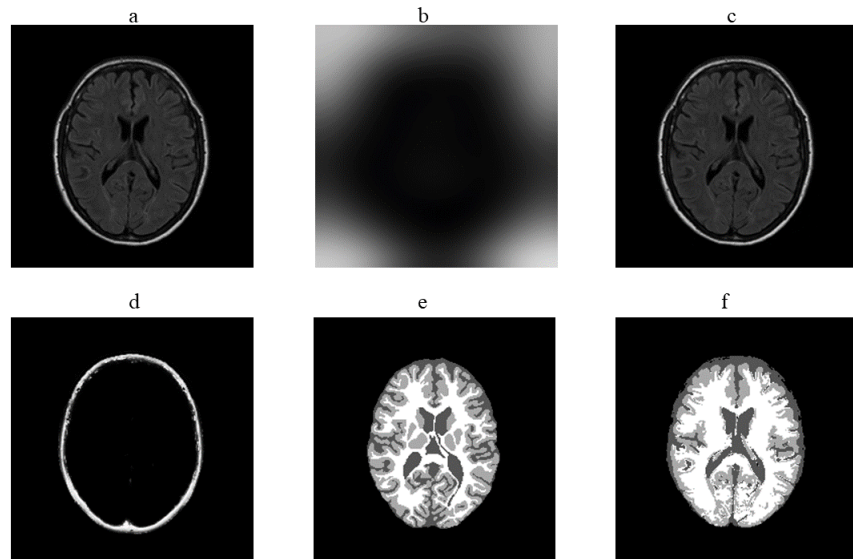


Fig. 8. Patient-4 (T2-FLAIR): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

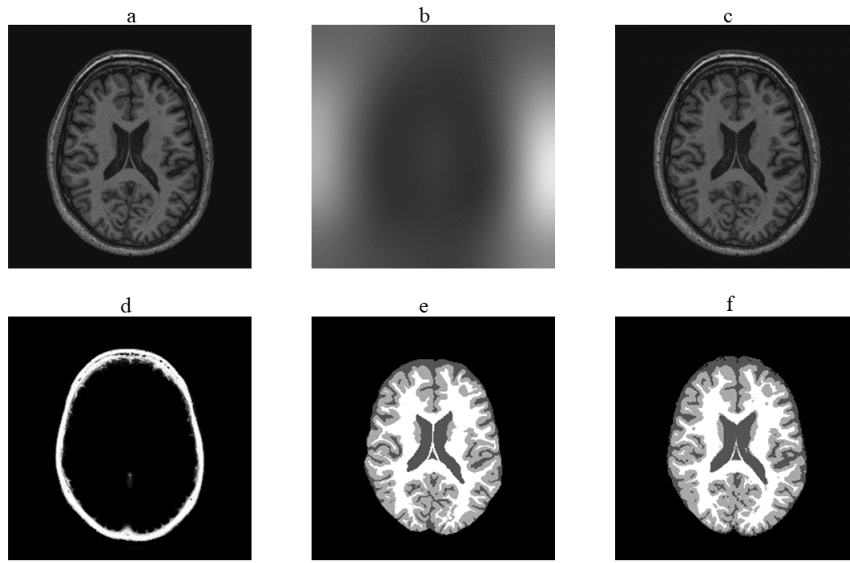


Fig. 9. Patient-5 (T1): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .

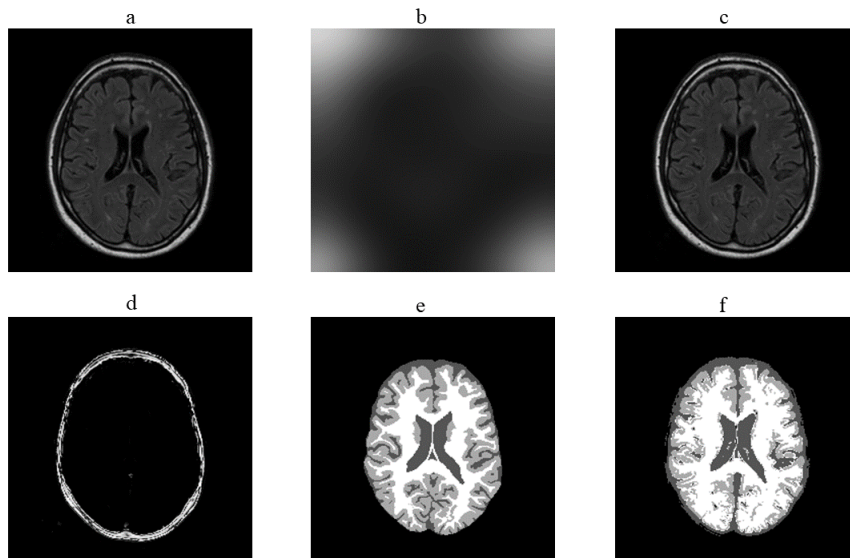


Fig. 10. Patient-5 (T2-FLAIR): a) Original Image, b) Bias Field, c) Bias Corrected Image, d) Skull Mask, e) Segmentation Result, f)Ground Truth .