Medical Image Segmentation & Applications

SPM: a neuroimaging tool

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1 Overview

Image segmentation plays an important role in medical image analysis. In the context of brain tissue segmentation, it is the process of partitioning tissues like white matter (WM), grey matter (GM), and cerebrospinal fluid (CSF) from brain images into a group of separate regions, where each region shares similar characteristics and features [1]. Accurate segmentation of magnetic resonance (MR) image tissues can be necessary in various brain disorders such as multiple sclerosis [2]. In intensity-based segmentation applications on MR images, bias can cause serious misclassification [2]. Another important example of whole-brain segmentation is called skull stripping, which segments the brain from non-brain tissues, e.g. skull, eyeballs, and skin [3]. In this presented work, we applied an automated tissue segmentation, bias field correction, and skull stripping technique on various subjects.

2 Objectives

The objectives of this laboratory are to explore Statistical Parametric Mapping (SPM) tool for brain tissue segmentation and as pre-processing steps, perform brain tissue segmentation, skull stripping, and bias field correction. The final deliverables include providing the segmented brain tissue nifti file, with reporting the experimental results of the segmentation and technique using different parameters.

3 MRI Dataset

The given dataset consists of 5 samples. Each sample contains both T1 and T2_FLAIR sequences, with a labels file that will be used later for evaluating the segmentation results. In the following sections, all of the results will be based on using only the T1 sequence for the tissue segmentation and evaluation.

4 Tools & Methods

The following steps were performed to achieve the demonstrated work in this report:

(a) SPM Matlab tool, ITK-SNAP visualization software, and the brain MRI dataset were installed.

(b) Setup SPM on Matlab and experiment with different options.

(c) Perform brain tissue segmentation and bias field correction using multiple parameters.

(d) Fusing the segmented masks and performing skull stripping using the results obtained by tuning the parameters.

(e) Evaluate the segmentation using the DICE score.

4.1 Brain Tissues Segmentation

The first task of this report is to use SPM tool to perform brain tissue segmentation for each of the dataset volumes. This had to be done by experimenting with different parameters available in SPM. This process resulted in automatically correcting the bias field, which will be discussed in section 4.2, and segmenting the brain volume into multiple tissues (GM, WM, CSF, bone, soft tissues, and air), each saved as a separate new volume. The following parameters were evaluated using different values, as described below:

1. Bias regularisation: which could vary from no regularisation (0), light regularisation (0.001) to extremely heavy regularisation (10).

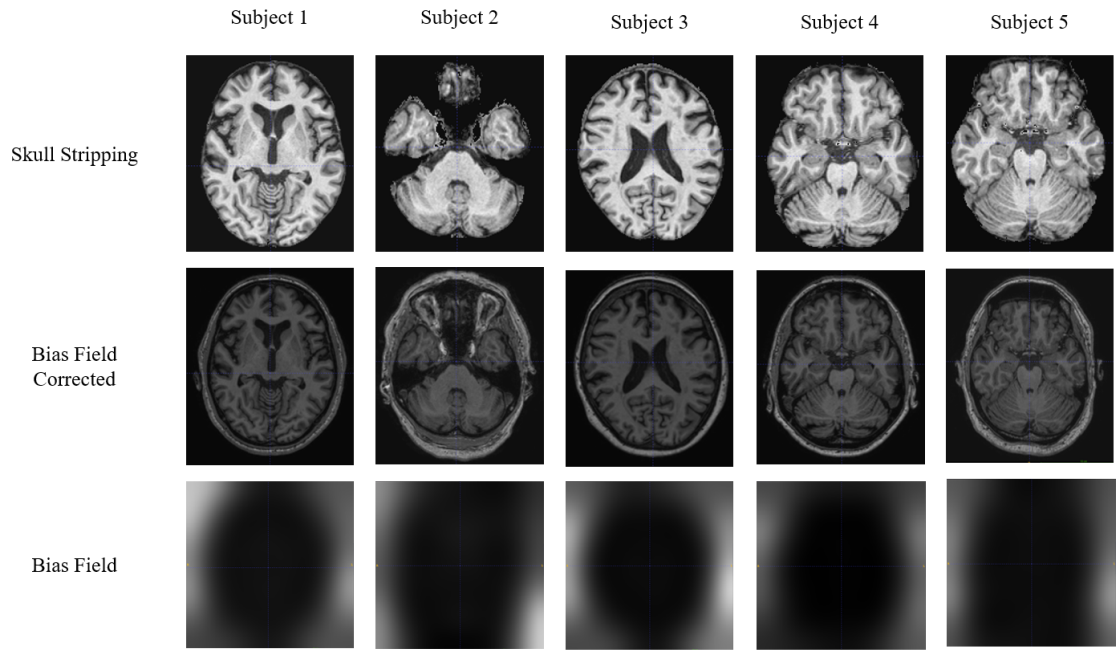

Figure 1: Final result for brain tissue segmentation, bias field correction, and bias field for all five patients using 0.0001 regularization parameter.

2. Bias FWHM: FWHM of bias Gaussian smoothness. It is used to guide the algorithm in modelling out the intensity variations due to different tissue types. A larger value is recommended by SPM to be used if the intensity non-uniformity is very smooth.

3. Save Bias Corrected, which is an option to save the bias corrected version of the images and their estimated bias fields.

Table 1 summarizes the parameters and values used in this work.

Table 1: Parameters used for segmentation and bias field correction.

Parameters	Values
Bias FWHM	60mm cutoff
Bais regularisation	No regularisation [a] Medium regularisation [b] Light regularisation [b] Very Light regularisation [c]
Save Bias	Save field and corrected

[a] Regularisation equal to 0.0.
[a] Regularisation equal to 0.01.
[b] Regularisation equal to 0.001.
[c] Regularisation equal to 0.0001.

4.2 Bias Field Correction

Bias field is a term that refers to an undesirable low frequency signal that corrupts MR signals due to the inhomogeneities in the magnetic field of the MR machines [4]. It reduces the high frequency information that determines the contours and edges, and alters the image pixels intensity values resulting in different grey level distribution for the pixels in the same tissue. Making it a challange for segmentation and classification algorithms [4], for this, bias field correction is an important pre-processing step.

As mentioned in Section 4.1, the bias field correction is made automatically during the tissue segmentation process. As a result, the corrected bias volume, and the bias field are exported with the remaining segmentation masks.

4.3 Skull Stripping

Skull stripping refers to the process of removing the non-brain tissues such as skin, fat, muscle, neck, and eye balls from MR brain images [5]. Pre-processing the brain images with skull stripping eventually leads to better segmentation of different brain regions resulting in accurate diagnosis of various brain-related diseases [5]. In this work, skull stripping is performed using SPM tool, the bias field corrected images, and the 3 tissues segmented masks for GM, WM, and CSF. The processing steps are as follows:

1. In SPM GUI, ImCalc button is used to open

Table 2: Mean dice score results for each patient for each brain tissue segmented using the bias corrected field image and segmented volumes.

	Regularization	GM	WM	CSF
Bias FWHM = 60mm	0.0	0.732568 ± 0.030546	0.80368 ± 0.028947	0.739264 ± 0.028534
	0.01	0.733544 ± 0.031073	0.80686 ± 0.028747	0.735134 ± 0.026908
	0.001	0.734064 ± 0.030911	0.806736 ± 0.029405	0.737742 ± 0.026732
	0.0001	$0.734864 \pm 0.0.02978$	0.806320 ± 0.029311	0.740066 ± 0.026871

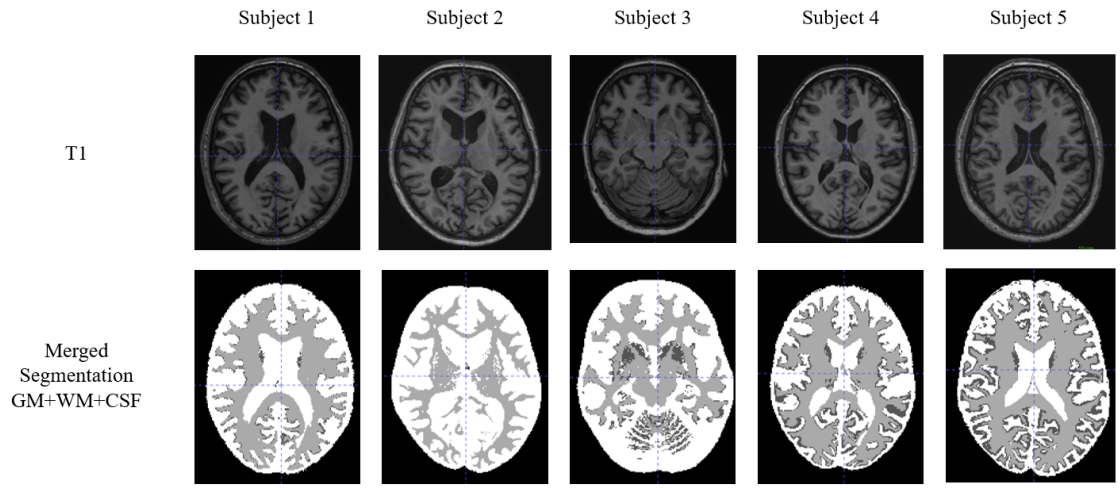

Figure 2: Qualitative segmentation results of the three brain tissues (GM, WM, and CSF), comparing to the original T1 images for all five patients using 0.0001 regularization parameter.

a new interface for this process.

2. The four volumes are loaded in order, starting with the bias corrected field volume, then the remaining 3 volumes for GM, WM, and CSF.

3. The expression in equation 1 is used to remove the skull and any other unwanted tissues. In the equation, $I1$ refers to the bias corrected brain image, while $I2$, $I3$, $I4$ are for GM, WM, and CSF respectively.

$$I1 \times ((I2 + I3 + I4) > 0.2) \quad (1)$$

The expression consists of 3 steps, firstly adding the segmentation results of the 3 tissues together, then binarizing them with a threshold equal to 0.2, making the regions of interest white, and everything else black with an intensity equal to 0. Finally, this binary mask is multiplied by the bias corrected volume, resulting in only maintaining the 3 tissue volumes and removing the rest.

5 Results and Discussion

As demonstrated in Table 2, which reports the mean and standard deviation of dice score evaluation for each brain tissue, the results of the tissue segmentation and the regularization parameter of 0.0001 had almost the highest mean and standard deviation dice score for all five subjects together, for both GM and CSF tissues. Only minor a difference is found comparing it to the regularization parameter 0.001 on WM tissue.

The result of this segmentation, skull stripping with the bias field corrected volume, and the bias field using a regularization parameter equal to 0.0001 can be seen in Figure 1 for the 3 tissues combined, given that this parameter resulted in the highest evaluation for most of the tissue cases. In addition, the segmentation masks for the three tissues were merged together in a single volume for each patient and compared to the original T1 images, as demonstrated in Figure 2. We can see from those segmentation masks that the tissue segmentation task performed well in segmenting each tissue, given also the mean dice scores reported in Table 2.

Conclusions

In this work, we have tested, presented, and evaluated results obtained SPM Matlab software and ITK-SNAP tool. Multiple experiments had been conducted using different parameters results on T1 images for all five subjects. A regu-

larization value of 0.0001 showed the best evaluation and segmentation result on GM and CSF tissues. To further improve and validate this approach, different evaluation and segmentation approaches could be taken into account to compare a software like SPM with an implemented approach. Overall, SPM software demonstrated satisfying results for brain tissue segmentation, bias field correction, and skull stripping tasks.

References

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