MODEL SELECTION PROPAGATION FOR APPLICATION ON LONGITUDINAL MS LESION SEGMENTATION

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ABSTRACT

Despite possible structural changes related to atrophy and edema, the structural anatomy of the brain should present time consistency for a given patient. Based on this assumption, we propose a lesion segmentation method that first derives a gaussian mixture model (GMM) separating healthy tissues from pathological and unexpected ones on a multi-time-point intra-subject groupwise image. This average patient-specific GMM is then propagated back to each time point where it serves as an initialization to the final time point specific GMM from which the final lesion segmentations are obtained.

***Index Terms*—** Groupwise registration, Model propagation, Model selection, Gaussian mixture model

1. INTRODUCTION

For an individual patient, even though global changes, such as atrophy, and local lesion changes, such as enlargement, shrinkage, appearance and disappearance, can occur, the overall anatomical structure of the brain can be assumed to remain stable. In the neuroimaging field, Gaussian mixture models have been used to model in MR imaging. These models have been shown to behave robustly to the presence of outliers, such as the presence of lesions [1]. It is for example possible to model separately the healthy tissues, hereafter called inliers (I), and their unexpected and pathological counterparts, called outliers (O) [2]. In the proposed model selection framework, the number of Gaussian components necessary to model correctly the inlier and outlier components of the four main anatomical regions (gray matter, white matter, corticospinal fluid and non-brain) is determined automatically, by finding a balance between model fit and complexity. In such a framework, the segmentation of the lesions can be obtained through the selection of the relevant derived Gaussian components as a post-processing stage of the model selection process.

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In this work, we first fit the model to the intra-subject groupwise average across the different time points. The resulting average tissue and inlier/outlier segmentation are then propagated back, along with the model parameters to initialize a time point specific model. Overall, the proposed model can be divided into four major steps whose rationale will be described hereafter.

2. DETAILED STEPS

2.1. Preprocessing

Although all available modalities and time points are coregistered to the baseline T1 image, and corrected for any intensity inhomogeneities, this preprocessing is refined (denoted pp+) so that the images are analysed in the space of the FLAIR images. For that purpose, the T1 and T2 modalities at each time point are rigidly aligned to the FLAIR image. ICBM atlases are also aligned to the new obtained T1 image and used as an initialization for an 3 modalities initial EM segmentation in a framework that will not only correct for possibly remaining bias field but also for an initial separation between inlier and outliers (I/Oinit). In this framework, the data intensities are log-transformed and bounded.

2.2. Groupwise image creation

From the refined preprocessed images at the different time points, an intra-subject multi-time-point groupwise average is created. This is performed through an iterative set of affine registrations refined afterwards by non-rigid deformations using the NiftyReg package [3]. The non-rigid step is performed to account for atrophy but in order to prevent an unwanted effect on the lesions appearance, constraints are added at this stage. Furthermore, in order to standardize the information about the intensities while avoiding artefacts, an histogram matching is progressively performed between the individual time points and the groupwise image using only the model inliers and applying a polynomial fit of degree 2. This intensity matching step will allow for a more straightforward projection of the selected groupwise model to the specific time

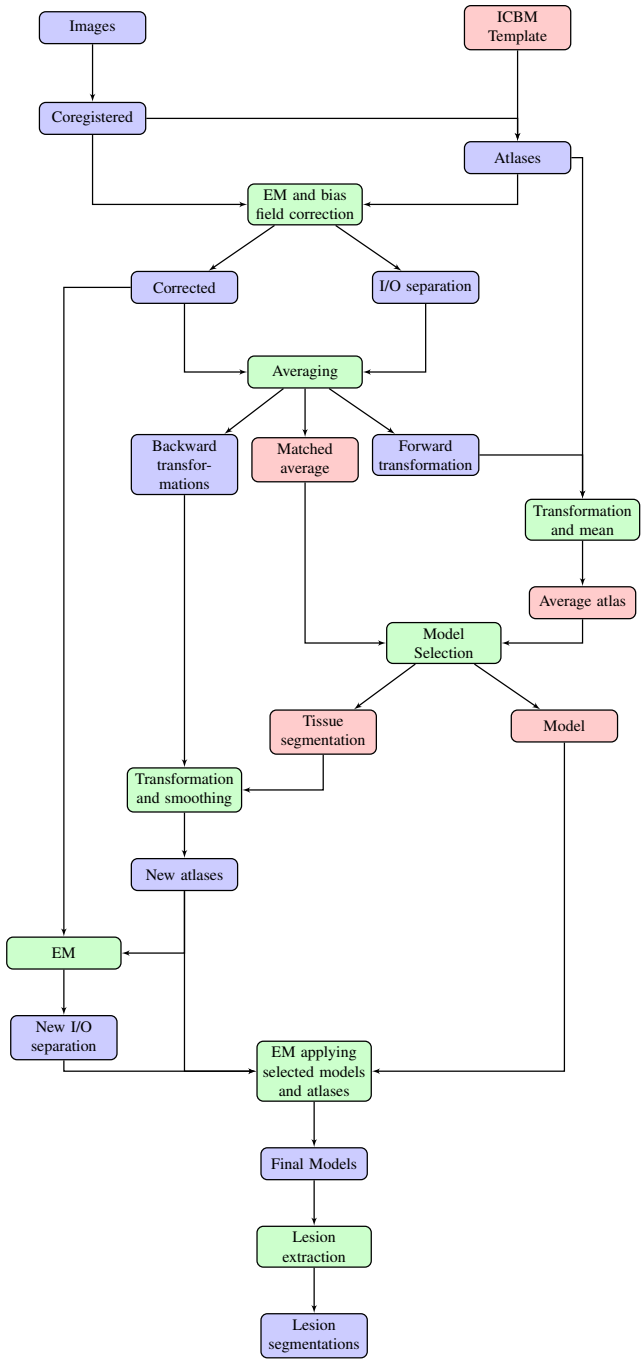

Fig. 1. Graphical representation of the pipeline of the method. Blue boxes refer to sets of elements related to specific time points while red ones are related to the groupwise space. In turn, green boxes refer to performed actions. EM refers to the application until convergence of an Expectation-Maximization algorithm.

points. The obtained atlases for each time point are accordingly transformed to the groupwise space and averaged together to produce groupwise tissue atlases. Similar operation is performed on the brainmasks.

2.3. Model selection and reused outputs

From the matched groupwise images (T1, FLAIR and T2), corresponding tissue atlases and brainmask, the process of GMM model selection is performed. Here the model fit makes use of joint T1, T2 and FLAIR data. Once the final model converges, one can obtain a groupwise tissue segmentation and an inlier/outlier classification.

2.4. Time point specific analysis

The groupwise tissue segmentation is transformed back towards a specific time point and smoothed using a Gaussian filter. For each time point, this smoothed segmentation is used as tissue atlas for a new GMM model fit improving on the inlier/outlier separation. Once the model selection has been applied for each time point space, a lesion extraction process relies simply on the choice of the relevant Gaussian components from the outlier part of the model based on location and intensity heuristics. The global detailed pipeline is presented in Figure 1.

3. REFERENCES

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