AUTOMATIC SEGMENTATION OF CORTICAL REGION OF THE BRAIN FROM MR IMAGES

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ABSTRACT: In this paper we describe a fully automated method for segmentation of cortical regions from 3D magnetic resonance images (MRI) of the brain using a pre-labelled anatomic atlas of the brain that guides the segmentation process. First, the method uses a linear transformation to establish a correspondence between the atlas and the subject to segment. Then, a classification algorithm performs a global segmentation to identify the anatomic tissues. Finally, an iterative process is performed between the tissue classified and nonlinear transformation to align locally the template with the tissue classified and to obtain spatial information to identify the interest structure; at each iteration the atlas is updated in order to improve the segmentation of the region of interest (e.g. the cortical region, sub cortical region and the ventricular system). This method can be used in the context of analysis and valuation of medical images. We validated the technique with real MR images of the brain and the results show that it can successfully segment structures of the brain, which has important medical applications.

KEY WORDS: classification, nonlinear registration, anatomical atlas.

1. Introduction

The study of the normal and abnormal brain is of great importance in medical research and clinical studies, where the identification of the brain structures is the base of the analysis from medical images. However, the automatic segmentation of these structures is still a difficult task to solve due to the anatomical variability between individuals. Nowadays, there are several types of segmentation methods for medical images that can be applied to the anatomical brain MRI. The intensity-based classification methods have widely been used for the identification of tissues types, such as the non-parametric classifier KNN (k nearest neighbors) by Cocosco et al. [1] or Expectation Maximization used by Nathan Moon et al. [2], and Wells in [3] and the MRF’s (Markov random Fields) used by Leemput in [4]. These methods interleave intensity correction and classification in an iterative fashion using a prior tissue probability map as its model. All MRI classification methods are sensitive to overlapping areas in the tissue distribution. Such overlap is caused by inherent limitations of the image acquisition process such as noise or non-uniform intensity, also known as field bias.

Another segmentation approach includes the registration methods. These methods use a previously segmented brain image and align it with the subject image. The goal of registration is to remove structural variations between individuals by matching an atlas image to each individual and the result of this alignment is the segmentation. There have also been developed many approaches to non-rigid registration in recent years, Cuisenaire et al. [5], Sandor and Leahy [6], Thirion and Calmon [7], and Thirion [8] are examples where deformable models have been successfully applied to the localization of particular anatomical structures. These classification methods and deformable matching models (registration) are insufficient when they are used in a separate way. In the case of tissue classification, there are errors to identify structures of the same subject (in different slices) when different types of structures have similar spectral properties or between subjects when the same structure has different spectral properties. In the case of deformable models, the problem is that they need an accurate initialization and also are usually optimized to identify particular structures. In addition, deformable models can fail in the presence of abnormal anatomical variability or even in the presence of variable normal structures. In practice, statistical classification and nonlinear registration are often complementary segmentation strategies. This approach was used by Warfield et al. [9], he combined the elastic atlas registration algorithm with a statistical classification algorithm. Warfield creates a statistical model from the intensity values of the image, and then he uses an atlas to generate the anatomical localization of the image through a distance transformation in combination with an elastic match algorithm to enhance the classification process. However, the initialization of the probability density functions still requires a supervised selection of training data.
regions. Wang and Staib [10] use a physical model created with a Bayesian formulation, an atlas (or anatomical reference), and deformable elastic solids. Phol et al. [11] used the Expectation Maximization-Mean Field Approximation method with a Local Prior Map and deformable registration for tissue classification. In this work, we propose a fully automatic method for segmentation of the cortical region, ventricular system and subcortical region using non-supervised classification and non-linear registration based in a diffusion model (demons deformable registration proposed by Thirion) with the purpose of adapting the segmentation iteratively.

2. Method

Our method involves a classification algorithm to assign labels to the different tissue types and a nonlinear registration algorithm to align locally a digital anatomic atlas with the classified tissues. The non-supervised classification is applied to obtain a global segmentation, it divides an image into different tissue classes based on the signal intensity value, these classes are Cerebro-Spinal Fluid (CSF), grey matter, and white matter. However, we still need to perform a local segmentation process to identify specific structures belonging to those classes. For this, we use additional information about the spatial location of anatomical structures derived from a registered anatomical atlas. The method iteratively uses the classified tissues and the characteristics that describe the spatial location of the specific region to segment. These spatial location characteristics are generated through the conversion of the registered anatomical template into a distance transformation. The segmentation is then put through a feedback path, where an elastic matching algorithm is used to refine the alignment of the template to the classified tissues and at the same time refine the segmentation at each iteration. Figure 1 illustrates the developed method.

2.1 Image Preprocessing

Different steps are involved in the initialization of the images to feed the algorithm. This initialization consist of the image acquisition and the use of image enhancement algorithms to improve the contrast of the structures of interest, to decrease the intrasubject and intersubject intensity non-homogeneities (e.g. nonlinear anisotropic diffusion for noise smoothing, enhancement of the contrast of local structures), and apply an initial alignment strategy to align the patient scan to the template (e.g. transformations in position and orientation through rigid registration) and then transform the atlas to the patient scan (e.g. transform in form and size with affine registration). We use the mutual information similarity metric in both registration methods.

2.2 Atlas Generation

The atlas consists of a 3D representation of a human brain. In order to generate the atlas we label each voxel of the volume according to the current anatomical structure. This generation is semiautomatic with the help of an expert and bibliographic references in the medical area. The atlas was constructed from normal anatomy scans of a 35 year old woman. The volume consists of 18 transverse slices and each slice of 256 x 256 pixels and voxels have a dimension of 0.90 x .90 x 7.2 mm³. The volume was preprocessed using local segmentation techniques followed by manual editing. The final atlas is composed of a set of pre labeled templates that form the 3D volume.

2.3 Classification

For the classification process we used the k-means algorithm, which is a popular clustering algorithm because it is simple and usually converges to a reasonable solution. The input parameters are k that represents the number of clusters to be generated and an approximation of the initial mean for each cluster (the center for each class). An object is assigned to the most similar cluster based on the distance between the object and the cluster mean. Then the algorithm computes the new mean for each cluster. This process iterates until the termination condition converges. This algorithm is used to segment the white matter, grey matter and CSF. The input parameters, k, were analyzed in different volumes to establish the k means in general form. The k-means clustering algorithm is computationally very expensive because it has to recalculate the mean at each iteration. We used the itk implementation [12], based in Kanungo et al. [13] that uses a special data structure known as k-d tree with additional information to reduce the computational cost of the distance calculation and means. The additional information includes the number and the vector sum of measurement vectors under each node of the tree architecture. The algorithm then compares each node of the k-d tree and the k-means. This idea of using a k-d tree can be found in different papers such as [13], and [14].

2.4 Nonlinear registration

We use the concept of demons deformable registration based on the work of J.P. Thirion [8] as an elastic matching algorithm. Given a source data set S(\(x\)) and a target data set \(M(x)\) and a target data set \(S(x)\), the goal of the elastic matching algorithm consists on finding a deformable vector field \(U(x)\) such that the function \(M(x - U(x))\) is as similar to the function \(S(x)\) as possible. Each image is viewed as a set of iso-intensity contours. The main idea is that a regular grid
Fig. 1 General structure of the method. The method consists of the image acquisition and an initial registration of a template created from an image of normal anatomy. A global segmentation is computed by the k-means algorithm. Then, the anatomical template is converted into a distance map describing the anatomical localization with a distance transformation. The segmentation is then put through a feedback path that is used to refine the segmentation with the help of an elastic matching algorithm to adjust the template of normal anatomy to the classified patient data. The anatomical localization is recomputed with the refined atlas in an iterative process.

of forces deforms an image by pushing the contours in the normal direction. The orientation and magnitude of the displacement is derived from the instantaneous optical flow equation and re-normalized by Thirion’s algorithm to avoid large displacements. The general deformation formula is shown in equation 1.

\[
U(x) = \frac{(M(x) - S(x)) \nabla S(x)}{|| \nabla S ||^2 + (M(x) - S(x))^2} 
\]

Starting with an initial deformation field \( u^0(x) \), the demons algorithm iteratively updates the field using equation 2 to calculate the field at the \( N \)-th iteration.

\[
U^N(x) = U^{N-1}(x) - \frac{(M(x + U^{N-1}(x)) - S(x)) \nabla S(x)}{|| \nabla S ||^2 + (M(x + U^{N-1}(x)) - S(x))^2} 
\]

Finally the deformation field needs to be normalized at each iteration through smoothing with a Gaussian filter. For this, we used the “itk” implementation of the demons deformation registration algorithm [12].

2.5 Anatomical Localization

The anatomical localization is obtained by converting each of the relevant structures of aligned templates into a distance map. First, the templates are intersected with the classified tissue obtaining only matches in small regions due to highly variability of the structures, such as the cortex. Then, a distance transformation is applied to the intersected regions, with the objective of spreading these regions to take the closest pixels that belong to the classified tissue regions. After this, a nonlinear transformation is applied using an elastic matching algorithm to deform these regions to update the template at each iteration. Finally, the template is used to generate a new anatomical localization.

The whole process described before follows these steps. We perform a classification of the different brain tissues mentioned before and use that classification to update a template alignment and vice versa the template eliminates incorrect classified regions of the classification process such as the image background and others regions that are not of a specific type of tissue. To recap, a global segmentation is computed using the k-means algorithm to obtain the different types tissues, then we make an iteratively local segmentation based on the classified tissue the spatial localization derived from the anatomical template. The process converges when a satisfactory local segmentation is found, this happens with around eight or fewer iterations of the process.

3. Experiments and Result

We have applied our method to a dataset of 12 real MR scans of normal patients that were acquired on a Signa 1.5 Tesla. The images resolution is of 256 x 256 pixels with a voxel resolution of 0.90 x 0.90 x 7.2 mm³ on T1 single mode. The figure 2 show the results of segment the cortical region with our method and a comparison between automatic and manual segmentation. In this section we illustrate one of these tests due to space limitations. For the method validation we used three different techniques. The first one involves comparing two regions (manual and automatic segmentation), the second compares contours between three different manual segmentations and the automatic segmentation. Finally we use the maximum Hausdorff distance measure applied
to regions and contours to obtain the maximum distance between the regions of the automatic segmentation that does not overlap with the manual segmentation.

Comparing regions

We used the Dice Similarity Measure (DSC) described by Zijdenbos et al. [15] to compare the manual segmentation done by a human expert and our automatic segmentation according to equation 3.

\[
DSC = \frac{2 * |A_1 \cap A_2|}{|A_1| + |A_2|}
\]  

(3)

where \(A_1\) and \(A_2\) are the two segmented areas. This index ranges from zero to one; zero indicates that there is not any overlap between the regions and one indicates a perfect match between the two areas. A DSC > 70% is considered as an excellent agreement between the two [15].

Comparing contours

We compared the automatically generated contours with those obtained manually. For this, we joined the three manual contours to form a single region. Then, we computed the number of pixels of this new region that overlap with the automatic contour using a intersection operator. We also computed the maximum distance for pixels falling outside this joined-region.

Table 1 shows the results of applying the three metrics described before (DSC, distance Hausdorff and overlap contours) in one single scan to compare the segmentation of the cortical region, sub-cortical region and the ventricular system by our method with manual tracings made by a human expert.

<table>
<thead>
<tr>
<th>Validation Metric</th>
<th>Cortical Region</th>
<th>Sub-cortical Region</th>
<th>Ventricular System</th>
</tr>
</thead>
<tbody>
<tr>
<td>DSC regions</td>
<td>0.82</td>
<td>0.91</td>
<td>0.94</td>
</tr>
<tr>
<td>Contour overlap</td>
<td>0.85</td>
<td>0.82</td>
<td>0.88</td>
</tr>
<tr>
<td>Hausdorff regions</td>
<td>8.01</td>
<td>6.19</td>
<td>2.53</td>
</tr>
<tr>
<td>Hausdorff Contours</td>
<td>7.00</td>
<td>6.53</td>
<td>1.88</td>
</tr>
</tbody>
</table>

Table 1. Validation metrics to compare the similarity between our automatic segmentation method and the manual segmentation.

The DSC metric gave us an average value of 0.89 for the three segmented regions, which is considered as perfect [15]. This result is strengthen by the contour overlap value that shows an excellent percentage of the overlapping regions between the automatic and manual segmentations with an average value of 0.85. Finally, table 1 shows the results of applying the maximum hausdorff distance metric between regions and contours of the automatic and manual segmentations. The distance values show that there are really small differences between the regions. Figures 2 to 4 illustrate the automatic segmentation and the difference between the automatic and manual segmentations.

All these results demonstrate that our method is robust and that it can be applied to the real world.

4. Conclusion

We have developed a fully automatic method for segmentation of the cortical and sub-cortical regions and the ventricular system for normal anatomy of the brain. Our method combines two strategies, classification and nonlinear registration. We use them as complementary strategies in order to accomplish a local segmentation of specific brain structures guided by the anatomical information derived from an atlas of the brain.

We validated the method with real MR images and demonstrate that it can achieve a better segmentation than either classification method or nonlinear registration in relation to specific structures. Our method is robust against significant morphological differences between subjects. Moreover, the classification step does not need to use a training set because of its non-parametric characteristics and it does not make any assumption about the tissue intensity distribution in the image.

However, the method is highly dependent on anatomical information and it might not segment regions that are not included in the template. Currently the classification step does not consider pathologies present in the images. In our future work, we will incorporate a method based on non-homogeneity intensity correction to enhance the quality of our results. We also plan to use a probabilistic atlas to incorporate a spatial prior probability field to predict the spatial distribution of tissue classes and to apply this method to recognize certain types of pathologies.

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References


Fig. 2 Two T1 slices of a volume that shows the segmentation of the cortical region
(a) Original image. (b) Manual segmentation by a human expert. (c) Automatic segmentation. (d) Difference between automatic and manual segmentation.

Fig. 3 Three T1 slices of a volume that shows the segmentation of the ventricular region (a) original image. (b) Manual segmentation by a human expert. (c) Automatic segmentation. (d) Difference between automatic and manual segmentation.

Fig. 4 Two T1 slices of a volume that shows the segmentation of the sub cortical region (a) original image. (b) Manual segmentation by a human expert. (c) Automatic segmentation. (d) Difference between automatic and manual segmentation.