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Brain Tissue Classification in Magnetic Resonance Images

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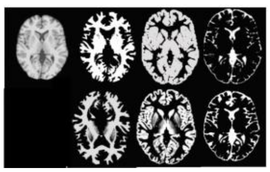
Graphical abstract



Abstract

Automatic segmentation of brain images is a challenging problem due to the complex structure of brain images, as well as to the absence of anatomy models. Brain segmentation into white matter, gray matter, and cerebral spinal fluid, is an important stage for many problems, including the studies in 3-D visualizations for disease detection and surgical planning. In this paper we present a novel fully automated framework for tissue classification of brain in MR Images that is a combination of two techniques: GLCM and SVM, each of which has been customized for the problem of brain tissue segmentation such that the results are more robust than its individual components that is demonstrated through experiments. The proposed framework has been validated on brainweb dataset of different modalities, with desirable performance in the presence of noise and bias field. To evaluate the performance of the proposed method the Kappa similarity index is computed. Our method achieves higher kappa index (91.5) compared with other methods currently in use. As an application, our method has been used for segmentation of MR images with promising results.

Keywords: Automatic brain segmentation; gray level cooccurrence matrices; tissue classification; magnetic resonance images

1.0 INTRODUCTION

The field of medical image processing gains its significance with increase in the need of automated and efficient diagnosis. Magnetic Resonance Images (MRI) are used as a valuable tool in the clinical environment due to its characteristics such as high spatial resolution, high contrast and soft tissue differentiation. MRIs are assessed by experts based on visual interpretation of the image to detect the presence of abnormal tissues, which is a time consuming and labor-intensive task. These manual techniques suffer from inter- and intra-observer variability. In addition, the sensitivity of the human eye reduces with increasing number of cases.

Therefore there is a need for automatic or semi techniques for analysis of MR images. Changes in the composition of white matter (WM), gray matter [1] and cerebro-spinal fluid (CSF) in the brain volume can be used to define disease entities or to determine disease severity [2, 3]. In this paper, we proposed an automatic framework for brain segmentation into WM, GM and CSF. Many automatic image-processing methods have been proposed for brain MRI segmentation. Since the intensity distribution of tissues in brain MR images is complex, it leads to difficulties for defining the threshold value.

Therefore, thresholding techniques are restrictive and have to be combined with other techniques. Region growing methods is an extension of thresholding techniques by combining it with region homogeneity criteria. Successful methods require anatomical knowledge to locate seed points for each region and together with their associated homogeneity [4]. Clustering techniques are the most popular algorithms for MRI segmentation, with fuzzy c-means (FCM) and expectation–maximization (EM) methods. The advantages of the EM algorithm are its ease of implementation, conceptual simplicity, and also the fact that each of the iterations improves the results. A common drawback of EM is that the intensity distribution of images is modeled as a normal Gaussian distribution that is untrue, especially for noisy images.

The FCM algorithm has been proposed by many researchers [5] such as knowledge-based segmentation and tissue labeling technique, to initially segment brain MRI. Segmented brain MRI via artificial neural network and compared the result with FCM. FCM algorithm was demonstrated to be superior on normal brains, but worse on abnormal brains. One of the main problems of the FCM methods is that the results are influenced by artifacts such as noise [4]. Since MR images always include considerable unknown noise, this leads to further degradation with segmentation using FCM.

Many extensions of FCM technique have been reported in the literature to overcome the effects of noise, but most of them still have major disadvantages. Machine-learning methods have proven to yield acceptable results in many cases. The SVM method is considered as a desirable candidate because of its high generalization performance without the need prior knowledge, even when the dimension of the input space is very high [6]. Some studies have reported that the SVM is commonly more able to deliver higher performance in terms of classification precision than the other classification methods. In this study, SVMs are obtained by learning from the training samples in the last stage.

The key aspect of the proposed method is that we combined two methods to have an accurate classification, each of which individually extracts a different set of constraints of the problem and the results of each step simplifies the one that follows it. The rest of this paper is organized as follows:

In section 2 we present the new automatic framework for classification of brain tissues that combines two methods and that is more robust than its individual components and other currently used methods. We give a step-by-step explanation for estimating model parameters. In Section 3, we present experimental results of the proposed technique. We discuss issues regarding verification of medical image segmentation, and also present a comparison of our results in a database on 18 simulated image volumes. The segmentation performance is evaluated for the proposed method. Section 4 contains discussion and concluding remarks.

The proposed method is an accurate and fast way to find optimal segmentations, given the intensity models, which incorporate the spatial coherence assumptions.

2.0 METHODOLOGY

In this study we proposed a hybrid of texture analyses and machine learning based segmentation method to segment three tissue classes (WM, GM and CSF) in MR Images.

Extracting proper features has a strong effect on brain MRI segmentation. It should be considered that a set of features that can classify brain tissues efficiently. The three constructing tissues of brain not only have various intensities, but also their intensity varies among different slices. In some slices, the voxel intensities of GM tissues are very close; Thus, identification of brain tissues according to the intensity features singly is not recommended. In this paper we used different features to have appropriate segmentation for all cases.

2.1 Feature Extraction

In this study the statistical features based on intensity of image such as mean and variance and features from gray level cooccurrence matrices (GLCM) such as contrast, entropy, correlation and inverse difference moment are used to investigate the adequacy for accurate segmentation. In other word we carried out texture analysis for describing texture of the images to have adequate feature for accurate segmentation.

The following statistical features are computed as presented as follow:

$$\text{Mean (M)} \quad \overline{x} = \frac{1}{X*Y}\sum_{i=1}^{X}\sum_{j=1}^{Y} x(i,j) \tag{1}$$

$$\text{Variance (V)} \quad V = \frac{1}{X*Y}\sum_{i=1}^{X}\sum_{j=1}^{Y}\left(x(i,j)-\overline{x}\right)^2 \tag{2}$$

Where,
X and Y: The number of pixels
x(i, j) : the image intensity

The intensities of the extracted pixels and the spatial coordinates were preserved to construct the GLC matrix. The GLCM are created by mapping the gray level co-occurrence probabilities based on spatial relations of voxels in various angular directions.

Four angles (0, 45, 90, and 135) as well as a predefined offset distance of a pixel in the formation of symmetric GLC matrices are considered (see Figure 1).

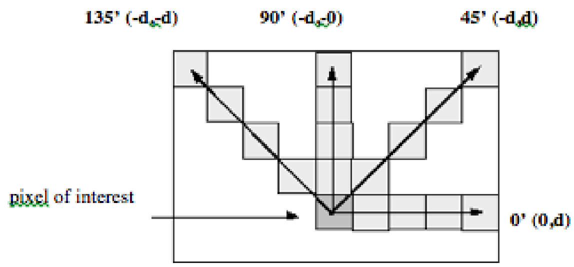


Figure 1 Spatial relationships of pixels, which are defined by the array of offsets, and d represents the distance from the pixel of interest

We computed four GLCM matrices, set of features and five texture measures in this paper, which are entropy, contrast, energy, Inverse Difference Moment and correlation.

$$\text{Entropy} \quad = -\sum_{i=1}^{N}\sum_{j=1}^{N}\left(\frac{P(i,j)}{R}\right)\log\left(\frac{P(i,j)}{R}\right). \tag{3}$$

$$\text{Contrast} = \sum_{i=1}^{N}\sum_{j=1}^{N}(i-j)^2\left(\frac{P(i,j)}{R}\right) \tag{4}$$

$$\text{Energy} = \sum_{i=1}^{N}\sum_{j=1}^{N}\left(\frac{P(i,j)}{R}\right)^2 \tag{5}$$

Inverse Difference Moment

$$= \sum_{i=1}^{N}\sum_{j=1}^{N}\frac{[P(i,j)/R]}{1+(i-j)^2}, \quad i \neq j. \tag{6}$$

$$\text{Correlation} = \frac{\sum_{i=1}^{N}\sum_{j=1}^{N}[ijP(i,j)/R]-\mu_x\mu_y}{\sigma_x\sigma_y}. \tag{7}$$

Where,

$$\mu_x = \sum_{i=1}^{N} i\sum_{j=1}^{N} P(i,j)/R$$

$$\mu_y = \sum_{j=1}^{N} j\sum_{i=1}^{N} P(i,j)/R$$

$$\sigma_x{}^2 = \sum_{i=1}^{N}(i-\mu_x)^2\sum_{j=1}^{N} P(i,j)/R$$

$$\sigma_y{}^2 = \sum_{j=1}^{N}(j-\mu_y)^2\sum_{i=1}^{N} P(i,j)/R$$

In addition the standard deviation and mean valus of GLCM accumulated in the x and y directions [7]. These features will be used as inputs of SVM to have an accurate segmentation.

2.2 Segmentation by SVM

SVMs are currently the state-of-the-art technique to solve binary classification problems. SVMs work well for classification of the objects, which are not linearly separable. These objects are mapped into a high-dimensional feature space through the kernel transformations. They have shown good results in the literature for different pattern recognition tasks. Due to the generalization ability, the SVM has accomplished great success in different applications.[1, 8, 9].

In this study we used SVM to enhance the segmentation process, to rank computed features from the extracted regions and to classify particularly the brain borders and overlapped regions. After feature extraction to assign a label of each overlapped voxels a support vector machine classifier is used. SVM classifiers are trained for each brain tissue based on the set of extracted features from the previous section.

The SVM classifiers have a training step to determine a separating hyper plane for the data in the feature space. The hyperplanes separate different classes so that the margin between the classes is the maximum margin (see Figure 2).

The optimal hyperplane is achieved by solving the optimization problem:

$$\min_{\mathbf{w},b,\xi} \frac{1}{2}\mathbf{w}^T\mathbf{w} + C\sum_{i=1}^{l}\xi_i \tag{8}$$

$$\text{subject to } y_i(\mathbf{w}^T\phi(\mathbf{x}_i)+b) \geq 1-\xi_i, \; i=1,\dots,m. \text{ with } \xi_i \geq 0 \tag{9}$$

Let w be the normal vector of the separating hyper plane and WT*W maximizes the margin around the decision function. *C* is the penalty parameter for the error term. $\varphi(x_i)$ is the non-linear transformation that maps the samples into a higher-dimensional feature space. b is the offset of the hyper plane and (x_i, Y_i) are the pairs of the dataset and the appealing specifications of this approach is that they offer the possibility to apply a kernel function $(K(x_i, x_j) = \varphi(x_i)\, T\, \varphi(x_j))$ to transform the data into a higher-dimensional feature space. The kernel causes the data can be linearly separated through a maximum margin. In this paper, we used radial basis function kernel for parameter selection of SVM classifier. In this study an iterative labeling of neighboring voxels in the brain margins is performed applying the SVM classifier.

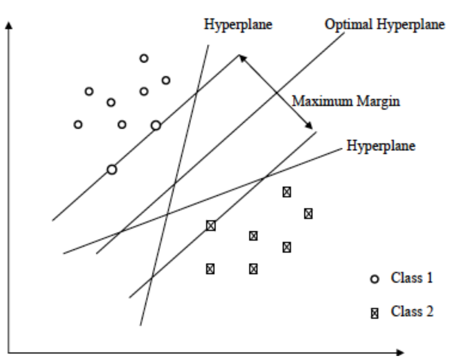


Figure 2 SVM classification

In this study the training process is conducted in two atages. Firstly we extracted optimal features from each subject and consequently we trained each of the subjects individually.

In the second step, we applied all subjects for training process to have a robust classifier. In this section 18 samples of T1-weighted images of BrainWeb are used for training. 11 subjects are applied as training dataset and 7 subjects to test the performance of the training process in each dataset.

The classifier is trained for a total of 10 000 samples per training image that are randomly selected from the provided brain mask. Laplacian RBF kernels reduce the Gaussian RBF error rate from 30% down to less than 10%. This improvement is because of the selection of the suitable metric and the proper generalization of SVMs.

3.0 RESULTS AND DISCUSSION

The proposed framework has been evaluated on T1-weighted brain images from braiweb dataset. Knowing the anatomical model we can have a quantitative verification of the performance of the different algorithms.

BrainWeb dataset provide synthetic MRI which are available at (http://www.bic.mni. mcgill.ca/ brainweb/) [10, 11]. A combination of different noise levels and bias field gives 18 simulated image volumes having voxel dimension of 1.0×1.0×1.0mm.

Each MR Image is provided with an anatomical model that provides main tissues class label for each voxel. In this paper, we applied 18 volumes (181*217*181). For both the ground truth labeling and our labeled results, we obtained three-class labeling (see Figure 3). The experiments indicate that the segmentation results are close to ground truth.

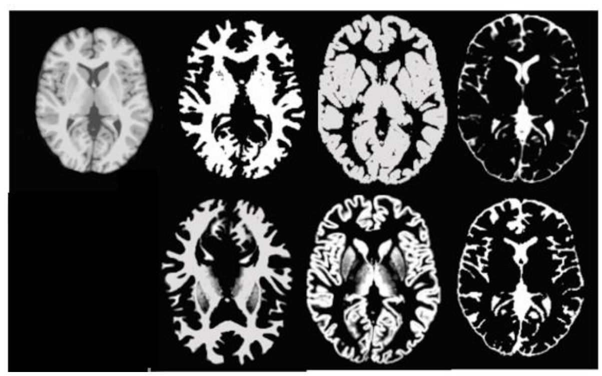


Figure 3 Results of segmentations on the brainweb images, Left to right, Top to bottom; Original image, Estimated WM, Estimated GM, Estimated CSF, ground truth of WM, ground truth of GM, ground truth of CSF

Since in these cases, the ground truth is accessible, it is possible to have a quantitative evaluation of the performance of the method. For quantitative evaluation the kappa index is calculated for WM and GM tissues for each volume compared to ground truth that is determined as Equation 10 [12-14].

$$k(S1,S2) = \frac{|S1 \cap S2|}{|S1 \cup S2| - 1/2(\,|s1 \backslash s2| + |s2 \backslash s1|\,)} \tag{10}$$

In this section to point out the contribution of the proposed method, it would be compared with fuzzy and non-fuzzy method such as EMS, SPM and NL-FCM[4] [28]. The averages of Kappa indexes for WM in brainweb images with different Rician noise and 20% bias field for EMS, SPM5, NL-FCM and the proposed methods as plotted in Figure 4 are: 89.26, 91.07, 90.86 and 92.60 respectively. The averages of Kappa indexes of GM segmentation of these techniques are: 88.61, 91.1, 90.9 and the proposed-algorithm is 91.5. The amounts of kappa indexes demonstrate that the proposed. In terms of application, our method can be helpful in the case of low contrast images with low contrast tissue boundaries. Extension of proposed method for disease detection is the next challenging task for future.

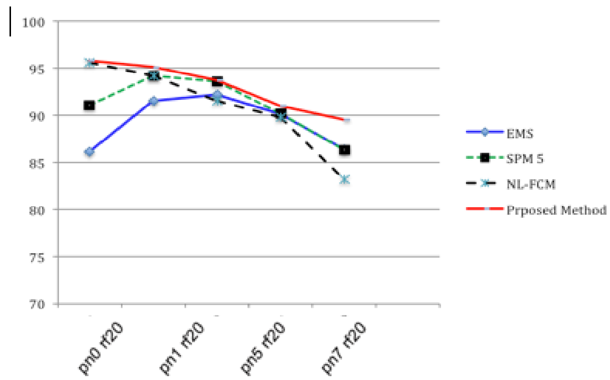


Figure 4 Kappa indexes for the synthetic images. Top to bottom: The Kappa indexes of WM segmentation of the brainweb dataset

■4.0 CONCLUSION

In this paper, we proposed a hybrid method for brain MRI segmentation, by a new combination proposed GLCM and SVM. The experimental results indicate that this method can improve the overall segmentation performance.

This is because the proposed method takes the advantages of the classification ability of machine learning method, in addition to location information, which are consequential information to classify the bran in a 3D MRI into the multiple classes.

In order to investigate the proposed technique, it has thus been used to brain tissue segmentation using brainweb dataset, creating satisfactory results with respect to segmentation performance. The experiments demonstrated that the segmentation results are much closer to ground truth. Incorporating spatial techniques like GLCM approach into the proposed method could lead to interesting alternatives.

The proposed technique not only preserves the simplicity, but also has the potential to generalize to multivariate versions adapted for classification-applying multimodality scans. The experiments run on different noise level and 20% inhomogeneity on Brainweb MRI. These experiments show the robustness and precision of our approach in the presence of bias field and different levels of noise.

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