Statistical Structure Analysis in MRI Brain Tumor Segmentation

Xiao Xuan, Qingmin Liao
Department of Electronic Engineering and Graduate School at Shenzhen
Tsinghua University, China.
xuanxiao@mails.thu.edu.cn

Abstract

Automated MRI (Magnetic Resonance Imaging) brain tumor segmentation is a difficult task due to the variance and complexity of tumors. In this paper, a statistical structure analysis based tumor segmentation scheme is presented, which focuses on the structural analysis on both tumorous and normal tissues. Firstly, 3 kinds of features including intensity-based, symmetry-based and texture-based are extracted from structural elements. Then a classification technique using AdaBoost that learns by selecting the most discriminative features is proposed to classify the structural elements into normal tissues and abnormal tissues. Experimental results on 140 tumor-contained brain MR images achieve an average accuracy of 96.82% on tumor segmentation.

1. Introduction

Automated MRI brain tumor segmentation provides useful information for medical diagnosis and surgical planning. However, it is a difficult task due to the large variance and complexity of tumor characteristics in images, such as sizes, shapes, locations and intensities. So in practice, segmentation of brain tumor continues to depend on manual tracing and delineating. Many image processing techniques have been proposed for MRI brain tumor segmentation, such as deformable model [1], fuzzy connectedness [2] and atlas-guided method [3]. Most of the previously-reported work falls into the category of pattern recognition methods [4-6]. The key issue of successful pattern recognition methods is to extract effective features. Intensity-based statistical features are the most straightforward and have been widely used [4]. But due to the complexity of the pathology in human brain and the high quality required by clinical diagnosis, only intensity features can not achieve acceptable result. Thus many texture features have been presented for tumor segmentation. Co-occurrence matrix [5] and wavelet-based texture features [6] are often used and achieve promising results. The problem in most previous work is the lack of effective feature selection strategies. Texture features are usually in large dimensions, but not each dimension can provide useful information for the segmentation.

In this paper, a statistical structure analysis method is presented and applied to MRI brain tumor segmentation. Firstly, MR images are divided into small structure elements, and then three different kinds of features are extracted from each element, which quantify the intensity, symmetry, and texture properties of different tissues. Secondly the AdaBoost algorithm is performed to select the most discriminative features and classify tumor and normal structures. AdaBoost introduced in 1995 by Freund and Schapire [7], has been applied to solving many machine learning problems. Xin Yuan, et al. [8] used AdaBoost to select texture features for microcalcification detection in mammography; Oriol Pujol, et al. [9] presented an ultrasound vessel segmentation method based on AdaBoost feature selection; Anant Madabhushi, et al. [10] applied AdaBoost to prostatic adenocarcinoma detection. However, the application of AdaBoost in medical image analysis is still rare, especially in MRI brain tumor segmentation. We apply AdaBoost to our problem due to its merit of the feature selective ability. Compared with other feature selection methods such as PCA, the features selected by AdaBoost have specific physical meanings and lower computing cost.

In the following section, the statistical structure analysis method is firstly presented in section 2, including the structure elements division, feature extraction, selection and classification. Section 3 applies the presented method on tumor segmentation and experimental results are shown and discussed. Finally, the conclusion is given in section 4.

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2. Methodology

The main idea of our method is to view the image as structure elements rather than pixels, because it is difficult to determine which tissue a pixel represents if you only focus on the pixel, but it is much easier when the structure information of the pixel's neighborhood is considered. In this paper, each pixel together with a small square neighborhood is defined as a structure element, which is called 'block'. Further steps are all based on the blocks. For training process, firstly, 3 kinds of features are extracted block by block in one image. Secondly, AdaBoost algorithm is applied to select the most discriminative features and design a classifier to categorize the blocks into normal and tumorous groups. When a new image comes, only those selected features are extracted and the trained classifier is used to categorize the tumor in the image. The training and detection process flow of the proposed method is shown in figure 1. It should be noticed that the input images are preprocessed beforehand, including skull stripping which eliminates the skull from the brain image and scale normalization to adjust the intensity scale of the input images.

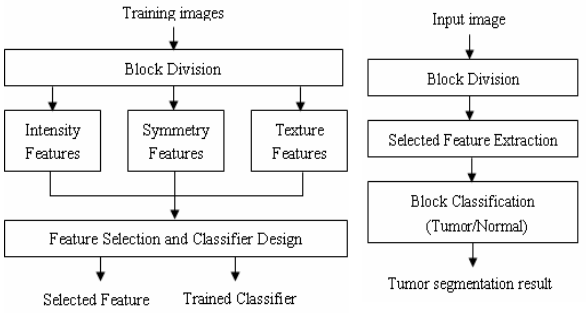

Figure 1. **(Left) The training process flow (Right)The tumor segmentation process flow**

2.1. Block size

The block size must be chosen carefully. If it is too small, the block cannot show the characteristics of structures; if it is too big, it will include too many kinds of structures and also increase the computing cost. In this paper, the basic rule to select the block size is to make sure the blocks which locate within white and gray matters include gyri, because gyri contain important texture information of white and gray matters.

The block size is determined as follows: first, erode the skull stripped T2 MR brain image to find a curve that is parallel to the contour of the brain. The intensity signal along the curve is shown in Figure 2, in which the peaks are gyri in the image. Then the mean distance M of every two neighbor peaks is calculated, and the size of the block is defined as $M \times M$.

In the experiment on 140 MR brain images from 10 adults, we found that the result varies little (25 ± 1 pixels), so it is reasonable to use fixed block size rather than a variable one. Furthermore, the fixed block size is easy for computing and further processing such as feature extraction and classification.

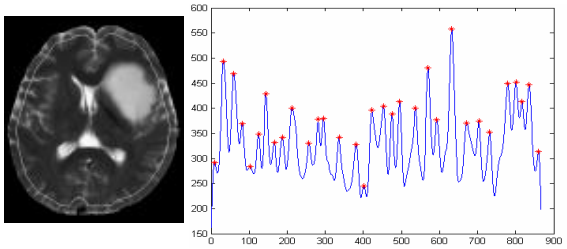

Figure 2. **(Left) The detected curve (white curve) that parallels to the brain contour. (Right) The intensity signal along the curve, * marks the peak point.**

2.2. Feature extraction

2.2.1 Intensity-based features

10 intensity-based statistical features are extracted from each block, including the mean intensity, maximum intensity, minimum intensity, range (maximum intensity minus minimum intensity), central pixel's intensity, variance, standard variance, median intensity, skewness, and kurtosis. The intensity values directly reflect the physical characteristics of tissues in MRI, however, different tissues may have overlapping of intensity values. In order to achieve good segmentation performance, other information such as anatomic knowledge should also be considered.

2.2.2 Symmetry-based features

A remarkable characteristic of normal brain MR images is the symmetry of two cerebral hemispheres. The brain image with tumor will turn asymmetric because tumor usually occurs in one cerebral hemisphere and holds the normal structure's place. The simplest way to detect the asymmetry is subtracting one hemisphere from the other pixel by pixel. However, the human brain is not exactly symmetric, and there are always some slight variances. Thus in this paper, an asymmetry map S is calculated based on the original MR image I.

$$S(i,j) = \min_{(k,l)\in N(i',\ j')} |I(i,j) - I(k,l)| \quad (1)$$

(i', j') is the symmetric pixel of (i, j); $N(i', j')$ is a small neighborhood of pixel (i', j'), defined by equation (2); δ is the radius of N, which is a small value selected empirically.

$$N(i',j') = \{(k,l) \mid \|(k,l),(i',j')\| \le \delta\} \quad (2)$$

The symmetry-based feature is defined as the asymmetry map S value of the central pixel in each block.

2.2.3 Texture-based features

In normal MR brain images, the relative positions of different tissues are generally fixed, so there are certain texture patterns within one tissue and among different tissues, such as the gyrus, which is important for detecting white and gray matters. Homogeneous texture descriptor (HTD) in MPEG-7 is applied to this work to represent the block texture [11]. Since HTD can capture the most salient features of a texture pattern, different texture patterns in one image can be distinguished by it.

HTD is extracted by Gabor filter banks which partition the frequency space with equal angle of 30 degrees in angular direction and with octave division in radial direction. According to some previous results, the best numbers of angular and directional parameters are 6 and 5 respectively, resulting in 30 channels in total.

In each channel, the following 2-D Gabor function is applied to filter the image:

$$G_{\rho_s,\gamma}(\omega,\theta) = \exp[\frac{-(\omega-\omega_s)^2}{2\sigma_{\rho_s}^2}]\exp[\frac{-(\theta-\theta_r)^2}{2\sigma_{\theta_r}^2}] \quad (3)$$

where $\{\omega_s = \omega_0 2^{-s}$, s = 0, 1, 2, 3, 4$\}$ are the center frequencies in the radial direction, and ω_0 is the center frequency of the highest frequency channel, specified by 3/4. The corresponding bandwidths are $\{B_s = B_0 2^{-s}$, s = 0, 1, 2, 3, 4$\}$, and B_0 is the largest bandwidth specified by 1/2. $\{\theta_r = 30^\circ \times r$, r = 0, 1, 2, 3, 4, 5$\}$ are the center angles in the angular direction. In addition, $\sigma_{\rho_s} = B_s/(2\sqrt{2\ln 2})$, where σ_{θ_r} is a constant $30^\circ/(2\sqrt{2\ln 2})$.

After filtering, the first and second moments in 30 frequency channels are computed, to compose the HTD represented as a 60-dimensional vector.

Accordingly, 3 kinds of features are extracted, which describe the structure's information of intensity, symmetry and texture. These features certainly have some redundance, but the purpose of this step is to find the potential useful features. In the next step, the feature selection will be performed to reduce the redundance.

2.3. AdaBoost

As the feature extraction strategy mentioned above, 3 kinds of features are extracted. However, not all the features are equally effective. AdaBoost learns the classification by selecting only those individual features that can best discriminate among classes. Furthermore it provides a final classifier as well as the feature selection strategy.

The AdaBoost algorithm takes as input a training set $(x_1, y_1), \cdots, (x_m, y_m)$, where each x_i belongs to the feature space X, and each *label* y_i is in label set $Y = \{-1, +1\}$. -1 represents normal structures, and +1 represents tumorous structures. AdaBoost calls a given weak classifiers repeatedly in a series of rounds $t = 1, \cdots, T$. One of the main ideas of the algorithm is to maintain a distribution or a set of weights over the training set. The weight of this distribution on training example i on round t is denoted by $D_t(i)$. Initially, all weights are set equally. On each round, the most effective weak classifier is selected based on the current distribution, then the weights of incorrectly classified examples are increased so that the weak classifier is forced to focus on the hard examples. The final classifier is created by combining the weak classifier selected on each round. The outline for AdaBoost is given as below [7].

Given $(x_1, y_1), \cdots, (x_m, y_m)$ where $x_i \in X, y_i \in Y = \{-1, +1\}$

- Initialize $D_1(i) = 1/m$.
- For t = 1, …, T: choose the classifier h_t: $X \to \{-1, +1\}$ with minimum classification error $\varepsilon_t = \sum_{i=1}^{m} \omega_i |h_t(x_i) - y_i|$;
- $\alpha_t = (1/2)\ln[(1-\varepsilon_t)/\varepsilon_t]$; $D_{t+1}(i) = [D_t(i)\exp(-\alpha_t y_i\, h_t(x_i))]/Z_t$ where Z_t is a normalization factor (chosen so that D_{t+1} will be a distribution).
- Output the final classifier: $H(x) = sign(\sum_{t=1}^{T} \alpha_t h_t(x))$.

If on each round, only one feature is used to do the classification, the algorithm is also a feature selection process. In this work, h_t is defined as equation (4)

$$h_t(x_i) = \begin{cases} 1, & f_t(x_i) < \mathrm{P}_t \\ -1, & otherwise \end{cases} \quad (4)$$

where f_t is the feature selected on the tth round, and it should be set to 0 on the next round; P_t is the threshold with the minimum classification error for f_t.

3. Experimental results

We conducted our experiments on MR images from 10 different patients with gliomas. Each patient has 3 volumes of MR images, T1, T2, and FLAIR. Each volume contains 24 slices in axial plain with 5 mm slice thickness. MR imaging was performed on 3.0T Siemens devices. The imaging conditions of different protocols are: T1 weighted (TR=1680ms, TE=13ms, TI =800ms), T2 weighted (TR=5800ms, TE=103ms)

and FLAIR weighted (TR=9000ms, TE=100ms, TI=2500ms).

According to section 2, firstly the images are divided into small structure elements (blocks), and then 3 kinds of features are extracted from each block. It should be noticed that all the features are extracted respectively from multi-protocol MR images, T1, T2 and FLAIR, so the dimension number should be multiplied by 3. In total, a 213-dimensional feature vector is extracted from each block.

Half of the experimental images are selected randomly as the training set and another half constitute the test set. The ground truth is the tumor contour delineated by experienced doctors. From all the training images, 40000 blocks (20000 positive and 20000 negative) are extracted to train the AdaBoost classifier. Positive means normal tissues and negative means tumorous tissues. In order to test the classifier, 40000 blocks (20000 positive and 20000 negative) are extracted from the images in test set.

The training and test error curves of the AdaBoost classifier as a function of the boosting round number are shown in figure 3. The curves indicate that along with the increasing of rounds, the training error tends toward zero, but after the number of rounds exceeds 40, the test error does not change much any more, which means the left features can not provide more information for classification. So when processing a new image, we only need to extract 40 selected features, and use the classifier created by the first 40 rounds of AdaBoost algorithm.

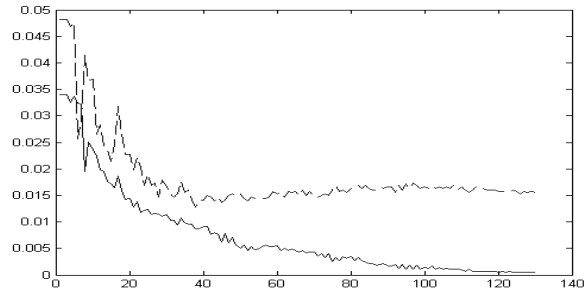

Figure 3. **(Lower) AdaBoost training error curve (Upper) Test error curve**

In all the 40 selected features, there are 13 intensity-based features, 1 symmetry-based feature, and 26 texture-based features. It proves that the 3 kinds of features extracted in our work are all useful for the classification. Besides, the distribution of the 40 features in different protocols, T1, T2, and FLAIR, are 9, 12, 19 respectively. It means FLAIR provides the most information for tumor segmentation, T2 provides less and T1 provides the least. This result is in accordance with the conclusion in medical imaging, that FLAIR and T2 are more sensitive in pathological discrimination than T1. The distribution of the selected features is shown in table 1.

Table 1. **The distribution of selected features**

Number of Features	T1	T2	FLAIR	Total
Intensity Features	2	5	6	13
Symmetry Features	0	0	1	1
Texture Features	7	7	12	26
Total	9	12	19	40

On each round, AdaBoost selects a weak classifier with the minimum classification error in current distribution. Each weak classifier has a weight which determines its effectiveness in the final strong classifier. One weak classifier is produced by one feature, so the weight value also represents the importance of the feature for segmentation. 3 features with the highest weights selected by AdaBoost (denoted by *F1*, *F2*, and *F3*) together with the original MR images are illustrated in figure 4 respectively. *F1* is the texture feature extracted from FLAIR image with ω_s =3/4 and $\theta_r = 90^o$. *F2* is the maximum intensity value extracted from T1 image. *F3* is the median intensity value extracted from T2 image. Tumorous tissues have relatively high *F1* values but most necrotic tissue included inside the tumor and cerebral fluid are relatively low. *F2* is able to discriminate the necrotic tissue and *F3* provides the information about cerebral fluid. So these 3 features contribute irrelevant and complementary information to the tumor segmentation.

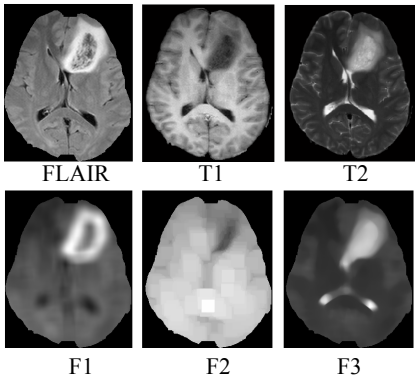

Figure 4. **Original MR images(upper line) and 3 most effective features selected by AdaBoost *F1*, *F2* and *F3*(lower line)**

Using the 40 selected features, the block classification accuracy on the test set by our algorithm is 98.74%. We compared this result with kNN (k nearest neighbors) algorithm and SVM (Support Vector Machine), which are widely used in medical image analysis. On the same training and test set, classification accuracies achieved by AdaBoost, kNN and SVM are shown in table 2. While using the 40 selected features, the accuracy on the test set by AdaBoost is 98.74%, which is better than 98.48% by kNN (choose k=7 which achieves the best result while ranging from 1~15) and 98.69% by SVM. The differences among three methods are not remarkable, but AdaBoost performs slightly better. The reason is that AdaBoost set different weights to different features, but kNN and SVM deal with all the features equally. Especially in this problem, features have different dimensions and physical meanings, setting appropriate weight to each feature may achieve good results. If all the 213 features are used without selection, the classification result of AdaBoost has no change, but the accuracies of both kNN and SVM decrease significantly. The phenomenon shows that the redundancy and correlation exist in the 213 features, and influence the classification. The feature selection by AdaBoost is able to eliminate this kind of influence, and in the same time increase the efficiency of computing.

Table 2. **The classification accuracy of AdaBoost, kNN and SVM**

Classification accuracy	With feature selection	Without feature selection
AdaBoost	98.74%	98.55%
kNN	98.48%	95.47%
SVM	98.69%	96.46%

Some tumor segmentation results by the method presented in this paper are shown in figure 5. It can be observed that the results are very close to the delineations by doctors, which means our method is effective in MRI brain tumor segmentation. The correct rate, false positive rate (*FP*) and false negative rate (*FN*) of tumor segmentation are defined as below:

$$FP = \frac{false\ positive\ pixel's\ number}{tumor\ size} \quad (5)$$

$$FN = \frac{false\ negative\ pixel's\ number}{tumor\ size} \quad (6)$$

$$correct\ rate = FP + FN \quad (7)$$

The average correct rate by the presented method is 96.82%, with *FP* of 1.3% and *FN* of 3.69%. The main factor influencing the accuracy is the presence of edema, which leads to high *FN* value, because the edema usually occurs beside the tumor and has similar appearance to the white matter. Both tumor and edema are abnormal tissues, so doctors are inclined to include the edema when delineating the tumor contours. We compared our method to ACM (Active Contour Model) based and fuzzy connectedness based segmentation methods. The segmentation results on the same test set are shown in table 3. ACM is widely used in image segmentation, and the principle of which is to evolve the contour curve until it achieves the lowest energy. Fuzzy connectedness based segmentation method firstly calculate the fuzzy connected component of each pixel to the seed point using both intensity and space information, and then segment the fuzzy connected component image by region growing or threshold. In this paper, the seed point and the optimal segmenting threshold are manually selected. In table 3, it can be observed that our method performs better than both ACM and fuzzy connectedness based methods in tumor segmentation. The *FN* of our method is much lower than the other two methods. Because ACM and fuzzy connectedness methods both rely on some edge information between tumor and normal tissues, but the presence of edema obscure the edge between tumorous and normal tissues. The above comparison proves the effectiveness of the structure analysis in our method, which is able to discriminate tumor and normal tissues by comprehensive information.

Table 3. **The segmentation accuracy of our method, ACM and fuzzy connectedness based method**

Segmentation Accuracy	*FP*	FN	Correct rate
Our Method	1.3%	3.69%	96.82%
ACM	1.84%	7.51%	90.65%
Fuzzy Connectedness	2.95%	5.02%	92.04%

4. Conclusions

Automated MRI brain tumor segmentation is a useful technique for diagnosis. In this paper, a statistical structure analysis method and its application to MRI brain tumor segmentation is presented.

The method mainly includes 3 steps: structure elements subdivision, feature extraction, feature selection and classification. Experimental results demonstrate the features selected by our method can contribute effective and complementary information to discriminating tumor and normal tissues. The selected features include intensity, symmetry and texture based features extracted from multi-protocol MR images. By

the comparisons with kNN and SVM methods, it shows that feature selection reduces the dimensionality of the feature space and improves the performance of the classifier. The proposed method performs better than the existing segmentation methods such as ACM and fuzzy connectedness based methods, and achieves very accurate segmentation results. In the future, the application of the presented method to multi-tissue segmentation will be considered, and the information of new imaging techniques such as fMRI will be added into the scheme to achieve more accurate results.

5. References

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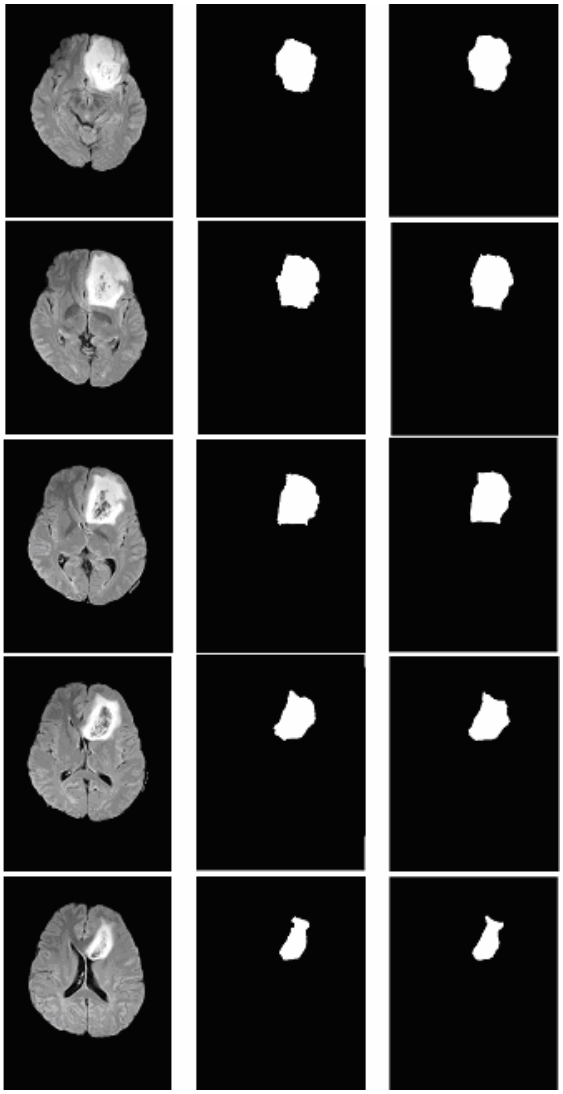

Figure 5. **(Left column) Original FLAIR image; (Middle column) Tumor segmentation result by our method; (Right column) Ground truth**