TUMOR SEGMENTATION FROM A MULTISPECTRAL MRI IMAGES BY USING SUPPORT VECTOR MACHINE CLASSIFICATION

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ABSTRACT

The goal of this paper is to present a supervised system aimed at tracking the tumor volume during a therapeutic treatment from multispectral MRI volumes. Four types of MRI are used in our study: T1, T2, Proton Density (PD) and Fluid Attenuated Inversion Recovery (FLAIR). For decreasing the processing time, the proposed method employs a multi-scale scheme to identify firstly the abnormal field and extract then the tumor region. Both steps use Support Vector Machines (SVMs). The training is carried out only on the first MRI examination (at the beginning of the treatment). The tracking process at the time point \( t \) takes the tumor region obtained in the examination at \( t-1 \) as its initialization. Only the second step is performed for others examinations to extract the tumor region. The results obtained show that the proposed system achieves promising results in terms of effectiveness and time consummating.

1. INTRODUCTION

Magnetic resonance imaging (MRI) is a highly successful diagnostic imaging modality, largely due to its ability to derive contrast from a number of physical parameters. The different types of MR images obtained from the different of excitation sequences, also called multispectral images, can provide different image intensity information for a given anatomical region and subject. As a tumor consists of different biologic tissues, one type of MRI cannot give complete information about abnormal tissues. Therefore, radiology experts always combine the multispectral MRI volumes of one patient to take a decision on the location, extension, prognosis and diagnosis of the tumors. That is why it is necessary to fuse multispectral MRI information to segment tumor regions.

Accurate and robust brain tissue segmentation is a very important issue in many applications of medical image system for quantitative studies and particularly in the study of some brain disorders [1]. One example is to analyze and estimate quantitatively the growth process of brain tumors, and to evaluate effects of some pharmaceutical treatments in clinic. As known, manual tracing by an expert of a tumor in 3D for all types of MR modalities involved in studies is not only exceedingly time consuming, but also exhausting for experts leading to human errors. Therefore, a segmentation tool with minimum manually intervention is necessary. A lot of studies of brain segmentation have been carried out and are reported in the literature. The methods based on elastic registration using elastic matching techniques, or deformable models [2] have proven the efficiency for small and local shape changes, especially for normal tissue segmentation. The methods based on statistical models, such as Gaussian intensity models [3], explicit models [4], Markov random field models [5] work well in case of normal tissue segmentation. In the pathological cases, the methods based on supervised or unsupervised classification integrating anatomical templates [6] have shown their robustness. Level set methods are also used for brain tumor segmentation [7] with some successes. Mancas and Gosselin [8] used the iterative watersheds to segment the brain tumor with a given initialization. Based on the concept of fuzzy logic, Dou [9] used the fuzzy fusion technique for the abnormal tissue segmentation and classification. Kernel based methods such as SVMs [10] have gained much attention from the machine learning and pattern recognition community in recent years. It is also developed for tumor segmentation with some success [11].

In conclusion, the full automatic segmentation of tumor tissues is still a difficult problem. The use of the experiences of the experts to get learning data sets can allow to increase the segmentation precision. In addition, the leaning processes can be done by a very essay and quick way. The proposed method is based on this idea. The learning is only applied to one type of MRI image at one time point. In
general, SVM may pose heavy computational challenges for large data sets. As four types of MRI data are used in our study, the time costing is a problem for a real application. Therefore we propose a SVM based classification using a two-steps with multi-scales to decrease the processing time. The first step consists in cutting the image into a set of small windows, and then classifying these windows by using the SVM classifier that uses the texture parameters of each window, such as mean and variance. An abnormal field is obtained after this first step. Based on this field, the SVM is again performed in each pixel by using intensity information to obtain precisely the tumor region. The paper is organized as follows: in the next section, We present an overview of the segmentation framework from multiple MR image sequences. Then section 3 shows the principal of the SVM classification. Some experiment results using four routine MRI sequences are shown in section 4. We finally conclude in section 5.

2. OVERVIEW OF THE SEGMENTATION SYSTEM

The framework consists of 4 main steps (Figure.1): registration, learning, classification base on SVM, quantification of the tumor volume variation. The software SPM [12] is used to register the all data sets. The learning is carried out on one slice of the Flair MRI data using the mouse to chose some tumor pixels and non tumor pixels. As all data sets are registered, the learning on the others types of MRI data can be automatically done. The information to be learned concerns about the mean and the variance of the window, and the intensity of the pixel. The first classification step consists in cutting each slice into a set of small window and classifying them into two classes: tumor and non tumor. Each window includes in fact four ones relative to four types of MRI. Therefore the SVM uses the information of the four windows to classifier. As the classification is carried out only to the windows, it works quickly. However the low scale does not lead to a good precision. The second step is necessary to perform to obtain better results. It consists in finding the abnormal field which is formed by a set of connected windows by 8 convexity. The SVM is again applied only on the abnormal field to classifier this time each pixel which represents four intensities corresponding to the four types of MRI data.

When the patient is asked to do another examination after the first one. The tracking of the tumor uses only the second classification step, because the tumor region obtained in the precedent examination is considered as the initial field. The quantification of the volume variation provides the important information to evaluate the current medical treatment.

Figure 1. Over view of the proposed framework

3. SUPPORT VECTOR MACHINE

Founded on the Statistical Learning Theory [10], SVMs are currently the state-of-the-art algorithm for solving binary classification problems and have shown excellent results for various pattern recognition tasks. The Support Vector Machines algorithm exploits kernel functions for nonlinear classification. A kernel is a function $K : \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R}$ such that for some mapping function $\Psi : \mathbb{R}^n \to \mathbb{R}^m$, the value of the dot product in $\mathbb{R}^m$ can be computed by applying $K$ to vectors in $\mathbb{R}^n$:

$$K(u,v) = \langle \Phi(u), \Phi(v) \rangle, \quad \forall u,v \in \mathbb{R}^n$$

Given a training set of $N$ pairs $\{(x_k, y_k)\}_{k=1}^N$, where $x_k \in \mathbb{R}^n$ are observations and $y_k \in \{-1, 1\}$ are corresponding labels, SVMs find the discriminating hyperplane that separates the classes with maximal margin, i.e. maximal distance to the nearest examples, by optimizing the classification function:

$$f_K(x) = \sum_{k=1}^N \alpha_k y_k \langle \Phi(x)\Phi(x_k) \rangle + b = \sum_{k=1}^N \alpha_k y_k K(x,x_k) + b$$

In the higher dimensional space defined by the mapping $\Phi$, the separation boundary is a hyperplane whose normal is a linear combination of $\Phi(x_k)$'s:

$$w = \sum_{k=1}^N \alpha_k y_k \Phi(x_k)$$

but it can be an arbitrary complex surface in the original space. In case of such separating hyperplane does not exist, we introduce a so called slack variable $\xi_k$ such that:

$$f_K(x) = \sum_{k=1}^N \alpha_k y_k \langle \Phi(x)\Phi(x_k) \rangle + b + \xi_k$$
Optimizing the classification function becomes the following minimization problem related to:

\[
\frac{1}{2} w^T w + c \sum_{k=1}^{N} \xi_k
\]

Once the optimal values of the parameters \( \alpha \) are obtained, given a new example \( x \), we can classify it according to the following decision function:

\[
y(x) = \text{sign}(f(x))
\]

Different kernels are proposed in the literature to a nonlinear classification. In this work, we use a family of Gaussian kernel functions:

\[
K(u, v) = e^{-\frac{1}{2\sigma^2} ||u-v||^2}
\]

Where the \( \sigma \) determines the width of the kernel. One of the important properties of this family of classifiers is its locality: moving a support vector slightly affects the separation boundary close to the vector, but does not change it in regions distant from the vector. This is a desirable property in the presence of noise in the training examples [13].

4. EXPERIMENTATION

4.1. Data

MRI images are acquired on a 1.5T GE (General Electric Co.) machine using an axial 3D IR (Inversion Recuperation) T1-weighted sequence, an axial FSE (Fast Spin Echo) T2-weighted, an axial FSE PD-weighted sequence and an axial FLAIR. The total number of slices is 124 for T1 images with a voxel size of 0.94×0.94×1.5mm3; 24 slices for T2, PD and FLAIR images with a voxel size of 0.47×0.47×5.5 mm3.

4.2. Training data

The learning is carried out only on the one slice of T2 image which is in the middle of the tumor volume, because of a good visibility. Fifty pixels belonging to the tumor and fifty pixels not are chosen randomly. The learning from others types of MRI images are obtained automatically, because the four volumes are registered. The training data consists of 20 points for each type MRI. For the following MRI examination of the same patient, the new learning is not necessary.

4.3. SVM classification

After learning, the system classifies the MRI data sets according to the decision boundary specified by (6). Because each type of MRI provides useful information, all four types of image volumes are used for classification. That leads to a large data for the SVM. The proposed two-step classification allows us to decrease the time consuming 2.5 times less. In the first classification step, each image of the each volume is cut to a set of windows with a size of 11x11 voxels. The choice of the size does not influence significantly to the final results because a coarse field is needed in this step. As the size of images is decreased five time less, the costuming time of the algorithm decreases also. The parameters used in the SVM classifier are chosen by the experience: \( c = 5 \), \( \sigma = 2 \). The results are shown in the figure.3. Some classification errors can be observed. Any classification method could yield classification errors. To remove errors (figure.3), the method is to merge the connected windows yielding to a set of isolated regions. The big one is chosen as the abnormal field under the assumption of only one tumor in the brain.

The second step performs the classification on each voxel, which is within the obtained field in the first step. The Figure.3 shows the results of this step where the tumor contour in white color is superposed in the input images.

The segmentation results (Figure.4) are acceptable by radiologists in the field.

Based on the learning knowledge of the first examination, only the second step is performed for following examinations to segment the tumor volumes. The same patient in Figure.2 was given another examination six months after, shown in Figure. 5. Using the two segmented tumor volumes, the volume variation can be then easily calculated. The variation of this patient is decreased 15.42% six months after. This measure provides a very important information for the experts to evaluate the medical treatment.

Figure 2. Four registered slices of MRI image data corresponding to: T2 (a), PD (b), FLAIR (c), T1 (d).
4.3. Evaluation

The tumor is manually delineated on 3 slices of each type by an expert to obtain the ground truth. T1 sequence is not taken into account to this manual elaboration due to the bad contrast. Quantitative measurement of segmentation accuracy are then calculated in terms of true positive (TP), false positive (FP) and false negative (FN) with respect to the ground truth. In our experiments, the results achieve a high percentage of correct match to the ground true with TP=98.6%; FP=11.6%, FN=1.4%.

5. CONCLUSION

Segmentation of a concerned region from medical images is a challenging yet unsolved task due to large variations and complexity of the human anatomy and pathological lesions. In this paper, we have presented a brain tumor segmentation based on SVM classification from multispectral MR images. The proposed segmentation approach has the ability of dealing with a large data using a simple learning process. The fact that the classification is carried out in multi-scale allows to decrease significantly the time consuming. The obtained results are confirmed by radiologists in the field. The future work consist of testing and evaluating the algorithm from a large database.

6. REFERENCES