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A NOVEL DETECTION ON AUTOMATIC BRAIN TUMOR TISSUE BASED ON HIERARCHICAL CENTROID SHAPE DESCRIPTOR IN T1-WEIGHTED MR IMAGES

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ABSTRACT

The brain tumor tissue detection allows localizing a mass of abnormal cells in a slice of Magnetic Resonance (MR). The automatization of this process is useful for post processing of the extracted region of interest like the tumor segmentation. In order to detect this abnormal growth of tissue in an image, this paper presents a novel scheme which uses a two-step procedure; the k-means method and the Hierarchical Centroid Shape Descriptor (HCSD). The clustering stage is applied to discriminate structures based on pixel intensity while the HCSD allow to select only those having a specific shape. A bounding box is then automatically placed to delineate the region in which the tumor was found. Compared to the tumor delineation performed by an expert, a similarity measure of 91% was reached by using the Dice coefficient. The tests were carried out on 254 T1-weighted MRI images of 14 patients with brain tumors.

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INTRODUCTION

Magnetic Resonance Imaging is a standard modality used in medicine for brain diagnosis and treatment. It offers the advantage to be a noninvasive technique that enables the analysis of brain tissues. The early detection of tumor in the brain leads on saving the patients' life through proper care. Due to the increasing of medical data flow, the accurate detection of tumors in the MRI slices becomes a fastidious task to perform. Furthermore the tumor detection in an image is useful not only for medical experts, but also for other purposes like segmentation and 3D reconstruction. The method proposed in this work allows to automatically and accurately detect the abnormal tissues in preoperative images. The manual delineation and visual inspection will be limited in order to avoid time consumption by medical doctors. The automatic detection and segmentation of brain tumor plays an important role in medicine because it leads to critical decisions. In these past years, several works were focused on this problem which is not entirely solved. Therefore, our contribution by this work is the automatic detection of the tumor in T1-weighted Magnetic Resonance Images by using a

robust method against shape variation, texture, size, pixel intensity and tumor location. For achieving this goal, the k-means algorithm was associated with a shape feature based on hierarchical centroids. A preprocessing step is performed for removing the skull and extracting only the brain. The brain anatomy can be classified based on its intensity in three groups. If pathological tissues like tumors appear, the group number increases to four and contains the Gray Matter (GM), White Matter (WM), Cerebrospinal Fluid (CSF) and the tumor. But because the CSF has a low intensity in T1-weighted modality, it is generally classified in the same cluster that the black background image. Hence, the cluster number is settled as $k=4$. The remainder of this paper is structured as follows. Section 2 presents some previous works related to the brain tumor. Section 3 describes the cooperation of the k-means algorithm and the hierarchical Centroid Shape Descriptor in order to select accurately the target tissue. In Section 4, the results show the improvement of brain tumor detection by using the proposed approach. Finally, Section 5 gives conclusions.

Related Work

In [4], the authors show that the automatic tumor detection can be achieved by using some features like texture, shape, intensity and symmetry. Different kinds of tumors lead to an

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inhomogeneity of their sizes, shapes, textures, locations and intensities, whence the automatic detection of abnormal tissues is a challenging task. An automatic brain tumor detection technique was presented by [5], which incorporates the methods of modified texture based region growing and cellular automata edge detection. A stochastic model to extract tumor texture was proposed in [6]. However, the use of the texture by itself is not sufficient because some real data do not have enough texture features leading to unsatisfying results. The variety of tumor texture can generate a confusion with other tissues if considered alone. The Fuzzy C means algorithm is used in [7] for classifying brain tumor images and it works well for tumor detection. Like the mean-shift [8], this method has a high computation complexity; however it is suitable when the number of clusters are unknown a priori. In [9], the brain symmetry was used for tumor segmentation and detection by using the texture and intensity. Another automatic method for tumor detection based on the brain symmetry is introduced by [10]. The application of this kind of feature is limited on axial and coronal planes because there is no symmetric structures in the sagittal plane.

The authors in [11] propose to classify brain image as normal or abnormal by using neural network. The work realized by [12] describes a computer-aided detection system for detecting tumors. This framework is based on histogram equalization and morphological mathematical operations. The mentioned experiments were performed on 125 MR images. The Watershed segmentation method is presented in [13] for brain tumor detection. In [14] the thresholding method of Otsu associated with the Particle Swarm Optimization algorithm for maximizing the optimal threshold values was applied on medical images for tumors detection.

MATERIALS AND METHODS

The presence of pathological structures in the brain often leads to inaccurate results. As applied in various works [15]– [18], the thresholding technique and the morphological operations such as erosion, dilation, closing and opening are used in a pre-processing step for skull removing. To overcome the ineffectiveness of algorithms to automatically detect and localize tumor in human brain, we propose to use the k-means clustering method followed by the selection of the shape that can better describe the tumor. The choice of the k-means algorithm was motivated by the a priori knowledge of number of cluster for brain tissues and its low computational complexity. The Otsu algorithm [19] was also tested on this first stage and it provided results close to the those obtained with the k-means technique. By classifying pixels based on their intensities, the highlighted structures like tumors are found in the high intensity cluster. The image is binarized by using a threshold value in order to keep only pixels in the *k*th cluster. Considered as the first step of our method, some studies [20]–[22] show that this is sufficient for brain tumor detection while many times with real data, not only abnormal tissues are always selected. Due to this, a second stage is necessary for brain tumor detection task as shown in Fig. 1. In order to discriminate healthy tissues misclassified in the cluster of interest, a flexible descriptor based on the kd-tree decomposition algorithm [23] is used to select only tumor structures. This strategy enables to extract centroid-based Tree structure features as illustrated in the Fig. 3.

The vector obtained through the k-d tree decomposition process is described as

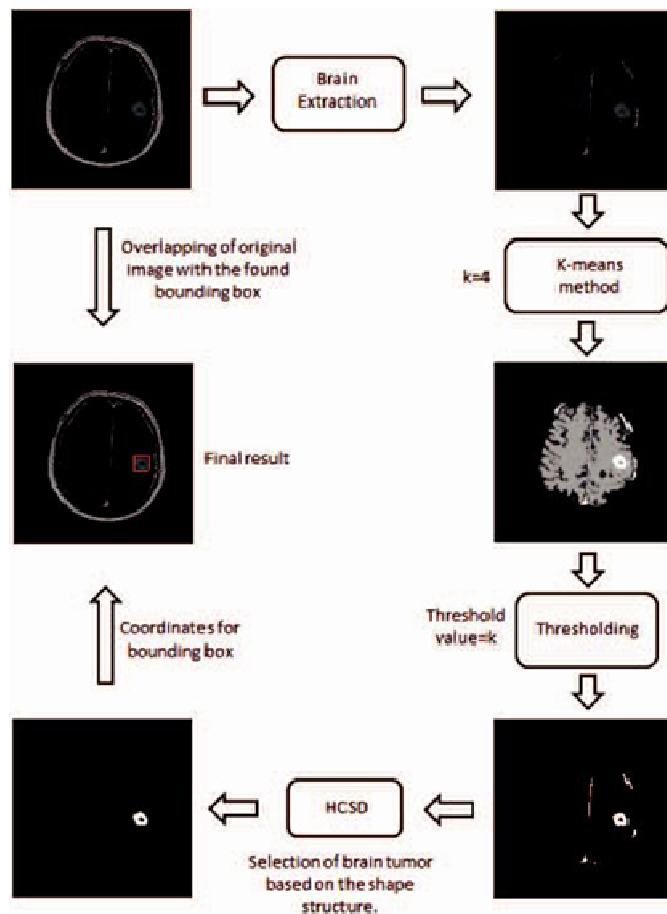


Figure 1. Proposed tumor detection algorithm

$$v = (x_0^0, y_0^1, y_1^1, x_0^2, x_1^2, x_2^2, x_3^2, y_0^3, y_1^3, \dots, y_7^3) \dots\dots\dots(a)$$

where x_0^0 represents the root level coordinate, y_m^n the *m*th *y* coordinate at level *n* and x_m^n the *m*th *x* coordinate at level *n*.

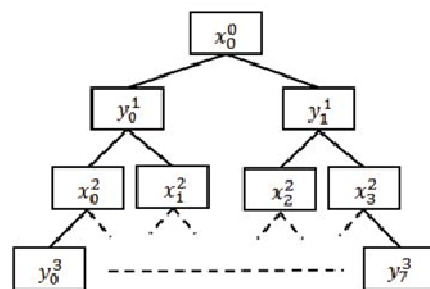


Figure 2. K-tree decomposition structure

k-means

Introduced by [24], the k-means received many contributions as in [25], [26] and it is one of the most popular clustering algorithms. Given y_i a vector of data ($i= 1..n$), the classification of its elements in *k* clusters starts by randomly defining *k* points as centroids of each regroupment in the data space. By an iteration process the elements are associated to the closest barycentre in *k* groups. By using (2), the groups means are updated by considering the new elements belonging

to each of them. The method seeks to minimize an objective function described as the sum of squared errors.

$$J = \sum_{j=1}^k \sum_{i=1}^n x_i^{(j)} \mu_j^2 \tag{2}$$

where μ_j is the centroid of the cluster c_j and x_i the data points that it contains. The metrics like Euclidean distance, Minkowski distance, cosine measure distance and Manhattan distance are often chosen for the minimization of the objective function. The data grouped in a cluster have a high similarity measure to the centroid, in other words they have a minimum distance to the mean point.

Hierarchical Centroid Shape Descriptor

The HCSD is a binary shape descriptor built with the centroid coordinates extracted from a binary image and it is based on the kd-tree technique decomposition. Presented in [27] and based on [23], the HCSD is a shape descriptor extracted recursively by decomposing the image in sub-images. Because an image can be described by the spatial distribution of pixels, this method is based on an image decomposition in the pixel domain by using the kd-tree algorithm. The neighborhood information like the centroid coordinates of local regions is extracted. A similar descriptor was proposed by [28]. The descriptor length is $2 \times (2^d - 2)$ where d is the depth of the features extraction process. The Fig .4 illustrates how the centers of gravity are extracted and the manner in which the image is divided. Let I the $M \times N$ binary image with foreground I_{fg} and background I_{bg} , the HCSD is built as follows

- Take the input I and compute its transposed I^T ,
- Calculate for each input, its centroid $C(x_c, y_c)$ at the root level by using (3) and (4).

$$x_c = \frac{m_{10}}{m_{00}} \tag{3}$$

$$y_c = \frac{m_{01}}{m_{00}} \tag{4}$$

where m_{10} , m_{01} and m_{00} are respectively the first order moment along the x-axis, the first order moment along the y-axis and the area of I_{fg} . The moment of order $(p+q)$ (raw moment) of a 2D continuous function $f(x, y)$ is defined as

$$m_{pq} = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} x^p y^q f(x, y) dx dy \tag{5}$$

The raw moments m_{pq} of a digital image with pixel intensities $I(i, j)$ are calculated by

$$m_{pq} = \sum_{i=0}^M \sum_{j=0}^N i^p j^q I(i, j) \tag{6}$$

RESULTS

The results of the proposed method are illustrated in this section. The implementation was done with an Intel Celeron, 1.5 Ghz and 2 GB of memory using Matlab v.2012 tool. All tests were performed on a set of 254 T1-weighted MR images containing brain tumors. These medical images have been provided by the University Hospital, Department of Neurosurgery, University of Leipzig, Germany. In order to validate the proposed method, the delineated detection regions (A) by an expert were compared with the regions obtained by the HCSD k-means method (B) by using the Jaccard $J(A, B)$ and Dice $D(A, B)$ indexes adopted as metrics. Computed on binary images by using (7) and (8), these indexes describe how well two images are similar in a range of [0,1]. The perfect overlapping is obtained when the similarity measure is equal to 1.

$$J = \frac{A \cap B}{A \cup B} \tag{7}$$

$$D = \frac{2(A \cap B)}{A + B} \tag{8}$$

Fig .5.(a) presents some images in which the brain tumors have to be detected and bounded. The structures detected as tumor by using the k-means algorithm are shown in Fig .5.(b). In the Fig .5.(c), the results of our method are presented and show how the tumors are selected among the remaining tissues after applying the k-means clustering. The HCSD k-means method outperforms the results obtained with the one-step method such as k-means or Otsu Multilevel thresholding. In addition, the comparison in Table I presents the average of Jaccard and Dice indexes of all experiments and it shows that the proposed method achieves better results than the two-stage method HCSD Otsu. These similarity measures were calculated by comparing the results observed with the regions bounded by an expert.

The score reached with our method is of 0.842 with the Jaccard index and 0.91 based on the Dice index, and it demonstrates that the proposed approach is effective for brain tumor detection. Several algorithms fail to detect tumor when it has an irregular shape or the image has a low contrast, but Fig. 6 illustrates how the HCSD k-means method is robust in detecting brain tumor tissue even in this kind of data. Unlike various work based on simulated database, the advantage of our study is that it was performed by using real patient data. In addition, the experiments showed the robustness of our technique in the presence of poor image quality (Fig. 7). As depicted in Table I, the use of one-step methods (clustering or thresholding) is not sufficient to achieve good results. However, the association of a method based on pixel intensity with another based on shape, for instance, increases the efficiency. The Otsu and k-means results are very similar because the segmented structures are often identical, but sometime they have different shapes (Fig. 8). In the case where their results are not the same, by applying the HCSD method, the segmented structures through the k-means algorithm have a particular shape allowing them to be selected as tumors compared to those obtained by using the Otsu method. Due to this, the scores difference after the second step between the HCSD Multilevel Otsu and HCSD k-means increases.

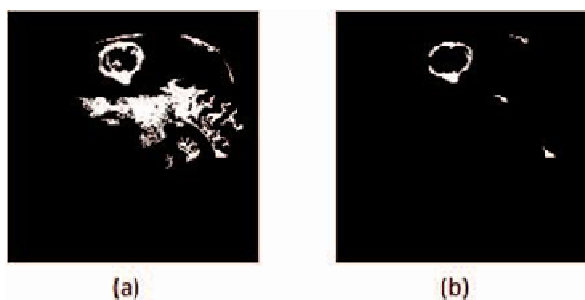


Figure 8. Comparison of the first stage results for two different images: (a) Otsu method and (b) k-means method

Conclusion

In this paper, a two-step method for brain tumor tissue detection was introduced. This method combines the k-means clustering algorithm followed by the use of a shape descriptor based on features called Hierarchical centroids. On the first step, the k-means algorithm groups image pixels in k clusters, then the image is binarized by using a threshold value equal to k . The tumor structures are found in remained binary elements but they are often surrounded by healthy structures. The second step method is used to discard other tissues in order to detect only those corresponding to the tumor. The experimental results have shown that this technique is robust in detecting and bounding the abnormal cells in MRI images despite the inhomogeneity intensity or the complicate shape of the tumor. Unlike one-stage techniques, the proposed approach is robust to the shape change and does not require a big dataset for the training.

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