Brain Tumors Detection on MRI Images through Extracting HOG Features

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Abstract

In this paper, a system of Computer Aided Diagnosis (CAD) is introduced for detecting brain tumors through MRI images. The proposed system consists of three main sections: segmentation, feature extraction, and categorization. In the segmentation phase, a system called Seeded Region Growing (SRG) is applied to separate brain tissue from other regions. In the feature extraction phase, the Histograms of Oriented Gradients (HOG) algorithm is used. Finally, in order to describe the images of the brain, we use Support Vector Machine (SVM) and classify the images in two tumor-free and tumor-grade groups, and then compare them with similar tasks. The results show a high efficiency of this approach compared to other methods. 850 MRI images have been applied to test and teach samples; the number of healthy brains is 300 and the number of defective brains is 550, and the system has achieved a precision rate of 93.2% in the categorization.

Keywords: Tumor detection, Histograms of Oriented Gradients, Feature extraction, Support Vector Machine
1. Introduction

Diseases of the brain like cancerous tumors are among the leading causes of death. High mortality rates caused by brain tumors require early diagnosis and treatment. Due to the complexity of the brain tissue, the traditional approaches for diagnosing brain tissues and cancerous tumor are very time consuming and inefficient. We need the experts to check the images and determine the problems. Therefore, the application of automatic methods will be very useful for accurate examination of brain tumors. Today, there are several techniques of brain imaging like magnetic resonance imaging (MRI) that uses strong magnets to monitor at organs and structures inside the body. It is one of the most common methods in this field [1-2]. The displayed images are usually received as T1 and T2, which have specific features. On T1 images, the white matter appears brighter than other parts and it functions as fat. Gray matter is moderately dark and the property of the Cerebrospinal Fluid (CSF) is similar to water and it appears darker than other tissues. On T2 images, the white matter is dark and the CSF is bright. T2-weighted images that have dense connective tissues tend to be white and bright. This feature makes it easier to detect cancerous tissues because cancer cells grown at high density in the target areas [2-3]. In the field of automatic detection of the brain tumors, many studies have been done and numerous results have been achieved. In the present paper, the method includes preprocessing, segmentation, feature extraction, dimension reduction, feature selection, and categorization through SVM. In order to extract the features, the HOG method is applied, that we explain in Section 3-3.

The preprocessing stage involves normalizing images, removing noise and highlighting the edges [4]. In order to subdivide the images, the SRG algorithm is applied, which is based on the Region Growing. It is the most important algorithm that acts based on the comparison of the color intensity of the pixels [5].

Feature extraction is the process of recovering the most important data of raw materials. There are various approaches for feature extraction, including Wavelet Transform [6, 7, 8], Gabor Filter [9], Image Blocking [11], Brain Symmetry and Static Features [12], Statistical Approaches [13], Fourier Transform [14] and many other ways which have different functions [15]. In this paper, the HOG is applied to extract the features of brain MRI images.
We reduce the dimensions through Principal Component Analysis (PCA) and extract the best features and then, we use SVM to do classification in order to detect tumorous MRI images of the from healthy ones.

1.1. Literature Review

An approach of automatic detection for brain tumors was offered in which the k-means clustering algorithm was applied to tag the objects in the brain. In the first stage, pre-processing including normalization, noise removal and histogram balancing was performed. Then, the objects were tagged as three classes of spinal cord, which was referred as the tumor, white matter and gray matter. As a result, the accuracy rate of 90% in tumor detection was reported (Vijay et al. 2009) [18].

Another approach proposed by Sharma et al. (2012) was Brain Tumor Segmentation which has four stages of preprocessing, image segmentation, feature extraction, and feature selection. In this method, three stages of stretching of the histogram, image binary and morphology operations are applied for pre-processing function. Morphological operations include expansion, opening, closing and erosion and in this approach, erosion was only used. The GLCM matrix has been applied for feature extraction and the parameters used in this matrix include: contrast, crossover, homogeneity, entropy, energy, mean, variance, and standard deviation. And, the genetic algorithm has been used for feature selection. Finally, SVM was used for classification [19]. The criteria of Accuracy, Sensitivity and Specificity have been used in order to evaluate the cluster.

In 2014, Caropadal et al. presented a new hybrid method of KNN (K-Nearest Neighbor) and FCM (Fuzzy C-Mean) for the detection and segmentation of brain tumors in MRI images. This method was auto-detection and fuzzy-based segmentation of brain tumor images, and it was called Fuzzy-KNN. The main purpose of this method was to detect and classify the brain tumors in MRI images automatically. This approach includes various steps, such as preprocessing, image segmentation, and feature extraction. In the preprocessing stage, the researchers used normalization and noise elimination. In image segmentation, they applied FCM algorithm. For feature extraction and categorization, Gabor filter and Fuzzy-KNN were applied, respectively. Finally, the criteria of Accuracy, Sensitivity and Specificity were used
to evaluate the cluster. The results indicated that the hybrid method of KNN and FCM has a better result than KNN [20].

In 2013, Robert et al. offered a method for brain tumor detection using a genetic algorithm. This method suggested a new algorithm using SVM in order to detect brain tumors in MRI images. In this algorithm, four types of features are considered and the best feature for the support vector machine is selected based on the genetic algorithm. The first type of features includes static ones such as entropy, energy, torque, correlation, variance, and skidding. The second type is extracted using the frequency domain. The third type of features is extracted from the coefficients of discrete wavelet transform and its dimension is reduced by the PCA technique. The fourth type is obtained through the histogram graph. Then, these four types are combined and the optimal features are extracted by genetic algorithm. These features are used for SVM testing and training 511 MRI images. Totally, the number of healthy brains is 198 and the number of defective brains is 313 [21].

2. Materials and Method

The method presented in this paper includes preprocessing, segmentation, feature extraction, dimension reduction, feature selection, and categorization through SVM. The various steps of the proposed algorithm are shown in Figure 1 and the explanation is offered.

2.1 Preprocessing

The preprocessing stage takes place in a CAD system to improve the areas of study. Various image processing techniques such as noise elimination, contrast improvement, and heterogeneous image correction techniques are performed. It should be noted that the preprocessing phase is carried out in a detection system designed to assist the computer in segmenting and extracting the features. The preprocessing operations carried out in this study include: normalizing images, removing noise, and highlighting edges. Figure (1) proposes the algorithm diagram.

2.1.1 Normalization

The normalization stage in the image processing changes the range of pixel intensity values. This stage is sometimes called the contrast reduction or pulling histogram process. In this paper, we have used linear normalization based on equation (1) to normalize the images.
\[ I(\text{new}) = (1 - \frac{\text{newMax} - \text{newMin}}{\text{Max} - \text{Min}}) + \text{newMin} \]  

(1)

Where, the new pixel value = \( I(\text{new}) \), the initial pixel value = \( I \) the new maximum value = \( \text{newMax} \), the new minimum value = \( \text{newMin} \), the initial maximum value = \( \text{Max} \), the initial minimum value = \( \text{Min} \).

Fig 1. Diagram of proposed algorithm

2.1.2 Noise Removal

Noise removal is considered as one of the most important parts of any process. Most often, the images are subject to the noise due to the structural constraints of imaging. One of the most widely used methods is the Perona-Malik noise removal, which is known as Anisotropic Diffusion Filter and it is applied for giving superiority to the high-contrast edges compared to the low contrast edges [23]. Perona -Malik model helps the segmentation process and also
contributes significantly to the extraction process because it performs proper filtering on other areas and remove their noise.

\[ C(x,y,t) = e^{-||I\nabla[k]\|^2} \]  

(2)

Where, \( I\nabla \) represents the image gradients and the guiding parameter. The K parameter controls the sensitivity to the edges. When we consider K to be very low, the weak edges can block the guidance. On the other hand, when k is considered very high, strong edges may not be maintained. Therefore, the value of k is calculated through the trial and error method, and the experiment of different values and their result suggests the value of k= 20, and the integral constant= 1/20. The frequency of this algorithm on the images is 20. Figure (2) shows the input and output of Perona- Malik Equation.

![a) Input image b) Output image after normalization and noise removal](image)

Fig. 2 Noise removal using Perona-Malik Equation

### 2.2 Image Segmentation

At this stage, the goal is to extract brain tissue from other parts. In the method used in this paper, the SRG algorithm is applied which is based on the regional growth. This algorithm has better performance for the images that have weak edges [5]. Regional growth is a process that categorizes the pixels or sub-areas into larger groups. The simplest approach is to join the pixels together and this process starts with a set of seed points. Then, the neighboring pixels join the seeds and the larger areas are created based on the similar features (such as brightness). In the SRG algorithm, a number of neighboring pixels are selected as the seeds. Then we select a pixel from the neighborhood and compare its brightness with the average brightness of the selected region. If the brightness of the pixel is similar (we will determine
the degree of similarity based on a threshold value), that pixel will join the selected area. The equation (3) is used for segmentation. In Figure 3, the extracted tissue is presented.

\[
S(x,y) = \begin{cases} 
S(x,y) + I(x,y) & \text{if } |M(x,y) - I(x,y)| = T \\
S(x,y) & \text{otherwise}
\end{cases}
\]  

(3)

Where, threshold= T, average seed= M(x,y), the pixel in the neighborhood of seed= I(x, y), and seed= S(x,y)

![Fig. 3 Extracted tissue](image_url)

**2.3 Feature Extraction**

The main idea of the HOG descriptors is that a shape can be well described by distributing the orientations of the edges or gradients. In this method, first the image is divided into several small areas, which is called a cell. Then gradients are calculated in two orientations of x and y per pixel. The next step is to get the histograms of each cell through the channels. We divide the distance from 0 to 180 degrees to 9 equal parts, each part creates a mid-histogram. Then for each cell, a histogram of edge orientations is calculated. Each pixel within the cell casts a weighted vote for an orientation-based histogram channel based on the values found in the gradient computation. Finally, histograms are normalized to compensate for the intensity of brightness. In this process, we consider several neighbor cells as a block and normalize their histograms. The accumulation of the histograms represents a HOG descriptor. Figure (4) shows the process of feature extraction using HOG.
Gamma correction and image normalization are the first steps of feature extraction in image processing. However, these steps can be removed from the calculation and implementation of the HOG descriptor [16]. Instead, calculating gradient values will be the first step in implementation. The most common method for calculating the gradients values is to apply the one-dimensional derivative masks \([-1,0,1]\) in the horizontal orientation and \([-1,0,1]^{T}\) in the vertical orientation.

\[
G_x(x,y) = I(x+1,y) - I(x-1,y) \quad (4)
\]
\[
G_y(x,y) = I(x,y+1) - I(x,y-1) \quad (5)
\]
\[
G(x,y) = \sqrt{G_x(x,y)^2 + G_y(x,y)^2} \quad (6)
\]
\[
\theta = \arctg \frac{G_y(x,y)}{G_x(x,y)} \quad (7)
\]

Where, brightness intensity = \(I(x,y)\), vertical gradient = \(G_y(x,y)\), horizontal gradient = \(G_x(x,y)\), Gradient size = \(G(x,y)\), gradient angle = \(\theta\).

The third step of this method is to compute the diagram of each cell’s histograms. Therefore, we determine the Mid-histogram channels. We divide the distance from 0 to 180 degrees to 9 equal parts, each part creates a Mid-histogram space. Then for each cell, a histogram of the
edge orientations is computed. Each pixel of the cell votes to a channel of the histogram based on the edge orientations and its gradient value.

The fourth step is to normalize the blocks. We use Equation (8) where \( V \) is a non-normalized vector containing all the histograms of the block. \( k = 1, 2 \) , \( ||V||_k \) is equal to k-norm block and \( e \) is a constant small value.

\[
\text{L2-norm: } f = \frac{v}{\sqrt{||V||_2^2 + e^2}} \tag{8}
\]

The fifth step is to collect the histograms. We collect the histogram of the blocks that were normalized in the previous step. A feature vector is created that describes the image. The parameters used to extract the features through the HOG method are presented in Table 1.

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Window size</td>
<td>128*64</td>
</tr>
<tr>
<td>Cell size</td>
<td>8*8</td>
</tr>
<tr>
<td>Block size</td>
<td>2*2</td>
</tr>
<tr>
<td>Overlap rate</td>
<td>.5</td>
</tr>
<tr>
<td>Histogram channels</td>
<td>9</td>
</tr>
<tr>
<td>Filter core</td>
<td>( hx=[-1,0,1] )</td>
</tr>
<tr>
<td>Normalization</td>
<td>L2-norm</td>
</tr>
</tbody>
</table>

At this stage, 3780 features have been extracted for each image. The process of the features computation is described in Fig. 5.
2.4 Dimension Reduction

In the previous step, a total number of 3,780 features were extracted through the HOG method. This number contains a large amount of repeated data that increase the computation time in the classification phase and also reduce the efficiency of the categorization. The Dimension Reduction process using the PCA has been applied to these features that reduce the features number to 900. Consequently, for each MRI image, we construct a feature vector that contains 900 components. In the following section we will describe how to use the PCA.

Different methods for computing basic components can be used. In this paper, we used eigenvalues and eigenvectors of the covariance matrix.

If we consider the input data as X:

\[ X = X_1, X_2, \ldots, X_n \]  \hspace{1cm} (9)

Where \( n \) is the number of samples and \( X_i \) is a sample of data with the dimension of D. First, the average sample of \( \bar{X} \) is deducted from each data sample.

\[ X_1 - \bar{X}, X_2 - \bar{X}, \ldots, X_n - \bar{X} \]  \hspace{1cm} (10)

Then the covariance matrix \( \Sigma \bar{X} \) is calculated by Equation (11).

\[ \Sigma \bar{X} = \frac{1}{n} \bar{X} \bar{X}^T \]  \hspace{1cm} (11)
Now, the main components are obtained by computing the eigenvectors of the covariance matrix $\phi_\tilde{X}$ in Equation (12).

$$\sum \tilde{X} \phi_\tilde{X} = \phi_\tilde{X}$$  \hspace{1cm} (12)

Where, $\Lambda_\tilde{X}$ is a diagonal matrix of eigenvalues corresponding to eigenvectors $\phi_\tilde{X}$.

$$\Lambda_\tilde{X} = \begin{bmatrix} \lambda_1 & 0 & \cdots & 0 \\ \vdots & \ddots & \vdots & \vdots \\ 0 & \cdots & 0 & \lambda_n \end{bmatrix}$$  \hspace{1cm} (13)

The eigenvector corresponding to the highest eigenvalue and the original vector with the highest variance of data are the primary components. The $i^{th}$ of the sample is $X_i$ that can be transferred to the PCA through Equation (14).

$$y_i = \phi^{-1}_x (X_i - \bar{X})$$  \hspace{1cm} (14)

When only one subset of eigenvectors is selected, the result will be obtained by depicting the data in a sub space of the PCA. This fact is very useful for reducing data redundancy; it means the removal of all eigenvectors that are zero.

2.5 Classification

In order to implement this stage, the SVM classification algorithm has been used in MATLAB. The feature vectors that were obtained in the feature extraction stage, are considered as SVM inputs, and classification is performed based on these features. Since the samples are linearly separated, we use the separable linear SVM. Figure 6 shows that we have two classes called Class1 and Class2, and the goal is to find a cloud-based interface that separates the two classes. The training data that will be in the top and bottom of this interface, are as follows: for $y=1$ is $w^T x + b > 0$ and for $y = -1$ is $w^T x + b < 0$, respectively. Therefore, for the optimal separator, we use Equation (15). The parameters of $w$ and $b$ should be calculated as each data is placed correctly in the related class and the distance between the nearest points of each data class and the separator is the maximum.

$$w^T x + b = 0$$  \hspace{1cm} (15)

The relation between the vector $x$ and the weight, such as $w$, is expressed in terms of the inner multiplication. The T sign indicates the weight of the matrix.
Figure 7 shows the classification performed by SVM. As it is observed, SVM has errors in some cases and these errors are due to the bugs in the extracted features.

3. Implementation and Results

MATLAB software is applied to implement the proposed method. Testing and training have been performed using 850 MRI images of tumorous and healthy brains extracted from database of Harvard University [22]. Figures 8 to 11 show the result of this system for one image.
The system uses extracted features to evaluate tumorous or healthy brain. Information obtained from MRI images is given to the SVM in order to decide on their status. This cluster recognizes the healthy or unhealthy brains based on the knowledge received from the training phase. There are several ways to evaluate the performance of the clusters. A general evaluation method is based on specificity, sensitivity and accuracy of the cluster.

Accuracy $= \frac{tp+tn}{tp+fp+tn+fn}$ \hspace{1cm} (16)

Sensitivity (TPR) $= \frac{tp}{tp+fn} \%$ \hspace{1cm} (17)

Specificity $= \frac{tn}{fp+tn} \%$ \hspace{1cm} (18)

tp is the number of patients who have tumorous brain diagnosed by the detection system correctly. fp is the number of patients who have tumorous brain but the system detects them healthy. tn is the number of healthy people detected by the system correctly. fn is the number of healthy people but the system detects them unhealthy. We will examine the results
obtained by the cluster through the extracted features. Table 2 compares the efficiency of the proposed approach with other methods. It should be noted that this approach uses the Harvard database, too.

Table 2: Comparison of proposed method with other methods

<table>
<thead>
<tr>
<th>Criterion</th>
<th>Sensitivity%</th>
<th>Specificity%</th>
<th>Accuracy%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reference</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>[20]</td>
<td>% 84/3</td>
<td>% 81/8</td>
<td>% 44/5</td>
</tr>
<tr>
<td>[19]</td>
<td>%87</td>
<td>%90</td>
<td>% 95</td>
</tr>
<tr>
<td>[10]</td>
<td>%71</td>
<td>%68</td>
<td>% 71</td>
</tr>
<tr>
<td>[18]</td>
<td>%89</td>
<td>%90</td>
<td>% 89</td>
</tr>
<tr>
<td>[21]</td>
<td>%89</td>
<td>%88</td>
<td>% 92</td>
</tr>
<tr>
<td>Proposed Approach</td>
<td>% 92/3</td>
<td>% 91/1</td>
<td>% 93/2</td>
</tr>
</tbody>
</table>

4. Results and Discussion

• In the preprocessing phase as Fig. 2B shows, the application of the Perona and Malik Equation eliminates noise and elevates the edges of the image. This greatly help the segmentation.

• In the segmentation phase, as shown in Figure 3, the method extracts the brain from other parts.

• In the feature extraction phase, the HOG can describe the shape of tumorous brains and detect them from the healthy brains. Although this method has been introduced to detect objects, this paper shows that it can describe the shape of the brain properly.

• In the classification phase and generally detection system, the results in Table 1 show the higher accuracy of this approach compared to other tested methods.
5. Conclusion

In this paper, a method is presented for brain tumors detection in MRI image through the HOG feature extraction. The results of the test on the database indicate that the system has achieved the accuracy rate of 93.2% in the classification. Also, this method has better performance in tumor detection.

Although the results obtained in this article suggest a high efficiency of the proposed system, it should be noted that the subject of medical detection does not end with the recognition of the two classes. In this article, two tumorous and non-tumorous classes are defined, while another type of brain injury might be seen practically. Our future goal is to design a system that can effectively diagnose a variety of diseases and offer suggestions for treatments. However, note that there is a long way to reach this point.

6. References


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