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An Automatic Classification of Brain Tumors through MRI Using Support Vector Machine

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Abstract

Brain tumor is a life threatening disease. It is any mass that outcomes from abnormal growths of cells in the brain. In this paper a brain tumor diagnostic system is developed. The system determines the type of the tumor which is benign or malignant using the Magnetic Resonance Imaging (MRI) images which are in the Digital Imaging and Communications in Medicine (DICOM) standard format. The system is assessed based on a series of brain tumor images. Experimental results demonstrate that the proposed system has a classification accuracy of 98.9%.

Keywords: *Support Vector Machine; Fast FourierTransform, Segmentation, MRI, Brain Tumor, DICOM*

1. Introduction

A primary brain or spinal cord tumor is one that begins in the brain or spinal cord. This year, an expected 78,000 individuals will be determined to have primary tumors of the brain and Central Nervous System (CNS). This number incorporates 23,770 grown-ups (13,350 men and 10,420 women) in the United States who will be determined to have primary cancerous tumors of the brain and spinal cord this year. This number additionally incorporates more than 4,000 teens and children who will be determined to have a brain or central nervous system tumor this year. In addition to primary brain tumors, there are also secondary brain tumors or brain metastases. This is the point at which the tumor began elsewhere in the body and spread to the brain. The most widely recognized malignancies that spread to the brain are bladder, breast, kidney, and lung cancers, leukemia, lymphoma, and melanoma. It is estimated that 16,050 adults (9,440 men and 6,610 women) will die from primary cancerous brain and CNS tumors this year. These Statistics adapted from the American Brain Tumor Association; the Central Brain Tumor Registry of the United States; the National Cancer Institute; National Institute of Health; and the American Cancer Society's publication, Cancer Facts and Figures 2016 [1].

Brain tumor is any mass that outcomes from unusual developments of cells in the brain. It might influence any individual at any age. Brain tumor impacts may not be the same for every individual, and they may even change from one treatment session to the next. Brain tumors can have an assortment of shapes and sizes; it can show up at any area and in various picture intensities. Brain tumors can be benign or malignant. Low grade Gliomas and Meningiomas [2], which are benign tumors, represent the most widely recognized brain tumor. Glioblastoma multiform [2] is a malignant tumor and represents the most widely recognized primary brain neoplasm. Benign brain tumors have a homogeneous structure and do not contain cancer cells. They may be either simply be monitored radiologically or surgically eradicated and they seldom grow back. Malignant brain tumors have a heterogeneous structure and contain cancer cells. They can be treated by radiotherapy, chemotherapy or a combination thereof and they are life threatening. Many procedure and diagnostic imaging techniques can be performed for the early detection of any abnormal changes in tissues and organs such as Computed Tomography (CT) scan and Magnetic Resonance Imaging (MRI) [3]. MRI is a briskly growing medical imaging technique and capture high resolution images of soft tissues [4]. Magnetic resonance imaging (MRI) is a non-invasive technique for classifying cells composed of tissues in human body [5]. Fig 1 shows the normal MR brain image and image with tumor.

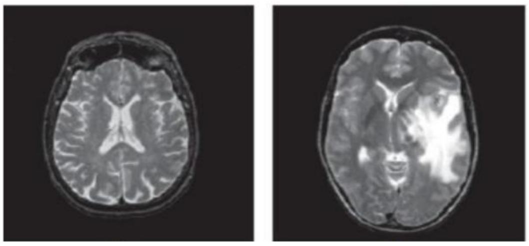


Fig 1: Normal (on the left) and Tumor (on the right) MRI image

This paper is organized as follows, section 2 presents the related work, section 3 discusses the proposed method, section 4 presents the results and discussions and finally section 5 contains the conclusions and future work.

2. Related Work

Many techniques have been reported for classification of brain tumors in MR images, most notably, Support Vector Machine (SVM) [6] Artificial Neural Network (ANN) [7], knowledge based techniques [8], Expectation–Maximization (EM) algorithms and Fuzzy C-Means (FCM) clustering. Gering and colleagues [9] applied the EM algorithms in the detection of abnormalities. These algorithms are capable of recognizing large tumors from the surrounding tissues of the brain by training on normal brain images in healthy individuals in order to perceive deviation from normality. This requires high computational effort. The knowledge based techniques permitted to make more efficient results for the segmentation and classification tasks but these techniques requires intensive training. In medical image analysis, the determination of tissue type (normal or pathological) and tissue pathology classification are done by using texture. MR image texture proved to be useful for determining the type of the tumor [10] and to detect Alzheimer's disease [11]. To solve problems of the texture classification, many approaches have been implemented over the years, such as multichannel methods, multi-resolution analysis, level set, Gabor filters, and wavelet transform [12, 13]. Gabor filters are poor because of their lack of orthogonality that results in redundant features that are of different scales or channels. Wavelet Transform is able to represent textures at the most suitable scale, by varying the spatial resolution and there is also many choices for the wavelet function. Selecting the optimal features to discriminate between classes is a big problem. The evaluation of different feature subsets is a hard task because it requires agreat computational effort. Siedlecki and Sklansky [14] compared the Genetic Algorithm (GA) with classical algorithms and they concluded the superiority of the

GA. GA proved to be a successful approachfor choosing the best feature subset while preservingan acceptable classification accuracy.

Praveen G.B. and Anita Agrawal [15] proposed a hybrid approach for brain tumor detection and classification in MR Images. First stage of the proposed approach concerns with image preprocessing which includes noise filtering, skull detection, etc. The second stage deals with feature extraction of MR brain images using gray level co-occurrence matrix. Third stage deals with classification of input data into normal or abnormal using Least Squares Support Vector Machine (LS-SVM) classifier with MultiLayer Perceptron (MLP) kernel. Final stage is the segmentation of the tumor part from the brain using fast bounding box. The experiments were performed on 100 images (25 normal and 75 abnormal) from a real human brain and synthetic MRI dataset. The accuracy on both training and test images was found to be 96.63%. A. Shenbagarajan and colleagues [16] proposed a MRI brain image analysis method, where, the MRI brain images are classified into normal (benign) and cancerous (malignant) brain tumor. In this proposed method, the region based Active Contour Method (ACM) is used for segmentation and ANN based Levenberg-Marquardt (LM) algorithm is used for classification process. The accuracy was found to be 93.74%. LuizaAntonie [17] proposed a method for automated segmentation and classification of brain MR images in which an SVM was used for images classification (normal and abnormal) with statistical features. S. Chaplot and colleagues [18] proposed brain tumor identification using wavelets transformation method and SVM. In this method, noise was detached from the signal and through wavelet, features were extracted and then an SVM is used for classification of brain images as normal and abnormal.R. Mishra [19] proposed tumor identification system based on wavelet packet and ANN in MR images. The feature extraction process is performed using wavelet packet and the classification of images as normal and abnormal is done using ANN. Wavelet packet gives wealthy investigation by decomposing estimation and detail component every time whencompared to wavelet transformation method.E. A. El-Dahshan and colleagues [20] proposed a hybrid system for tumor detection in MR imagesand categorize them using ANN and K-Nearest Neighbor (KNN). In this method,the feature extraction is done using Discrete Wavelet Transform (DWT) and then Principle Component Analysis (PCA) is used for selecting best features. The selected features were introduced as input to classifiers such as KNN and ANN. Both KNN and ANN involve two phases which are trainingand testing. These classifiers were used to categorize MR images as normal and abnormal. H. Selvarajand colleagues [21] proposed a system forclassification of MR Images by means of wavelet features that were given as input to SVMand ANN. In the proposed method, aSelf-Organizing Maps (SOM) is used as a classifier for brain tumor, it simply captures nonlinear computation and theaccuracy rate was 94% as compared toSVM which captures linear and nonlinear computation and the accuracy ratewas 98%. A.E. Laskhari [22] proposed a technique based on neural networks for braintumor detection in MR images using geometric and Zernike moments. MRImages were usedas input images. Feature extraction stage occupies statistics features collection by mean, median, entropy andstandard deviation as well as a non-statistic feature by geometric moment's invariants. Feature selection wasdone by kernel F-score technique and given as input to ANN classifier which classifies it into two classes either normal orcancerous brain tissues. A.Kharratand colleagues [23] proposed a system for brain tumor classification using GA and SVM. The feature extraction is carried out by two methods. First, extracting features from bothnormal and abnormal images by Spatial Gray Level Dependence Method (SGLDM). Second, theimage is decomposed at second level by performingDaubechies wavelet transform. The optimal set of features wereselected by GA.

The selected features were given as an input to SVM. The accuracyachieved was 94.44% to 98.14%.

3. Proposed System Methodology

This section explains the proposed system design and methodology. The proposed method consists of number of phases which are dataset acquisition,preprocessing, segmentation using the Expectation Maximization (EM) algorithm and adaptive thresholding, feature extraction from MRI data set using Fast Fourier Transform (FFT), feature selection using Minimal-Redundancy-Maximal-Relevance criterion (MRMR) to select most valuable features and finally the classification stage in which SVMis used for classification of brain images as normal or abnormal. Figure 2 shows the flow diagram for the proposed method.

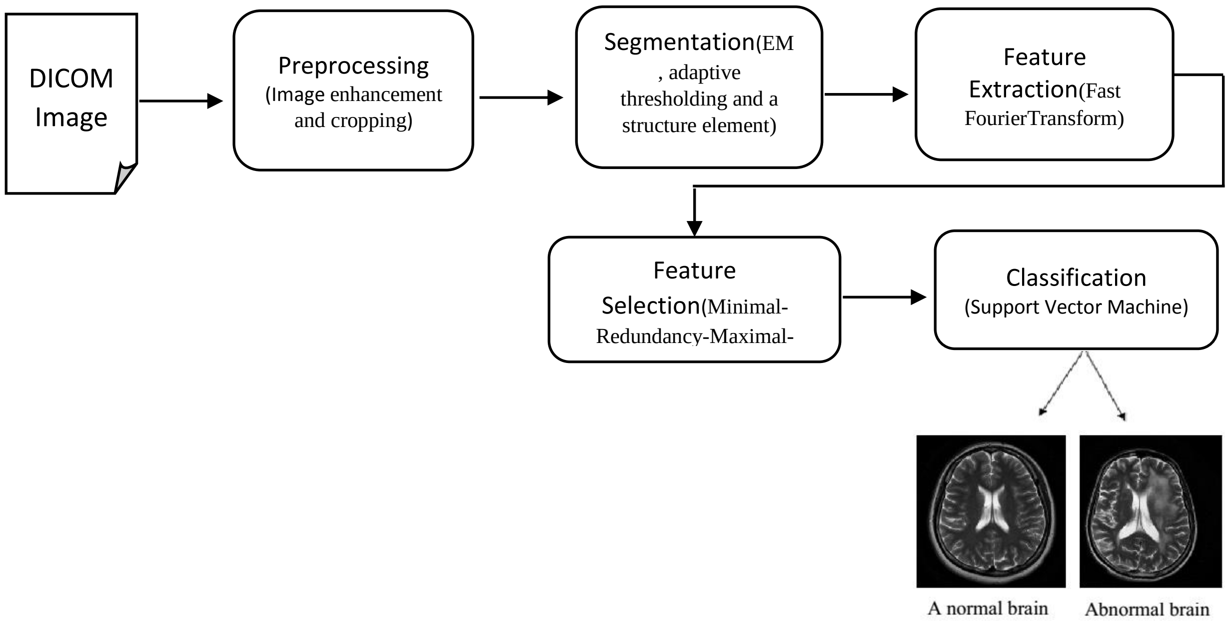


Fig. 2: The Flow Diagram of the Proposed System

3.1.Dataset Acquisition

A dataset are acquired for experimental evaluation. It consists of 100 MR images, out of which 80images have tumor and there maining 20are normal. The age of the patients ranges between 35-70 years. The size of each image is 512 x 512 having DICOM format. The dataset consists of multi-contrast MR scans.

3.2.Preprocessing

One of the most important tasks for the tumor detection is preprocessing. Usually medical images appear inhomogeneous and of poor contrast which requires preprocessing for image enhancement. In this work, preprocessing include enhancement and cropping, which helps in more accurate tumor diagnosis. The enhancement is carried out by median filter and high pass filter in order to remove noise and clean-up the background of the image. The high pass filter can be used for removing a small amount of low frequency noise from an N dimensional signal. The cutoff frequency of the filter used is 0.1. The median filtering is applied in order to remove the high frequency components in MR images. The median filter is the most used method to reduce noise and improve image quality. It preserves the edges of the image. The median is calculated by first sorting all the pixel values from the encompassing neighborhood into numerical order and then changing the pixel being considered with the middle pixel value. A 3×3 square neighborhood is used here. The piecewise linear transformations are applied in order to enhance image contrast.

3.3.Segmentation

Image segmentation is used to separate the main part of brain from undesired pieces. The EM, adaptive thresholding and a structure element are used to remove these pieces. The EM algorithm is widely used in medical image reconstruction [24]. Adaptive thresholding takes an image(grayscale or color) as input and outputs a binary image. A threshold has to be calculated for each pixel in the image. If the pixel value is less than the threshold it is set to the background value, otherwise it is set to the foreground value. There are two main approaches for finding the threshold: (i) the Chow and Kaneko approach [25] and (ii) local thresholding [26]. The assumption behind both techniques is that smaller image regions are probably have approximately uniform illumination which make them more suitable for thresholding. Chow and Kaneko divide an image into an array of overlapping sub images and then for each sub image, it finds the optimum thresholdvia investigating its histogram. For each single pixel, the threshold is found by interpolating the results of the sub images. This method is computationally expensive and is not appropriate for real-time applications. There is an alternative approach that can be used to find the local threshold by statistically examining the intensity values of the local neighborhood of each pixel. The statistics which is most appropriate depends largely on the input image. Simple and fast functions include the mean of the local intensity distribution, T=mean, the median value, T=median or the mean of the minimum and maximum values, T= (Max+Min)/2. The size of the neighborhood has to be large enough to cover sufficient foreground and background pixels, otherwise a poor threshold is chosen. On the other hand, choosing regions which are too large can violate the assumption of approximately uniform illumination. The adaptive thresholding in this method applies the *mean* of an 8×8 neighborhood. This method is less computationally intensive than the Chow and Kaneko method and produces sufficient results for most applications.To find appropriate size for structure element, first a small structure is defined to separate potential connected pieces. Erosion and dilation methods are applied to separate pieces without damaging main parts thenobjects' area is obtained. A 4×4 structuring element is used. Figures 3shows an image with a tumor in the left side of the brain before and after applying the EM algorithm. Figure 4A shows the same image after applying the adaptive thresholding while figure4B shows the image after applying erosion and dilation.

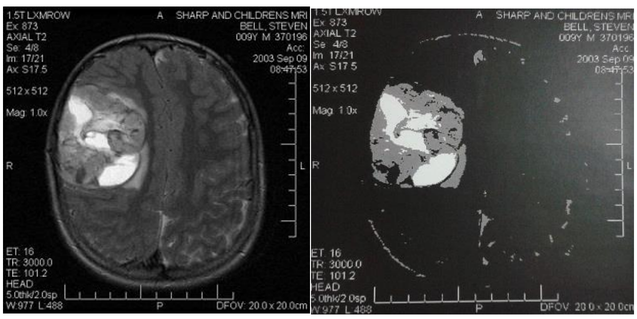
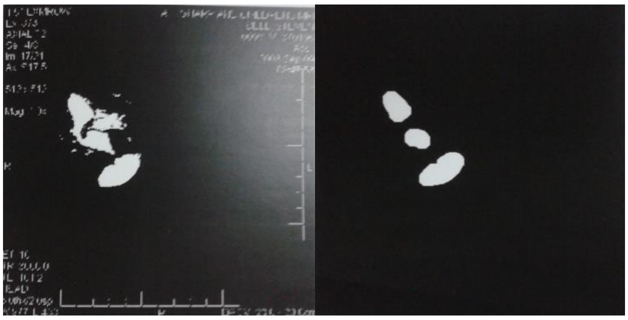


Fig.3: An image of the brain with a tumor before(left) and after (right)applying EM algorithm.



(A) (B)

Fig.4: The image after applying (A) the adaptive thresholding and (B) the erosion and dilation

3.4.Feature Extraction

Feature extraction is the first step of classification in which features of each image is extracted from MR images by Fast Fourier transform (FFT) algorithm [27]. FFT is applied to convert an image from the spatial domain to the frequency domain. It decomposes an image into its real and imaginary components which considered as a representation of the image in the frequency domain. The Fourier Transform (FT) of an image f (i, j) is given by:

$$F(k,l)=\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}f(i,j)e^{-i2\pi\left(\frac{ki}{N}+\frac{lj}{N}\right)}$$

where f(i,j) is the image in its spatial domain and the exponential term is the basis function corresponding to each point F(k,l) in the Fourier space. The inverse transform (IFT) converts the frequencies to the image in the spatial domain as:

$$f(i,j)=\sum_{i=0}^{N-1}\sum_{j=0}^{N-1}F(k,l)e^{i2\pi\left(\frac{ki}{N}+\frac{lj}{N}\right)}$$

FT transforms intensity variations of an image occurring in spatial domain to frequency variations. In frequency domain, sudden variation in intensity appears as high frequency component while low variation in intensity appears as low frequency component.

3.5.Feature Selection

Feature selection identifies subsets of data that are relevant to the parameters used and is normally called Maximum Relevance. These subsets often contain material which is relevant but redundant. We applied Minimal-Redundancy-Maximal-Relevance (MRMR) [28] in order to address this problem by removing those redundant subsets. MRMR has many applications in different domains such as cancer diagnosis and speech recognition. MRMR has two important properties, the first property is that features which are highly correlated among themselves should not be used thus keeping only features which are maximally dissimilar to each other. Let U denote a set of unidimensional discrete random variables $\{X1, X2, . . . ,\}$ and let C be a distinguished class variable which takes its values in the set $\{c1, c2, . . . , ck\}$.

$S \subseteq$ U will represent any subset of U. A way of measuring redundancy among the variables in S is:

$$W_I(S) = \frac{1}{|S|^2} \sum_{X_i, X_j \in S} MI(X_i, X_j)$$

where$(Xi,\ Xj)$ represents the measure of mutual information between the variables Xi and Xj.The second property of MRMR is that minimum redundancy should be supplemented by the use of a maximum relevance criterion of the features with respect to the class variable. A measure of relevance of the variables in S with respect to C is:

$$V_I(S) = \frac{1}{|S|} \sum_{X_i \in S} MI(C, X_i)$$

The simplest way of combining redundancy and relevance to obtain a good subset of features is:

$$S^* = \arg\max_{S \subseteq \mathbf{U}} (V_I(S) - W_I(S))$$

The selected subset is obtained in an incremental way, starting with the feature having maximum value of $(C;\ Xi)(S0\ =\ \{Xi0\})$ and progressively adding to the current subset$Sm{-}1$ the feature which maximizes:

$$\max_{X_j \in \mathbf{U} \setminus S_{m-1}} \left(MI(C, X_j) - \frac{1}{m-1} \sum_{X_i \in S_{m-1}} MI(X_j, X_i) \right)$$

3.6.Classification

In order to classify the input image as normal or abnormal, we applied SVM. SVM is a systematic technique for two class problems. The SVM classifier is used in many research areas because it gives high performance in pattern recognition and image processing tasks. SVM is most likely used in problems with small training dataset and high dimensional feature space. Like neural networks, SVM needs two stages; training and testing. The SVM can be trained by features given as an input to its learning algorithm. During training, the SVM finds the suitable margins between two classes. Features are named according to class associative with specific class.

ANN has many drawbacks such as having local minima and the selection of number of neurons for each problem. SVM occupies no local minima and by initiating the idea of hyper planes, it overcomes the problem of neurons selection.

In our SVM, input data is mapped into higher dimensional space using RBF kernel. In this transformed space, a hyper plane linear classifier is applied utilizing those patterns vectors that are closest to the decision boundary. Let *m*-dimensional inputs x*i* (*i*= 1, . . .,*M*) belong to Class 1 or 2 and the associated labels be *yi*= 1 for Class I and −1 for Class II. Decision function for SVM is:

$$D(\mathbf{x}) = \mathbf{w}^t \mathbf{x} + b$$

where w is an *m*-dimensional vector, *b* is a scalar. The separating hyper plane satisfies:

$$y_i(\mathbf{w}^t \mathbf{x}_i + b) \geq 1 \quad \text{for} \quad i = 1, \ldots, M.$$

The distance between the separating hyper plane $D(x) = 0$ and the training datum nearest to the hyper plane is called the margin. The hyper plane $D(x) = 0$ that has the maximum margin is called the optimal separating hyper plane.T able 1 shows the values of the SVM parameters as used in the Weka tool [29].

Table 1: The values of the SVM parameters

Parameter	value
Type of SVM	C-SVC
Type of kernel function	Radial Basis Function
Degree in kernel function	3
Tolerance of termination criterion	0.001
The parameter C of C-SVC	1
Missing value replacement	off

4. Results and Discussions

The proposed system follows an approach in which feature extraction is done using FFT then feature reduction is done using MRMR and finally the SVM has been utilized using these set of features for classification. The dataset collected are used for testing. The size of each image is 512 x 512 having DICOM format. Only 16 × 16 features are extracted for each image. The support vector machine classifier gives accuracy of 98.9%. Table 2 shows a comparison between the proposed method and other brain tumor classification techniques.

Table 2: A comparison between different approaches of brain tumor classification

Approach	Methodology	Dataset Size	Accuracy (%)
Praveen G.B. & Anita A. [15]	LS-SVM + MLP	100	96.63
A. Shenbagarajan et al [16]	ACM + ANNLM	80	93.74
Antonie L [17]	SVM	50	70
Chaplot S. et al [18]	Wavelets+SVM	52	98
R. Mishra [19]	Wavelet packets + ANN	Six images from one MRI sheet were selected	95
E. A. El-Dihshan et al [20]	DWT + PCA + ANN DWT + PCA + k-NN	70	97 98.6
Selvaraj H et al [21]	LS-SVM + RBF kernel	The test sets are extracted from a MRI dataset which contains 1100 slices	98.64 to 98.92
A. E. Lashkari[22]	ANN	160	98.2
A. Kharrat et al [23]	GA + SVM	83	94.44 to 98.14
Proposed Method	FFT + MRMR + SVM	100	98.9

From table 2, we can conclude that the proposed system and the system by Selvaraj H and colleagues [21] give the highest accuracy rate. The highest results given by Selvaraj H and colleagues is due to selecting a test set from the dataset which could not have a lot of varieties.

5. Conclusions and Future Work

Brain tumor is a main cause of death. Many approaches are used to detect the tumor as early as possible because early detection is important in the cure of this disease. Medical imaging can be used for the identification of brain tumor. For MRI-based brain tumor identification, the proposed system is proved to be quite efficient. The proposed system gives 98.9% accuracy on the collected dataset. The system provides an efficient solution as compared to other existing approaches. The system is quite useful in the context of detection and classification of brain tumors. As a future work, we are aiming to increase the size of the dataset by including more patients of different ages, symptoms, and gender.

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