



Brain Tumor Detection Using Hybrid Techniques and Support Vector Machine

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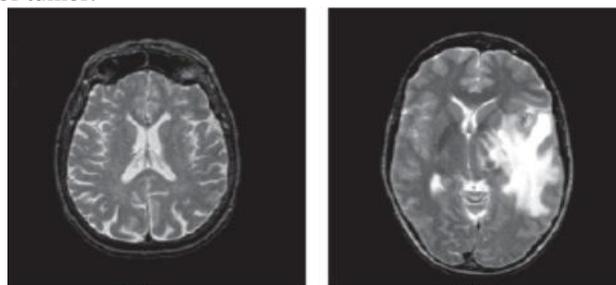
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Abstract— Brain tumor is a life threatening disease. The brain contains more than 10 billion working brain cells. The damaged brain cells are diagnosed themselves by splitting to make more cells. This regeneration takes place in an orderly and controlled manner. If the regeneration of the cells gets out of control, the cells will continue to divide developing a lump which is called tumor. In proposed method feature extraction is done by hybrid method. In this paper support vector machine and naïve bayes is used for detection of tumor and non tumor Image segmentation by using fuzzy c-means Segmentation Method. In this paper the Gray Level Co-occurrence Matrix (GLCM) is used as a feature. Main advantage of this method is that it will give fast and accurate result with the help of training data set and it reduces time and computation power.

Keywords— Feature extraction using Wavelet and Quad tree transform, C-means Segmentation algorithm, detection using SVM and Naïve Bayes.

I. INTRODUCTION

Abnormal growth of cells developed inside human body is called as Tumor. Brain Tumor is an intra-cranial solid neoplasm occurs within the brain or the central spinal canal. Brain tumor is implicitly serious and life-ominous disease because brain is very fragile part of human body to treat for. However, Brain tumors can be malignant that is cancerous or benign that is non-cancerous.[1] Treatment of brain tumor depends on proper diagnosis and depends on the different factor like the type of tumor, location, size and state of development. MRI is technique used to measuring density of photons in tissue; it is based on fundamental property of photon that spins and possesses magnetic movement. It is done to visualize the internal structure of human body, gives superior image quality. Fig 1 shows the normal MR brain image and image with tumor. Early and proper detection of tumor is the key for the proper treatment. Previously stage of tumor is used to be detected manually with the help of observation of image by doctors and sometimes it takes more time and sometimes results may inaccurate. There are many different types of brain tumor and only experienced and expert doctor can able to give the accurate result. So we require accurate diagnosis tool for proper treatment. Detection involves finding the presence of tumor; segmentation involves the detection of size and location of tumor and classification involves the detection of stage of tumor.



(A) (B)
Fig 1: Normal and Tumor MRI image

Now a day's many computer added tool is used in medical field. These tools possess a property of quick and accurate result. The known MRI images are first processed through various image processing steps such as histogram equalization and sharpening filter etc. and then features are extracted using wavelet and quadtree transform in that the specific feature is Gray Level Co-occurrence Matrix.[2,3] The features extracted are used in the Knowledge Base which helps in successful classification of unknown Images. These features are normalized in the range -1 to 1 and given as an input to support vector machine Classifier [4, 5]. This paper proposes a genetic algorithm and SVM based classification of brain tumor. It is concluded that, Gabor filters are poor due to their lack of orthogonality that results in redundant features at different scales or channels. While Wavelet and quadtree Transform is capable of representing textures at the most suitable scale[6], by varying the spatial resolution and there is also a wide range of choices for the wavelet and quadtree function.

II. LITERATURE SURVEY

In various recent research on segmentation, feature extraction and classification of MR brain image many different combination of segmentation and classification is used by various author. Discrete cosine transform for segmentation and Probabilistic neural network for classification is developed in matlab by author D. Sridhar and evaluation was performed on 20 set of images dividing in to different combination of test set and training set of data. Homogeneity predicates are usually based on image intensity, color, texture, etc. [1] According to Harlick and Shapiro [4], image segmentation can be classified into three categories: spatial clustering split and merge schemes, and region growing schemes. Classification of brain MRI using the LH and HL wavelet transform sub-bands was performed by Salim Lahmiri and Mounir Boukadoum [7], in 2011. This approach shows that feature extraction from the LH (Low-High) and HL (High-Low) sub-bands using first order statistics has higher performance than features from LL (Low-low) bands. In 2010, Ahmed kharrat, Karim Gasmi, Mohamed Ben Messaoud [8], presented their work on A Hybrid Approach for Automatic Classification of Brain MRI Using Genetic Algorithm and SVM. From the literature survey, firstly, it can be concluded that, various research works have been performed in classifying MR brain images into normal and abnormal [9],[4]. Whereas, classifying MR brain images into normal, cancerous and non cancerous brain tumors in particular, is a crucial task, which is considered in this proposed method.[11][12] Secondly, it is found that existing methods of brain tumor diagnosis and classification involve invasive techniques such as biopsy and spinal tap method [13]. It is essential to prevent and replace the invasive methods of brain tumor classification using a non invasive method of brain tumor diagnosis, which has been focused in this method. Thirdly, Discrete Wavelet Transform is found to be an important tool in decomposing the images into different levels of resolution, from which the significant features can be extracted [14], [15]. Fourthly, Statistical texture analysis techniques are constantly being refined by researchers and the range of applications is increasing [16], [17], [19]. Gray level co-occurrence matrix method is considered to be one of the important texture analysis techniques used for obtaining statistical properties for further classification, which is employed in this research work. Fifthly, Probabilistic Neural Network is found to be superior over other conventional neural networks such as Support Vector Machine and Back propagation Neural Network in terms of its accuracy in classifying brain tumors [18]. Hence a wavelet and co occurrence matrix method based texture feature extraction and Probabilistic Neural Network for classification has been used in this method of brain tumor classification.[20]

III. PROPOSED METHOD

In proposed method we are doing brain tumor detection using hybrid techniques. In this method we are using two kind of transform those transforms are wavelet and quadtree transform.[4] Those two feature extracted images are fused together and it is fed in to the support vector machine algorithm for classification tumor in trained images. Including that we have induce naïve bayes classifier for the proposed method. In svm single and multilevel methods are used.[5][6] We are using single level svm so we are induce another kind of method to classify a tumor. In machine learning, naive Bayes classifiers are a family of simple probabilistic classifiers based on applying Bayes' theorem with strong (naïve) independence assumptions between the features. Than it will given to the fuzzy c-means segmentation [7][8] The flow diagram for proposed method

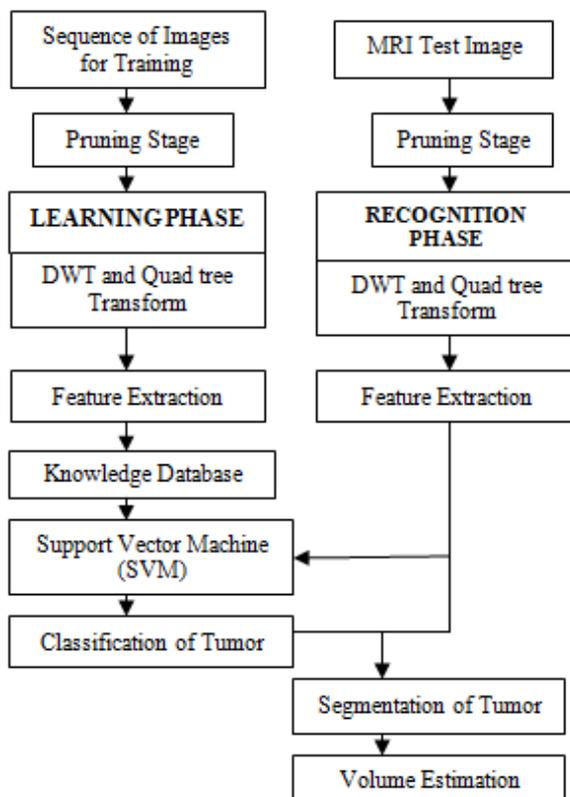


Fig 3: Flow diagram for proposed method

A. Discrete Wavelet Transform:

Wavelet transform performs multi-resolution of images that is simultaneous representation of images on different resolution levels. The wavelet compression techniques uses wavelet filters for decomposition into sub images. First, filter is applied along the rows, then along the columns thus resulting in four sub-bands that is low-low, low-high, high-low and high- high. Hence, M x N image is filtered and then down sampled into N x M/2 images. Then each column is filtered and down sampled into N/2 x M/2 images.[3][4]

i. Wavelet Decomposition

Daubechies wavelet filter of order two is used and found to yield good results in classification and segmentation of tumor from the brain CT images. By applying 2D DWT[15], two level wavelet decomposition of region of interest(ROI) is performed which results in four sub bands.[6][8] In 2D wavelet decomposition the image is represented by one approximation and three detail images ,representing the low and high frequency contents image respectively. The approximation can be further to produce one approximation and three detail images at the next level of decomposition, wavelet decomposition process is shown in Figure 1. LL1, LL2 represent the wavelet approximations at 1st and 2nd level respectively, and are low frequency part of the images. LH1,HL1,HH1,LH2,HL2,HH2 represent the details of horizontal, vertical and diagonal directions at 1st and 2nd level respectively, and are high frequency part of the images.

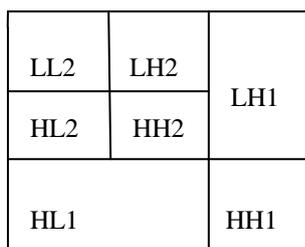


Fig 3.1: Wavelet Image decomposition at 2nd level

$$\psi_{a,b}(t) = \frac{1}{\sqrt{a}} \psi\left(\frac{t-b}{a}\right)$$

Among the high frequency sub bands, the one whose histogram presents the maximum variance is the sub band that represents the most clear appearance of the changes between the different textures. The WST features are extracted from the 3rd level of both low and high frequency sub bands and WCT features are extracted from 2nd level of high frequency sub bands are useful to classify and segment the tumor region from brain CT images.[12][14]

3 level Wavelet Decomposition

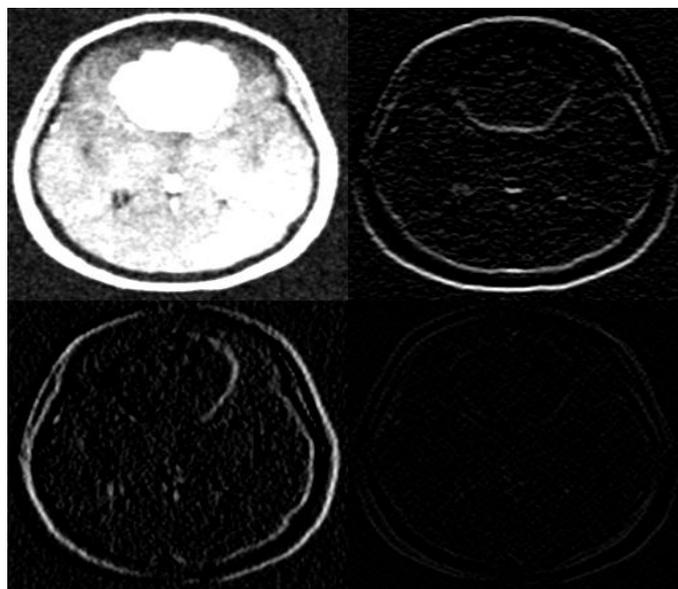


Fig 3.1: 3-level of decomposition

B. Quad tree transform

i. Decomposition

Fractal Geometry has become an important branch of modern mathematics and nonlinear science, it has been widely used covering many branches of science and engineering. At present, among the studies of fractal compression encoding, there are two research focuses on the application of fractal on the field of image compression. The main problem is that the fractal encoding is taking too much time. Many approaches to reduce the encoding time has bad affection on the image quality after iteration, therefore the hybrid encoding method of combining fractal coding and other coding methods becomes an important direction of fractal methods. The Quad tree approach divides a square image into four equal sized

square blocks, and then tests each block to see if meets some criterion of homogeneity. If a block meets the criterion it is not divided any further, and the test criterion is applied to those blocks. This process is repeated iteratively until each block meets the criterion. The result may have blocks of several different sizes [3][4][6].

ii. Quadtree Decomposition Partitioning

2.1.Partition the image into a set of large range blocks

2.2.If a range is fail to find a match, the process is repeated after partitioning that particular range block into four quadrants

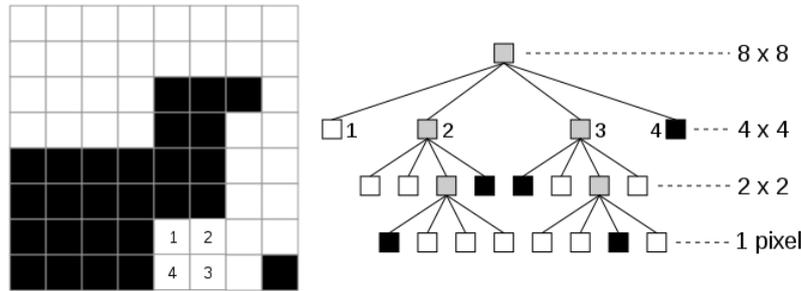


Fig 3.2.2 : decomposition in tree structure

iii. Grayshade blocks and edge blocks

All range and domain blocks are compared with a constant grayshade block. Blocks that exhibit an MSE error less than the user-specified tolerance are classified as grayshade blocks. Remaining blocks are classified as edge blocks.

3.3.2. Grayshade range blocks don't require search for a matching domain block.

3.3.4. Grayshade domain blocks are excluded from the domain pool used in the matching process

Quadtree Decomposition

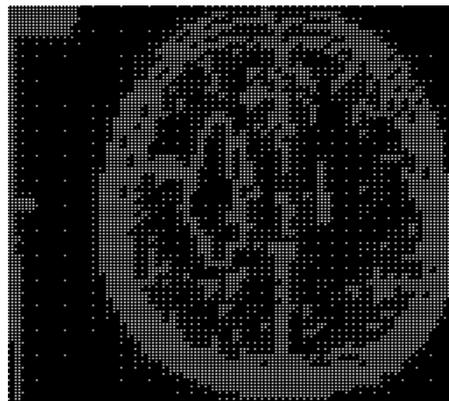


Fig 3.2: Quadtree decomposition

iv. Feature Extraction

Texture analysis is a quantitative method that can be used to tissues .As the tissues present in brain are difficult to classify using shape or intensity level of information, the texture feature extraction is founded to be very important for further classification.[5][7] The purpose of feature extraction is to reduce original data set by measuring certain features that distinguish one region of interest from another. 3-level Discrete Wavelet Transformed (DWT) low and high frequency sub bands and Gray level co occurrence matrix (GLCM) obtained from third level Discrete Wavelet Transformed (DWT) high frequency sub bands decomposition and quadtree transform.[3][8]

Algorithm for Feature Extraction is as Follows

(i) Obtain the sub-image blocks, starting from the top left corner.

(ii) Decompose sub-image blocks using 2-D DWT.

(iii) Another decomposition is done by quadtree transform.

Derive GLCM or Co-occurrence matrices [10] for two level high frequency sub bands of DWT with 1 for distance and 0,45,90 and 135 degrees for θ and averaged.

(iii) From these co-occurrence matrices is called Gray level co occurrence matrix (GLCM) are extracted.

(iv) from the GLCM features we can conclude

- (1) Homogeneity
- (2) Correlation
- (3) Entropy
- (4) Energy

IV. SUPPORT VECTOR MACHINE

Support vector machines (SVMs) are a relatively new learning process in statistical learning theory and gain popularity in computer processing power in recent years. The SVM motivated from the idea of the structural risk minimization that was developed by Vapnik [5]. Support vector machines are mainly two class classifiers, linear or non-linear class boundaries. The idea behind svm is to form a hyper plane in between the data sets to express which class it belongs to. The task is to train the machine with known data and then svm find the optimal hyperplane which gives maximum distance to the nearest training data points of any class. We consider data points of the form $\{(x_1, y_1), (x_2, y_2), (x_3, y_3) \dots \dots \dots (x_i, y_i)\}$ Where $y_i = \pm 1$, a constant denoting the class to which that point x_i belongs. $i =$ number of sample. Each x_i is p -dimensional real vector. The task is to find the maximum-margin hyperplane that divides the points having $y_i = 1$ from those having $y_i = -1$. Any hyperplane that satisfy the set of points x can be written as [10]

$$w \cdot x + b = 0 \quad (1)$$

Where b is scalar and w is p -dimensional Vector. If the training data are linearly separable, svm can chose two hyperplanes that divide the data in a way that have no points between them, and also have maximum distance between both hyperplanes[10]. The regions bounded by both hyperplanes are called "the margin". These equations for both hyperplane can be defined as

$$w \cdot x + b = 1 \quad (2)$$

$$w \cdot x + b = -1 \quad (3)$$

By geometry, the distance between the hyperplane is $2 / |w|$. Now add the following constraint: for each i either

$$w \cdot x_i + b = 1 \quad (4)$$

$$w \cdot x_i + b = -1 \quad (5)$$

It is equivalent to

$$y_i (w \cdot x + b) \geq 1 \quad (6)$$

The classifier written as

$$f(x) = \text{sign}(w \cdot x + b) \quad (7)$$

A. NAÏVE BAYES

It was introduced under a different name into the text retrieval community and remains a popular (baseline) method for text categorization, the problem of judging documents as belonging to one category or the other with word frequencies as the features. With appropriate preprocessing, it is competitive in this domain with more advanced methods including support vector machines. It also finds application in automatic medical diagnosis.[11] Naive Bayes classifiers are highly scalable, requiring a number of parameters linear in the number of variables (features/predictors) in a learning problem. Maximum-likelihood training can be done by evaluating a closed-form expression, which takes linear time, rather than by expensive iterative approximation as used for many other types of classifiers.[12] In the statistics and computer science literature, Naive Bayes models are known under a variety of names, including simple Bayes and independence Bayes. All these names reference the use of Bayes' theorem in the classifier's decision rule, but naive Bayes is not (necessarily) a Bayesian method, Russell and Norvig note that "[naive Bayes] is sometimes called a Bayesian classifier,[16] a somewhat careless usage that has prompted true Bayesians to call it the idiot Bayes model." [17]

V. SEGMENTATION

In this paper we are using fuzzy c-means algorithm. Which define as clustering algorithm. [6][8]

The goal of clustering is to

- I. group data points that are close (or **similar**) to each other
- II. identify such groupings (or clusters) in an **unsupervised** manner

Unsupervised: no information is provided to the algorithm on which data points belong to which clusters One of the major applications of clustering in bioinformatics is on microarray data to cluster similar genes

- Hypotheses:
 - Genes with **similar** expression patterns implies that the coexpression of these genes
 - Coexpressed genes *can* imply that
 - 1) they are involved in similar functions
 - 2) they are somehow related, for instance because their proteins directly/indirectly interact with each other
 - It is widely believed that coexpressed genes implies that they are involved in similar functions

Here we are using fuzzy c_means clustering algorithm for segmentation .

A. FUZZY C-MEANS CLUSTERING

In fuzzy clustering, every point has a degree of belonging to clusters, as in fuzzy logic, rather than belonging completely to just one cluster. Thus, points on the edge of a cluster, may be in the cluster to a lesser degree than points in the center of cluster. An overview and comparison of different fuzzy clustering algorithms is available.

Any point x has a set of coefficients giving the degree of being in the k th cluster $w_k(x)$. With fuzzy c -means, the centroid of a cluster is the mean of all points, weighted by their degree of belonging to the cluster:

The degree of belonging, $w_k(x)$, is related inversely to the distance from x to the cluster center as calculated on the previous pass. It also depends on a parameter m that controls how much weight is given to the closest center. The fuzzy c -means algorithm is very similar to the k -means algorithm:

- Choose a number of clusters.
- Assign randomly to each point coefficients for being in the clusters.
- Repeat until the algorithm has converged (that is, the coefficients' change between two iterations is no more than ϵ , the given sensitivity threshold) :
 - Compute the centroid for each cluster, using the formula above.
 - For each point, compute its coefficients of being in the clusters, using the formula above.

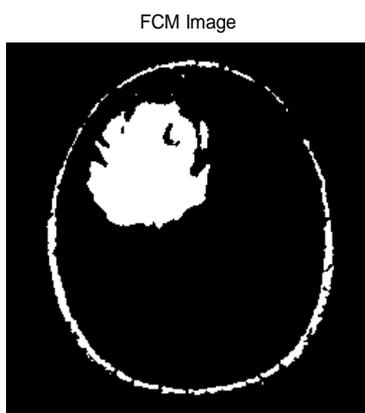


Fig 5.1: FCM output

VI. RESULTS

I have selected 50 MRI images from the TCIA database [11]. Out of 30 MRI images, 15 images are cancerous and 15 images are non cancerous. We have used all the images for training & testing of classification framework. Out of 50 images, 30 images are used for training and 25 images are used for testing. To estimate the performance of proposed method we used some metric. They are precision (P), recall (R) and accuracy (AC) and the respective definition are as follows:

$$AC = (TP+TN) / (TP+TN+FP+FN) * 100 \quad (8)$$

$$P = TP / (TP+FP) * 100$$

$$R = TP / (TP+FN) * 100 \quad (10)$$

Where TP is the number of true positives, TN is the number of true negatives, FN is the number of false negatives, and FP is the number of false positives, are defined as:

TP: Predicts cancerous as cancerous.

TN: Predicts noncancerous as noncancerous.

FN: Predicts cancerous as noncancerous.

FP: Predicts noncancerous as cancerous.

Accuracy measure how many instances that are correctly classified. Precision is the percentage of the instances which actually have class label A with all those which were classified as class label A. Recall is the percentage of the instances which were classified as class A, with all instances which truly have class A.

Table I Results after testing the classifier

Images	Precision	Recall	Accuracy
25	80	100	88

Table 1 gives results after testing the approach and it found that proposed method gives satisfactory results.

VII. A ROC CURVE

Receiver Operating Characteristics (ROC) graphs is visualizing the performance of the classifier. ROC curve draw between the true positive rate (TPR) and false positive rate (FPR). The TPR represent how many correct positive results come from all positive samples which are available during test. FPR on the other hand, represent how many incorrect positive results come from all negative samples which are available during test. In ROC curve the diagonal line shows random classification, if curve is draw above the diagonal line it shows better classification. Figure 5 shows the ROC curve for proposed classifier. The following ROC curve shows the good performance for the identification of brain tumor.

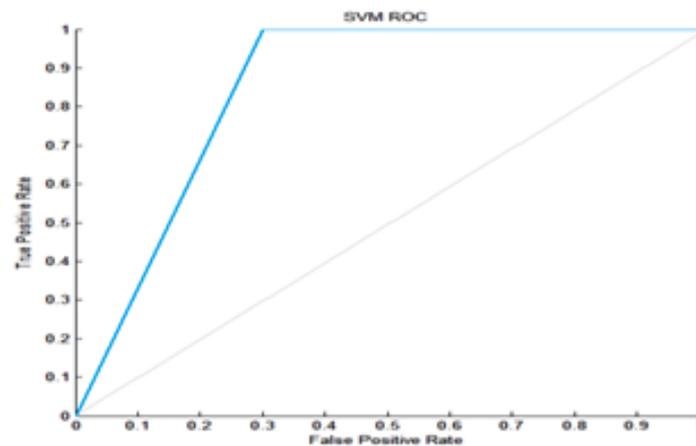


Fig 7: A ROC curve

VIII. CONCLUSION

Brain Tumor is a major cause of death. Many techniques are used to detect the tumor as early as possible because early detection is cure of this disease. Medical Imaging provides many techniques for the identification of tumor. The proposed system follows an approach in which feature extraction is done using wavelet and quadtree transform with GLCM features. then support vector machine and naive bayes has been utilized using these extracted features for identification. From the results, it is found that the proposed system gives satisfactory performance.

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