Automated Brain Image classification using Neural Network Approach and Abnormality Analysis

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Abstract— Image segmentation of surgical images plays an important role in diagnosis and analysis the anatomical structure of human body. Magnetic Resonance Imaging (MRI) helps in obtaining a structural image of internal parts of the body. This paper aims at developing an automatic support system for stage classification using learning machine and to detect brain Tumor by fuzzy clustering methods to detect the brain Tumor in its early stages and to analyze anatomical structures. The three stages involved are: feature extraction using GLCM and the tumor classification using PNN-RBF network and segmentation using SFCM. Here fast discrete curvelet transformation is used to analyze texture of an image which be used as a base for a Computer Aided Diagnosis (CAD) system .The Probabilistic Neural Network with radial basis function is employed to implement an automated Brain Tumor classification. It classifies the stage of Brain Tumor that is benign, malignant or normal automatically. Then the segmentation of the brain abnormality using Spatial FCM and the severity of the tumor is analysed using the number of tumor cells in the detected abnormal region.The proposed method reports promising results in terms of training performance and classification accuracies.

Keyword- MRI brain image, Segmentation and classification, Probabilistic Neural Network (PNN), Radial Bias Function(RBF), Fast Discrete Curvelet Transform(FDCT), feature selection

I. INTRODUCTION

Magnetic Resonance Imaging (MRI) is the state-of -the- art medical imaging technology which allows cross sectional view of the body with unprecedented tissue contrast. MRI plays an important role in assessing pathological conditions and is rapidly evolved into an accepted modality for medical imaging of disease analysis in the musculoskeletal system, specifically the foot and brain due to the use of non-ionizing radiation. MRI provides the digital representation of tissue characteristic that can be obtained from any tissue plane. The MRI scanner produces the images produced that can be best described as slices through the brain in both horizontal and vertical planes.

Tumor is due to the uncontrolled growth of the tissues in any part of the body. The brain tumors are classified as benign (Non-cancerous) which means they do not spread or invade the surrounding tissue and malignant (cancerous) which spreads or invades the surrounding tissue. It is categorized as primary and secondary tumor [1]. Different types of algorithm were developed for brain tumor detection. Segmentation is an important process to extract information from complex medical images.

Segmentation has wide applications in medical field. The objective of image segmentation is to partition an image into mutually exclusive and exhausted regions such that each region of interest is spatially contiguous and the pixels within the region are homogeneous with respect to a predefined criterion. The methods for segmentation of images are of two types: conventional and nonconventional (intelligent) methods. The different conventional methods used may be standard mask operators, detection of edge linking and boundary methods, discontinuities detection,thresholding, clustering, region of interest based segmentation, watershed segmentation and statistical methods, etc. and the nonconventional methods are of: Artificial Neural Networks(ANNs), fuzzy logic algorithms [2].

In the past, many researchers in the field of medical imaging and computer vision have made significant survey in the field of image segmentation. In the segmentation of medical images, the main objective is identifying different regions, and internal parts of the body from data acquired via MRI or other medical imaging technique [3]. In this paper, a clustering based method for image segmentation is proposed to extract tumor regions from MRI images. Clustering approach is widely used in biomedical applications especially for brain tumor detection in abnormal Magnetic Resonance (MR) images. Many clustering methods such as hard clustering and fuzzy clustering (soft clustering) can be used. Each object of the dataset is restricted to belong to only one cluster in the case of the hard clustering approach whereas in soft or fuzzy based clustering, each object can belong to more than one clusters depending upon the degree of membership associated. In most of the real situations, like images, an object restricted to only one cluster will make the task very difficult. So in the practical cases, fuzzy clustering is more naturally preferred to the hard clustering [4, 5]

The paper is organized as follows: The First section deals with the introduction and second section describes about the related works and third section explains the proposed methodology and fourth section displays the results and discussion and followed by the conclusion of the work.

II. RELATED WORK

. According to the degree of human interaction required, brain tumor segmentation methods can be classified into three categories as manual segmentation [6], semiautomatic segmentation [7], and fully automatic segmentation [8]. The different types of medical image segmentation methods that are applied to brain MRI: edge-based methods, region-based methods, and pixel-based methods and model based methods .The edge-based method uses the edge information to determine boundaries to form the closed regions belonging to the objects in the image. Some researchers have applied this method to divide MRI into regions with connected boundaries [9, 10]. But, it suffers from spurious edges and sometimes resulted in erratic performance.

Kaus et al. [11] implemented a region based method, wherein the technique involved statistical classification to divide an image into different tissue classes on the basis of the signal intensity value. The main disadvantage of region growing method is the partial volume effect (PVE) [12, 13] which reduces the accuracy. Also it blurs the intensity distinction between tissue classes at the border of the two tissues types, because the volume element may represent more than one kind of tissue types. Another type of region based method is watershed transform segmentation where it segments multiple regions at the same time. A complete contour of the images is produced and avoids the need for any kind of contour joining and this method suffers from over segmentation.

The pixel-based method used histogram based statistics to define single or multiple thresholds to classify an image pixel-by-pixel. These methods failed as they were limited by intensity inhomogeneities, partial volume effects and susceptibility artifacts. All these methods were degraded by noise in low contrast and low signal-to-noise ratio (SNR) images [14]. So, statistical methods were also developed [15].

To make consistent with the mathematical modelling and human knowledge in the engineering applications, fuzzy sets were introduced. Fuzzy models and algorithms for pattern recognition are widely used in advanced technologies. One of the most popularly known methods in clustering analysis is Fuzzy C-Means (FCM) which was proposed by Dunn extended by Bezdek. FCM clustering depends on the Euclidean distance between samples based on the assumption that each feature has equal importance. In most of the real-world problems, features are not considered to be important. So, this affects the performance of clustering. To improve the performance of FCM, many techniques have been developed [16-18].

Keller et al developed a possibility-based approach that corresponds with an intuitive concept of degree of belonging or compatibility, reducing problems in the noise environment. In practice, a suitable parameter value is needed to select values for different data sets by trial-and-error. So, the possibility-based approach became impractical in the real world [16]. Wang *et al* proposed a feature-weight assignment method which improved the performance of FCM clustering [17]. Liew*et al.* presented a spatial fuzzy clustering algorithm that exploited the spatial contextual information into image data, where the influence of the neighboring pixels is suppressed in non-homogeneous regions of the image [18].This method utilizes the difference between the pixel intensity and the centroid of a cluster, which is also called as dissimilarity index. It takes into account the influence of the neighboring pixels on the center pixel. The dissimilarity index is calculated from the new weighting function which does not depend on the relative location. The correct information for the sigmoid distribution in all areas of the image was not provided by this function. Thus, the weighting function should be dynamically calculated from the characteristics of the pixels.

Padma Nanthagopal, et al proposed a method in which the Segmentation of tumor has been done using Support Vector Machine (SVM) classifier which segments the shape of tumor information. SVM performs robust non-linear classification with kernel tricks. SVM is dimensional-independent and it is a combination of linear algorithms with linear or non-linear kernel functions which makes it a powerful tool in medical imaging applications. It was pre-processed using 2D discrete wavelet decomposition which extracts the texture features of an image. The two level of decomposition gives rise to four sub-bands. Spatial features were extracted from the two-level wavelet approximation tumor image by using both dominant grey-level run length and co-occurrence matrix method. Then finally classification process where a given number of test samples were assigned to a class based on knowledge gained by the classifier during the training of the neural network [19].

Discrete Wavelet Transform (DWT) is a tool for mathematical analysis and signal processing, but it has the disadvantage of poor directionality, and it can be improved by the complex wavelet transform. It improve directional selectivity and only requires O(N) computational cost. But it is difficult to design complex wavelets with perfect reconstruction properties and good fillter characteristics [20]. The 2D complex wavelets are essentially constructed by using tensor-product 1D wavelets. The directional selectivity provided by complex wavelets (six directions) is much better than that obtained by the classical DWT (three directions).

III. PROPOSED METHOD

A. *Methodology overview*

Basically, in an image processing system, the first stage image acquisition and image enhancement are the steps to be done as pre-processing. All the MR images are collected from publicly available resource. First the image is converted into a format that is capable of being manipulated by the computer. The MR images are converted into matrices form by using MATLAB. Then the features of the images are extracted using the Fast Discrete Curvelet Transform. Here fast discrete curvelet transformation is used to analyse texture of an image which be used as a base for a Computer Aided Diagnosis (CAD) system .The features extracted contains a dataset which is further divided into training dataset and test dataset. The training images are converted into the transformed domain and the coefficients are used as the prototypes for probabilistic neural network. For the testing set, the images are converted to the transformed domain and the approximate coefficients serves as the feature set. The test images are fed into the PNN combined with Radial Bias Function classifier for being classified. It classifies the stage of Brain Tumor that is benign, malignant or normal automatically. Then the MR image segmentation is done using Spatial FCM which segments the abnormal region of the brain and the results are compared with the previous results i.e. segmentation with K-Means Clustering algorithm. Lastly, performance based on the result will be analysed for the proposed method and it shows promising results than K-Means Clustering algorithm.

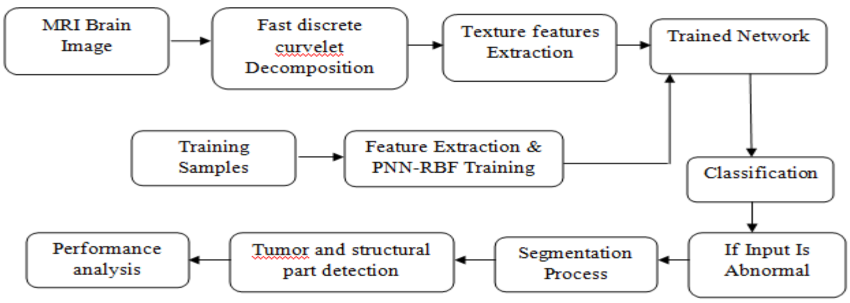

Figure 1. Block Diagram of the proposed work

B. *Images Acquisition*

The proposed approach is applied to analyse the simulated MRI images taken from publicly available sources. This dataset consists of 50 brain MR images in which 40 images with tumor and the remaining brain images are normal and the dataset is divided as training dataset and testing dataset.

C. *Feature extraction and analysis*

Feature analysis is a quantitative method to quantify and detect structural abnormalities in different brain tissues. As the tissues present in the brain are very difficult to classify using the shape or the grey-level intensities, texture feature extraction is very important for further classification. Texture is that innate property of all surfaces that describes visual pattern that contains important information about the structural arrangement of the surface also characterized by the spatial distribution of gray levels in a neighborhood. The spatial features are extracted by using the curvelet decomposition and also grey-level co-occurrence matrix (GLCM).

(i) Fast discrete curvelet Decomposition

An anisotropic geometric wavelet transform, named ridgelet transform, was proposed by Candes and Donoho. The ridgelet transform is optimal for representing straight-line singularities. This transform with arbitrary directional selectivity provides a key to the analysis of higher dimensional singularities. But, the ridgelet transform can be applicable onlyto objects with global straight-line singularities, which are rarely observed in real applications. In order to analyse local line or curve singularities, an idea is to consider a partition for the image, and then to apply the ridgelet transform to the obtained sub-images. This block ridgelet based transform, which was named curvelet transform. But the application of this first-generation curvelet transform is limited because the geometry of ridgelets is unclear, as they are not true ridge functions in digital images. Later, a modified, simpler second- generation curvelet transform based on a frequency partition technique was proposed by the same authors [20-22].

The curvelet transform is a multiscale pyramid with many directions and positions at each length scale, and needle-shaped elements at fine scales. This pyramid is nonstandard, but curvelets have useful geometric features and the curvelets obey a parabolic scaling relation which says that at scale 2^{-j} , each element has an envelope which is aligned along a "ridge" of length 2−j/2 and width 2−j .Curvelets are quite interesting because it is used for optimal sparse representation of objects with edges, optimal sparse representation of wave propagators and also optimal image reconstruction in severely ill-posed problems.

The two fast discrete curvelet transforms (FDCTs) which are simpler, faster, and less redundant are of: Curvelets via USFFT, and Curvelets via Wrapping. Both FDCTs run in O (n^2 log n) flops for n by n Cartesian arrays, and are also invertible, with rapid inversion algorithms of about the same complexity. The curvelet transform which are faithful to the mathematical transformation. These digital transformations are linear and take as input Cartesian arrays of the form f[t1, t2], 0 ≤ t1, t2 < n, which allows us to think of the output as a collection of coefficients $c_D(j, \ell, k)$ obtained by the equation,

$$cD(j,\ell,k) := \sum_{0\leq t1,t2<n} f[t1,t2]\,\overline{\varphi^{D}_{j,\ell,k}[t1,t2]} \qquad \rightarrow (1)$$

Where each $\varphi^{D}_{j,l,k}[t1, t2]$ is a digital curvelet waveform. In this work, the FDCT via wrapping is used and its algorithm is as follows:

Fast Discrete Curvelet Transform via Wrapping:

The "wrapping" approach assumes the same digital coronization but makes somewhat simpler choice of spatial grid to translate curvelets at each scale and angle. Instead of a tilted grid, we assume a regular rectangular grid and define "Cartesian" curvelets in the same way as before,

$$c(j.k,\ell) = \int \hat{f}\,(\omega)\hat{U}_j \;\; S^{-1}_{\theta\ell} e^{i(b,\omega)} d\omega \qquad \rightarrow (2)$$

by taking on values on a rectangular grid. The algorithm for FDCT via wrapping is as follows:

1. Apply the 2D FFT and obtain Fourier samples $\hat{f}$[n1, n2], −n/2 ≤ n1, n2 < n/2.

2. For each scale j and angle l,, form the product $\widetilde{UJ}, \ell$[n1, n2] $\hat{f}$[n1, n2].

3. Wrap this product around the origin and obtain $\tilde{f}_{j,}\,\ell$ [n1, n2] = W($\widetilde{UJ}, \ell\,\hat{f}$)[n1, n2], where the range for n1 and n2 is now 0 ≤ n1 < L1,j and 0 ≤ n2 < L2,j (for θ in the range (−π/4, π/4)).

4. Apply the inverse 2D FFT to each $\tilde{f}$j, ℓ hence collecting the discrete coefficients $c_D(j, \ell, k)$.

(ii)Grey-Level Co-Occurrence Matrix (GLCM)

A mathematical definition of the co-occurrence matrix was proposed by R.M. Haralick. Haralick et al. [23] proposed 14 features computed using the Gray Level Co-occurrence Matrix (GLCM), which is a structure that describes the co-occurring intensity values at a given offset. In other words, the GLCM provides information on how often a gray level occurs at different directions. Usually, four directions are considered in the 2D case: ϕ = 0°, ϕ = 45°, ϕ = 90°, and ϕ = 135°.

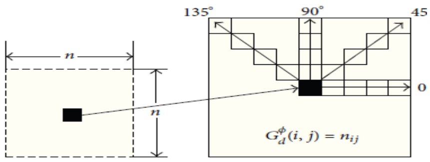

Fig 2: 2D Gray Level Co-occurrence Matrix (GLCM) computation Main directions (0°, 45°, 90°, and 135°)

However, Haralick suggests using the mean value of the features computed for the four directions to guarantee rotation invariance. Moreover, symmetric GLCM (i.e., taking into account voxels separated by $-d$and d voxels) is a common choice in image analysis. The structure of the 2D-GLCM is shown in Figure 2**,** where $n_{ij}$is the number of co-occurrences of gray levels $i$and $j$at a distance $d$and a specific direction. Thus, the GLCM, matrix defined as $G_{\phi}{}^{d}(i, j)$, is a square matrix of size N, where $N$is the total number of voxels in the window, so that (i, j) entry represents the number of co-occurrences of gray levels $i$and $j$for voxels separated at a distance $d$in direction ϕ The dominant grey-level run length matrix φ(d, θ) is given by the formula,

$$(d,\theta) = \left[p\left(i,j\,\middle|\,d,\theta\right)\right], 0 < i \leq \mathrm{Ng}, 0 < j \leq \mathrm{Rmax} \qquad \rightarrow (3)$$

The grey-level co-occurrence matrix ¢ (d, θ) is,

$$(d,\theta) = \left[p\left(i,j\,\middle|\,d,\theta\right)\right], 0 < i \leq \mathrm{Ng}, 0 < j \leq \mathrm{Ng} \qquad \rightarrow (4)$$

Once the co-occurrence matrix is constructed, based on the orientation and distance between image pixels, then we extract meaningful statistics from the matrix as the texture representation by using the following texture features: Energy, contrast, correlation, and homogeneity and the resulting sets of statistical measures are computed, called feature vectors.

Energy: It is a gray-scale image texture measure of homogeneity changing, reflecting the distribution of image gray-scale uniformity of weight and texture.

$$E = \sum_x \sum_y p(x,y)^2 \qquad \rightarrow (5)$$

Where, p(x, y) is the GLCM

Contrast: Contrast is the main diagonal near the moment of inertia, which measure the value of the matrix is distributed and images of local changes in number, reflecting the image clarity and texture of shadow depth.

$$I = \sum \sum (x-y)^2 p(x,y) \qquad \rightarrow (6)$$

Correlation Coefficient: Measures the joint probability occurrence of the specified pixel pairs.

Correlation: $\sum\sum(x - \mu x)(y - \mu y)p(x, y)/\sigma x \sigma y) \qquad \rightarrow (7)$

Homogeneity: Measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal.

Homogeneity =∑∑ (p(x, y)/(1 + [x-y])) → (8)

(iii) Probabilistic Neural Network classifier

The Probabilistic Neural Network (PNN) was first proposed in [24-26]. In this neural network, the operations are organized into multilayered feed forward network with four layers: input layer, pattern layer, summation layer and output layer. PNNs are a special form of Radial Basis Function (RBF) network used for classification. The architecture of a typical PNN is shown in Fig: 3

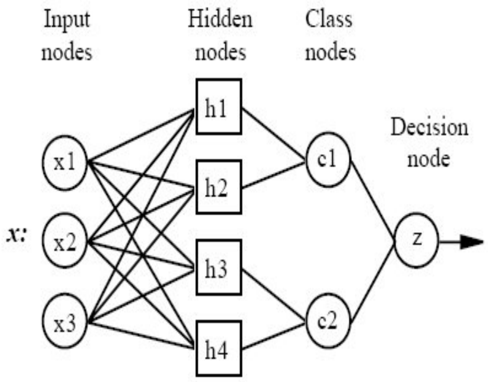

Fig 3: Architecture of Probabilistic Neural network

The input layer unit does not perform any computation and simply distributes the input to the neurons in the pattern layer. On receiving a **X** pattern from the input layer, the neuron **Xij** of the pattern layer computes its output,

$$\phi_{ij}(x) = \frac{1}{(2\pi)^{\frac{d}{2}}\sigma^d} \exp\left[-\left(x - x_{ij}\right)^T \frac{\left(x - x_{ij}\right)}{2\sigma^2}\right]$$

where'd 'denotes the dimension of the pattern vector x , σ is the smoothing parameter and **Xij** is the neuron vector. The summation layer neurons compute the maximum likelihood of pattern X being classified into C_i by summarizing and averaging the output of all neurons that belong to the same class

$$P_i(x) = \frac{1}{(2\pi)^{\frac{d}{2}}\sigma^d} \frac{1}{N_i} \sum_{j=1}^{N_i} \exp\left[-\left(x - x_{ij}\right)^T \frac{\left(x - x_{ij}\right)}{2\sigma^2}\right]$$

Where $\mathbf{N_i}$ denotes the total number of samples in class C_i . And the decision layer classifies the output based on the summation of all neurons, based on Bayesian classification as

$$\hat{C}(x) = \arg\max\{P_i(x)\}, \ i = 1,2, \dots . m$$

Where$\hat{C}$(x) denotes the estimated class of the pattern X and m is the total number of classes in the training samples. The PNNs are a special form of RBF network which maps any input pattern to a number of classifications. If the output depends on the distance of the input from the given stored vector, then it is called radial basis. It is a kind of FFNN where each unit in the hidden layer includes a RBF, as the activation function. The positions and the weight associated are learnt from training patterns. The PNN network architecture with RBF is shown in fig 4. Here the classification problem considered is the two class problem, namely benign class and malignant class. The dataset is divided as training dataset and testing dataset. The output resulted as benign case, malignant or normal case. The weight of the hidden layer needs to be set by using "training data". Therefore, the images were divided into training and testing datasets. Out of 50 images, 5 were selected as "test data" while the remaining were used for training. The training data was used to the PNN as inputs and the weights of the hidden layer are calculated and the classification of the images was done.

(iv)Segmentation with Spatial FCM

One of the important characteristics of an image is that neighboring pixels are highly correlated. That is, these neighboring pixels possess similar features, and the probability that they belong to the same cluster is greater.[27,28] This spatial relationship is important for clustering, but it is not utilized in the standard FCM algorithm. To exploit the spatial information, spatial function is defined as

$$h_{ij} = \sum_{k \in NB(x_j)} u_{ik}$$

where NB(x**j**) represents a square window centered on pixel $\mathbf{x_j}$ in the spatial domain. Similar to the membership function, the spatial function $\mathbf{h_{ij}}$ represents the probability that pixel xj belongs to $\mathbf{i^{th}}$ cluster. The spatial function of a pixel for a cluster is larger if the majority of its neighborhood belongs to the same clusters. The spatial function is incorporated into membership function as follows:

$$u_{ij}{}' = \frac{u_{ij}^p h_{ij}^q}{\sum_{k=1}^{c} u_{kj}^p \, h_{kj}^q}$$

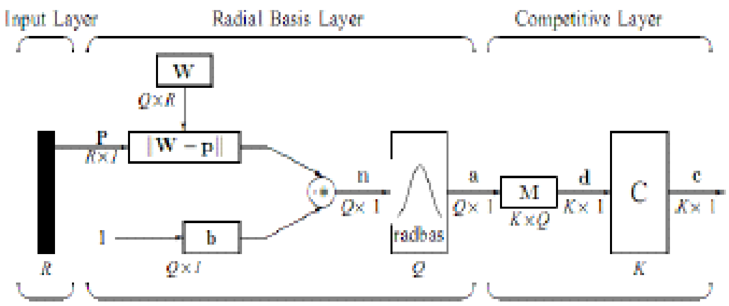

Fig4: The PNN with RBF Network Architecture

where p and q are parameters to control the relative importance of both functions. In a homogenous region, the spatial functions simply fortify the original membership, and the clustering result remains unchanged. The clustering is a two-pass process at each iteration. The first pass is the same as that in standard FCM to calculate the membership function in the spectral domain. In the second pass, the membership information of each pixel is mapped to the spatial domain, and the spatial function is computed from that. The FCM iteration proceeds with the new membership that is incorporated with the spatial function. The iteration is stopped when the maximum difference between two cluster centers at two successive iterations is less than a threshold (0.02). After the convergence, defuzzification is applied to assign each pixel to a specific cluster for which the membership is maximal.

IV. EXPERIMENTAL RESULTS

The proposed algorithm is implemented using MATLAB and tested on brain MRI images to explore the quality of the proposed method. The algorithm performance is quantified in terms of three parameters defined [28] as:

$$\text{Sensitivity} = \frac{\text{True positive(TP)}}{True\ Positive(TP)+False\ Negative(FN)}$$

$$\text{Specicivity} = \frac{\text{True Negative(TN)}}{True\ \text{Negative(TN)}+False\ \text{positive}(FP)}$$

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN}$$

The results of the proposed method are compared with K-Means Clustering algorithm results and it is shown that the SFCM method gives promising results. The simulated results shows that test image taken, curvelet decompositions, classification of tumor stage segmented abnormal region for the different classes of tumors namely benign and malignant classes.

TABLE I. COMPARISON BETWEEN K-MEANS AND SFCM

PARAMETERS	K-MEANS	SFCM (Proposed method)
Accuracy	81.8182	90.9091
Specificity	80	100
Sensitivity	83.3333	85.7143
Execution time in sec	20.646	15.666

V. SIMULATION RESULTS

A. Normal case:

Figure5: (a-c) Test image,Curvelet Decomposition, Segmented results for Normal case using SFCM method; (d-f) Test image,Curvelet Decomposition, Segmented results for Normal case using K-Means clustering.

SFCM SEGMENTATION

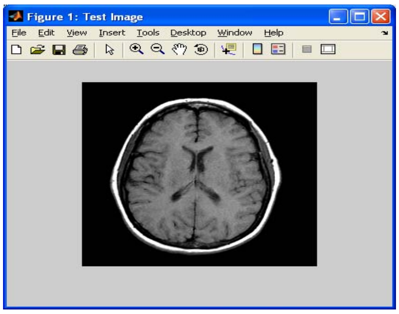

Fig5a. Test Image

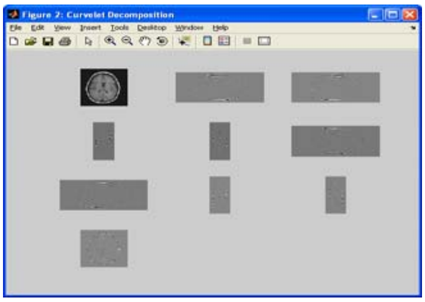

Fig5b.Curvelet Decomposition

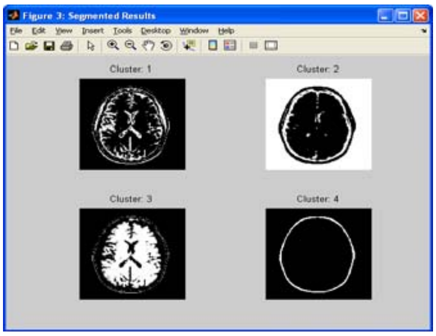

Fig5c. *Segmented results*

K-MEANS SEGMENTATION

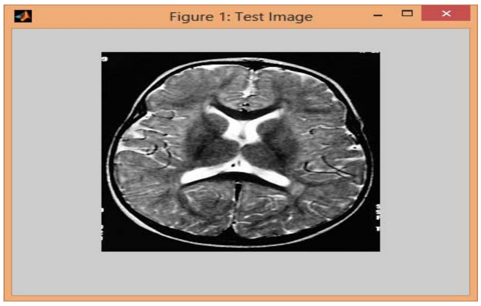

Fig5d : Test image

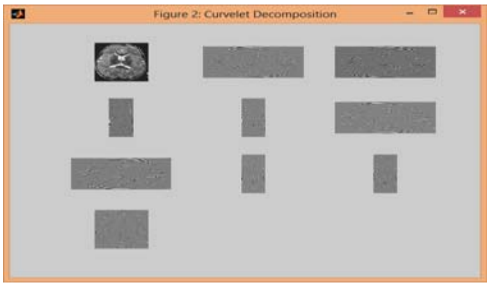

Fig5e.Curvelet Decomposition

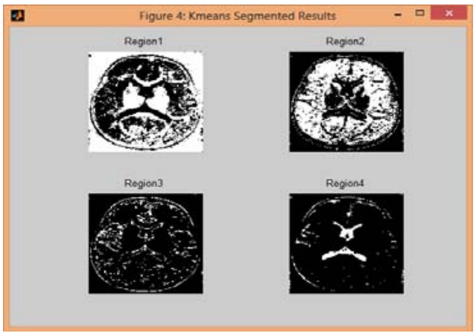

Fig5f. *Segmented results*

B. Benign Case:

Figure6:(a-d)Test image,Curvelet decomposition, Segmented results for Benign case using SFCM method; (e-h) Test image,Curvelet Decomposition, Segmented results for benign case using K-Means clustering:

SFCM SEGMENTATION

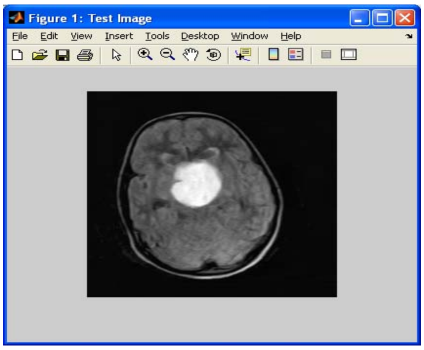

Fig 6a: Test image

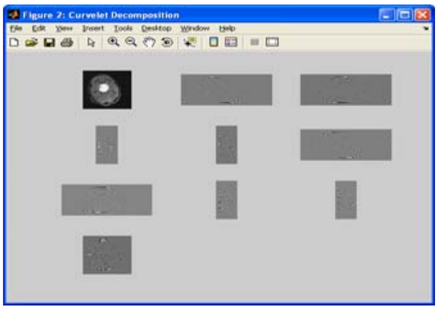

Fig6b.Curvelet Decomposition

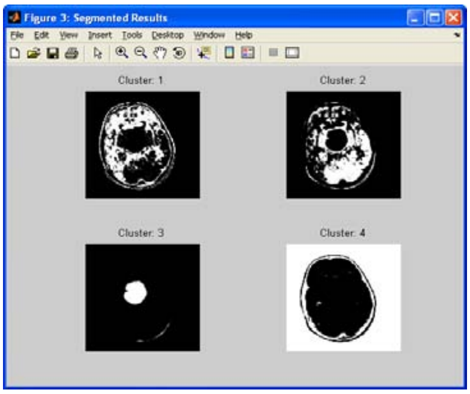

Fig 6c. Segmented results

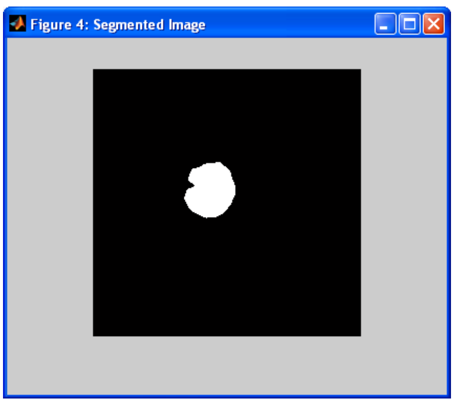

Fig6d.Abnormalabnormal region detected

K-MEANS SEGMENTATION

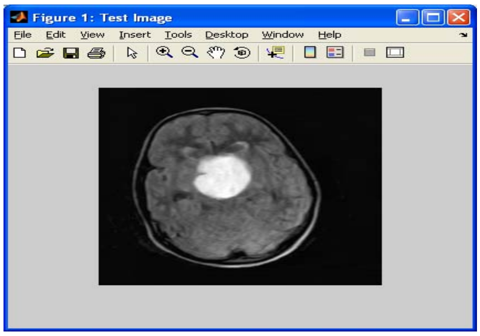

Fig 6e: Test image

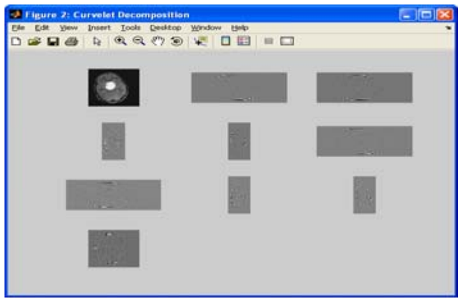

Fig6f.Curvelet Decomposition

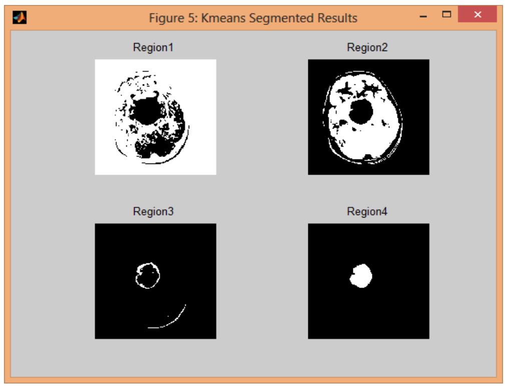

Fig 6g. Segmented results

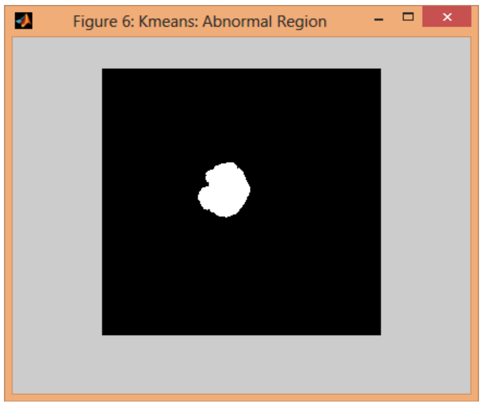

Fig6h.Abnormalabnormal region detected

C.Malignant Case:

Figure7:(a-d)Test image, Curvelet Decomposition, Segmented results for Malignant case using SFCM method; (e-h) Test image,Curvelet Decomposition, Segmented results for Malignant case using K-Means clustering.

SFCM SEGMENTATION K-MEANS SEGMENTATION

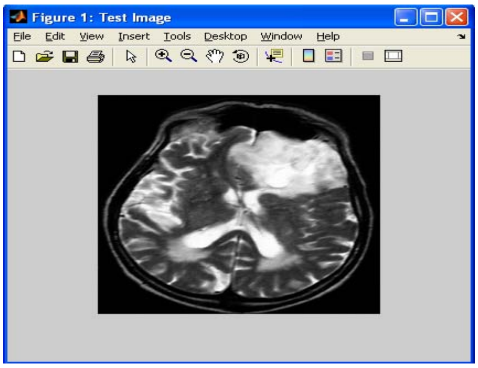

Fig 7a: Test image

Fig 7e: Test image

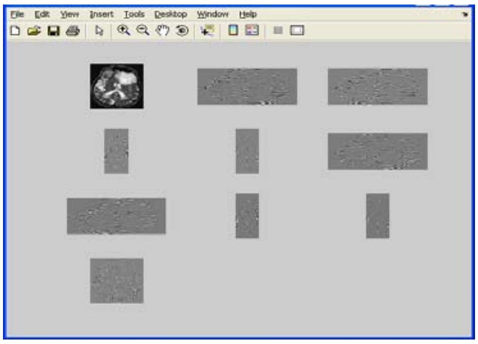

Fig7b.Curvelet Decomposition

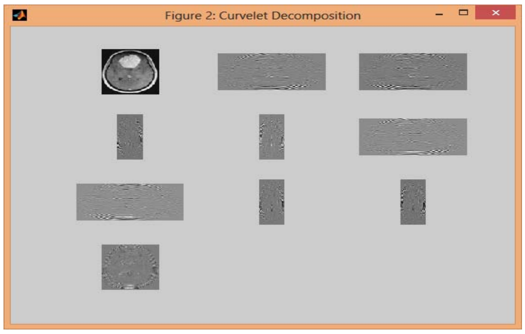

Fig7f.Curvelet Decomposition

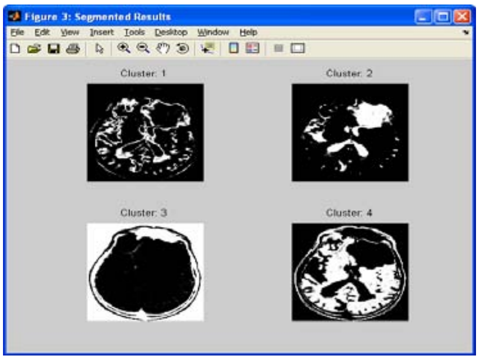

Fig 7c. Segmented results

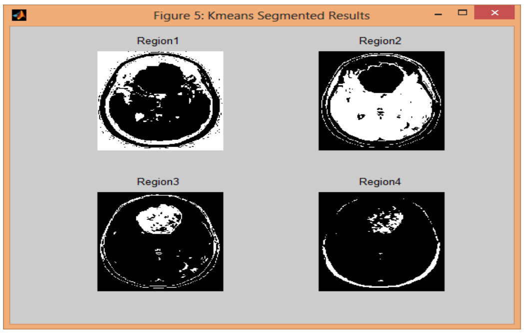

Fig 7g. Segmented results

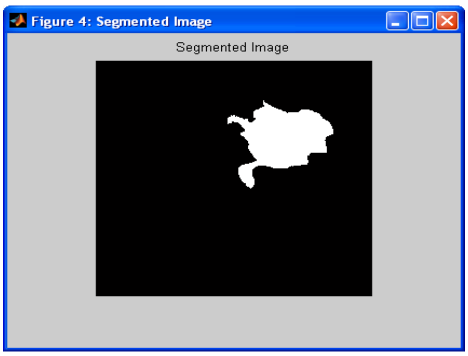

Fig7d.Abnormal region detected

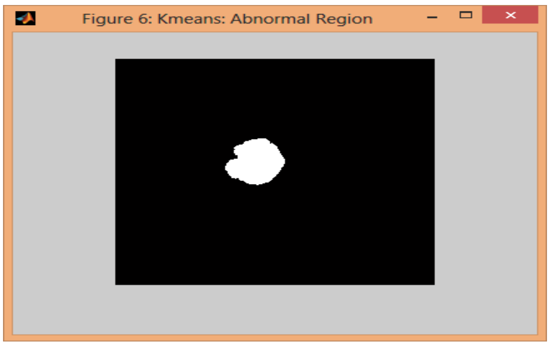

Fig7h.Abnormal region detected

VI. CONCLUSION

The paper presented that automated brain image classification for early stage abnormality detection with use of neural network classifier and spotting of tumor was done with image segmentation. Proposed is a new tumor classification based on discrete curvelet transform in which multi-level transformation is possible. Pattern recognition was performed using probabilistic neural network with radial basis function and pattern will be characterized with the help of fast discrete curvelet transform and Haralick features analysis. Here spatial fuzzy clustering algorithm was utilized effectively for accurate tumor detection to measure the area of abnormal region. From an experiment, system proved that it provides better classification accuracy with various stages of test samples and it consumed less time for process. As another extension, a toolbox can be developed in MATLAB to convert 2-dimensional images into 3-dimensional. A 3D image will be useful for the oncologists at the time of surgery. Since, it could show even the microscopic part of the MR images which is a major drawback of 2D.

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