Semantic Classification and Region Growing of Brain MRI using Canfis Model for Tumor Identification

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Abstract: Semantic interpretation and understanding of medical images is an important goal of visual recognition and offers a large variety of possible applications. This research involves semantic segmentation for pixel-wise classification of images for tumor identification. Classification of brain MRI is a difficult task for tumor identification due to variance in features. Hence, the exact features that involve in the classification and identification of region of interest have to be identified. Statistical features using wavelet and semantic features using novel method are extracted from the input MRI image. These features are fed into the neurofuzzy classifier for normal and abnormal image identification. Further, the pathological tissue segmentation is done using semantic region growing approach and identification of tumor is done. The results of implementation shows the efficiency of semantic segmentation technique in identifying the pathological tissues accurately from the MRI images. The performance of the segmentation technique is evaluated by performance measures such as accuracy, specificity and sensitivity.

Key words: Segmentation, pathological tissues, artificial neural network, white matter, gray matter, cerebrospinal fluid, tumor

INTRODUCTION

The front most part of the central nervous system is the brain. The maladies caused in the brain are brain tumors. The tumors that nurture in the brain are brain tumors. A strange development caused by cells reproducing themselves in an unrestrained way is known as tumor. A gentle brain tumor contains benign (harmless) cells and has separate boundaries. By means of Magnetic Resonance Imaging (MRI), the configuration and function of the brain can be learned non-invasively by doctors and researchers. The MRI image is really a lean horizontal piece of the brain. The white region at lower left is the cancer. It appears white since, MRI scans increase tissue differences. The cancer is really on the right side of the brain. Lately, to examine the relation between white matter growth and neural maladies, several people exploit the MRI data the precision of fragmenting white matter is the main problem. To fragment white matter, Attention Deficit Hyperactivity Disorder (ADHD) is moreover required. Despite many algorithms for fragmenting MRI of data, the Watershed algorithm, eSneke algorithm and generic algorithm are widely used. Besides, those algorithms are based on the homogeneity of image. Based on the Expectation-Maximization (EM) Algorithm (Mayer and Greenspan, 2009), wells progressed a novel statistical strategy but the results are too reliant on the early values, very consuming the time and now appearing for limited maximum point. Concerning one or more features, the fundamental objective in fragmentation process is to divide an image into areas that are uniform.

Fragmentation is an essential device in medical image processing and it has been constructive in several applications such as: detection of umors, detection of the oronary border in angiograms, surgical planning, measuring tumor volume and its response to therapy, automated classification of blood cells, detection of micro calcifications on mammograms, heart image extraction from cardiac cine angiograms, etc. (Hussain *et al.*, 2012).

It may be helpful to categorize image pixels into anatomical areas in various applications such as bones, muscles and blood vessels, though in others into pathological areas such as cancer, tissue deformities and multiple sclerosis lesions. To separate perfectly the whole image into sub areas is the goal in Magnetic Resonance (MR) images processing, integrated Gray Matter (GM), White Matter (WM) and Cerebrospinal Fluid (CSF) spaces of the brain. For instance, in a number of neurological turmoil such as Multiple Sclerosis (MS) and Alzheimer's disease (Cherifi *et al.*, 2011), the capacity varies in total brain, WM and GM can give main data about neuronal and axonal loss. A lot of algorithms have

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been suggested for brain MRI segmentation in latest years. The most famous techniques are integrated thresholding, region-growing and clustering (Shih and Cheng, 2005). The complete computerized intensity-based algorithms have elevated sensitivity to different noise relics such as intra-tissue noise and inter-tissue intensity difference reduction.

MATERIALS AND METHODS

In the proposed methodology, both the normal tissues such as WM (White Matter), GM (Gray Matter) and CSF (Cerebrospinal Fluid) and the pathological tissues for identification of tumorin the MRI brain images are segmented effectively. Initially, the wavelet transform features and the semantic features from the MRI brain images are extracted. These extracted features are the input to the next process. Then, the proposed segmentation technique performs classification process by utilizing neuro fuzzy classifier. The classifier is helpful for classifying whether the image is normal or abnormal. Based on the results the segmentation is carried out. In segmentation, the normal tissues such as WM, GM and CSF are segmented from the normal MRI images and the pathological tissue (tumor) is segmented from the abnormal images. The diagram for proposed methodology is given in Fig. 1.

The proposed technique is classified into three stages for the efficient segmentation of the MRI brain images into normal as well as pathological tissues. The three stages of the proposed technique are given:

- Feature extraction
- Classification
- Tumor segmentation

Feature extraction

Wavelet transform features extraction: In order to extract the wavelet transform features, the Haar Wavelet is applied to the input MRI. Later a two level wavelet transform is performed to the n×n dimension image. The features such as horizontal, vertical and diagonal bands of wavelet transform are obtained as the result of two level wavelet transform that is applied on the input images. Wavelet transform features such as horizontal, vertical and diagonal bands are calculated for the pixel co-efficients using the following equations (Alsultanny, 2008):

$$\text{Horizontal band (H)} = \frac{1}{r} \sum_{r=1}^{m} h_r \qquad (1)$$

$$\text{Vertical band (V)} = \frac{1}{r} \sum_{r=1}^{m} v_r \qquad (2)$$
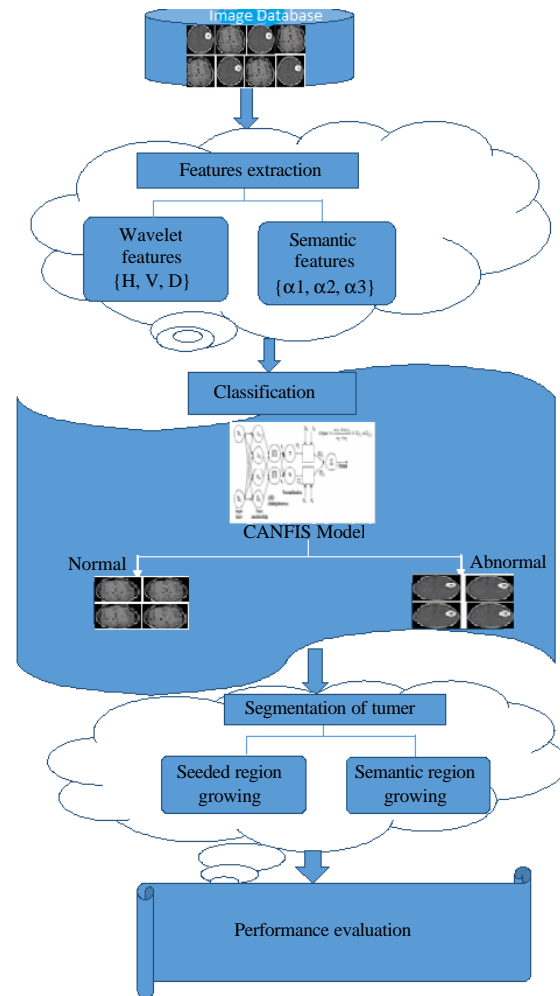

Fig. 1: Diagram for proposed methodology

$$\text{Diagonal band (D)} = \frac{1}{r} \sum_{r=1}^{m} d_r \qquad (3)$$

In Eq. 1-3, the value m indicates the pixel co-efficients and the parameters h_r, v_r and d_r, represents the coefficients of the horizontal, vertical and diagonal bands. Each feature has four pixel co-efficients.

Semantic features extraction: For extracting the semantic features the following steps are proceeded to map the low-level features with the high-level semantic features:

- Shape as low-level feature
- Key word as high-level feature
- Interpretation of low-level and high-level features

Shape as low-level feature: In this study, one of the low-level features named as shape feature is used to map

with the semantic information of the image. The edge detection is performed using Slope Magnitude Method. The edges of the shape feature that are extracted by the extraction process of input image should be connected. This makes the image to reflect the object boundaries. For extracting shape features in the form of connected boundaries, from the given MRI brain image, Sobel gradient operator is utilized.

Sobel gradient operator: It is a discrete differentiation operator that is used to performan approximation of the gradient of the image intensity function. Convolving the image with a small, separable and integer valued filter in horizontal and in vertical direction is the operation performed by the sobel operator. Based on computations, Sobel operator is inexpensive.

Steps to apply Slope Magnitude Method
Step 1: Convolve the original image with the Sobel mask S_x and S_y. The S_x mask is used to obtain the x gradient and S_y mask is used to obtain the y gradient:

$$S_x = \begin{bmatrix} +1 & 0 & -1 \\ +2 & 0 & -2 \\ +1 & 0 & -1 \end{bmatrix} \qquad (4)$$

$$S_y = \begin{bmatrix} +1 & +2 & +1 \\ 0 & 0 & 0 \\ -1 & -1 & -1 \end{bmatrix} \qquad (5)$$

Step 2: Get the individual squares of both values as S_x^2 and S_y^2 in Eq. 4 and 5.

Step 3: Add the two squared terms as: $S_x^2 + S_y^2$.

Step 4: Take square root of the sum and then researchers get the equation as:

$$S = \sqrt{S_x^2 + S_y^2} \qquad (6)$$

Thus, low-level shape feature is obtained using the Slope Magnitude Method.

Keyword as high-level feature: Keywords are the features that are helpful for describing the high-level domain concepts. The attributes of semantics includes some subjectivity, uncertainty, etc. The shape edge property is directly extracted using edge detection. High level semantic property can be extracted as the keyword, on the basis of low-level visual feature, shape. In the MRI brain image, the shape edge is initially extracted and according

to the clearance of shape edge. The semantic terms that are related with the clearance of the shape edge are:

$$ST = \{\text{"low, medium, high"}\}$$

Interpretation of low-level and high-level features: Initially find out the bounds of the semantic class, clearance, i.e.:

$$\{\text{"low} = \alpha_1, \text{medium} = \alpha_2, \text{high} = \alpha_3\text{"}\} \qquad (7)$$

For mapping the shape feature edge S into semantic term ST, the following inference rules or the degree of clearance are used:

$$I \rightarrow \begin{cases} \text{low} & \text{if } S < \inf \\ \text{medium} & \text{if } \inf < S < \sup \\ \text{high} & \text{otherwise} \end{cases} \qquad (8)$$

The upper sup and lower inf bounds are representation of shape feature edge and both are related to α_1 and α_2, respectively. Thus, the high level semantic features α_1-α_3 are extracted. Hence, the wavelet transform features as well as the semantic features are extracted effectively from the MRI brain images.

Classification using CANFIS: From the input MRI brain image I, both wavelet transform as well as semantic features are extracted, directly. Using Eq. 1, 2, 3, 7 and 8, the features are extracted for the entire image. The features that are extracted using direct extraction are represented as:

$$F = \{H, V, D, \alpha_1, \alpha_2, \alpha_3\} \qquad (9)$$

For the classification of the MRI brain images into normal and abnormal tissues, the extracted features using Block-wise Process and also the features that are extracted directly are given as the input to the neuro fuzzy classifier (Hemachandra and Satyanarayana, 2013).

Classification using CANFIS: The features that are extracted directly from the input MRI image are three statistical features and three semantic features are used for classification purpose. The extracted features namely $F = \{H, V, D, \alpha_1, \alpha_2, \alpha_3\}$ are fed as input to the Co Active Neuro-Fuzzy Inference System (CANFIS) Model. The architecture of the CANFIS is shown. The central component of CANFIS is a fuzzy axon, it applies the membership functions to the input responses. The following formula illustrates the output of the fuzzy axon:

$$f_j(x,w) = \min \quad \forall i = MF(x_i, w_{i,j}) \qquad (10)$$

Where:

i = Input index
j = Output index
x_i = Input i
w_{ij} = Weights (MF parameters) corresponding to the jth MF of input i
MF = Membership function of the particular subclass of the fuzzy axon

This system is a special three-layer feed forward neural network. In the first layer input variables are represented and in the middle (hidden) layer the fuzzy rules are represented. The third layer signifies the output variables. Consider a CANFIS structure with n inputs and one output (Fig. 2).

Layers of CANFIS: Layers in CANFIS structure can be adaptive or fixed and their functions are:

Layer 1 (premise parameters): Each node of this layer is a complex-valued membership function μ_{ij} with a node function:

$$O_{1,ij} = \left| \mu A_{ij}\left(z_i \right) \right| \angle \mu A_{ij}\left(z_i \right) \text{ for } 1 \le i \le n, 1 \le j \le m$$

$$(11)$$

Each node in layer 1 is the membership grade of a fuzzy set (A_{ij}) and specifies the degree to which the given input belongs to one of the fuzzy sets.

Layer 2 (firing strength): Every node in this layer is product of all the incoming signals. The product of all the output pairs from the first layer is given as input to this layer:

$$O_{2,j} = w_j = \mu A_{i1}(z_1)\mu A_{i2}(z_2),..., \mu A_{i1n}(z_n)$$
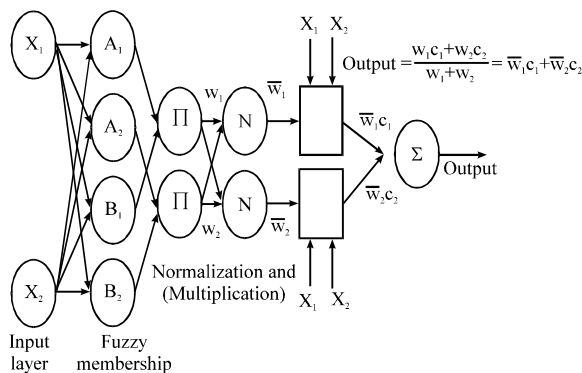$$\text{for } 1 \le i \le n, 1 \le j \le m \qquad (12)$$

Fig. 2: Two-input one-output CANFIS network and output calculation

Layer 3 (normalized firing strength): All the nodes in this layer are used to calculate rational firing strength:

$$O_{3,j} = \overline{W_J} = \frac{W_j}{\sum_{j=1}^{m} W_j} \quad \text{for } 1 \le j \le m \qquad (13)$$

Layer 4 (consequence parameters): Each node in this layer is obtained from the multiplication of normalized firing strength from the third layer and output of neural network:

$$O_{4,j} = \overline{W_J} u_j = \overline{W_J}(P_{J1}Z_1 + P_{J2}Z_2 +,... + P_{Jn}Z_{2n} + q_j)$$
$$\text{for } 1 \le i \le n, 1 \le j \le m \qquad (14)$$

Layer 5 (overall output):
The node here computes the output of CANFIS network:

$$O_{5,1} = \sum \overline{W}_j u_j$$

If-then rules:
For model initialize, a common rule set with n inputs and m IF-THEN rules as follows:

Rule 1: If z_1 is A_{11} and z_2 is A_{12}... and z_{nis} A_{1n} then $u_1 = P_{11}z_1 + P_{12}z_2 +... + P_{1n} z_n + q_1$

Rule 2: If z_1 is A_{21} and z_2 is A_{22}... and z_{nis} A_{2n} then $u_2 = P_{21}z_1 + P_{22}z_2 +... + P_{2n} z_n + q_2$
.
.
.

Rule m: If z_1 is A_{m1} and z_2 is A_{m2}... and z_{nis} A_{mn} then $u_m = P_{m1}z_1 + P_{m2}z_2 +... + P_{mn}z_n + q_m$

The data are fed as input to the CANFIS Model

Experimental study: In this study, the CANFIS architecture is used and the problem is proposed to network models by means of five inputs and one output parameter. The system produces the output either 1 or 0 that represents normal or abnormal. All experimental data were randomly placed in these sets. Before applying the CANFIS to the data, the training, cross-validation, testing and production subsets were scaled (normalized) to the range of 0-1 using the following equation:

$$X_{norm} = 0.5 + 0.5\left(\frac{X - \overline{X}}{X_{max} - X_{min}}\right) \qquad (15)$$

Where
X = The input value
X_{norm} = The scaled input value of the input value X
X_{max} and
X_{min} = The respective maximum and minimum values of the unscaled measured data

In this study, the Bell membership functions and TSK fuzzy models were used. For small to medium-sized data sets, the number of membership functions assigned to each network input will usually be between 1 and 10. The various algorithms (i.e., Levenberg-Marquardt, Delta-Bar-Delta, Step, Momentum, Conjugate Gradient and Quick prop) were applied in order to identify the one which trains a given network more efficiently. Besides, different transfer functions (i.e., Sigmoid, Linear sigmoid, Tanh, Linear Tanh, Linear and Bias) were used in order to identify the one which gives the best results in depicting the non-linearity of the modelled natural system. The best architecture of the network was determined by trial and error. In fact, the optimal network architecture for each model was selected from the one which resulted in minimum errors and best correlation in the data set. The process of designing the networks is managed by NeuroSolution for Excel Release 6 Software produced by Neuro Dimension, Inc.

Criteria of evaluation: To evaluate the success of CANFIS in learning, several statistical measures could be used. The comparison of the actual and desired values will be obtained. The statistical criteria considered here were minimum Mean Square Error (MSE), mean absolute error, minimum absolute error, maximum absolute error and Percentage Error of estimate (PE). Also, the MSE and PE are used to determine how much the network has reached to desired output values. The performance evaluation criteria used in this study can be calculated utilizing the following equations:

$$MSE = \frac{\sum_{i=1}^{n}(P_i - O_i)^2}{n} \qquad (16)$$

$$PE = \left|\frac{\overline{P} - \overline{O}}{\overline{O}}\right| \times 100\% \qquad (17)$$

Where:
P_i and O_i = The predicted and observed values, respectively
$\overline{P}$ and $\overline{O}$ = The average of P_i and O_i
n = The total number of data

The data used for developing this model was obtained from the experimental study and the prediction capability of the model was done by statistical and semantic features of input MRI as parameters.

Segmentation: Segmentation is the important part of this proposed methodology since this research involves semantics. Medical image segmentation is a complex and challenging task due to the indefinite nature of input images for further processing. This research involves the partitioning of the input image space into non-overlapping meaningful homogeneous regions. In general, these regions will have a strong correlation with the objects in the image. The success of an image analysis system depends on the equality of segmentation of the images.

After the classification of the images, normal and abnormal images are obtained. Segmentation is done on both these normal and abnormal images. In the normal images, the normal tissues such as WM (White Matter), GM (Gray Matter) and CSF (Cerebrospinal Fluid) are segmented and in abnormal images, the pathological tissues such as Tumor, Edema and Atrophy are segmented. In segmentation, the following two stages are performed:

- Pre-processing stage
- Tissue segmentation stage
  - Normal tissue's segmentation
  - Abnormal tissue's segmentation

Pre-processing stage: In this study, Skull Stripping Method is used for pre-processing the normal brain tissues. In the MRI images, the brain cortex is normally a separate dark ring surrounding the brain tissues. This separate dark ring surrounding the brain tissues are removed with the usage of Skull Stripping Method. Initially, in Skull Stripping Method, the normal brain tissue images are converted into gray scale image and then in the gray scale image, a morphological operationis performed. Then, with the help of region based binary mask extraction, the brain cortex is stripped in the gray scale image. The preprocessing process is performed only in the classified normal images and not in the abnormal images. Because, the pre-processing task help the normal tissue CSF (Cerebrospinal Fluid) to be lightly placed in the cortex surrounding area. The representation of the obtained normal image after Skull Stripping Method is I_S.

Tissue segmentation stage: After the pre-processing stage using Skull Stripping Method, the tissue segmentation is performed in the MRI brain images. Different methods are helpful to segment both normal as well as the pathological brain tissues (Hussain *et al.*, 2012). From the normal brain tissue images, the segmentation of the normal tissues such as WM (White Matter), GM (Gray Matter) and CSF (Cerebrospinal Fluid) are obtained in two ways:

- White matter and gray matter segmentation using Gradient Method
- Cerebrospinal fluid segmentation using OPT Method

White matter and gray matter segmentation using Gradient Method: The input for this white matter and gray matter segmentation is the skull stripped image I_S. Using Gradient Method, the WM and GM normal brain tissues are segmented from the image I_G. By utilizing Gaussian Convolution filter, the smoothing process is performed in the input image I_G. The resulting image I_G is the smoothed image that is obtained from the Gaussian Convolution filter. Then, the Gradient Operation is applied to the smoothed image, I_G. The representation of the gradient of two variables x and y is as follows:

$$\nabla I_G(x,y) = \frac{\partial I_G}{\partial x}\hat{e} + \frac{\partial I_G}{\partial y}\hat{f} \qquad (18)$$

The current edges in the image are marked as the following equations by applying the values of gradient:

$$G = x_{(e)^2} + y_{(f)^2} \qquad (19)$$

$$EM = \frac{1}{1+G} \qquad (20)$$

After that, the process of binarization is performed in the edge marked image EM. During the binarization process, by using a global threshold T_G, the gray level value of each pixel in the image is observed EM and the final binarized image is I_K. Then, morphological opening and closing operations are applied to the binarizedimage I_K. These opening and closing operations are used to remove small holes and small objects from the image I_K. Based on the intensity values, the WM and GM normal brain tissues are segmented:

$$I_{wg} = \begin{cases} WM & \text{if } I_{K_i} = 1 \\ GM & \text{if } I_{K_i} = 0 \end{cases} \qquad (21)$$

Cerebrospinal fluid segmentation using OPT Method: Skull stripped image I_S is subjected to Orthogonal Polynomial Transform (OPT) for segmenting the normal brain tissue cerebrospinal fluid. The computation of the image in OPT is as follows:

$$I_{CFS} = Sin\left(\frac{I_{S_{(i)}}^3}{100}\right)^2 + \left(0.05 \times rand(|I_S|)\right) \qquad (22)$$

After the polynomial transform, the corresponding cerebrospinal fluid region is segmented in the resultant image I_{CSF}. From the classified abnormal MRI brain images,

the abnormal tissues of tumor is segmented. The segmentation of pathological tissues is performed by Region Growing Method. This region growing involves the semantic approach for the effective segmentation.

Tumor segmentation using RGM: From the pathological MRI brain image I_A, the tumor tissues are segmented. For segmenting the abnormal tumor tissue image I_A, Seeded Region Growing Method (RGM) is used here. Region Growing Method is a region based image segmentation method; it selects the initial seed points from the input image I_A. The RGM observes the neighbor pixel values with the initial seed points that is it checks whether the neighbor pixels are included in this region or not.

Semantic region merging: The segmented image has clusters of data that are heterogeneous, the clustered information has to be grouped to make them enable for classification, here researchers propose a semantic approach for grouping the neighbours. The non-semantic and semantic portion for clustering is given.

Non-semantic criteria-seeded region growing: T1 and T2 are preset thresholds:

1   Merge region i, j as long as they have 1 weak separating edge until no two regions pass this test
2   Merge regions i, j where, $s(i, j) \leq T\_2$, $S(i, j) = (c\_1 + \alpha\_{ij})/(c\_2 + \alpha\_{ij})$, c1 and c2 are constants, $\alpha_{ij} = ((area\_i)^{(1/2)} + (area\_j)^{(1/2)})/(perimeter\_i. perimeter\_j)$ until no two regions pass this test

Semantic criteria:
3   Let Bij be the boundary between Ri and Rj. Evaluate each Bij with a Bayesian decision function that measures the (conditional) probability that Bij separates two region Ri and Rj of the same interpretation. Merge Ri and Rj this contitional probability is less than some threshold. Repeat steps 3 until no regions pass the threshold test
4   Evaluate the interpretation of each region Ri with a Bayesian decision function that measures the (conditional) probabilty that an interpretation is the correct one for that region. Assign the interpretation to the region with the highest confidence of correct interpretation. Update the conditional probabilities for different interpretations of neighbors. Repeat the p until all regions have interpretation assignments

The semantic portion of the above algorithm maximizes the evaluation function by measuring the

probability of a correct interpretation (labeled partition), given the measurements on the boundaries and region of the partition. The resultant segmented pathological tumor tissue image is represented as I_T.

RESULTS AND DISCUSSION

The proposed Segmentation Method is implemented in MATLAB platform. MRI brain images are gathered from various database and given as the input to this implementation. Initially normal and abnormal images are present in the whole MRI brain images. After the classification, the group of images is classified into normal and abnormal. Figure 3 shows the sample MRI brain images that are used as input for the classification purpose.

The given MRI brain images are classified using CANFIS classifiers. Six features such as 3 wavelet transform features and 3 semantic features are the inputs of the neuro fuzzy classifier. The testing images are the classified images that are shown in the Fig. 4 and 5. Then, the abnormal images are segmented into tumor and edema pathological tissues using RGM and multi-level thresholding function. The segmentation process for the pathological tissues is explained in study. The results of tumor and edema tissue segmentation is given in Fig. 6.

Performance analysis: The performance of the Brain Tissue Segmentation Method is analyzed by various statistical measures. The statistical performance measures that are obtained for the normal and abnormal MRI brain images are shown in Table 1.
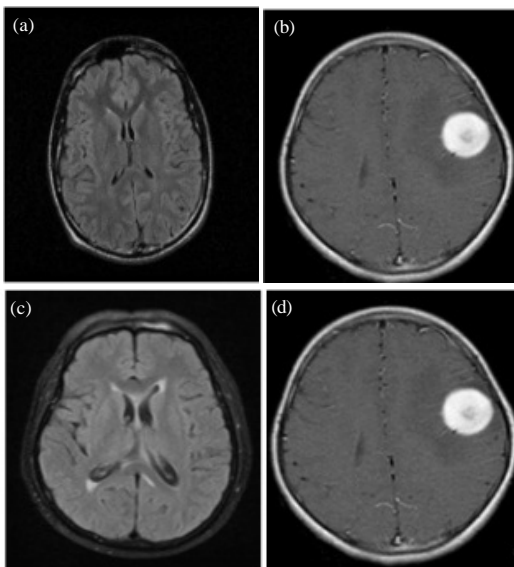

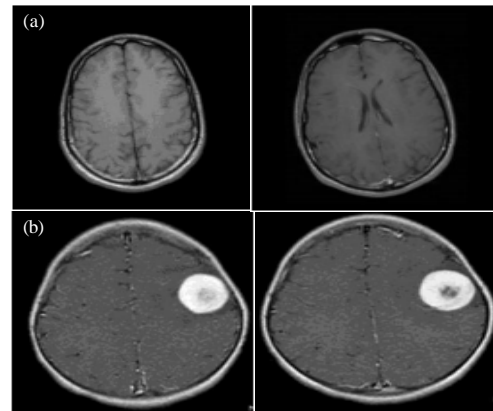Fig. 3: a-d) Sample MRI brain images in the database

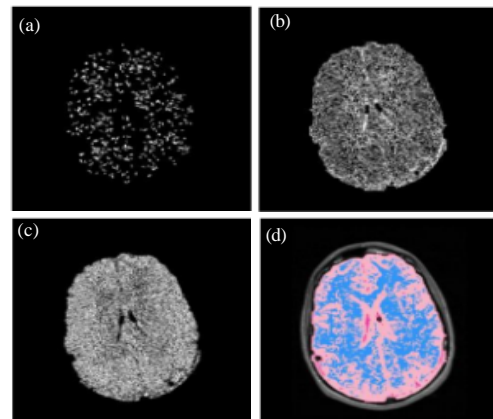Fig. 4: Classified images; a) normal and b) abnormal

Fig. 5: Segmentation outputs of b) normal tissues; b) WM Segmentation; c) GM segmentation and d) CSF segmentation
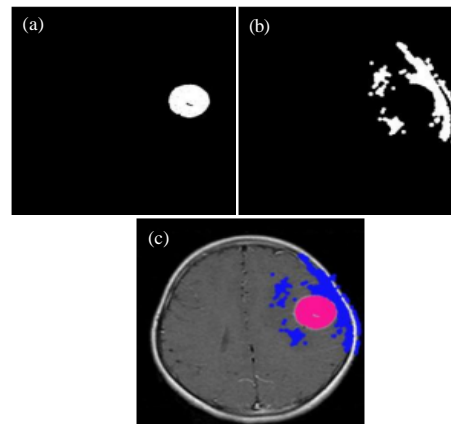

Fig. 6: Segmentation of abnormal tissues output; a) segmented tumor region image; b) segmented edema region image and c) original image for the abnormal tissues tumor and edema

Table 1: Statistical performance measures of normal and abnormal tissues of MRI brain images

Tissues	Measures		
	Sensitivity	Specificity	Accuracy
WM	80.0	100.000	98.41
GM	74.2	99.100	94.45
CSF	72.2	99.125	99.50
Tumor	48.0	95.600	94.10

Table 2: Performance comparison of existing K-means and fuzzy-ANN with the proposed method, in segmenting, WM, GM, CSF and Tumor

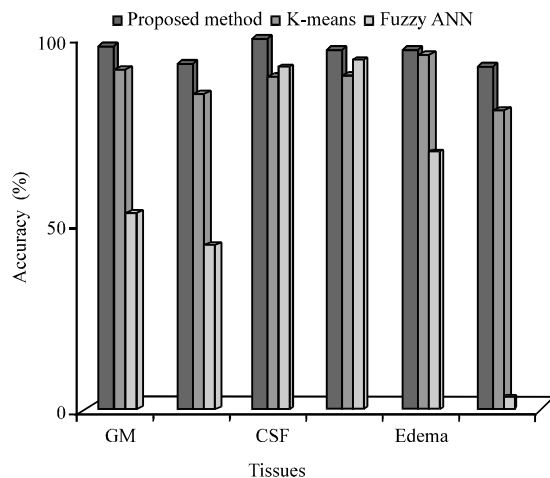| Tissues	Methods		
	Proposed method	K-means	Fuzzy ANN
GM	98.41	92.6	52.998
WM	94.45	84.6	43.164
CSF	99.50	90.8	93.296
Tumor	94.10	80.6	0.000

Fig. 7: Graph result for comparing accuracy of segmenting the tissues GM, WM, CSF and tumor of proposed method with K-Means and Fuzzy ANN

Comparative analysis: To analyze the performance of tissue segmentation, the proposed method is compared with K-Means Clustering and existing fuzzy ANN based Segmentation Method. K-Means Clustering and Fuzzy ANN Method is applied to five MRI brain images in order to segment the normal and abnormal tissues. The clustering method segmentation performance is shown in Table 2.

Figure 7 shows the result of a graph while comparing the accuracy for segmenting the normal tissues such as WF, GF and CSF and also the abnormal tissues such as Atrophy, Edema, Tumor. From the Fig. 7, it is observed that the accuracy of the proposed method is higher than the existing methods such as K-Means and Fuzzy ANN.

CONCLUSION

The normal tissues such as WF, GF and CSF and abnormal tissues of tumor were effectively segmented from the given MRI brain images with the help of the proposed Segmentation Method. The features were extracted in using wavelet and semantic approach. With those extracted features, the normal and abnormal images were classified using neuro fuzzy classifier. After classification, the normal images were given under pre-processing operation and then Segmentation was performed to segment WF, GF and CSF tissues. Then, the segmentation process was done on abnormal tissues for segmenting the tumor tissues, here the segmentation based upon normal region growing and semantic region growing is done. In this proposed method, the normal and abnormal images were utilized for analyzing the performance of the proposed Segmentation Method. The results of the proposed methodology for segmentation showed that the segmentation is more accurate and very sensitive since it involves semantics in two levels (i.e.) for feature extraction and region growing.

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