Segmentation of Tissues in Brain MRI Images using Dynamic Neuro-Fuzzy Technique

S.Javeed Hussain, T. Satya Savithri, P. V. Sree Devi

Abstract- In this paper, an efficient technique is proposed for the precise segmentation of normal and pathological tissues in the MRI brain images. The proposed segmentation technique initially performs classification process by utilizing Fuzzy Inference System (FIS) and FFBNN. Both classifiers are utilizing the extracted image features as an input for the classification process. The features that are extracted in two ways from the MRI brain images. The FIS are used to make the classification process by generating the fuzzy rules using extracted features. Five features are extracted from the MRI images: they are two dynamic statistical features and three 2D wavelet decomposition features. In Segmentation, the normal tissues such as WM (White Matter), GM (Gray Matter) and CSF (Cerebrospinal Fluid) are segmented from the normal MRI images and pathological tissues such as Edema and Tumor are segmented from the abnormal images. The non-cortical tissues in the normal images are removed by the preprocessing stage. The implementation result shows the efficiency of proposed tissue segmentation technique in segmenting the tissues accurately from the MRI images. The performance of the segmentation technique is evaluated by performance measures such as accuracy, specificity and sensitivity. The performance of segmentation process is analyzed using a defined set of MRI brain image and compared against K-means clustering and Fuzzy ANN based segmentation methods.

Keyword: MRI, FFBNN, FIS

I. INTRODUCTION

Segmentation of brain tissue on magnetic resonance (MR) images normally determines the type of tissue present for each pixel or voxel in a 2D or 3D data set respectively, based on the information gathered from both MR images and prior knowledge of the brain. It is one of the most vital preprocessing steps in several medical research and clinical applications, such as quantification of tissue volume, visualization and analysis of anatomical structures, multimodality fusion and registration, functional brain mapping, identification of pathology, surgical planning, surgical navigation, and brain substructure segmentation [1]. Segmentation at preliminary stage is important and necessary for the analysis of medical images for computer-aided diagnosis and treatment. As the images are inherent in nature, medical image segmentation is a difficult and challenging task [2] [14] [15]. Magnetic resonance imaging (MRI) is a significant diagnostic imaging method, which is employed for the early detection of abnormal changes in tissues and organs [3] [16] as well as it is a non-invasive imaging technique, so it allows a radiologist to create an image of the inner aspects of living tissue [12].

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Normally the structure of brain is complex and its accurate segmentation is very crucial for finding the tumors, edema and necrotic tissues in order to specify proper therapy [4]. The brain matters are mainly categorized as white matter, gray matter, cerebrospinal fluid (CSF) or vasculature. Mostly the brain structures are clearly described by the boundaries of the tissue classes, so a technique to segment tissues based on these categories is a major step in quantitative morphology of brain [6]. Apart from other diagnostic methods, Magnetic resonance imaging (MRI) systems can generate many images and each image indicates a different essential parameter of inner anatomical structures in the same body section with multiple differences, based on the local variations of spin–spin relaxation time (T2), spin–lattice relaxation time (T1), and proton density (PD) [5]. The presence of noise, errors in the scanners, and the structural variations of the imaging objects are the major obstruction to the segmentation of MR images, such obstructions are categorized into four types: thermal/electronic noise, magnetic field inhomogeneities, biological tissue variations, and incomplete volume effects [7].

Moreover, recognition and analysis of the lesions manually from MR brain images are generally time consuming, expensive and can produce unacceptably high intraobserver and interobserver variability [8]. The segmented MR images used in the medical diagnostic process depends on a combination of two, often conflicting, requirements, that is, the removal of the unnecessary information present in the original MR images and the maintenance of the significant details in the resulting segmented images [13] [17]. MR-image segmentation methods are usually evaluated based on their ability to differentiate i) between cerebro-spinal fluid (CSF), white matter, and gray matter and ii) between normal tissues and abnormalities [9]. Many techniques proposed in the recent years, which are used for the segmentation of brain tissues from MR image, are classical pattern recognition methods, rule-based systems, image analysis methods, crisp and fuzzy clustering procedures, feed-forward neural networks, fuzzy reasoning, geometric models to determine lesion boundaries, connected component analysis, deterministic annealing, atlas based methods and contouring approaches [10] [11]. Lots of researches have been performed for the segmentation of normal and abnormal tissues in MRI brain images. Some of the recent related works regarding the segmentation of brain tissues are reviewed in the following section.

II. PROPOSED METHODOLOGY FOR TISSUE SEGMENTATION IN MRI BRAIN IMAGES

In this paper, we propose an efficient method to segment the normal and pathological tissues in the MRI brain images. Two major stages are involved in our proposed methodology:

Classification
- Segmentation

Initially, the classification process is done on the given MRI brain images. In classification, the feature extraction process is performed in two ways and then these extracted features are given to the FIS and FFBNN for classification. Utilizing both classifier results, the MRI brain images (input image) are classified into normal and abnormal. Next, the segmentation process is performed over these classified images. Before the segmentation process, the non cortical tissues in the normal images are removed by performing preprocessing. Normal tissues such as WM, GM and CSF are segmented from the normal images and pathological tissues such as edema and tumor are segmented from the abnormal images.

2.1 Classification

In classification stage, the MRI brain images are classified into normal and abnormal brain images. Two phases are involved in this classification that are mentioned below

(i) Feature extraction
(ii) Fuzzy Rules Generation
(iii) Network training and testing

2.1.1 Feature Extraction

The features are extracted from the database MRI brain images. This process is done in two ways: (i) features that are extracted from the input images are processed blockwise; (ii) features are extracted directly from the input images. These two features extraction customs extract same features.

2. 1.1.1 Block wise Feature Extraction:

Let I be the brain image that is divided into N number of blocks, which is represented as $B = \{b_k\}; k = 1 \cdots N.$ .For feature extraction process, we have considered only a few numbers of blocks (not all blocks) by performing Euclidian distance measure. For this, we have taken one block b_k and checked its neighbor blocks. If the entire neighbor blocks value is 0, then these blocks are not considered for feature extraction process or else determine the distance between the chosen block b_k and neighbor blocks by exploiting Euclidian distance.

$$D_{kl} = b_k - b_l; l = 1 \cdots N, (k \neq l) \quad (1)$$

The distance value of each block D_{kl} is compared with the user defined threshold value t_1. During this comparison, if the distance value D_{kl} of all blocks is less than this threshold t_1, then it is adequate to store one block instead of storing all the blocks or else store the block's values individually. As a result of the above process, we obtain the block values that are stored in a variable $B_s = \{k^{'}\}; k^{'} = 1 \cdots N^{'}$ and the Feature extraction process is carried out for those stored blocks only. The features are extracted from each block in the block variable B_s and each block is of $n \times n$ dimension. Each block contains η number of pixels. Particularly in each block, 5 features are extracted namely, statistical features such as mean and variance, and multilevel 2D wavelet decomposition features such as horizontal, vertical, diagonal bands of wavelet transform. The feature vector of each block is

$$F_k = \{M_{k^{'}}, E_{k^{'}}, H_{k^{'}}, V_{k^{'}}, D_{k^{'}}\} \quad (2)$$

Pixel values are represented as p_u and the features such as mean and variance are calculated for these pixels in the blocks. Features are calculated by using the following equations

$$M_{k^{'}} = \frac{1}{\eta} \sum_{u=1}^{\eta} p_u \quad (3)$$

$$E_{k^{'}} = \left(\frac{1}{\eta} \left(\sum_{u=1}^{\eta} (p_u - M_k)^2 \right) \right) \quad (4)$$

To obtain the wavelet features, here haar wavelet is applied to the blocks and performed a two level wavelet transform. The two level wavelet transform is applied to the $n \times n$ size block images. After the two level wavelet transform, three features are extracted from the result image. Each feature has four pixel coefficients as m, and the computation of these three features $H_{k^{'}}, V_{k^{'}}, D_{k^{'}}$ are described in the following equations

$$H_{k^{'}} = \frac{1}{c} \sum_{c=1}^{m} h_c \quad (5)$$

$$V_{k^{'}} = \frac{1}{c} \sum_{c=1}^{m} v_c \quad (6)$$

$$D_{k^{'}} = \frac{1}{c} \sum_{c=1}^{m} d_c \quad (7)$$

In equations (5), (6), (7) the parameters h_c, v_c and d_c are the coefficients of the horizontal, vertical, and diagonal bands of one block $k^{'}$.

2.1.1.2 Direct Feature Extraction from Input Image

Features are extracted directly from the input image I. Features are extracted by utilizing the equations (3), (4) (5), (6) and (7) but they are extracted for the whole image not for blocks. The extracted features are M, E, H, V and D. In feature extraction phase, the extracted features in 3.1.1.1 FFBNN and the features from 3.1.1.2 are given to the FIS to accomplish the classification process.

2.1.2 Fuzzy Inference System (FIS)

The fuzzy inference system normally contains three major operations: Fuzzification, Rules Evaluation and Defuzzification. Fuzzy inference is the process of creating a mapping from a given input to an output by means of a fuzzy logic.

Then, the mapping provides a basis from which decisions can be made, or patterns discerned. The process of fuzzy inference involves Membership Functions, Logical Operations, and If-Then Rules. The schematic diagram of the fuzzy inference system (FIS) is shown in Fig. 2.

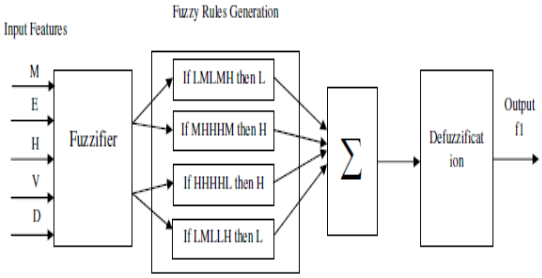

Figure 1: Fuzzy Inference System Structure

Fuzzification

In fuzzification process, the crusty quantities are changed into fuzzy. In our proposed method, the fuzzification process is carried out by employing the features that are extracted in section 3.1.1.2. The extracted features are M, E, H, V *and* D, for each feature we perform the fuzzification process. For the fuzzification process, we collect all the M, E, H, V *and* D features values of training images and computed each feature minimum (min) and maximum (max) values. The fuzzification process is performed by using the following equations.

$$ML^{(M)} = \min + \left(\frac{\max - \min}{3}\right) \qquad (8)$$

$$XL^{(M)} = ML + \left(\frac{\max - \min}{3}\right) \qquad (9)$$

In above equations (8) & (9), $ML^{(M)}$ *and* $XL^{(M)}$ are the minimum and maximum limit values of the feature M. The same equations are used for the features E, H, V *and* D to compute the minimum and maximum limit values.

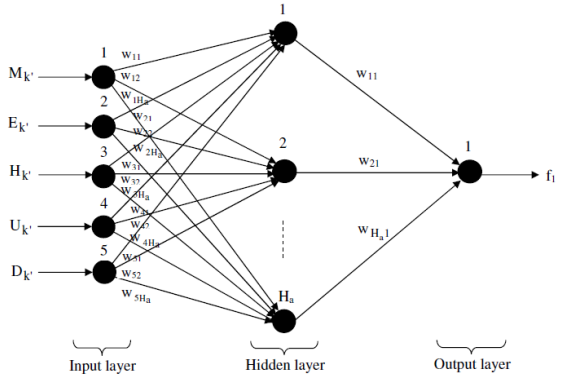

Figure 2: Basic Structure of the F1 FFBNN

The following steps describe the function of the Neural Network:

Step 1: Put the input weights to every neuron except the neurons in the input layer.

Step 2: The neural network is designed with five inputs layers, H_a hidden layers and one output layer. The weights are then added to the neural network and it is biased.

Step 3: The planned bias function and activation function for the neural network is described below.

The input layer bias function is given $M_{k'}(k'n')$, $E_{k'}(k'n')$, $H_{k'}(k'n')$, $V_{k'}(k'n')$ and $D_{k'}(k'n')$ are the extracted features of the block k'. The activation function for the output layer is given in Eq. (10).

Step 4: Compute the learning error for the neural network.

$$L^{(e)} = \frac{1}{H_a} \sum_{n'=0}^{N_a - 1} D_{n'} - Z_{n'} \qquad (10)$$

In Eq. (11), $L^{(e)}$ is the FFBNN network output, $D_{n'}$ *and* $Z_{n'}$ are the desired and actual outputs respectively.

Dual FFBNN networks $F1$*and* $F2$ are well trained with these extracted features and different number of unknown brain MRI images is tested. After generating both networks, we compute average value between $F1$*and* $F2$ networks results f_1, f_2.

$$A = \frac{f_1 + f_2}{2} \qquad (13)$$

The result of these $F1$*and* $F2$ networks average value is represented as A and this value A is compared with threshold value t_2.

$$result = \begin{cases} Abnormal;\ A \geq t_2 \\ Normal;\ A \leq t_2 \end{cases} \qquad (14)$$

In this way, the brain MRI images are classified into normal and abnormal. Next, the segmentation process is performed for these classified images.

3.2 Segmentation

Segmentation process is performed in both normal and abnormal images. In normal images, the normal tissues such as WM, GM and CSF are segmented and in abnormal images, the edema and tumor tissues are segmented. Following are the two steps involved in the segmentation process

(i) Preprocessing
(ii) Tissue Segmentation
(a) Normal tissue segmentation
(b) Pathological tissue Segmentation

3.2.1 Preprocessing

Various preprocessing methods have been proposed to deal with the MRI brain images used for segmentation. Among all preprocessing methods, Skull stripping is used for the segmentation of brain tissues.

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The brain cortex can be visualized as a distinct dark ring surrounding the brain tissues in the MRI images. The distinct dark ring surrounding the brain tissues are removed by skull stripping method. In skull stripping, initially the given MRI brain image is converted into gray scale image and then a morphological operation [25] is performed in the gray scale image. Then the brain cortex in the gray scale image is stripped by using region based binary mask extraction. The preprocessing process is performed in the classified normal images, not abnormal images. Because preprocessing process helps to improve the normal tissue CSF is lightly placed in the cortex surrounding area. The normal is image obtained after skull stripping is denoted as I_s.

3.2.2 Tissue Segmentation

After skull stripping, the brain MRI images are involved in the tissue segmentation process. Different methods are used to segment the WM, GM, CSF, edema and tumor tissues.

3.2.2.1 Normal Tissue Segmentation

Segmentation of Normal tissues such as WM, GM and CSF are performed from the normal images. Here, segmentation process is performed in two ways namely,

(i) WM and GM segmentation
(ii) CSF segmentation

WM and GM segmentation

The skull stripped image I_s is given as input to the WM and GM segmentation process. Here, the major step is to segment the WM and GM tissues from the image I_s by utilizing Gradient Method. The smoothing process is performed in the input image I_s by applying Gaussian convolution filter. Smoothed image obtained from the Gaussian convolution filter is I_G. After that, gradient operation is applied to the image I_G. The gradient of two variables x and y is defined as follows,

$$\nabla I_G(x,y) = \frac{\partial I_G}{\partial x}\hat{i} + \frac{\partial I_G}{\partial y}\hat{j} \qquad (15)$$

Using the gradient values, the current edges in the image are marked using the Equ. (16) & (17).

$$G = x_{(i)}{}^2 + y_{(j)}{}^2 \qquad (16)$$

$$E_m = \frac{1}{1+G} \qquad (17)$$

Then, the binarization process is performed in the edge marked image E_m. In binarization process, the gray level value of each pixel in the image E_m is observed by using global threshold T_g and the resultant binarized image is I_b. Then the binarized image I_b is subjected to morphological opening and closing operation. Opening and closing operation is utilized to remove small objects and small holes from the image I_b. Finally, MRI brain image WM and GM tissues are segmented based on their intensity values.

$$I_{wg} = \begin{cases} WM;\ if\ I_{b_i} = 1 \\ GM;\ if\ I_{b_i} = 0 \end{cases} \qquad (18)$$

CSF segmentation

To segment the cerebrospinal fluid from the brain MRI image, an Orthogonal Polynomial Transform (OPT) is applied to the skull stripped image I_s. In orthogonal polynomial transformation, image I_s is computed using the following formula,

$$I_{cf} = Sin\left(\frac{I_{s(i)}{}^3}{100}\right)^2 + (0.05 * rand(|I_s|)) \qquad (19)$$

After the polynomial transform, the corresponding CSF region is segmented in the resultant image I_{cf}.

3.2.2.2 Pathological Tissue Segmentation

Pathological tissues such as edema and tumor are segmented from the classified abnormal images and these tissues are segmented by two different methods:

(i) Tumor segmentation
(ii) Edema segmentation

Tumor Segmentation

The tumor tissue segmentation is performed in the abnormal brain MRI images. The main objective is to segment the tumor tissue in the abnormal image I_a. Here we utilize the Region Growing Method (RGM) to segment the tumor tissue. 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 [24]. The tumor segmentation result is represented as I_T.

Edema Segmentation

Edema tissue is segmented from the abnormal image I_a. Before the edema segmentation process, histogram equalization process is executed over the image I_a. The quality of image I_a is enhanced by the histogram equalization and it is denoted as I_a'. Then the enhanced I_a' image is converted into indexed image by using multilevel thresholding function. Grayslice function converts the grayscale I_a' image into indexed image using multilevel threshold and the result image is I_a''.

After that, the image I_a'' is converted into HSV (Hue, Saturation and Value) color model and it is represented as I_a'''. Next, the threshold process is performed in the image I_a'''. We define separate threshold value for Hue, Saturation, and Value.

Each pixel in the image is compared with these threshold values to select the pixels.

$$H \to t_3, S \to t_4, V \to t_5$$

$$X = \begin{cases} p_u ; p_u \le t_3, t_5 \& \ge t_4 \\ 0; otherwise \end{cases} \quad (20)$$

In the above eqn [15], X is the pixel values that satisfy the above conditions. Morphological closing operation is applied on the mask X and the resultant image is denoted as $X^{(c)}$. Now, the image $X^{(c)}$ contains z number of regions and then we compute the centroid value for each region, which is represented as $X_h^{(c)}(x, y), h = 1,2,\cdots z$. Subsequently, the distance is determined between the coordinates of center pixels of the regions in $X_h^{(c)}(x, y)$ and the tumor centroid coordinate value $t(x, y)$.

$$O_h(x, y) = X_h^{(c)}(x, y) - t(x, y) \quad (21)$$

The resultant $O_h(x, y)$ is then verified with threshold value t_6 and an edema region coordinate values are obtained,

$$I_e = \begin{cases} O_h(x, y) \ge t_6 \\ 0; otherwise \end{cases} \quad (22)$$

Then the morphological dilation and closing operations are performed in the image I_e.

III. EXPERIMENTAL RESULTS

The proposed brain tissue segmentation technique is implemented in the working platform MATLAB (version 7.10) and it is evaluated using 10 medical brain MRI images, which are collected from various medical diagnosis centers. Among 10 MRI images, 5 images are normal and the remaining is abnormal. The fig. 4 shows the given input MRI brain images used for the MRI image classification process.

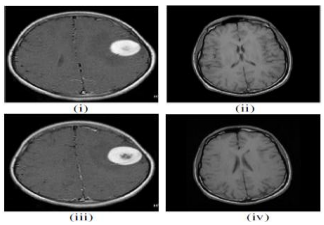


Figure 4: Classification result of normal and abnormal images

The input images are classified by two FFBNN networks. Input values for both FFBNN networks are five features such as mean, variance, horizontal, vertical and diagonal functions of 2D wavelet decomposition and these features is given as input to the dual FFBNN networks. These networks are trained using back propagation algorithm. The result of dual FFBNN network is evaluated by unknown testing images. The classification results of dual FFBNN networks are shown in Fig.4.

Then, the segmentation process is performed on the classified images. The normal images are segmented into three normal tissues such as WM, GM and CSF and the abnormal images are segmented into two pathological tissues such as edema, tumor. Preprocessing process is performed in the classified normal images before the segmentation process. In preprocessing, skull stripping process is performed to remove the non cortical tissues from the images. Fig. 6 shows output of the preprocessed MRI normal image.

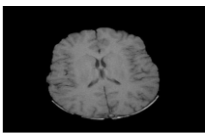


Figure 6: Preprocessed MRI normal image output

Normal tissues GM and WM are segmented by the gradient method and CSF is segmented by OPT. The segmented normal tissue results are shown in Fig. 7.

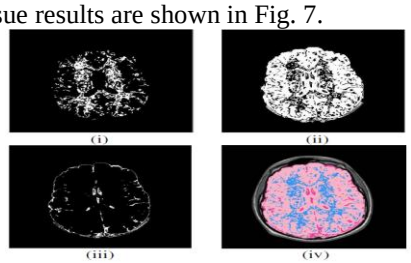


Figure 7: Segmentation outputs of normal tissues (i) WM segmentation (ii) GM segmentation (iii) CSF segmentation and (iv) WM, GM and CSF in original normal image

Pathological tissues such as tumor and edema are segmented by RGM and thresholding process. Various thresholding and morphological operations are performed during the edema segmentation, which are explained in section 2.2.2.2. Figure 8 shows the intermediary result of the edema segmentation. The segmented pathological tissues are shown in Figure 9.

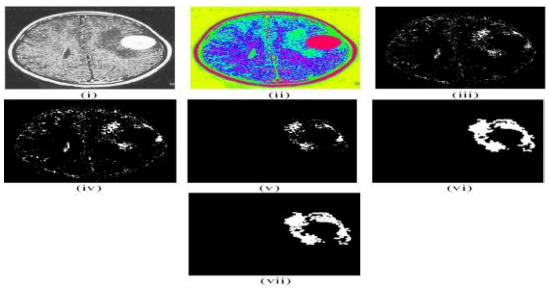
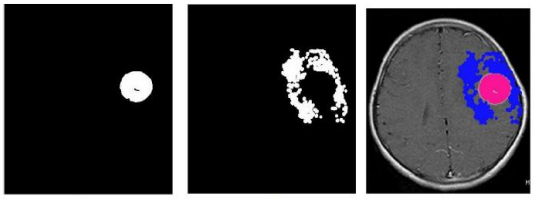


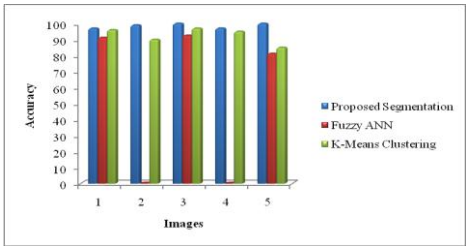
Figure 8: Images obtained from (i) Histogram Equalized Image (ii) HSV color model Image result (iii) Image obtained from HSV Thresholding Process (iv) Closing Operation result image (vi) Edema region result (vi) Closing Operation and (vii) Dilation Operation



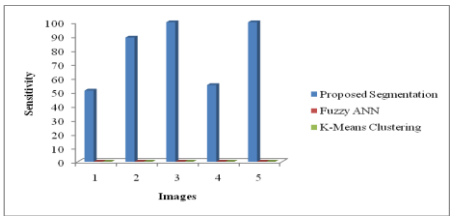
(i) (ii) (iii)

Figure 9: Segmentation result of pathological tissues (i) Tumor (ii) Edema and (iii) Tumor and Edema in abnormal image

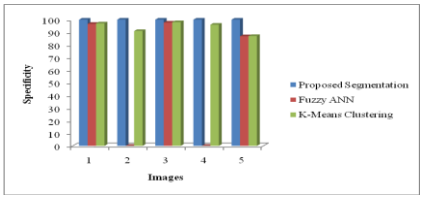
The performance measures values in Tables 1, 2 and 3 shows that the proposed segmentation method gives high percentage accuracy result than the K-means clustering and Fuzzy ANN method. The performance measures values corresponding graphs of both proposed and K-means clustering, Fuzzy ANN is listed below.



(i)

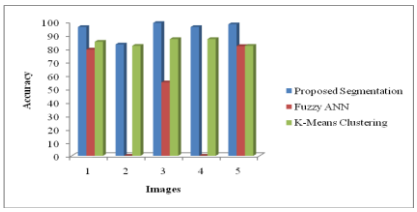


(ii)

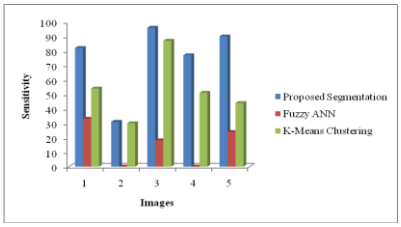


(iii)

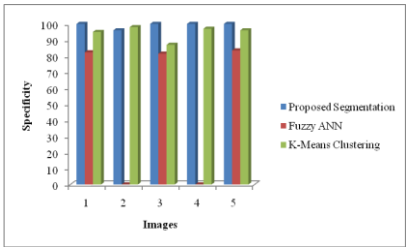
Figure 10: WM Tissues Segmentation result (i) Accuracy (ii) Sensitivity (iii) Specificity



(i)

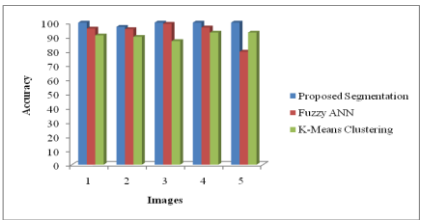


(ii)

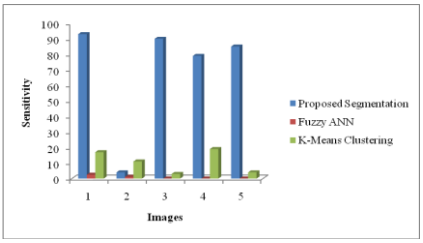


(iii)

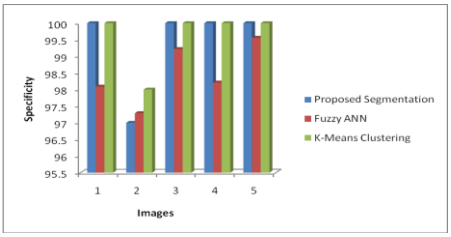
Figure 11: GM Tissues Segmentation result (i) Accuracy (ii) Sensitivity (iii) Specificity



(i)

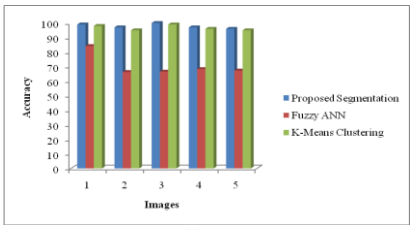


(ii)

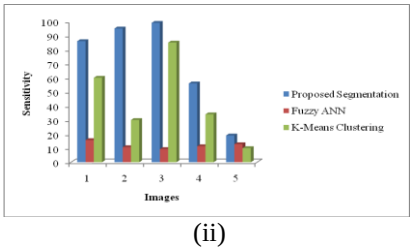


(iii)

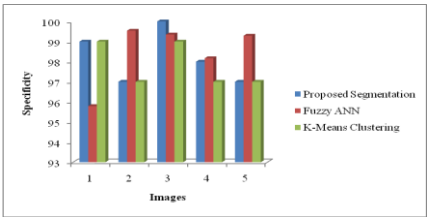
Figure 12: CSF Tissues Segmentation result (i) Accuracy (ii) Sensitivity (iii) Specificity



(i)

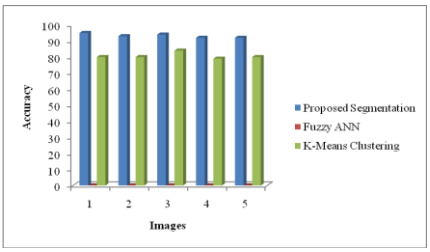


(ii)

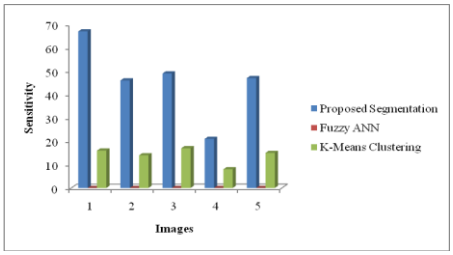


(iii)

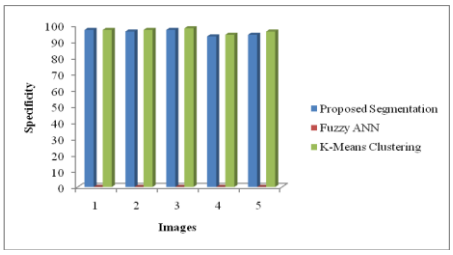
Figure 13: Edema Tissues Segmentation result (i)Accuracy(ii)Sensitivity(iii)Specificity



(i)



(ii)



(iii)

Figure 14: Tumor Tissues Segmentation result (i) Accuracy (ii) Sensitivity (iii) Specificity

The Figure 10 to 14 shows the graphical representation of WM, GM, CSF, Edema and tumor tissue segmentation performance compared to the Fuzzy ANN and K-means clustering method. It shows that the accuracy, sensitivity and specificity measure in this tissue segmentation processes are nearly same (or) higher than the Fuzzy ANN and K-means clustering methods. Also, the GM, CSF, Edema and Tumor tissue segmentation process has given high accuracy and sensitivity result than the Fuzzy ANN and K-means clustering methods, but these tissues performance lacks in specificity measure. However, this low performance of specificity measure will not affect the segmentation process because the specificity is only slightly lower than the Fuzzy ANN and K-means clustering as well as the accuracy level of both tissues are nearly same (or) high when compared to this low level result of Fuzzy ANN, K-means clustering methods.

IV. CONCLUSION

In this paper, an efficient segmentation was developed to segment the normal and pathological tissues from the MRI brain images. The performance of the proposed segmentation was analyzed using defined set of MRI normal and abnormal images. Statistical measures were utilized to measure the performance of the proposed tissue segmentation method. The performance of the proposed segmentation method was analyzed and compared against the K-means clustering method and existing Fuzzy ANN based segmentation method. The comparative results showed that the proposed method outperforms in terms of accuracy and sensitivity rather than the Fuzzy ANN and K-means clustering. It lacked in performing in terms of specificity values for certain images. Even though there is a lack in specificity values, the greater improvement in accuracy and sensitivity values makes that tolerable. Hence the performance of the method was understood from the experimental results and analysis.

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