Brain Tumor Segmentation and Its Area Calculation in Brain MR Images using K-Mean Clustering and Fuzzy C-Mean Algorithm

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***Abstract*- This paper deals with the implementation of Simple Algorithm for detection of range and shape of tumor in brain MR images. Tumor is an uncontrolled growth of tissues in any part of the body. Tumors are of different types and they have different Characteristics and different treatment. As it is known, brain tumor is inherently serious and life-threatening because of its character in the limited space of the intracranial cavity (space formed inside the skull). Most Research in developed countries show that the number of people who have brain tumors were died due to the fact of inaccurate detection. Generally, CT scan or MRI that is directed into intracranial cavity produces a complete image of brain. This image is visually examined by the physician for detection & diagnosis of brain tumor. However this method of detection resists the accurate determination of stage & size of tumor. To avoid that, this project uses computer aided method for segmentation (detection) of brain tumor based on the combination of two algorithms. This method allows the segmentation of tumor tissue with accuracy and reproducibility comparable to manual segmentation. In addition, it also reduces the time for analysis. At the end of the process the tumor is extracted from the MR image and its exact position and the shape also determined. The stage of the tumor is displayed based on the amount of area calculated from the cluster.**

***Key words*-Abnormalities, Magnetic Resonance Imaging (MRI), Brain tumor, Pre-processing, K-means, Fuzzy C-means, Thresholding**

I. INTRODUCTION

This paper deals with the concept for automatic brain tumor segmentation. Normally the anatomy of the Brain can be viewed by the MRI scan or CT scan. In this paper the MRI scanned image is taken for the entire process. The MRI scan is more comfortable than CT scan for diagnosis. It is not affect the human body. Because it doesn't use any radiation. It is based on the magnetic field and radio waves. There are different types of algorithm were developed for brain tumor detection. But they may have some drawback in detection and extraction. In this paper, two algorithms are used for segmentation. So it gives the accurate result for tumor segmentation. Tumor is due to the uncontrolled growth of the tissues in any part of the body. The tumor may be primary or secondary. If it is an origin, then it is known as primary. If the part of the tumor is spread to another place and grown as its own then it is known as secondary. Normally brain tumor affects CSF (Cerebral Spinal Fluid). It causes for strokes. The physician gives the treatment for the strokes rather than the treatment for tumor. So detection of tumor is important for that treatment. The lifetime of the person who affected by the brain tumor will increase if it is detected at current stage. That will increase the lifetime about 1 to 2 years. Normally tumor cells are of two types. They are Mass and Malignant. The detection of the malignant tumor is somewhat difficult to mass tumor. For the accurate detection of the malignant tumor that needs a 3-D representation of brain and 3-D analyzer tool. In this paper we focused on detection of mass tumor detection. The developing platform for the detection is mat lab. Because it is easy to develop and execute. At the end, we are providing systems that detect the tumor and its shape.

II. EXISTING METHOD

The existing method is based on the thresholding and region growing. The thresholding method was ignored the spatial characteristics. Normally spatial characteristics are important for the malignant tumor detection. In the thresholding based segmentation the image is considered as having only two values either black or white. But the bit map image contains 0 to 255 gray scale values. So sometimes it ignores the tumor cells also. In case of the region growing based segmentation it needs more user interaction for the selection of the seed. Seed is nothing but the center of the tumor cells; it may cause intensity in homogeneity problem. And also it will not provide the acceptable result for all the images. The typical output for the thresholding is given below.

Fig.1 input image for thresholding

Fig.2 output Image for thresholding

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Fig1 is the input image for thresholding. From theMR image it self we can see the tumor area but it is not enough for futher traetment. For that it is given to the threholding process. Fig2 is the output image for the thresholding. It consists of only two gray values .That is white as 1 and black as 0. The background value is assigned to binary value 0 and object gets the value 1. So we cannot extract the tumor from the image. This is the main drawback of the existing system. Due to that we go for the proposed method for tumor segmentation.

III. PROPOSED METHOD

The proposed system has mainly four modules: pre-processing, segmentation, Feature extraction, and approximate reasoning. Pre processing is done by filtering. Segmentation is carried out by advanced K-means and Fuzzy C-means algorithms. Feature extraction is by thresholding and finally, Approximate reasoning method to recognize the tumor shape and position in MRI image using edge detection method. The proposed method is a combination of two algorithms. In the literature survey many algorithms were developed for segmentation. But they are not good for all types of the MRI images.

A. Proposed method block diagram

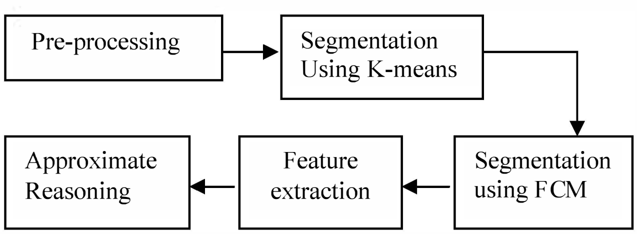


Fig.3 block diagram of proposed method

Fig 3 is the block diagram for proposed system. It uses the combination of two algorithms for segmentation. The proposed method consists of five modules. Each module and its function will be explained below.

IV.PRE-PROCESSING

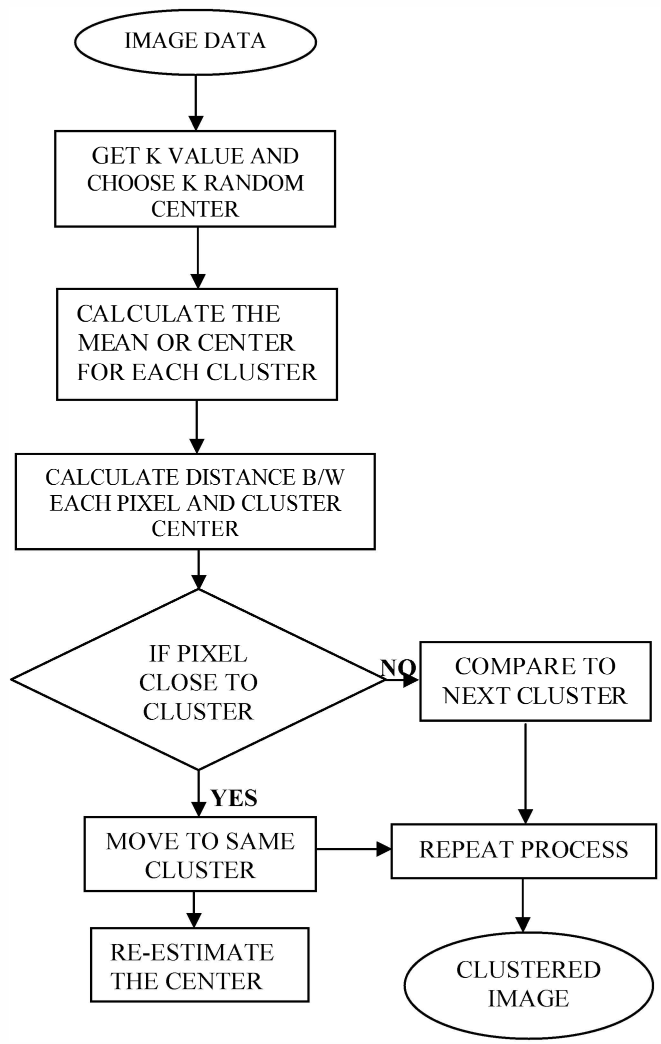
According to the need of the next level the pre processing step convert the image. It performs filtering of noise and other artifacts in the image and sharpening the edges in the image. RGB to grey conversion and Re-shaping also takes place here. It includes median filter for noise removal. The possibilities of arrival of noise in modern MRI scan are very less. It may arrive due to the thermal effect. The main aim of this paper is to detect and segment the tumor cells. But for the complete system it needs the process of noise removal. For better understanding the function of median filter, we added the salt and pepper noise artificially and removing it using median filter.

V. K-MEANS SEGMENTATION

A. K-means clustering detail

K-Means is the one of the unsupervised learning algorithm for clusters. Clustering the image is grouping the pixels according to the some characteristics. In the k-means algorithm initially we have to define the number of clusters k. Then k-cluster center are chosen randomly. The distance between the each pixel to each cluster centers are calculated. The distance may be of simple Euclidean function. Single pixel is compared to all cluster centers using the distance formula. The pixel is moved to particular cluster which has shortest distance among all. Then the centroid is re-estimated. Again each pixel is compared to all centroids. The process continuous until the center converges.

B. Flowchart of k-means algorithm



It is the diagrammatic representation of the k-means algorithm and its flow.

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C. Mathematical representation

For a given image, compute the cluster means *m*

$$M=\frac{\sum_{i:c(i)=k} x_i}{N_k} \quad ,k=1,\ldots,K. \longrightarrow (1)$$

Calculate the distance between the cluster center to each pixel

$$D(i) = \arg\min \left\| x_i - M_k \right\|^2 \text{ , i=1,……,N} \longrightarrow (2)$$

Repeat the above two steps until mean value convergence.

D. Algorithm:

1. Give the no of cluster value as *k*.
2. Randomly choose the *k* cluster centers
3. Calculate mean or center of the cluster
4. Calculate the distance b/w each pixel to each cluster center
5. If the distance is near to the center then move to that cluster.
6. Otherwise move to next cluster.
7. Re-estimate the center.
8. Repeat the process until the center doesn't move

E. Screen shot for pre-processing and K-means

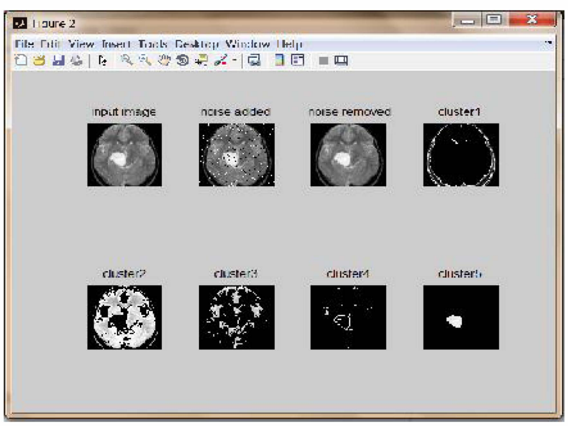

Fig. 4 Output image for pre-processing and k-means for k=5

Fig.4 is the MR image given as input to the pre-processing and K-means algorithm. Here 0.02% of salt and pepper noise is added and that has been removed using the median filter. The K-mean algorithm clusters the image according to some characteristics. Figure is the output for K-Means algorithm with five clusters. At the fifth cluster the tumor is extracted

VI. SEGMENTATION USING FUZZY C-MEANS

A. Fuzzy Clustering:

. The fuzzy logic is a way to processing the data by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set is ranges from 0 to 1. Fuzzy clustering is basically a multi valued logic that allows intermediate values i.e., member of one fuzzy set can also be member of other fuzzy sets in the same image. There is no abrupt transition between full membership and non membership. The membership function defines the fuzziness of an image and also to define the information contained in the image. These are three main basic features involved in characterized by membership function. They are support, Boundary. The core is a fully member of the fuzzy set. The support is non membership value of the set and boundary is the intermediate or partial membership with value between o and 1

B. Mathematical representation

Fuzzy c-means (FCM) is the clustering algorithm which allows one piece of data may be member of more than one clusters. It is based on reducing the following function

$$Y_m = \sum_{i=1}^{N}\sum_{j=1}^{C} M_{ij}^{m} \left\| x_i - c_j \right\|^2 \longrightarrow (3)$$

Where

m- any real number greater than 1,

M_{ij}- degree of membership of x_i in the cluster *j*,

x_i- data measured in d-dimensional,

R_j - d-dimension center of the cluster,

The update of membership M_{ij} and the cluster centers R_j are given by:

$$M_{ij} = \frac{1}{\sum_{K=1}^{C}\left(\frac{\left\| x_i - c_j \right\|}{\left\| x_i - c_j \right\|}\right)^{\frac{2}{m-1}}} \longrightarrow (4)$$

$$R_j = \frac{\sum_{i=1}^{N} x_i . M_{ij}^{m}}{\sum_{i=1}^{N} M_{ij}^{m}} \longrightarrow (5)$$

The above process ends when,

$$\max_{ij}\left\{ \left| M_{ij}^{(K+1)} - M_{ij}^{(k)} \right| \right\} < \delta \longrightarrow (6)$$

Where

ξ = termination value or constant between 0 and 1, *K= no of* iteration steps.

C. The Fuzzy c-means Algorithm

The algorithm contain following steps:

1. *Initialize* $M=[M_{ij}]$ *matrix*, $M^{(0)}$
2. *At k-step: calculate the centers vectors* $R^{(k)}=[R_j]$ *with*$M^{(k)}$

$$R_j = \frac{\sum_{i=1}^{N} x_i . M_{ij}^{m}}{\sum_{i=1}^{N} M_{ij}^{m}} \longrightarrow (7)$$

3. *Update* $U^{(k)}$, $U^{(k+1)}$

$$M_{ij} = \frac{1}{\sum_{K=1}^{C}\left(\frac{\|x_i - c_j\|}{\|x_i - c_j\|}\right)^{\frac{2}{m-1}}} \longrightarrow (8)$$

4. *If* $\| M^{(k+1)} - M^{(k)}\| < \varepsilon$ *then STOP; otherwise return to step 2.*

C. Output screenshot for FCM

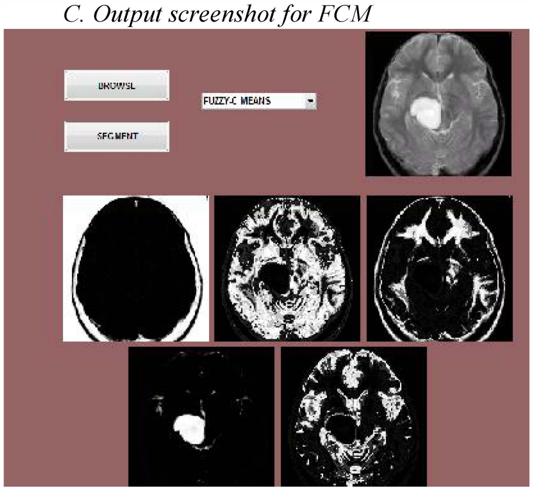

Fig.5 Output image of FCM

Fig.5 is the output image for Fuzzy C Means. It is mainly developed for the accurate prediction of tumor cells which are not predicted by K-means algorithm. It gives the accurate result for that compared to the K-Means.

VIII. FEATURE EXTRACTION

The feature extraction is extracting the cluster which shows the predicted tumor at the FCM output. The extracted cluster is given to the thresholding process. It applies binary mask over the entire image. It makes the dark pixel become darker and white become brighter. In threshold coding, each transform coefficient is compared with a threshold. If it is less than the threshold value then it is considered as zero. If it is larger than the threshold, it will be considered as one. The thresholding method is an adaptive method where only those coefficients whose magnitudes are above a threshold are retained within each block. Let us consider an image 'f' that have the k gray level. An integer value of threshold T, which lies in the gray scale range of k. The thresholding process is a comparison. Each pixel in 'f 'is compared to T. Based on that, binary decision is made. That defines the value of the particular pixel in an output binary image 'g':

$$g(n) = \begin{cases} \text{'0' if } f(n) >= T \\ \text{'1' if } f(n) < T \end{cases} \longrightarrow (9)$$

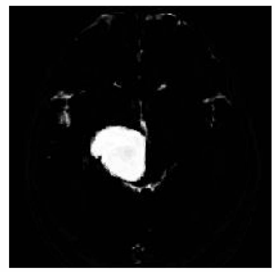

Fig.6 Output image of Thresholding

Fig.6 is the extracted tumor shape from the given image using the Fuzzy C- Means algorithm. The unpredicted tumor cells in the K-means algorithm can also be found using the Fuzzy C-Means algorithm.

IX. APPROXIMATE REASONING

In the approximate reasoning step the tumor area is calculated using the binarization method. That is the image having only two values either black or white (0 or 1). Here 256×256 jpeg image is a maximum image size. The binary image can be represented as a summation of total number of white and black pixels.

$$image, I = \sum_{W=0}^{255}\sum_{H=0}^{255}[f(0)+f(1)] \longrightarrow (10)$$

Pixels = Width (W) X Height (H) = 256 X 256
f (0) = white pixel (digit 0)
f (1) = black pixel (digit 1)

$$No\_of\_whitepixel, P = \sum_{W=0}^{255}\sum_{H=0}^{255}[f(0)] \longrightarrow (11)$$

Where,
P = number of white pixels (width*height)
1 Pixel = 0.264 mm

The area calculation formula is

$$Size\_of\_tumor, S = \left[\left(\sqrt{P}\right)^{*} 0.264\right] mm^{2} \longrightarrow (12)$$

P= no-of white pixels; W=width; H=height.

A.ALGORITHM

The algorithmic steps involved for brain tumor shape detection is as follows,

Step 1: Start the process.

Step 2: Get the MRI scan image input in JPEG format.

Step 3: Check whether the input image is in required format and move to step 4 if not display error message.

Step 4: If image is in RGB format covert it into gray scale else move to next step.

Step 5: Find the edge of the grayscale image.

Step 6: Calculate the number of white points in the image.

Step 7: Calculate the size of the tumor using the formula.

Step 8: Display the size and stage of tumor.

Step 9: Stop the program.

This algorithm scans the RGB or grayscale image, converts the image into binary image by binarization technique and detects the edge of tumor pixels in the binary image. Also it calculates the size of tumor by calculating the number of white pixels (digit 0) in binary image.

B. Output screenshot for tumor area calculation

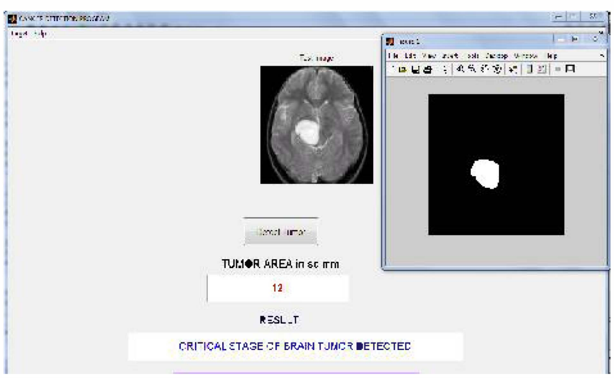

Fig.7 Output image of tumor area calculation

The predicted tumor area is calculated at approximate reasoning step fig 7 shows the output result for tumor area and its stage calculation. The stage of tumor is based on the area of tumor. We considered that, if the area is greater than 6 mm^2 it will be the critical position.

X. CONCLUSION AND FUTURE WORK

There are different types of tumors are available. They may be as mass in brain or malignant over the brain. Suppose if it is a mass then K- means algorithm is enough to extract it from the brain cells. If there is any noise are present in the MR image it is removed before the K-means process. The noise free image is given as a input to the k-means and tumor is extracted from the MRI image. And then segmentation using Fuzzy C means for accurate tumor shape extraction of malignant tumor and thresholding of output in feature extraction. Finally approximate reasoning for calculating tumor shape and position calculation. The experimental results are compared with other algorithms. The proposed method gives more accurate result. In future 3D assessment of brain using 3D slicers with matlab can be developed

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