Review on Brain Tumor Segmentation Using K-Means Clustering and Fuzzy C-Means Algorithms and Its Area Calculation

R. D. Walse[1], Prof. B.S. Sonawane[2] & A. L. Korde[3]

[1]P.G. Scholar Maharashtra Institute of Technology, Aurangabad.
[2,3]Professor at MIT Aurangabad and Professor at KSIET - Hingoli.

Abstract: The Tumor is an uncontrolled growth of tissue in any part of the body. The tumor is of different types and they have different characteristics and different treatment. This paper is to implement of Simple Algorithm for detection of range and shape of tumor in brain MR Images. Normally the anatomy of the Brain can be viewed by the MRI scan or CT scan. MRI scanned image is used for the entire process. The MRI scan is more comfortable than any other scans for diagnosis. It will not affect the human body, because it doesn't practice any radiation. It is centered on the magnetic field and radio waves. There are dissimilar types of algorithm were developed for brain tumor detection. But they may have some drawback in detection and extraction. After the segmentation, which is done through k-means clustering and fuzzy c-means algorithms the brain tumor is detected and its exact location is identified. Comparing to the other algorithms the performance of fuzzy c-means plays a major role. The patient's stage is determined by this process, whether it can be cured with medicine or not.

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 [2]. 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 [3]. 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 [6]. 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[4].

Existing System

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.
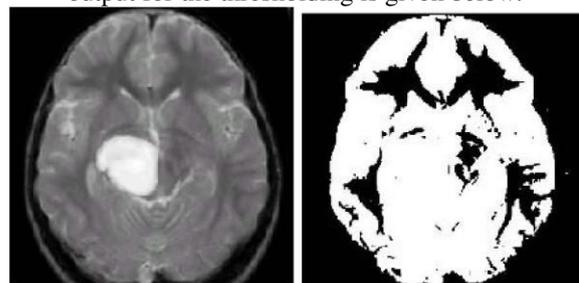
Fig.1 Input image for   Fig. 2 Output Image for thresholding

Figure 1 is the input image for thresholding [1]. From the MR image itself we can see the tumor area but it is not enough for further treatment. For that it is given to the threholding process. Figure 2 is the output image for the thresholding [1]. 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.

Proposed Method

The proposed system has mainly four modules: preprocessing, segmentation, Feature extraction, and approximate reasoning. Preprocessing is done by filtering. Segmentation is carried out by advanced K-means and Fuzzy C-means algorithms. Feature extraction is by thresholding and finally, approximates 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.
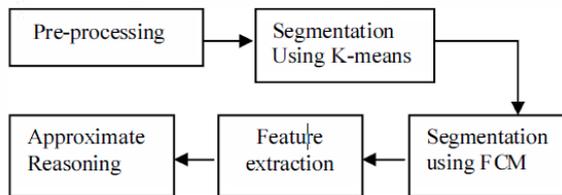
A.   Proposed method block diagram

Figure 3 Block diagram of proposed method [1].

Figure 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.

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 Reshaping 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 [11].

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 [10].
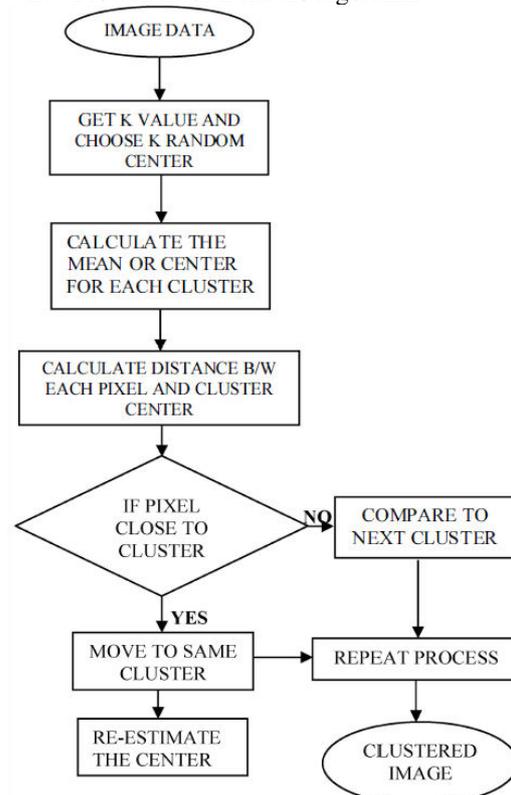
B.   Flowchart of k-means algorithm

Fig. 4 Flow of the k-means algorithm [1].

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

C. Mathematical representation

For a given image, compute the cluster means m

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

(1)
Calculate the distance between the cluster center to each Pixel

$$D(i) = \arg\min \| x_i - M_k \|^2 \quad . i = 1 \dots, N$$

(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
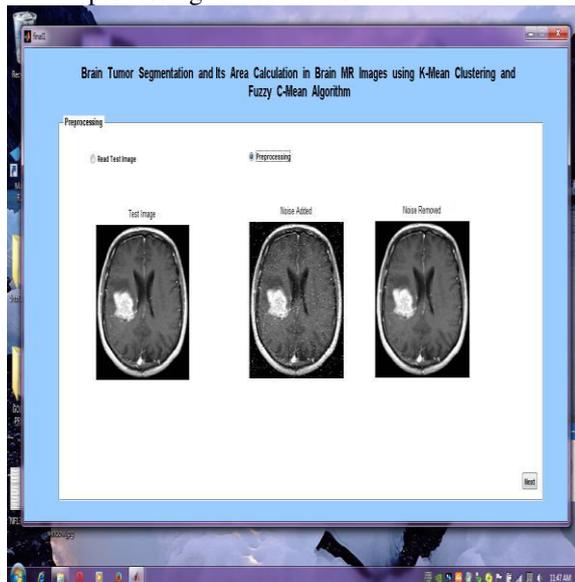
E. Pre-processing and K-means

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

Figure.5 It is the MR image given as input to the preprocessing 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.

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 0 and 1 [6].

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

$$Y_m = \sum_{i=1}^{N} \sum_{j=1}^{C} M_{ij}^m \| x_i - c_j \|^2$$

(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, are given by:

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

(4)

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

(5)

The above process ends when,

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

(6)

Where,
δ= termination value or constant between 0 and 1.
K= no. of iteration steps [1].

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 $M^{(k)}$.

$$R_j = \frac{\sum_{i=1}^{N} x_i \cdot M_{ij}^m}{\sum_{i=1}^{N} M_{ij}^m}$$

(7)

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

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

(8)

4. If $\| M^{(k-1)} - M^{(k)} \| < \delta$ then stop; otherwise return to step 2 [1].
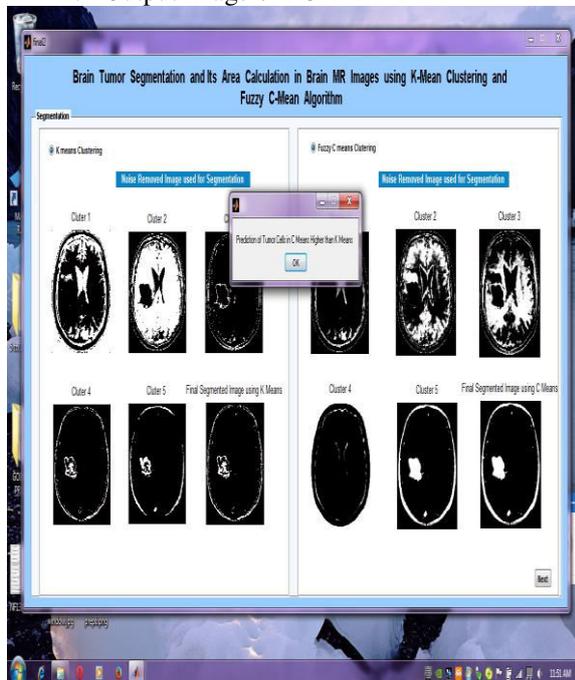
D. Output image of FCM

Fig. 6 Output image of FCM

Figure 6 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 [9].

Feature Extraction

The feature extraction is extracting the cluster which show 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:

$$g(n) = \begin{cases} `0' & if\ f(n) \geq T \\ `1' & if\ f(n) < T \end{cases}$$
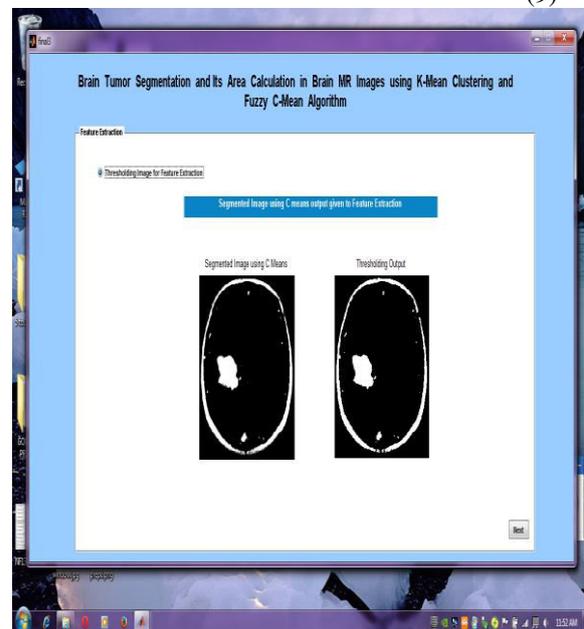
(9)

Fig. 7 Output image of thresholding.

Figure 7 It is the extracted tumor shape from the given image using the Fuzzy C- Means algorithm. The un- predicted tumor cells in the K-means algorithm can also be found using the Fuzzy C- Means algorithm.

Approximate Reasoning

In the approximate reasoning step the tumor area is Calculate using the binary 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 [8].

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

(10)

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

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

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

The area calculation formula is

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

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 gray scale 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 gray scale image, converts the image into binary image by binary technique and detects the edge of tumor pixels in the binary image. Also it calculates the size of tumor by calculate the number of white pixels (digit 0) in binary image [7].

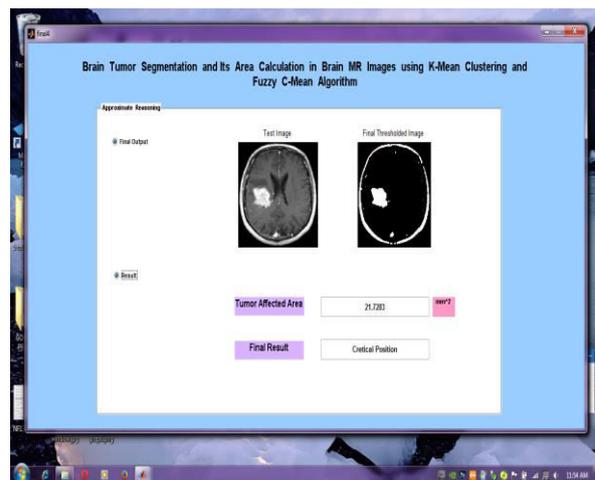B. Output screenshot for tumor area calculation

Figure 8 Final Threshold image and tumor affected area

The predicted tumor area is calculated at approximate reasoning step figure 8 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 21.7283 mm^2 it will be the critical position.

Conclusion and Future Work

There are different types of tumors available. They may be mass in the 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 present in the MR image it is removed before the K-means process. The noise free image is given as input to the k-means and tumors are extracted from the MRI image. The performance of brain tumor segmentation is evaluated based on K-means clustering. Dataset consists of Magnetic Resonance Imaging size of 181*272. The MRI image dataset that we have utilized in image segmentation technique is taken from the publicly available sources. This image dataset consists of 40 brain MRI images in which 20 brain images with tumor and remaining brain images without tumor. The brain image dataset is divided into two sets. Training dataset and testing dataset. Thus, the pre-processing is done by filtering. Segmentation is done by advanced K-means algorithm and fuzzy c means algorithm. Feature extractions is done by threading and finally, approximate reasoning method to recognize the tumor shape and position in MRI image using edge detection method. This method scans the RGB or gray scale, converts the image into binary image by binary technique and detects the edge of tumor pixels in the binary image. Also, it calculates the size of the tumor by calculating the number of white pixels (digit 0) in binary image. The stage of the tumor is based on the area of tumor.

Acknowledgements

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