Segmentation of Brain Tumour and Its Area Calculation

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Abstract— This paper deals with the implementation of Simple Algorithm for detection of range and shape of tumour in brain MR images. Tumour is an uncontrolled growth of tissues in any part of the body. Tumours are of different types and they have different Characteristics and different treatment. As it is known, brain tumour 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 tumours 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 tumour. However this method of detection resists the accurate determination of stage & size of tumour. To avoid that, this project uses computer aided method for segmentation (detection) of brain tumour based on the combination of two algorithms. This method allows the segmentation of tumour 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 tumour is extracted from the MR image and its exact position and the shape also determined. The stage of the tumour is displayed based on the amount of area calculated from the cluster.

Keywords— Abnormalities, Magnetic Resonance Imaging (MRI), Brain tumour, Pre-processing, K-means, Fuzzy C-means, Thresholding

I. INTRODUCTION

This paper deals with the concept for automatic brain tumour 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 [1]. There are different types of algorithm were developed for brain tumour 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 tumour segmentation [2]. Tumour is due to the uncontrolled growth of the tissues in any part of the body. The tumour may be primary or secondary. If it is an origin, then it is known as primary. If the part of the tumour is spread to another place and grown as its own then it is known as secondary. Normally brain tumour affects CSF (Cerebral Spinal Fluid). It causes for strokes. The physician gives the treatment for the strokes rather than the treatment for tumour. So detection of tumour is important for that treatment. The lifetime of the person who affected by the brain tumour will increase if it is detected at current stage. That will increase the lifetime about 1 to 2 years. Normally tumour cells are of two types. They are Mass and Malignant.

The detection of the malignant tumour is somewhat difficult to mass tumour. For the accurate detection of the malignant tumour that needs a 3-D representation of brain and 3-D analyser tool. Image segmentation plays a major role in the field of biomedical applications. The segmentation technique is widely used by the radiologists to segment the input medical image into meaningful regions [2, 3, 4].Clustering is one of the widely used image segmentation techniques which classify patterns in such a way that samples of the same group are more similar to one another than samples belonging to different groups [5, 6]. Three-dimensional (3-D) processing and visualization of medical images is a rapidly growing area of research and MRI has provided a means for imaging tissue at very high resolutions providing the desired information for use in fields like reparative surgery, radiotherapy treatment planning, stereotactic neurosurgery, and others [6,7] This paper focused on detection of mass tumour detection. The developing platform for the detection is mat lab. Because it is easy to develop and execute. At the end, this method are providing systems that detect the tumour and its shape.

II. 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 tumour detection. In the Thresholding based segmentation the image is considered as having only two values either black or white [2]. But the bit map image contains 0 to 255 gray scale values. So sometimes it ignores the tumour 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 centre of the tumour 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. An easy way to comply with the conference paper formatting requirements is to use this document as a template and simply type your text into it.
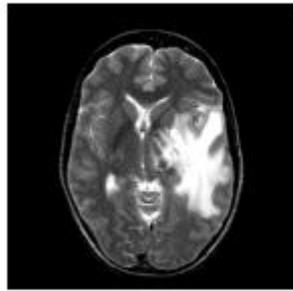

Fig1:Input Image For Thresholding   Fig 2: Output Image after Thresholding

Fig 1 is the input image for Thresholding. From the MR image itself doctor's can see the tumour area but it is not enough for further treatment. For that it is given to the Thresholding process. Fig 2 is the output image for the Thresholding. It consists of only two gray values .That is white as 1 and black as O. The background value is assigned to binary value 0 and object gets the value 1. So it cannot extract the tumour from the image. This is the main drawback of the existing system. Due to that it go for tumour segmentation method.

III. PROPOSED METHOD

Magnetic resonance imaging (MRI) segmentation is a complex issue. This paper proposes a new method for estimating the right number of segments and automatic segmentation of human normal and abnormal MR brain images. The purpose of automatic diagnosis of the segments is to find the number of divided image areas of an image according to its entropy and with correctly diagnose of the segment of an image also increased the precision of segmentation [7, 8]. The fig.3 shows the block diagram of method system. It 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 tumour shape and position in MRI image using edge detection method. In the literature survey many algorithms were developed for segmentation [9, 10]. But they are not good for all types of the MRI images.
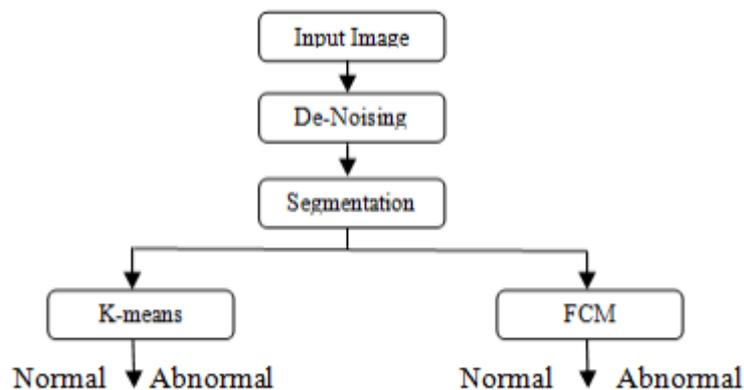

Fig.3 block diagram of proposed method.

IV. PREPROCESSING

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 tumors cells. But for the complete system it needs the process of noise removal. For better understanding the function of median filter, it added the salt and pepper noise artificially and removing it using median filter.

V. K-MEAN SEGMENTATION

A. *K-means clustering detail:*

K-Means is the one of the unsupervised learning algorithm for clusters [11]. Clustering the image is grouping the pixels according to the some characteristics. In this paper input image is converted into Standard format 512 X 512, then find the total no. of pixels using Length = Row X Column. Then covert 2D image into 1D and create no. of clusters depend on user. The k-means algorithm initially it has to define the number of clusters k [12,13,14]. Then k-

cluster centre 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 [16,17]. 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 al
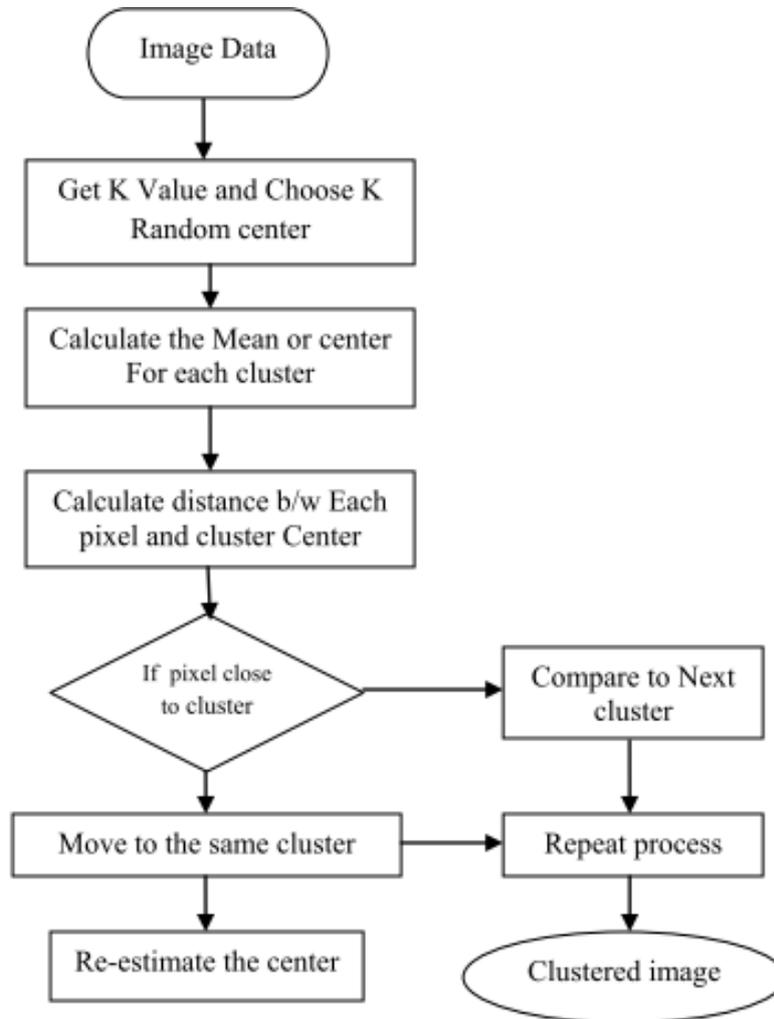
B. *Flowchart of k-means algorithm:*

Fig 4: 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:

$$M = \sum X_i \; i{:}c(i){=}k \; / \; N \; K \qquad (1)$$

Now, calculate the distance between the cluster center to each pixel:

$$D(i) = \arg\min \|x_i - R \; M_k\|^2 \qquad , i = 1,.....,N \qquad (2)$$

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/or pre-processing and K-means:*

Fig.5 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 [18]. Figure 5 is the output for K-Means algorithm with fore clusters. At the 4th cluster the tumors is extracted.
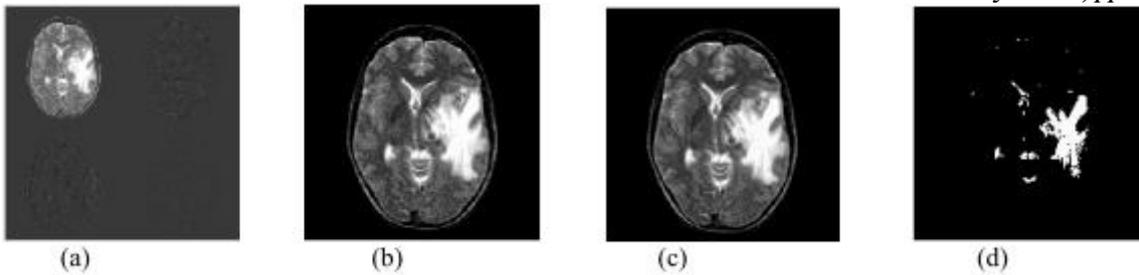
Fig.5: Performance analysis of various segmentation algorithms on MR brain image: (a) Transformed image
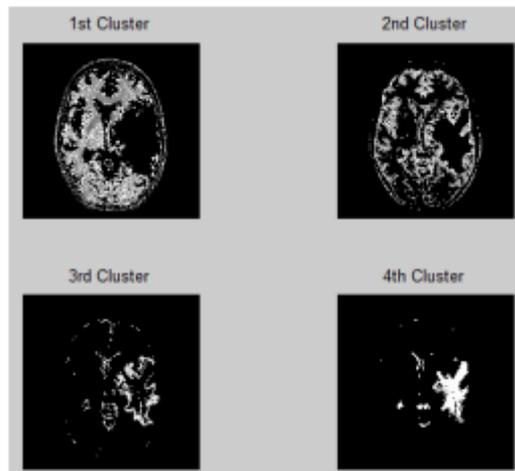(b) Denoised image (c)Inverse transformed image (d) Tumor image using K-means algorithm

Fig.6: Output Cluster images for pre-processing.

VI. SEGMENTATION USING FUZZY C-MEANS

A. *Fuzzy Clustering*:

Fuzzy C-Mean (FCM) is an unsupervised clustering algorithm that has been applied to wide range of problems involving feature analysis, clustering and classifier design. FCM has a wide domain of applications such as agricultural engineering, astronomy, chemistry, geology, image analysis, medical diagnosis, shape analysis, and target recognition [19]. The fuzzy logic is a way to processing the data by giving the partial membership value to each pixel in the image [20,21]. 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. The clusters are formed according to the distance between data points and cluster centers are formed for each cluster. The Algorithm Fuzzy C-Means (FCM) is a method of clustering which allows one piece of data to belong to two or more clusters [22]. This method is frequently used in pattern recognition. There is no abrupt transition between full membership and non membership.

Fuzzy c-means (FCM) is a data clustering technique in which a dataset is grouped into n clusters with every data point in the dataset belonging to every cluster to a certain degree. For example, a certain data point that lies close to the center of a cluster will have a high degree of belonging or membership to that cluster and another data point that lies far away from the center of a cluster will have a low degree of belonging or membership to that cluster. The Fuzzy Logic Toolbox™ function fcm performs FCM clustering. It starts with an initial guess for the cluster centers, which are intended to mark the mean location of each cluster. The initial guess for these cluster centers is most likely incorrect. Next, FCM assigns every data point a membership grade for each cluster. By iteratively updating the cluster centers and the membership grades for each data point, FCM iteratively moves the cluster centers to the right location within a data set. This iteration is based on minimizing an objective function that represents the distance from any given data point to a cluster center weighted by that data point's membership grade.

 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.

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

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

Where,

m - any real number greater than 1,

M ij- degree of membership of X; in the cluster j,
Xi-data measured in d-dimensional,
Rj - d-dimension center of the cluster,
The update of membership Mij and the cluster centers R, are given by:

$$M_{ij} = \frac{1}{\sum_{k=1}^{c}\left(\frac{\|xi - xj\|}{\|xi - cj\|}\right)^{2/m-1}} \tag{4}$$

$$R_i = \sum_{i=1}^{N} x_i \cdot M_{ii}{}^m / \sum_{i=1}^{N} M_{ii}{}^m \tag{5}$$

The above process ends when,

$$\text{Max}_{ij} \left| M_{ij}{}^{(k+1)} - M_{ij}{}^{(k)} \right| < \delta \tag{6}$$

Where,
δ = 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)

$$R_j = \sum_{i=1}^{N} x_i \cdot M_{ij}{}^m / \sum_{i=1}^{N} M_{ij}{}^m \tag{7}$$

3. Update U(k),U(k+1)

$$M_{ij} = \frac{1}{\sum_{k=1}^{c}\left(\frac{\|xi - xj\|}{\|xi - cj\|}\right)^{2/m-1}} \tag{8}$$

4.If $\left\| M^{(k+1)} - M^{(k)} \right\| < \delta$ then STOP ,otherwise return to step 2

D. *Output screenshot for Fuzzy C-means Algorithm:*
   Fig.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.
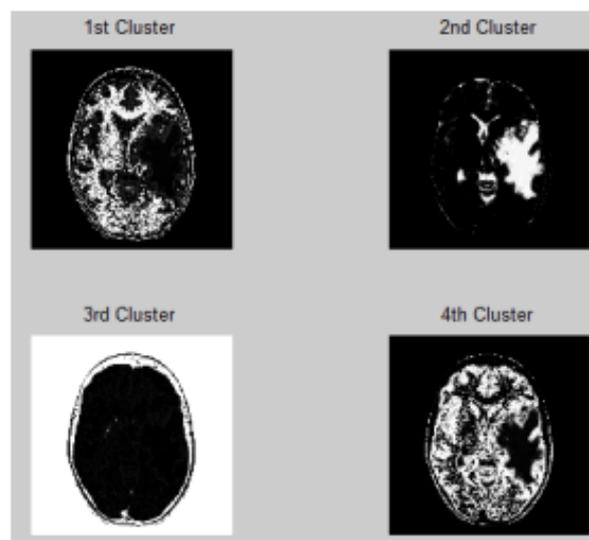

Fig.6: Output Cluster image of FCM.

VII. FEATURE EXTRACTION

   The feature extraction is extracting the cluster which shows the predicted tumour 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':

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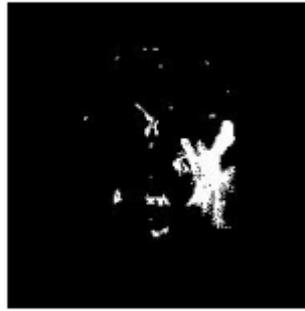

Fig.7: Output image of Thresholding

Fig.7 is the extracted tumor shape from the given image using the Fuzzy C- Means algorithm. The unpredicted tumour cells in the K-means algorithm can also be found using the Fuzzy C-Means algorithm.

VIII. APPROXIMATE REASONING

In the approximate reasoning step the tumor area is calculated using the linearization method. That is the image having only two values either black or white (0 or 1). Here 256x256 jpeg image is a maximum image size. The binary image can be represented as a summation of total number of white and black pixels.

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

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

$$\text{No\_ of\_ white pixel P} = \sum_{W=0}^{255} \sum_{H=0}^{255} [f(0)] \quad (11)$$

Where,
P = number of white pixels (width*height)
1 Pixel = 0.264 mm
The area calculation formula is

$$\text{Size\_ of\_ tumour, S} = [(\sqrt{P})^* \, 0.264] \text{ mm}^2 \quad (12)$$

Where,
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 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 linearization 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.8: 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. Here considered that, if the area is greater than $6.00mm^2$ it will be the critical position.

IX.   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. The heading of the Acknowledgment section and the References section must not be numbered.

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