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Using of Image Processing for Diagnostic the Brain Tumor by of Methods K-mean Clustering and C-mean Fuzzy

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ABSTRACT
Tumor is an uncontrolled growth of tissues in any part of the body. Tumors are of different varieties and that they have totally different Characteristics and different treatment. As it is thought, brain tumor is inherently serious and serious due to its character within the restricted area of the intracranial cavity (space shaped within the skull).Most analysis in developed countries show that the number of individuals who have brain tumors were died because of the actual fact of inaccurate detection. Generally, CT scan or mri that's directed into intracranial cavity produces an entire image of brain. This image is visually examined by the physician for detection & diagnosis of brain tumour. But this methodology of detection resists the accurate determination of stage & size of tumor. To avoid that, this project uses computer aided methodology for segmentation (detection) of brain tumour supported the combination of two algorithms. This technique permits the segmentation of tumor tissue with accuracy and reliability like manual segmentation. Additionally, it also reduces the time for analysis. At the top of the method the tumor is extracted from the mri image and its actual position and the form also determined. The stage of the tumor is displayed supported the quantity of space calculated from the cluster.

Keywords-Abnormalities, Magnetic Resonance Imaging (MRI), Brain tumor, Pre-processing, K-means, Fuzzy Cmeans, Thresholding.

INTRODUCTION

This paper deals with the concept for automatic braintumor 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 does 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 algorithmwere developed for brain tumor detection.But they mayhave some drawback in detection and extraction [1–4]. In thispaper, 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 ofthe body. The tumor may be primary or secondary.

If it is an origin, then it is called primary. If the part of the tumor is unfold to a different place and fully grown as its own then it is called secondary. Usually tumor affects CSF (Cerebral Spinal Fluid). It causes for strokes. The doctor offers the treatment for the strokes instead of the treatment for tumor. Thus detection of tumor is very important for that treatment. The period of time of the one who is suffering from the tumor can increase if it is detected at current stage.
That will increase the life time about 1 to 2 years. Normally, tumor cells are of two

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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 [5–9].

EXISTING METHOD

The existing method is based on the thresholding andregion growing. The thresholding method was ignored thespatial characteristics. Normally spatial characteristics are important for the malignant tumor detection. In the thresholding based segmentation the image is consideredas having only two values either black or white. But thebit 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 nothingbut the center of the tumor cells; it may cause intensity inhomogeneity problem. And also it will not provide the acceptable result for all the images. The typical output for the thresholding is given below.

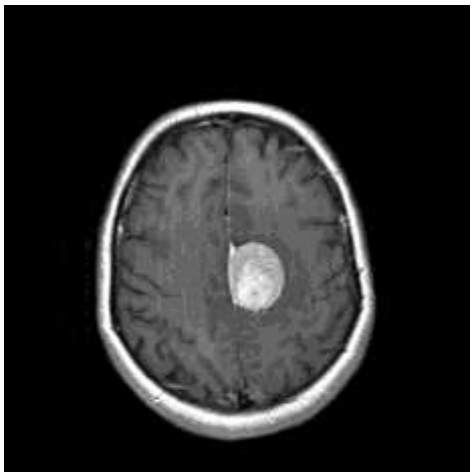

Fig.1 *input image for thresholding*

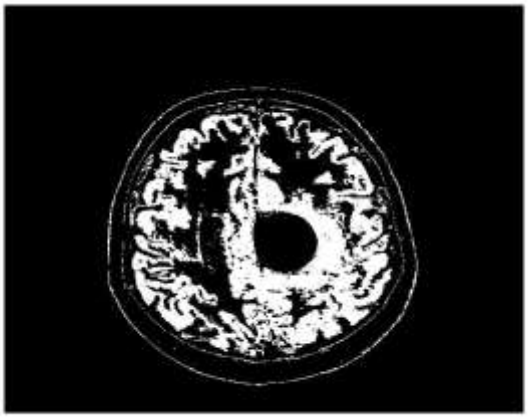

Fig.2 *output Image for thresholding*

Fig l is the input image for thresholding. From the MR image itself we can see the tumor area but it is notenough for further treatment. For that it is given to the thresholding process. Fig2 is the output image for thethresholding. It consists of only two gray values. That is white as 1 and black as O. The background value isassigned to binary value 0 and object gets the value 1. Sowe cannot extract the tumor from the image. This is themain drawback of the existing system. Due to that we go for the proposed method for tumor segmentation [10, 11].

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 extractionis by thresholding and finally, Approximate reasoning method to recognize the tumor shape and position in MRI image using edge detection method [12]. The proposed method is a combination of two algorithms. In the literature survey many algorithms were developed for

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segmentation. But they are not good for all types of the MR images [13, 14].

Proposed method block diagram

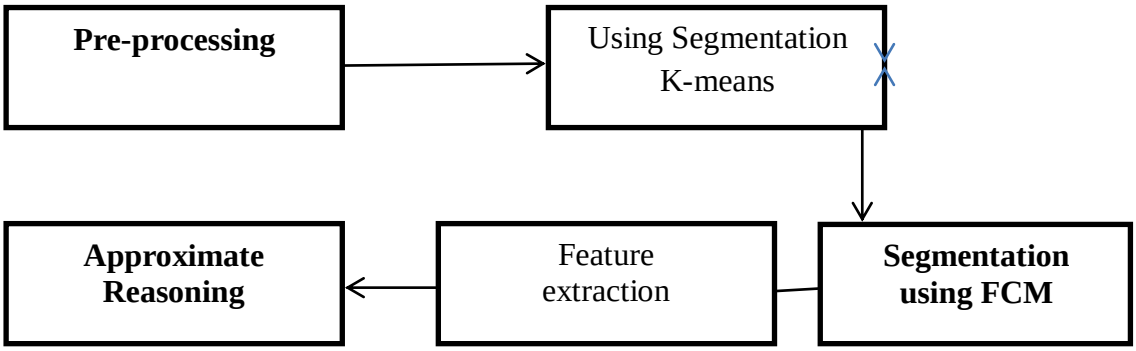

Fig.3 *block diagram of proposed method*

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

PRE-PROCESSING

According to the need of the next level the preprocessing step convert the image. It performs filtering ofnoise 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 inmodern MRI scan are very less. It may arrive due to the thermal effect. The main aim of this paper is to detect andsegment the tumor cells. But for the complete system it needs the process of noise removal. For betterunderstanding the function of median filter, we added thesalt and pepper noise artificially and removing it using median filter [15–17].

K-MEANS SEGMENTATION

K-meansclusteringdetail*:*

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 [18].

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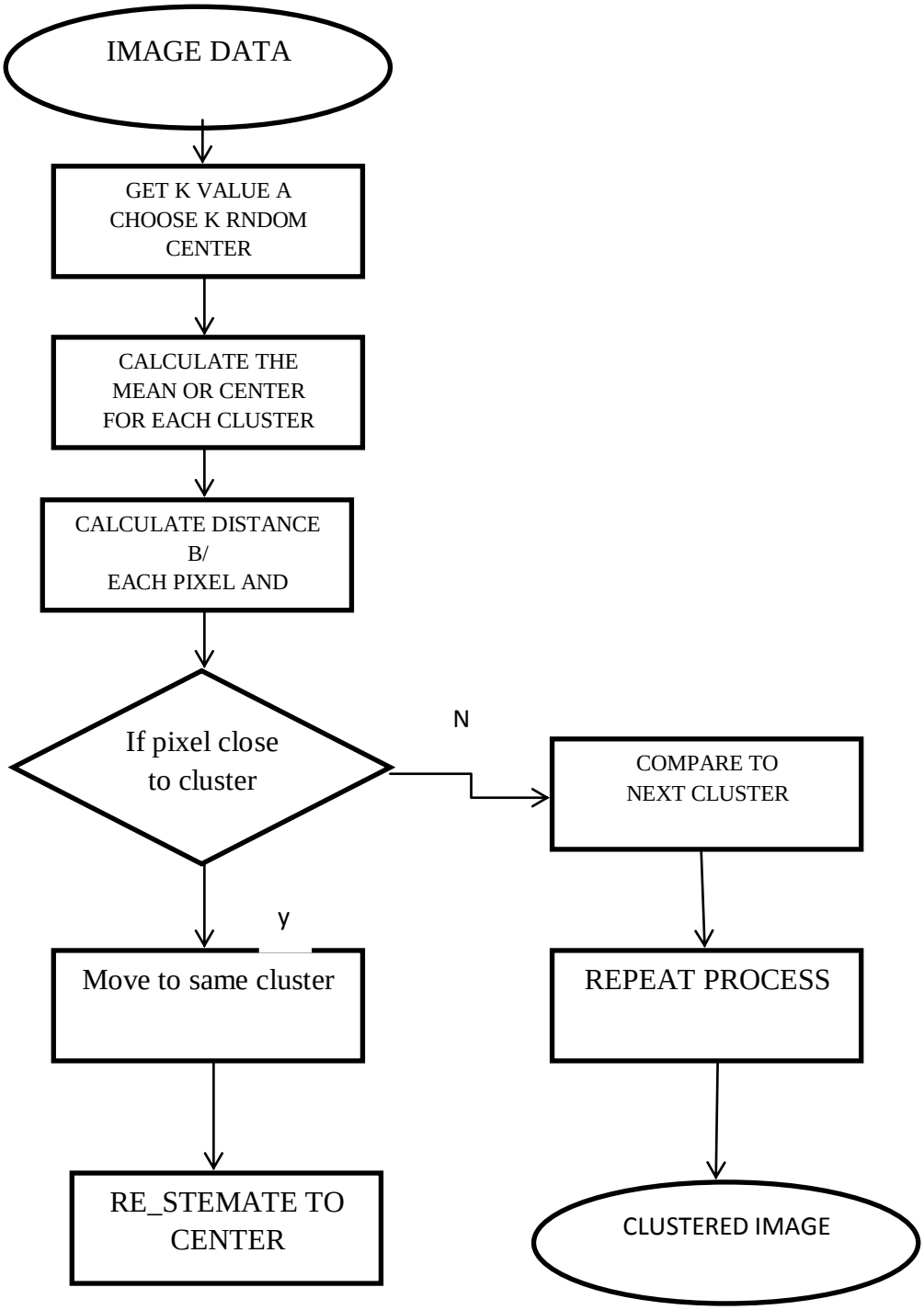
Flowchart of k-means algorithm:



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

Mathematical representation For a given image, compute the cluster means *m:*

$$m = \frac{\sum_{c(i)} x_i}{n_k} \quad , \quad k = 1, \ldots \ldots k \qquad (1)$$

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Calculate the distance between the cluster center to eachpixel

$$D(i) = argmin\|x_i - m_k\|^2 \text{i=1,……,n} \quad (2)$$

Repeat the above two steps until mean valueconvergence.

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:

:

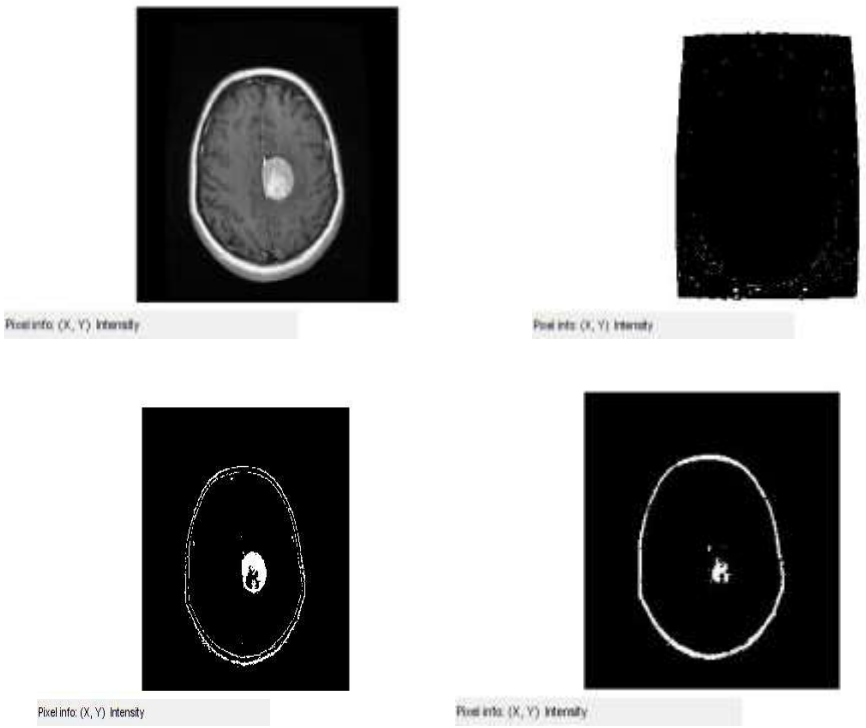

Fig. 4 *Output image for pre-processing and k-means for k=5*

Fig.4 is the MR image given as input to the preprocessing and K-means algorithm. Here 0.02% of saltand pepper noise is added and that has been removedusing the median filter. The K-mean algorithm clusters the image according to some characteristics. Figure is theoutput for K-Means algorithm with five clusters. At thefifth cluster the tumor is extracted [19–21].

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SEGMENTATION USING FUZZY C-MEANS

Fuzzy Clustering:

The fuzzy logic is a way to processing the data bygiving the partial membership value to each pixel in theimage. The membership value of the fuzzy set is rangesfrom 0 to 1. Fuzzy clustering is basically a multi valued.

Logic that allows intermediate values i.e., member of onefuzzy set can also be member of other fuzzy sets in thesame image. There is no abrupt transition between full membership and non membership. The membershipfunction defines the fuzziness of an image and also todefine the information contained in the image. These arethree main basic features involved in characterized bymembership function. They are support, Boundary. Thecore is a fully member of the fuzzy set. The support is nonmembership value of the set and boundary is theintermediate or partial membership with value between 0 and 1.

Mathematical representation:

Fuzzy c-means (FCM) is the clustering algorithmwhich allows one piece of data may be member of morethan one clusters. It is based on reducing the following function:

$$Y_m = \sum_{k=1}^{n}\sum_{j=1}^{c} m_{ij}^{m} \left\| x_i - c_j \right\|^2 \qquad (3)$$

Where

m- any real number greater than *1*,

m_j degree of membership of *X*; in the cluster *j*,

x_i- data measured in *d*-dimensional,

r_j - d-dimension center of the cluster,

The update of membership *M*i and the cluster centers *R*, are given by:

$$m_{ij} = \frac{1}{\sum_{k=1}^{c}\left(\frac{\|x_i - c_j\|}{\|x_i - c_j\|}\right)^{\frac{2}{m-1}}} \qquad (4)$$

$$r_j = \frac{\sum_{i=1}^{n} x_i . m_{ij}^{m}}{\sum_{i=1}^{n} m_{ij}^{m}} \qquad (5)$$

The above process ends when,

$$max_{ij}\{\left| m_{ij}^{(k+1)} - m_{ij}^{(k)} \right|\} < \partial \qquad (6)$$

Where:

∂ = termination value or constant between 0 and 1,

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K= no of iteration steps.
C The Fuzzy c-meansAlgorithm
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:

$$r_j = \frac{\sum_{i=1}^{n} x_i . m_{ij}^m}{\sum_{i=1}^{n} m_{ij}^m} \quad (7)$$

3.Update u^k, u^{k+1}

$$m_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{\|x_i - c_j\|}{\|x_i - c_j\|} \right)^{\frac{2}{m-1}}} \quad (8)$$

4. $\left\{ \left| m_{ij}^{(k+1)} - m_{ij}^{(k)} \right| \right\} < \partial$ then STOP; otherwise return to step.

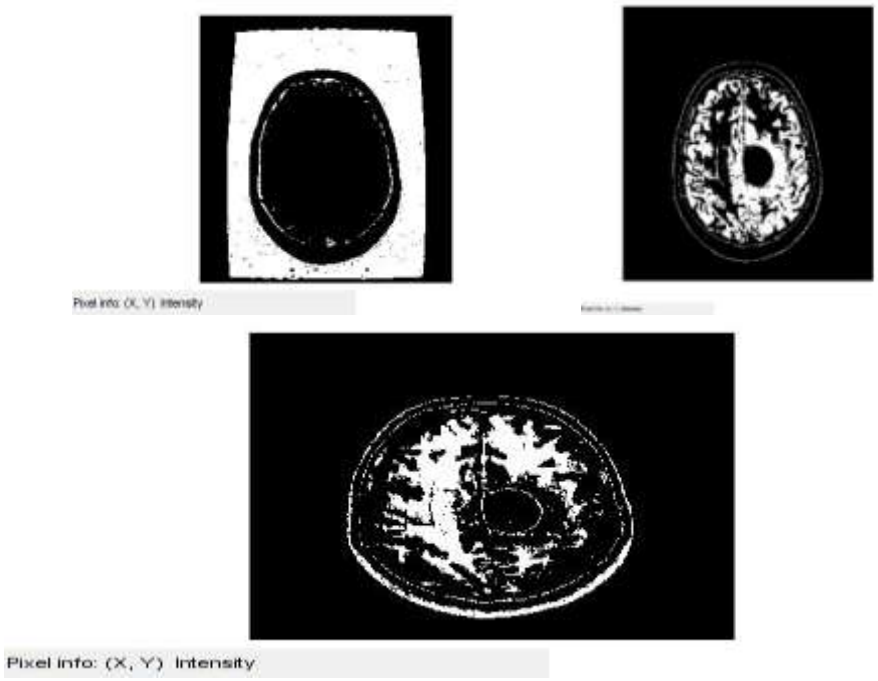

Fig.5 *Output image of FCM*

Fig.5 *is the output image for Fuzzy C Means. It ismainly developed for the accurate prediction of tumorcells which are not predicted by K-means algorithm. Itgives the accurate result for that compared to the K-Means.*

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FEATURE EXTRACTION

The feature extraction is extracting the cluster whichshows the predicted tumor at the FCM output. Theextracted cluster is given to the thresholding process.

It applies binary mask over the entire image. It makes thedark pixel become darker and white become brighter. Inthreshold coding, each transform coefficient is comparedwith a threshold. If it is less than the threshold value thenit is considered as zero. If it is larger than the threshold, itwill be considered as one. The thresholding method is anadaptive method where only those coefficients whose magnitudes are above a threshold are retained within each block. Let us consider an image 'f that has the k gray level. An integer value of threshold T, which lies in the gray scale range of k. The thresholding process is acomparison. Each pixel in 'f 'is compared to T. Based onthat, binary decision is made. That defines the value of theparticular pixel in an output binary image 'g':

$$g(n) = \begin{cases} 0 & if\ \ f(n) \geq T \\ 1 & if\ \ f(n < T \end{cases} \qquad (9)$$

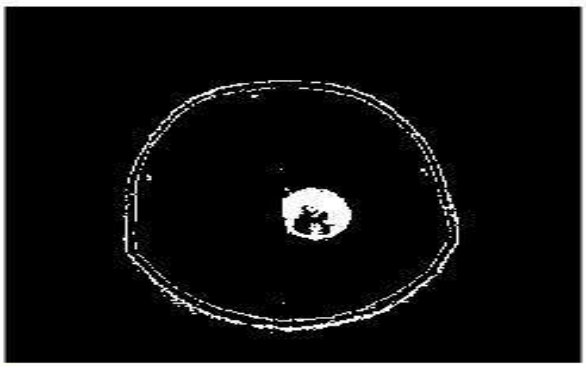

Fig.6 *Output image of Thresholding*

Fig.6 *is the extracted tumor shape from the givenimage using the Fuzzy C- Means algorithm. Theunpredicted 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 calculated using the binarization method. That is theimage having only two values either black or white (0 or1). Here 256x256 jpeg image is a maximum image size.The binary image can be represented as a summation oftotal number of white and black pixels.

$$IMAGE, I = \sum_{W=0}^{255} \sum_{H=0}^{255} [F(0) + F(1)] \qquad (10)$$

PIXEL=WITH(W)*HIGHT(H)=256*256
F(0)=WHITE PIXEL
F(1)= BLACK PIXEL

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$$NO-OF-WHITE\ PIXEL, P = \sum_{W=0}^{255}\sum_{H=0}^{255}[F(0)] \quad (11)$$

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

$$SIZE-OF-TUMOR, S = \left[\left(\sqrt{P}\right)^{*/264}\right] mm^2 \quad (12)$$

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

A.ALGORTHM

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 thebinary image. Also it calculates the size of tumor bycalculating the number of white pixels(digit 0) in binary image.

B. Output screenshot for tumor area calculation

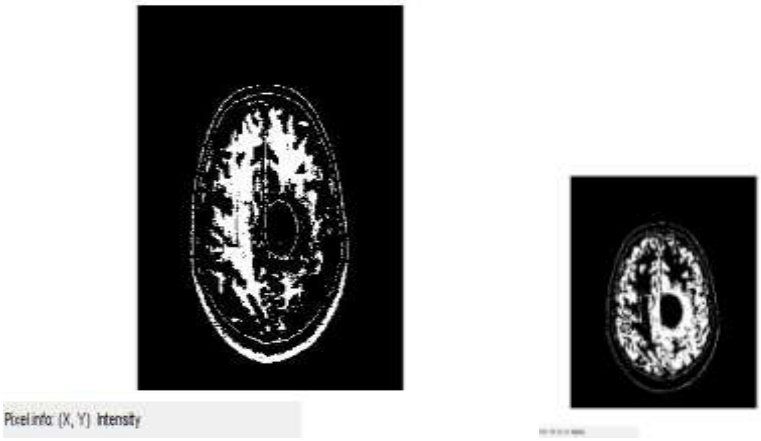

Fig.7 *Output image of tumor area calculation*

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The predicted tumor area is calculated at approximatereasoning step fig 7 shows the output result for tumor areaand its stage calculation. The stage of tumor is based on thearea of tumor. We considered that, if the area is greaterthan 6 mm"2 it will be the critical position.

CONCLUSION

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 enoughto extract it from the brain cells. If there is any noise arepresent in the MR image it is removed before the K-means process. The noise free image is given as an input to the k-means and tumor is extracted from the MRI_image.

And then segmentation using Fuzzy C means for accuratetumor shape extraction of malignant tumor andthresholding of output in feature extraction. Finally approximate reasoning for calculating tumor shape andposition calculation. The experimental results are compared with other algorithms. The proposed method gives more accurate result. In future 3D assessment ofbrain using 3D slicers with matlab can be developed.

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