



Research Article

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Segmentation of brain MR images for tumor area and size detection by using of clustering algorithm

Shinu Sadeyone¹ and S. Freeda²

¹EIE, Sathyabama University, Chennai

²EIE, A. C. T. Engineering College, Chngalpattu

ABSTRACT

There are different types of tumors are available. Astrocytoma is the most common type of tumor (30% of all brain tumor) and is usually a malignant one. Astrocytoma can be subdivided into four grades. Each grade has its own characteristics and unique treatment. If any wrong treatment is given to these grades that leads to death. So finding the position and shape of tumor is very important for the further treatment. The proposed system of this paper is to find the exact position and shape of the tumor cells. That helps the physician for further treatment. In the proposed system, it consists of four modules (i) Pre-processing, (ii) Segmentation of brain in MR Images, (iii) Quality extraction and (iv) Approximate reasoning. Pre processing is done by filtering. Segmentation is done by advanced K-means and Fuzzy C-means algorithms. Quality extraction is by thresholding. Finally, Approximate reasoning method to recognize the tumor shape and position in MRI image. If the tumor is a mass in shape then k-means algorithm is enough to extract it from brain cells. Suppose if it is a malignant (spread over the brain) one then the Fuzzy C-means algorithm will be used for accurate tumor diagnosis, since the Fuzzy method is used for floating point prediction of the tumor cells. At the end of the process the tumor shape, position, area and its stage will be determined. In this project the two strong algorithms are used for segmentation. So, the entire system for tumor segmentation is more accurate than other methods.

Key words: pre-processor, k-means clustering, fuzzy c-means clustering, grouping.

INTRODUCTION

The incidence of brain tumors has increased over the time and differs according to gender, age, race, and geography. Most of this to increase attributable to improvements in diagnostic imaging methods, increased availability of medical care and neurosurgeons, changing approaches in treatment of older patients, and changes in classifications of specific histology's of brain tumors. Survival time after brain tumor diagnosis varies greatly by histologic type and age at diagnosis [1]. Moreover, some of malignant brain tumors such as Glioblastomas may develop suddenly or by way of malignant progression from lower grades. Therefore, diagnosing the brain tumors in an appropriate time is very essential for further treatments. In recent years, neurology and basic neuroscience have been significantly advanced by imaging tools that enable in vivo monitoring of the brain. In particular, Magnetic Resonance Imaging (MRI) has proven to be a powerful and flexible brain imaging modality that allows non invasive longitudinal and 3D assessment of tissue morphology, metabolism, physiology, and function [2]. The information MRI provides, has greatly increased the knowledge of normal and diseased anatomy for medical research, and is a critical component in diagnosis and treatment planning. 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. So

we went for combination of two algorithms that will segment the malignant tumor such as astrocytoma tumor. The proposed method consists of five modules.

They are
Pre-processing
Segmentation using K-means
Segmentation using FCM
Feature extraction
Tumour Area calculation

I. System model

In this section fig 1. Gives the complete process done in the proposed work.

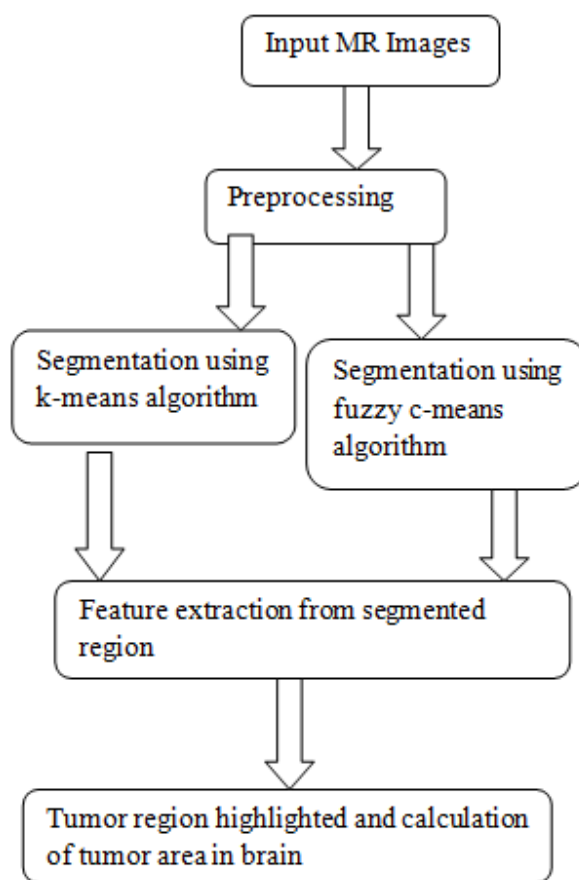


Fig 1. Proposed work flow chart

Segmentation of Brain MR Images for Tumor Extraction by Combining K-Means Clustering and Fuzzy C-Means can be done in four modules: pre-processing, segmentation, Feature extraction, and approximate reasoning. At first MR Images get pre-process, this is done to make an image perfect for the process done in the next level and the process done here is noise filter. Segmentation is carried out by both advanced K-means and Fuzzy C-means algorithms. Feature extraction is by thresholding and finally, approximate reasoning method is to recognize the tumor shape and position in MR image.

II. Pre-processing

Pre-processing is the process of making an image that is suitable for the next level. It performs filtering of noise and other artifacts in the image and sharpening the edges in the image. RGP to GRAY conversion and re-sharpening also take place here. The pre-processing of data takes under rule-based filtering (inference) system so the image is

enhanced. But the possibilities for the noise in MRI images are very less. Here we are using the medial filter for the noise removal.

a) Removing Noise by means of Median Filtering:

Median filtering is similar to using an averaging filter, in that each output pixel is set to an average of the pixel values in the neighbourhood of the corresponding input pixel. However, with median filtering, the value of an output pixel is determined by the median of the neighbourhood pixels, rather than the mean. The median is much less sensitive than the mean to extreme values (called *outliers*). Median filtering is therefore better able to remove these outliers without reducing the sharpness of the image. The `medfilt22` function implements median filtering.

Since there is no possibility for noise in the image. So the output of pre-processed image same as that of the original image. This image given as a input to the next level that is segmentation level done by both advanced k-means clustering and fuzzy c-means clustering. But for the whole system we artificially add and remove the noise.

III. K-means segmentation

K-means is one of the simplest unsupervised learning algorithms that solve the well known clustering problem [3][4].

Algorithm:

1. At first it decide on a value for k .
2. Initialize the k cluster centres (randomly, if necessary).
3. Decide the class memberships of the M objects by assigning them to the nearest cluster centre.
4. Re-estimate the k cluster centres, by assuming the memberships found above are correct.
5. If none of the M objects changed membership in the last iteration, exit. Otherwise go to step 3.

For a given assignment d , compute the cluster means α

$$\alpha = \frac{\sum_{i:d(i)=k} p_i}{M_k}, \quad k=1, \dots, K. \quad (1)$$

For a current set of cluster means, assign each observation as,

$$d(i) = \arg \min_k \|p_i - \alpha_k\|, \quad i=1, \dots, N \quad (2)$$

Iterate above two steps until convergence.

Advantages of using k-means algorithm Technique:

- With a large number of variables, K-Means may be computationally faster than hierarchical clustering (if K is small).
- K-Means may produce tighter clusters than hierarchical clustering, especially if the clusters are globular.

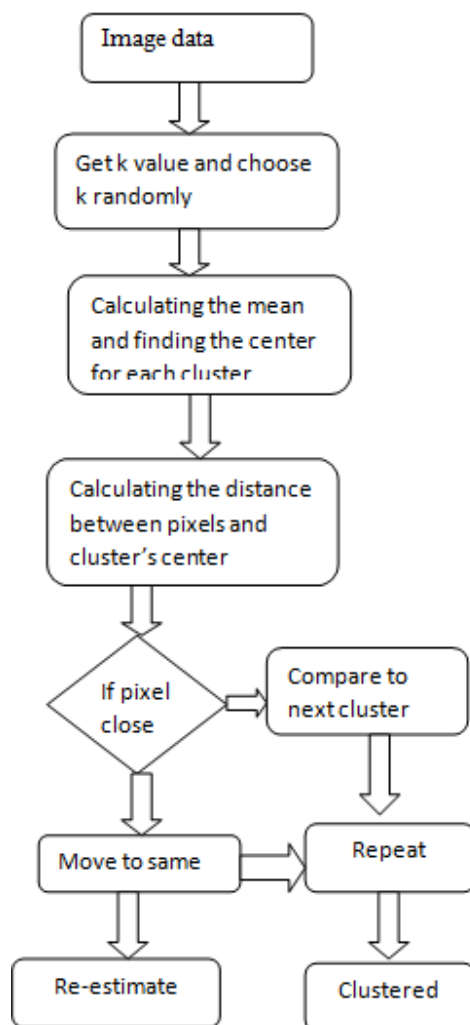


Fig2. Flowchart for k-means algorithm

After the removal of salt and pepper from the input image having noise 0.02% by using of median filter is taken to the segmentation process done by using of k-means clustering. The results shown from the segmentation of brain MR Image with k value as 5. K-means algorithm is to grouping pixels taking any as a centre point, distance is measured and pixels which are near to centre point get grouped in same [5].

IV. Fuzzy c-means segmentation

Fuzzy c-means (FCM) is a data clustering technique where in each data point belongs to a cluster to some degree that is specified by a membership grade. This algorithm works by assigning membership to each data point corresponding to each cluster centre on the basis of distance between the cluster centre and the data point [6]. More the data is near to the cluster centre more is its membership towards the particular cluster centre. It provides a method that shows how to group data points that populate some multidimensional space into a specific number of different clusters.

Fuzzy C-Means Algorithm:

Let $U = \{u_1, u_2, u_3, \dots, u_n\}$ be the set of data points and $V = \{v_1, v_2, v_3, \dots, v_c\}$ be the set of centres.

1. Randomly select 'c' cluster centres.
2. Calculate the fuzzy membership μ_{ij} using

$$\mu_{ij} = \frac{1}{\sum_{k=1}^c \frac{b_{ij}}{b_{ik}} \left(\frac{2}{q}-1\right)} \quad (3)$$

3. Compute the fuzzy centres 'v_j' using

$$v_j = \frac{\sum_{i=1}^n (\mu_{ij})^q y_i}{\sum_{i=1}^n (\mu_{ij})^q} \quad (4)$$

4. Repeat step 2 and 3 until the minimum 'j' value is achieved or $\|U^{(l+1)} - U^{(l)}\| < \eta$

(5)

where,

'l' is the iteration step.

'η' is the termination criterion between [0, 1].

'U' = (μ_{ij})_{n*c}' is the fuzzy membership matrix.

'j' is the objective function.

After each iteration membership and cluster centres are updated based on the above conditions.

Advantages of using this Technique:

- Gives best result for overlapped data set and comparatively better than k-means algorithm.
- Unlike k-means where data point must exclusively belong to one cluster centre here data point is assigned membership to each cluster centre as a result of which data point may belong to more than one cluster centre.

V. Tumor area calculation

The tumour detected image is converted to binary image by thresholding (binarisation). By using the tumour detection formula the area is calculated. Based on the area the various stages of tumours are identified [7] - [10].

Tumor Calculation formula:

Binary image = $\sum_{L=0}^{255} \sum_{B=0}^{255} [f(0) + f(1)]$ Where,

Pixels = Length (L) x Breadth (B) = 256 x 256.

f(0) = white pixel (digit 0)

f(1) = black pixel (digit 1)

Number of white pixels, W = $\sum_{L=0}^{255} \sum_{B=0}^{255} [f(0)]$

Size of tumor,

$$S = [(W) * 0.264] \text{ mm}^2$$

Where,

W = number of white pixels (width * height)

1 Pixel = 0.264 mm

Different stages of tumour:

- If the detected white pixels < 50, then no tumor was detected. The result gives 'activity found normal'.
- If the detected white pixels > 50, and detected <= 300, then tumor was in initial stage. The result gives 'initial stage of brain tumor detected'.
- If the detected white pixels > 300, and detected <= 500, then tumor was in intermediate stage. The result gives 'intermediate stage of brain tumor detected'.
- If the detected white pixels >= 500, then tumor was in critical stage. The result gives 'critical stage of brain tumor detected'.

RESULTS

The MR images does not have more noises in nature. In case when unintentional attacks happen, the images will get some noises. So the input image contains some artificial noises. It is taken to the pre-processing by using of median

filter, the output gives an image without noise. The advantage of median filter is, it can reduce small amount of noise present in an image.

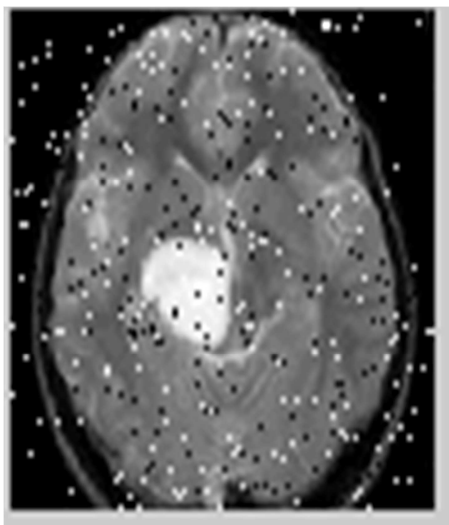


Fig 3. Image in which noise is added and given as an input to the pre-processing level

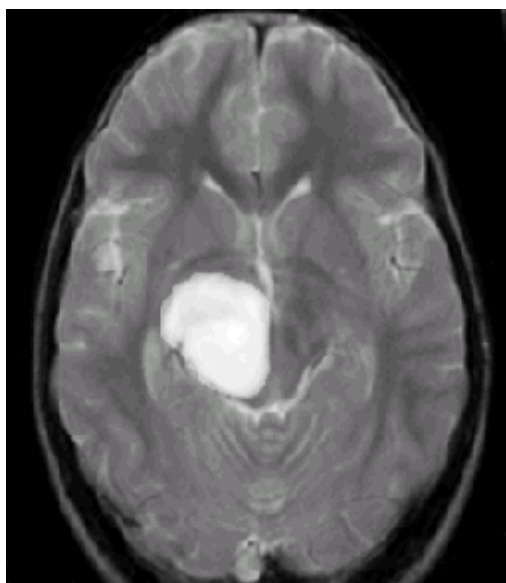


Fig4. Output of pre-processing level

In this section fig.3 is the image with salt and pepper noise of 0.02% is given to the pre-processing level to get an image without noise then fig.4 gives the noise removed image using median filter as an output from pre-processing level.

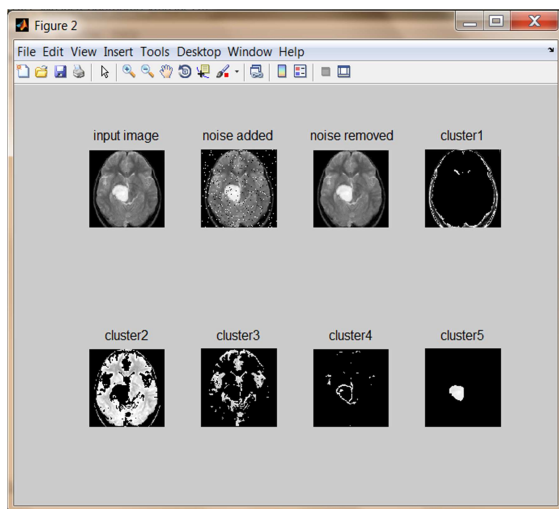


Fig5. Combined output for pre-processing and K-means with K=5

In this section, fig 5 gives the clustered images of MR Images. In which the pixels are get grouped on the basis of k-means clustering algorithm when the tumor is in mass level.

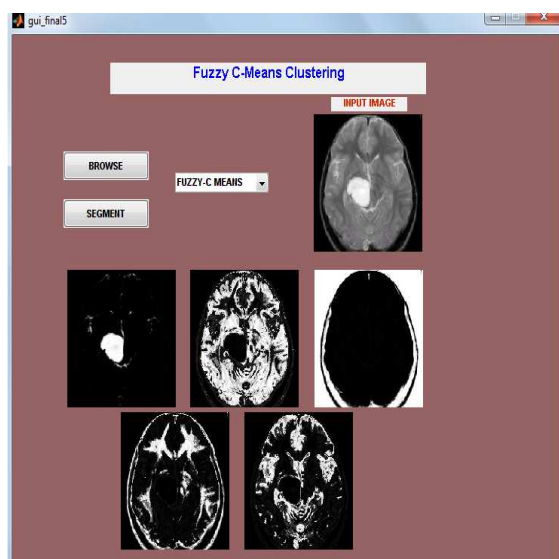


Fig6. Output image of for Fuzzy c-means algorithm

In this section, when the tumor is in malignant form then fuzzy c means algorithm is used. Fig 6 gives the clustered image based on the fuzzy c means clustering.

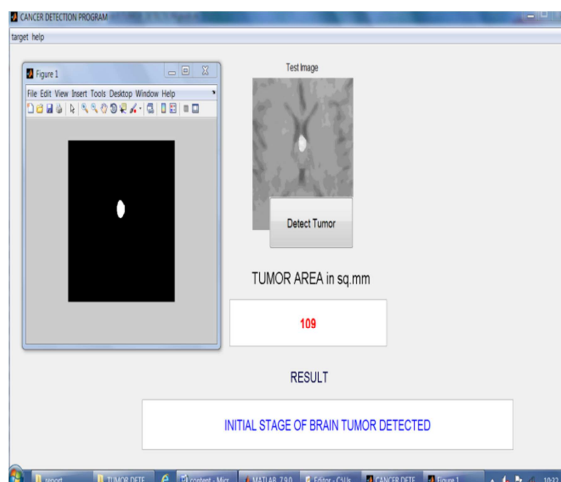


Fig7. Size detection (Output image detected white pixels > 50 & detected <= 300, Initial Stage of Brain Tumor)

In this section, it gives the output of stages of tumor level. Fig 7 gives the output of tumor level based on the quantity of white pixels.

CONCLUSION

There are different types of tumors are available. They may be as mass in brain or malignant over the brain. This project deals with the mass tumor detection and extraction. This project is used to extract the mass tumor from Brain MRI scan image and it can find out the area. This will help the physician for further treatment. In future, mass tumor volume can be calculated by using some morphological operation and 3D slicer.

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