



Brain Tumor Segmentation Mechanism by Using K Mean and Fuzzy C Means

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ABSTRACT: This paper manages the usage of Simple Algorithm for recognition of reach and state of tumor in cerebrum MR pictures. Tumor is an uncontrolled development of tissues in any part of the body. Tumors are of various sorts and they have diverse Characteristics and distinctive treatment. As it is known, mind tumor is intrinsically genuine and life-undermining in view of its character in the constrained space of the intracranial cavity (space shaped inside the skull). Most Research in created nations demonstrates that the quantity of individuals who have cerebrum tumors were kicked the bucket because of the certainty of off base recognition. For the most part, CT sweep or MRI that is coordinated into intracranial depression delivers a complete picture of mind. This picture is outwardly inspected by the doctor for discovery and conclusion of cerebrum tumor. Notwithstanding this strategy for discovery opposes the precise determination of stage and size of tumor. To stay away from that, this work utilizes PC supported technique for division (discovery) of mind tumor taking into account the Kmeans and fluffy c-implies calculations. This technique permits the division of tumor tissue with exactness and reproducibility similar to manual division. What's more, it likewise lessens the ideal opportunity for investigation.

KEYWORDS: Abnormalities, Magnetic Resonance Imaging (MRI), Brain tumor, Pre-processing, K-means, fuzzy c-means, Thresholding

I. INTRODUCTION

This paper manages the idea for programmed cerebrum tumor division. Regularly the life structures of the Brain can be seen by the MRI output or CT filters. In this paper the MRI filtered picture is taken for the whole procedure. The MRI sweep is more agreeable than CT check for conclusion. It is not influence the human body. Since it doesn't utilize any radiation. It depends on the attractive field and radio waves. There are diverse sorts of calculation were produced for cerebrum tumor identification. In any case, they may have some disadvantage in identification and extraction. In this paper, k-implies calculation and fluffy c-implies calculation is utilized for division. So it gives the exact result for tumor division. Tumor is because of the uncontrolled development of the tissues in any part of the body. The tumor might be essential or auxiliary. On the off chance that it is a source, then it is known as essential. In the event that the part of the tumor is spread to somewhere else and developed as its own particular influences CSF (Cerebral Spinal Fluid). It reasons for strokes. The doctor gives the treatment for the strokes as opposed to the treatment for tumor. So of the individual who influenced by the mind tumor will increment in the event that it is identified at current stage. That will build the lifetime around 1 to 2 years. Typically tumor cells are of two sorts. They are Mass and Malignant. The identification of the dangerous tumor is to some degree hard to mass tumor. For the precise identification of the harmful tumor that needs a 3-D representation of cerebrum and 3-D analyzer device. In this paper we concentrated on identification of mass tumor location. The creating stage for the location is mat lab [1].

II. RELATED WORK

The extracted cluster is given to the threshold process. It applies a binary mask over the entire image. In the approximate reasoning step the tumor area [6] is calculated using the binarization method. It makes the dark pixel



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become darker and white become brighter. Each transform coefficient is compared with a threshold in threshold coding. If it is smaller than the threshold value, then it is taken as zero. If it is larger than the threshold, it will be taken 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 grayscale range of k. The thresholding process is a comparison where each pixel in 'f' is compared to T. Based on which, binary decision is carried out. That defines the value of the particular pixel in an output binary image. The feature extraction is extracting the cluster, which shows the predicted tumor at the FCM (Fuzzy C-means) output. The extracted cluster is given to the threshold process. It applies a binary mask over the entire image. In the approximate reasoning step the tumor area [6] is calculated using the binarization method. It makes the dark pixel become darker and white become brighter. Each transform coefficient is compared with a threshold in threshold coding. If it is smaller than the threshold value, then it is taken as zero. If it is larger than the threshold, it will be taken 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 grayscale range of k. The thresholding process is a comparison where each pixel in 'f' is compared to T. Based on which, binary decision is carried out. That defines the value of the particular pixel in an output binary image. The feature extraction is extracting the cluster, which shows the predicted tumor at the FCM (Fuzzy C-means) output. The extracted cluster is given to the threshold process. It applies a binary mask over the entire image. In the approximate reasoning step the tumor area [6] is calculated using the binarization method. It makes the dark pixel become darker and white become brighter. Each transform coefficient is compared with a threshold in threshold coding. If it is smaller than the threshold value, then it is taken as zero. If it is larger than the threshold, it will be taken 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 grayscale range of k. The thresholding process is a comparison where each pixel in 'f' is compared to T. Based on which, binary decision is carried out. That defines the value of the particular pixel in an output binary image.

III. OBJECTIVE AND MOTIVATION

A number of institutions perform special medical checks for brain, known as "Brain Dock" in Japan, by using forward thinking skills like computed tomography (CT), magnetic resonance imaging (MRI) and positron emission CT (PET), because the Japanese are also keen in preventing various neurological conditions including stroke, dementia, etc. It is possible for radiologists to miss the lesions of patients, because of their heavy workloads. Therefore, for detecting the lesions of patients correctly and efficiently, radiologists would need to experience a number of training sessions. In addition, the number of images, which neuron-radiologists have to diagnose, has increased rapidly, because MRI [2] has shifted from two dimensional (2D) imaging to 3D imaging, and the determination as well as signal-to-noise ratio has become developed. Consequently, due to their heavy workloads in the field of NeuroRadiology neuron-radiologists have been demanding the new approach of "Computer-Aided Diagnosis (CAD)". CAD has become one of the major research subjects in medical imaging and diagnostic radiology. The basic concept of CAD was proposed by The University of Chicago, in the mid- 980s, whose idea it was to provide a computer output as a "second opinion" to assist radiologists

in interpreting images, so that the accuracy and consistency of radiological diagnosis could be improved, and also the image reading time could be reduced. Since then, a number of researchers have developed computer aided diagnostic CAD schemes for detection and classification of various kinds of abnormalities such as micro calcifications and masses in mammograms, pulmonary nodules. In recent years, various kinds of CAD methods have been developed in the euro radiology using MR images. Radiologists expect that CAD systems can improve their diagnostic abilities based on synergistic effects between the computer's and radiologists high abilities by using the information analysis including the medical images.

IV. EXISTING APPROACH

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

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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 [2]. 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.

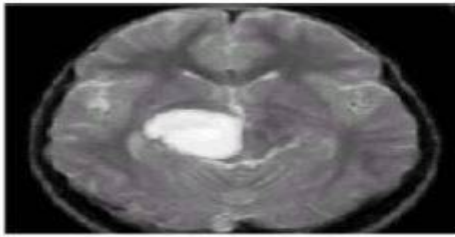


Fig-1 Input Image

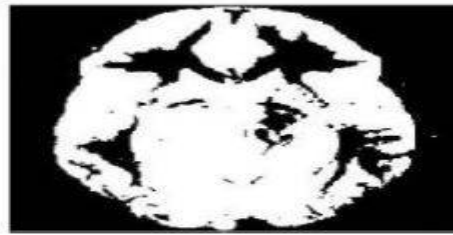
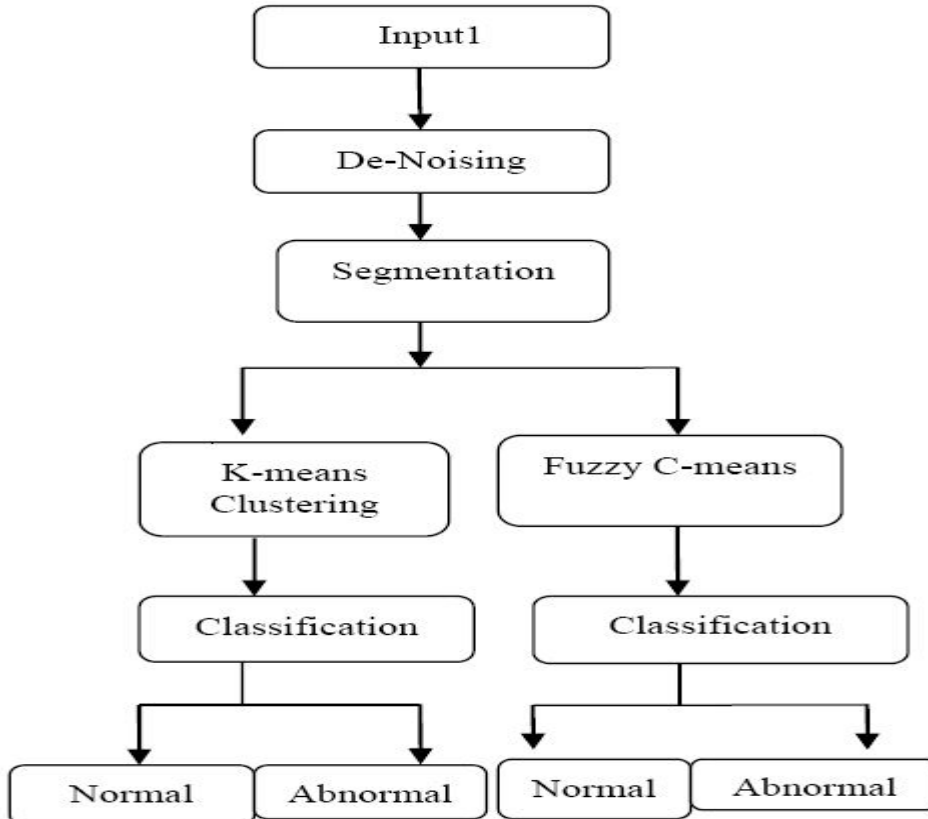


Fig .2 output image

Fig.1 is the input image for thresholding. 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 thresholding 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.

V. PROPOSED APPROACH

In the proposed method Segmentation is carried out by advanced K-means and fuzzy c-means algorithms. [3].





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According to the need of the next level the preprocessing 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.

VI. SEGMENTATION USING K-MEANS ALGORITHM

K-Means is one of the simplest unsupervised learning algorithms that solve the well-known clustering problem. The procedure follows a simple and easy way to classify a given data set through a certain number of clusters (assume k clusters) fixed a priori. The main idea is to define k centroids, one for each cluster. These centroids should be placed in a cunning way because of different location causes different result. So, the better choice is to place them as much as possible far away from each other [4]. The next step is to take each point belonging to a given data set and associate it to the nearest centroid. When no point is pending, the first step is completed and an early group age is done. At this point it is necessary to re-calculate k new centroids as bar centers of the clusters resulting from the previous step. After obtaining these k new centroids, a new binding has to be done between the same data set points and the nearest centroid. A loop has been generated. As a result of this loop, one may notice that the k centroids change their location step by step until no more changes are done. In other words centroids do not move any more. Finally, this algorithm aims at minimizing an objective function, in this case a squared error function ([5],[6],[7]).

Steps for k-means:

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

VII. SEGMENTATION USING FUZZY C-MEANS

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. With the developing of the fuzzy theory, the fuzzy c-means clustering algorithm based on Ruspini fuzzy clustering theory was proposed in 1980s. This algorithm is examined to analyze based on the distance between the various input data points. The clusters are formed according to the distance between data points and cluster centers are formed for each cluster. The basic structure of the FCM algorithm is discussed below. The Algorithm Fuzzy C-means (FCM) is a method of clustering which allows one piece of data to belong to two or more clusters ([8],[9]).

VIII. FLOW OF THE PROJECT

1. Preprocessing

Pre-processing step translate the image, it completes filtering of noise and other artifacts in the image and sharpening the edges in the image. The RGB to grey conversion and Reshaping also takes place here. It includes a median filter for noise deduction. The opportunities of arrival of noise in modern MRI scan [6] are very less. It may reach due to the thermal effect. The aim of this paper is to detect and segment the tumor cells, but for the complete stage it needs the process of noise removal. For better understanding the function of median filter we added the salt and pepper noiseartificially and removing it using median filter.



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2. K-means Clustering

A cluster is a collection of objects which are similar between them and are dissimilar to the objects belonging to other clusters. Clustering is an unsupervised learning method which deals with finding a structure in a collection of unlabeled data. A loose description of clustering could be the process of organizing objects into groups whose members are similar in some way. K-means clustering is an algorithm to group objects based on attributes/features into k number of groups where k is a positive integer. The grouping (clustering) is done by minimizing the Euclidean distance between the data and the corresponding cluster centroid. Thus the function of k-means clustering is to cluster the data.

3. Fuzzy C-means Algorithm

Fuzzy c-means (FCM) is a method of clustering [5] which allows one piece of data to belong to two or more clusters. The Fuzzy C-Means (FCM) clustering algorithm was first introduced by Dunn and later was extended by Bezdek. The algorithm is an iterative clustering method that produces an optimal c partition by minimizing the weighted within group sum of squared error objective function =

$$Y_m = \sum_{i=1}^N \sum_{j=1}^c u_{ij}^m \|X_i - C_j\|^2.$$

Where $X = \{x_1, x_2, \dots, x_n\} \subseteq R^p$ is the data set in the p-dimensional vector space, n is the number of data items c is the number of clusters with $2 \leq c < n$, u_{ik} is the degree of membership of x_k in the i th cluster q is a weighting exponent on each fuzzy membership v_i is the prototype of the centre of cluster i $d(x_k, v_i)$ is a distance measure between object x_k and cluster center v_i . The result of the objective function JFCM can be obtained via an iterative method.

4. Fuzzy C-Means Segmentation

The fuzzy logic is a way of processing the data by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set ranges from 0 to 1. Fuzzy clustering is basically a multi valued logic that allows intermediate values member of one fuzzy set can also be members 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 characterizing by membership function. They are supported Boundary. The core is a full member of the fuzzy set. The support is a non-membership value of the set and boundary is the intermediate or partial membership with value between 0 and 1.

5. Feature Extraction

The feature extraction is extracting the cluster, which shows the predicted tumor at the FCM (Fuzzy C-means) output. The extracted cluster is given to the threshold process. It applies a binary mask over the entire image. In the approximate reasoning step the tumor area [6] is calculated using the binarization method. It makes the dark pixel become darker and white become brighter. Each transform coefficient is compared with a threshold in threshold coding. If it is smaller than the threshold value, then it is taken as zero. If it is larger than the threshold, it will be taken 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 grayscale range of k. The thresholding process is a comparison where each pixel in 'f' is compared to T. Based on which, binary decision is carried out. That defines the value of the particular pixel in an output binary image.

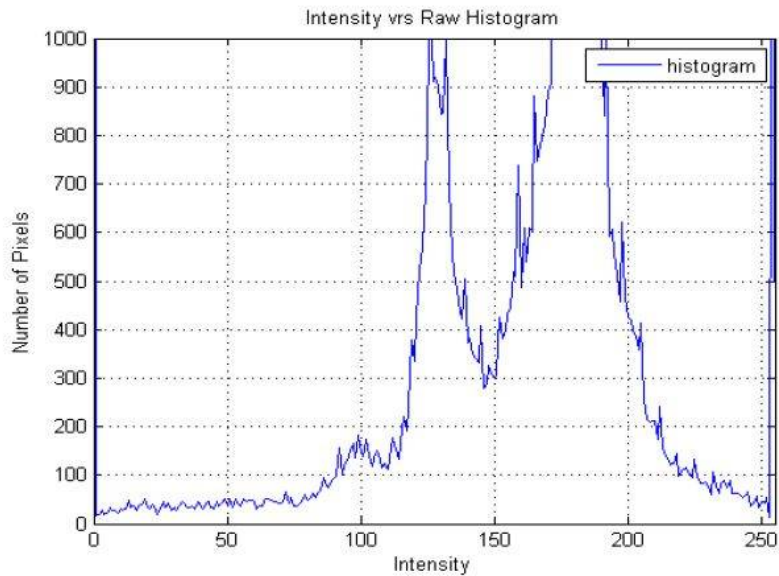
IX. EXPERIMENTAL RESULT

The figure shows the raw histogram of the image. The presence of consistent peaks throughout the histogram makes it difficult to identify tumor, white matter, grey matter and CSF.

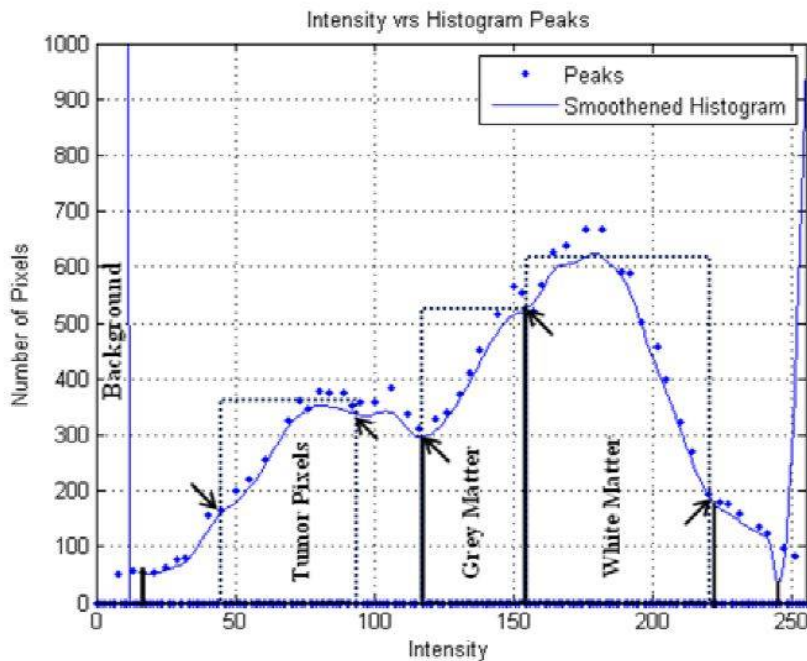
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Processed histogram for an efficient identification of tumor thresholds. The figure shows a detailed break-down of the histogram curve with each threshold range pertaining to A certain region of brain.

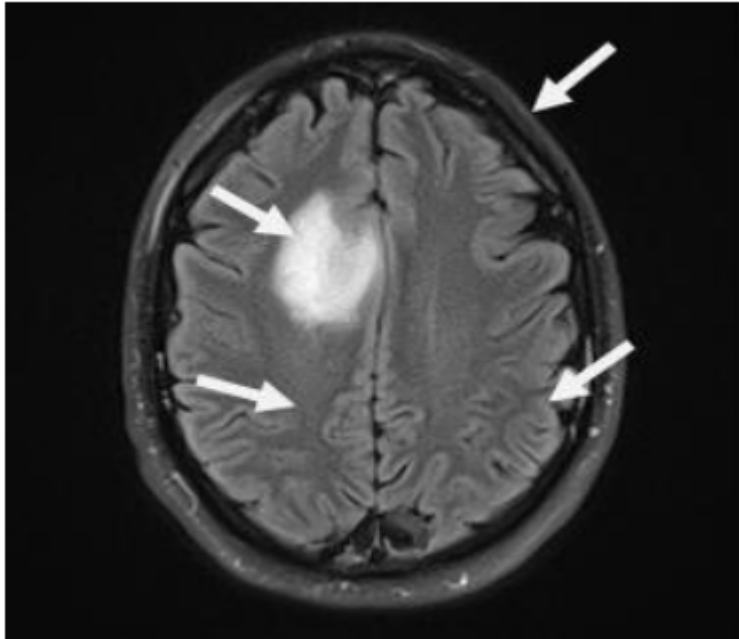


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OUTPUT RESULT-



X. CONCLUSIONS

From the consideration of all the above points we conclude that 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. 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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