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Brain Tumor Segmentation and Area Calculation of Tumor by Use of Unsupervised Clustering Algorithm

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

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

I. INTRODUCTION

Normally the anatomy of the Brain can be viewed by the MRI scan or CT scan. In this 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. There are different types of algorithm were developed for brain tumor detection. But they may have some drawback in detection and extraction. In this project, three 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 of the body. 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. For the accurate detection of the malignant tumor that needs a 3-D representation of brain and 3-D analyser tool. In this 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.

II. RELATED WORK

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[1]. 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[2][3]. 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.

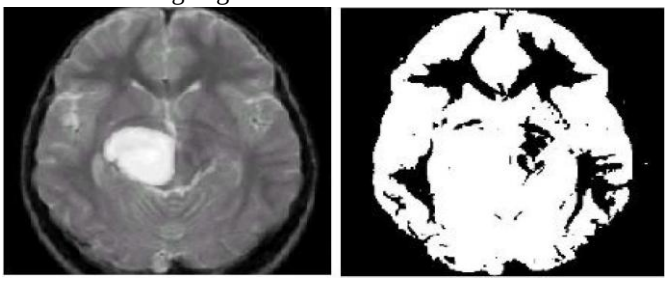

Fig. 1 (a) Input image for thresholding (b) Output Image for thresholding

Fig l (a) is the input image for thresholding. From the MR image it self we can see the tumor area but it is not enough for further treatment. For that it is given to the threholding process. Fig1 (b) 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 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.

III. MATERIAL AND METHODS

A. K-Means Clustering Method

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[7]. 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.

B. K-Means Clustering Algorithm

- Give the no of cluster value as k.
- Randomly choose the k cluster centers .
- Calculate mean or center of the cluster
- Calculate the distance b/w each pixel to each cluster center.
- If the distance is near to the center then move to that cluster.
- Otherwise move to next cluster.
- Re-estimate the center.
- Repeat the process until the center doesn't move

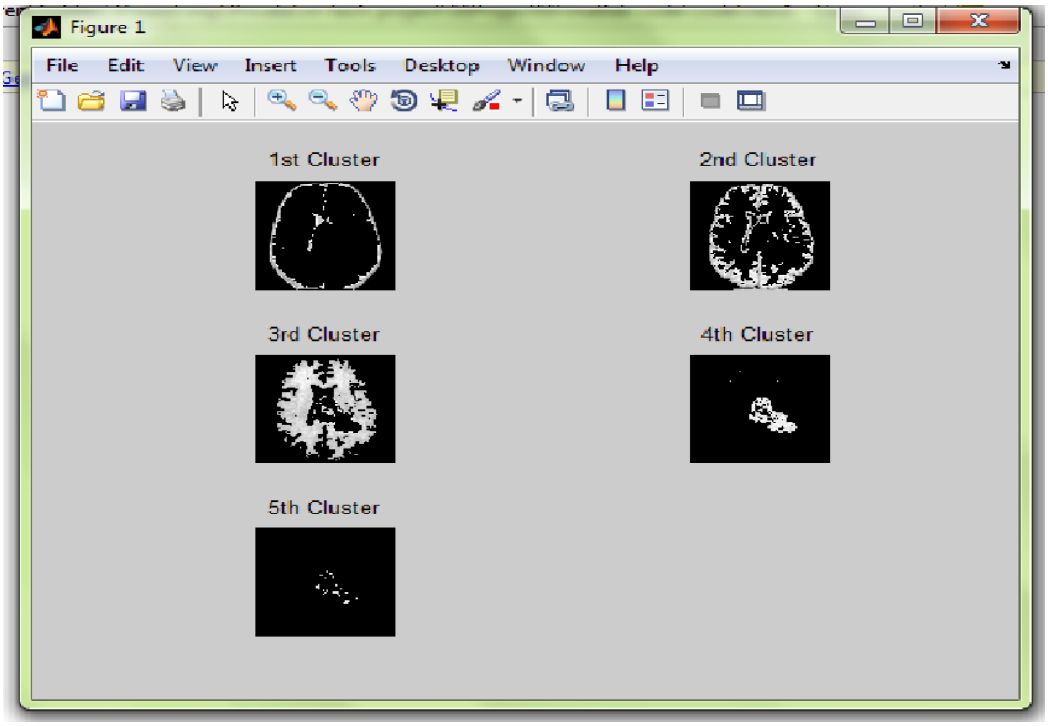

Fig. 2 Output image for pre-processing and k-means for k=5

Fig.2 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.

C. Segmentation Using Fuzzy C-Means

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 characterised 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.

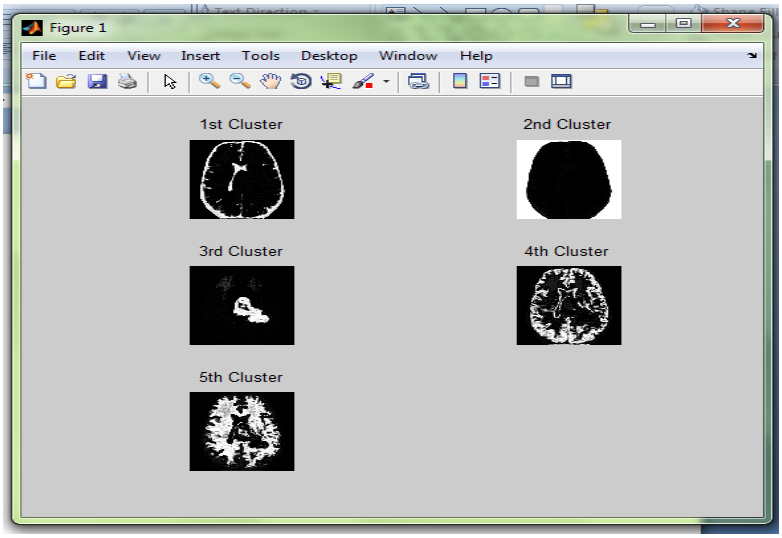

Fig. 3 Clustering Results of fuzzy C-mean

Fig.3 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.

IV. RESULTS

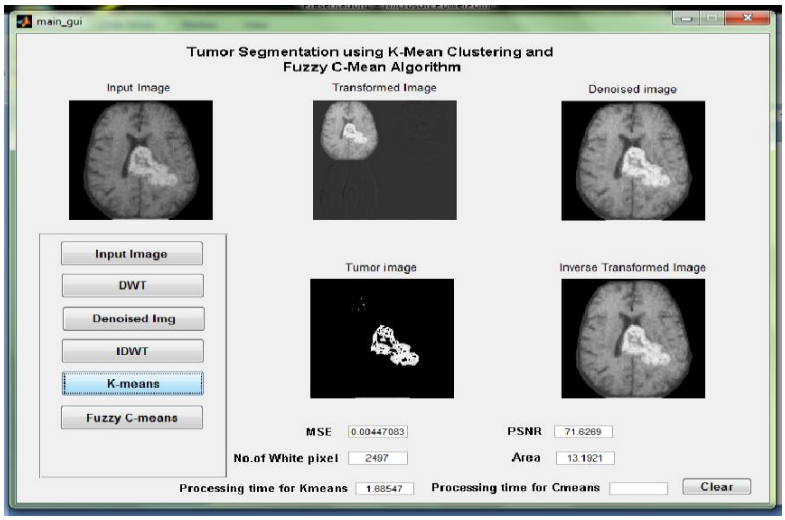

Fig. 4 Result of kmeans calculate different parameters

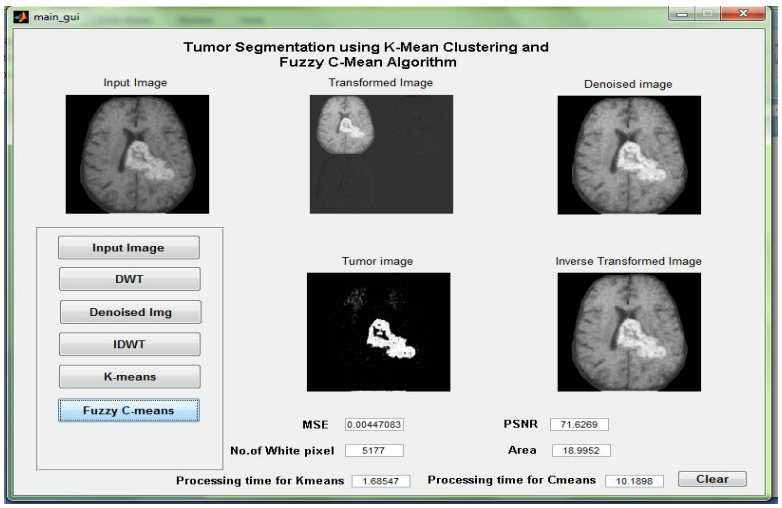

Fig. 5 Fuzzy C-means algorithm apply to image

The tumor area is calculated at approximate reasoning step Fig 4 and Fig 5 shows the output result for tumor area ,different parameters and its stage calculation. The stage of tumor is based on the area of tumor. We considered that, if the area is greater than 6 mm"2 it will be the critical position.

V. CONCLUSIONS

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 mat-lab can be developed

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