

# Brain Tumor Detection from MRI Images using Fuzzy C-Means Segmentation

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**Abstract:** The tumor is an undesirable growth of unhealthy tissues which increase intracranial pressure. Magnetic Resonance Imaging is a medical expertise, mainly used by the radiologists for diagnosis of an internal structure of the human body without any surgery. The method proposed in this paper is fuzzy c-means (FCM) and is compared with K-Means segmentation. Followed by tumor detection which will display the presence of a tumor as Abnormal brain whereas the absence of tumor as a normal brain. In the different clusters obtained, it shows different elements of the brain such as white matter, gray matter, edema and CSF (Cerebrospinal fluid) and tumor. A user-friendly environment is created by using GUI in MATLAB which in turn saves the precious time of doctor to diagnose the tumor automatically. Performance analysis using various parameters such as PSNR, Global Consistency error (GCE), Variation of Information (VOI), area, elapsed time, reproducibility, and Rand Index (RI) is done.

**Keywords:** Fuzzy C-Means, K-MEANS, Brain Tumor, PSNR, Rand Index, Variation of Information, GCE.

## I. INTRODUCTION

This paper deals with an automatic approach for brain tumor segmentation and detection. Basically, the tumor is an unconstrained growth of tissues in the brain. This tumor, when turns into cancer become potentially fatal. So in medical imaging, it is necessary to detect the perfect location of a tumor and its type. For detection and identification of brain tumor, MRI is the better option. A brain tumor is an intracranial mass produced by an unconstrained growth of cells either normally found in the brain such as neurons, cells, blood vessels, pituitary and pineal gland, lymphatic tissue, skull or spread from cancers predominantly located in other organs. Brain tumors are classified based on the location of the tumor, the type of tissue involved whether it is benign or malignant [1] [3].

1) Benign brain tumor: This type generally does not consist cancer cells and can be removed. It usually has an obvious border or edge. They don't spread to other parts of the body. However, benign tumors can cause serious health issues.

2) Malignant brain tumor: This consists cancerous cells and hence also called as brain cancer. They grow rapidly and can affect nearby healthy brain tissues. This can be a threat to life. Depending on the type of cell causing tumor, doctor groups brain tumor by grades. Over time, a low-grade tumor may become a high-grade tumor.

For diagnosis of brain tumor, MRI provides rich information about the basic structure, enabling quantitative pathological or clinical studies. The fundamental aspect that makes segmentation of medical images difficult is the complexity and instability of the anatomy that is being imaged. It may become impossible to locate certain

structures without detailed anatomical mastery. This makes general segmentation complicated, as the information must either be built into the system or provided by the operator.

For this, Matlab R2014b version 8.4 is used over the 64-bit operating system on intel (R) core i5 processor with inbuilt 4 GB RAM and 500GB hard disk.

## II. LITERATURE SURVEY

J.selvakumar et al. have used a method for brain tumor segmentation and detection based on the combination of two algorithms. This allows the tumor tissue segmentation with reproducibility and accuracy as compared to manual segmentation within a short span of time. The tumor is extracted from the MR image. The area of the tumor is calculated from the cluster the stage of the tumor is displayed [11]. Gauri P. Anandgaonka et al.[8] gave a method for the segmentation using Fuzzy C-Means algorithm and a method to find the area of the tumor which helped to decide the type of brain tumor.

## III. PROPOSED APPROACH

In this section, an idea used in the proposed technique is described. [7] The proposed system has mainly six modules: Image acquisition, pre-processing, segmentation, Post-processing, Feature extraction, Stage detection. In pre-processing filtering is performed on the MR image. K-means and Fuzzy C-means algorithm are used in segmentation work separately.

Thresholding is used for feature extraction. The flow for proposed system is shown in Figure 1.

## A. MRI image acquisition

- 1) **Data collection:** The input MRI images have been collected from different online open source database available for research work in DICOM, .MHA and .JPEG format.
- 2) **Image format Conversion:** The majority of the images collected was in .MHA format; hence they have been exported into a more usable format i.e. Medical Imaging Interaction Toolkit. For .DICOM image we used DICOM viewer software tool.

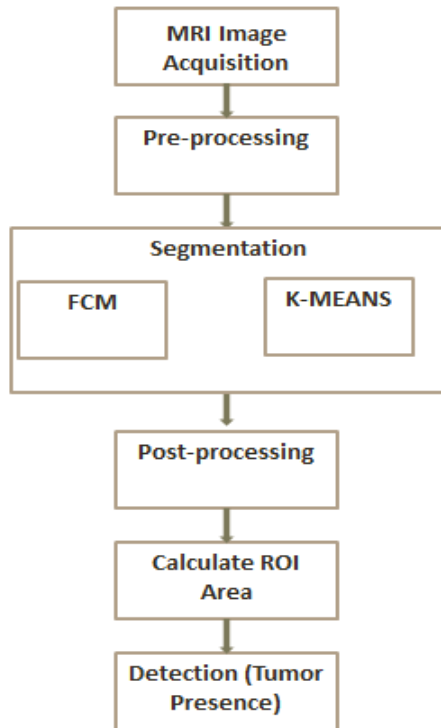


Fig 1: Flow Diagram for Proposed System

- 3) **Size normalization:** The images have been acquired from different sources; hence, they are of variable size. All images have been size normalized to be of size 255\*255 pixels.

## B. Image pre-processing

1. By changing the image mode to gray-scale, remove the color components for FCM and K-MEANS
2. Enhance the quality of the image by a median filter.
3. Plot the histogram to study and analyze the intensity distribution of the pixels.
4. Intensity adjustment if needed.
5. Histogram equalisation
6. This section formats the input image as per the need of further stages

## C. Segmentation

In this paper, two main clustering based segmentation methods named Fuzzy C-Means and K-Means are compared. In clustering process, partitioning or grouping of given unlabelled pattern sector into a number of clusters such as the similar patterns are assigned to a group. These groups are the known as clusters.

## 1) Fuzzy C-Mean (FCM):

In Fuzzy C-Mean, the data has to be processed by giving the partial membership value to each pixel in the image. The membership value of the fuzzy set is in the range of 0 to 1. In fuzzy clustering basically, a member of one fuzzy set can also be a member of other fuzzy sets in the same image. There are three basic features involved in characterization by a member function. The core is the full member of the fuzzy set, Support is the non-membership value of the set and Boundary is the partial membership with the value between 0 and 1 [11] [4] [8]. Generally, it is hard to determine whether a pixel belongs to a region or not. This is due to unsharp transitions at region boundaries. Fuzzy partition is carried out by an iterative optimization of object function, with the update of the membership function and cluster centre. Nearer the data point to the cluster centre the more possible its membership towards the particular centre. Compare to K-means, FCM provides better results for overlapped region and data point which belongs to one or more cluster. It is becoming a fruitful research area.

## Fuzzy c-mean Algorithm steps:

1. Browse the file path; select the image from database of MRI images to be processed (JPEG format)
2. Check if the image is RGB then convert it to gray image
3. Convert the image to double to increase the range of pixel values
4. For FCM, predefine the number of iterations and number of clusters
5. Get the size of the image
6. Convert input image matrix to a vector.
7. Randomly select the k cluster centre.
8. Calculate the fuzzy centre (vector) using the formula in equation (3).
9. Calculate the fuzzy membership function using distance formula in equation (2).
10. Repeat steps 8 and 9 until a minimum value is achieved of equation (1).
11. Terminate if stopping condition in equation (5) is true otherwise return to step 8.
12. Combine the membership grades and class values of clusters; map and reshape the respective pixels to form the final clustered image.

## Mathematical representation:

Fuzzy C-means (FCM) is the clustering algorithm which allows one piece of data may be the member of more than one clusters. It is based on reducing the following function:

$$Y_m = \sum_{i=1}^N \sum_{j=1}^C M_{ij}^m \|x_i - C_j\| \quad \text{--- (1)}$$

Where,

m - Any real number greater than 1,

M<sub>ij</sub> - degree of membership of x<sub>i</sub> in the cluster j,

x<sub>i</sub> - data measured in d-dimensional,

R<sub>j</sub> - d-dimension centre of the cluster (vector),

The update of Fuzzy membership M<sub>ij</sub> and the cluster

centres R are given by

$$M_{ij} = \frac{1}{\sum_{k=1}^C \left( \frac{\|x_i - x_k\|}{\|x_i - c_j\|} \right)^{\frac{2}{m-1}}} \quad \text{--- (2)}$$

$$R_i = \sum_{i=1}^N x_i \cdot M_{ij}^m / \sum_{i=1}^N M_{ij}^m \quad \text{--- (3)}$$

The above process ends when,

$$\text{Max}_{ij} |M_{ij}^{(k+1)} - M_{ij}^{(k)}| < \delta \quad \text{--- (4)}$$

Where,

$\delta$  = termination value or constant between 0 and 1, K= no of iteration steps.

2) K-means:

K-Means algorithm is an unsupervised clustering algorithm. [7] It classifies the input data points into multiple classes depending upon their intrinsic distance from each other. 'K' is a number of clusters and it is always less than data points 'n'. The algorithm assumes that the data features form a vector space and tries to find natural clustering in them. This algorithm selects the number of clusters k, then randomly generates clusters and determines the cluster centres. Then next step is to assign each data point to the nearest cluster centre and then recomputed the new cluster centres. These two steps are iterated until the minimum variance criterion achieved that means until the centre converges.

K-means Algorithm steps:

1. Give the number of cluster value as k. (k = 5)
2. Randomly choose the k cluster centres.
3. Calculate the centre of the cluster.
4. Calculate the distance between each pixel to each cluster centre.
5. If distance is near to the centre then move to that cluster.
6. Otherwise move to the next cluster.
7. Re-estimate the centre.
8. Repeat the process until the centre stops varying.

D. Post-processing

Clusters obtained from segmentation are reshaped to image file by Matlab function reshape ( ).

E. Feature extraction

In feature extraction, the tumor/ abnormal group of tissues are extracted from segmentation output image which is given to the thresholding process as input. [11] The binary mask is applied over the entire image. It makes the white become brighter and dark pixel become darker. Each transform coefficient denoted by 'T' is compared with a threshold in threshold coding. If 'T' is less than the threshold then it is considered as zero otherwise 'T' will be considered as one. Thresholding is an adaptive technique in which only those coefficients having value above a threshold are retained within each block.

F. Detection stage

In this stage, detection out of segmented image is made using the binarization method in the approximate reasoning step the area of the tumor is calculated. That means the image having two values either white or black (1 or 0). Here maximum image size is 256x256 jpeg image. We can represent a binary image as a summation of total number of black and white pixels [11].

$$\text{Image, } I = \sum_{W=0}^{255} \sum_{H=0}^{255} [f(0) + f(1)] \quad \text{-- (5)}$$

Pixels = Height (H) X Width (W) = 256 X 256

f (1) = black pixel (digit 1)

f (0) = white pixel (digit 0)

$$\text{No\_of\_white\_pixel, } P = \sum_{W=0}^{255} \sum_{H=0}^{255} [f(0)] \quad \text{--- (6)}$$

Where,

P = Total number of white pixels (height \* width)

1 Pixel = 0.264 mm

The formula for area calculation is

$$\text{Size\_of\_tumor, } S = [(\sqrt{P}) * 0.264] \text{ mm}^2 \quad \text{--- (7)}$$

P= Number of white pixels; H=height, W=width;

Detection stage Algorithm steps:

[8] The algorithmic steps involved for brain tumor detection is as follows-

1. Use .JPEG MRI images from a database or real-time system as input.
2. Checks whether the input image format is as specified and move to step 3, otherwise display an error message.
3. Verify that image is gray image. If not then convert to gray-scale using rgbtorgay ( ) function in Matlab.
4. Find the edge of the grayscale image using binarization and thresholding method.
5. Calculate the total number of white pixels (digit 0) in the image.
6. With the help of the formula, calculate the size of the tumor.
7. Compare the area obtained with 6mm<sup>2</sup>. If the area is greater than 6mm<sup>2</sup> then Brain MRI image has severe abnormality.
8. Display the tumor size and stage.
9. Stop the process.

## IV.EXPERIMENTAL RESULTS

The proposed approach was tested on the database of 30 images out of which 6 images output is discussed. The recorded entities were as follows: the image name, Area of tumor, execution time and the detection decision (tumor present and tumor absent). Some of the table entries are given below in Table I, II and III. Out of 6 images, two images named IN\_0000N.jpg, IN\_0007N.jpg are normal and rest are Abnormal MRI Brain images. Fig. 2 show the Database of 6 images considered.

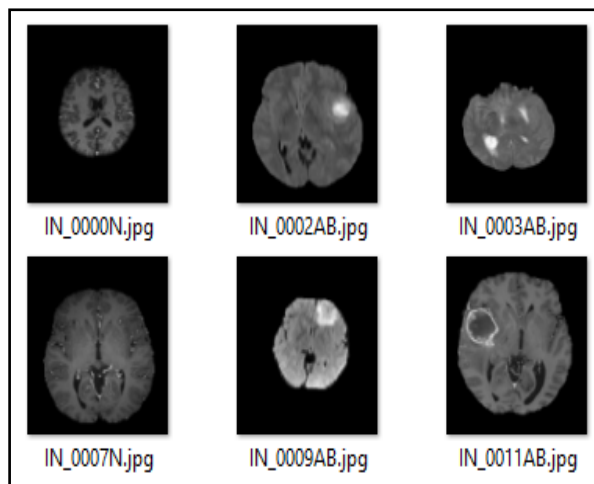


Fig 2: Database of images considered

TABLE I TABLE OF DETECTION RESULTS

IMAGE NAME	IMAGE SIZE	DETECTION RESULT
IN_0000N	255x255	Tumor Absent
IN_0002AB	255x255	Tumor Present
IN_0003AB	255x255	Tumor Present
IN_0007N	255x255	Tumor Absent
IN_0009AB	255x255	Tumor Present
IN_0011AB	255x255	Tumor Present

TABLE II TABLE OF TUMOR AREA COMPARISON

IMAGE NAME	IMAGE SIZE	AREA(mm <sup>2</sup> )		
		GROUND TRUTH	FCM ROI	K-MEANS ROI
IN_0002AB	255x255	418	589	1071
IN_0003AB	255x255	356	399	454
IN_0009AB	255x255	691	781	946
IN_0011AB	255x255	1002	984	2694

TABLE III TABLE OF ESTIMATED TIME COMPARISON

IMAGE NAME	ESTIMATED TIME (Sec)	
	FCM	K-MEANS
IN_0000N	3.96	0.38
IN_0002AB	5.16	0.31
IN_0003AB	5.55	0.31
IN_0007N	4.12	0.39
IN_0009AB	5.59	0.43
IN_0011AB	5.55	0.31

Table I give the idea of accurate detection of the normal and abnormal brain by showing a message of tumor present or absent. The proposed method gives 98% accuracy in detection and 96% and 89% accuracy in segmentation using FCM and K-means respectively.

Table II and III show the area and estimated time comparison respectively of both the proposed methods.



Fig. 3 Image IN\_0000N.jpg GUI output with message showing normal brain

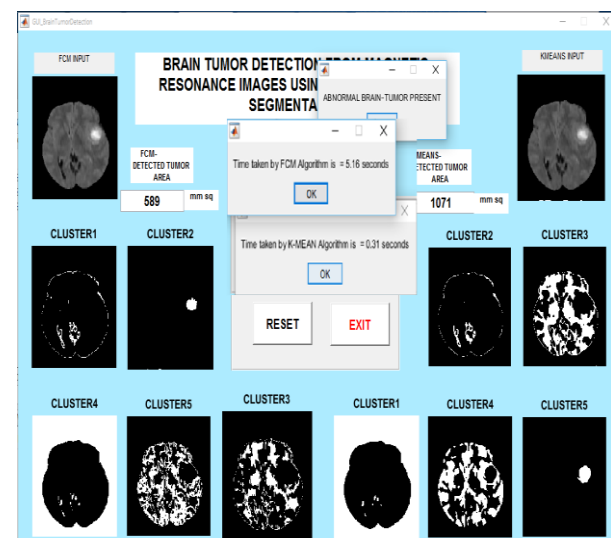


Fig. 4 Image IN\_0002N.jpg GUI output with message showing abnormal brain

Fig. 3 and 4 show the GUI made for the user-friendly operation of the automatically proposed method. It shows 5 clusters for both segmentation methods. All are shown on single GUI screen for comparing easily. Different Clusters gives the different elements of the brain such as white matter, gray matter, edema and CSF (Cerebrospinal fluid) and tumor if present, etc.

On GUI screen, a message is shown for time and tumor detection separately for FCM and K-means and area calculated is shown in edit box as shown in figure above.

## V. PERFORMANCE ANALYSIS

In this section, the comparison between FCM and K-means segmentation is performed. Fig. 5 and 6 show the bar graph comparison of estimated time (sec) and final detected tumor area (mm<sup>2</sup>) respectively.

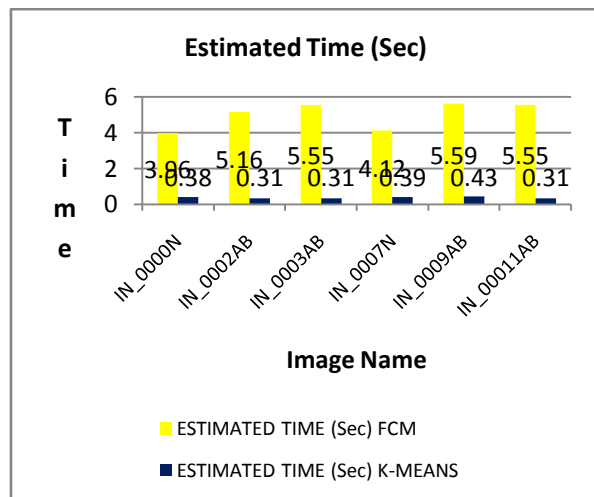


Fig.5. A bar graph of estimated time comparison

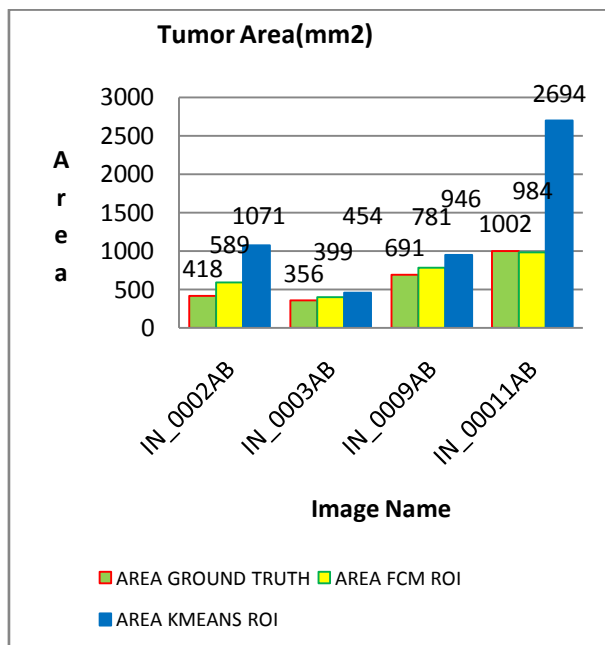


Fig. 6 A bar graph of detected tumor and ground truth area comparison

TABLE IV VARIATION OF STATISTICAL PARAMETERS

IMAGE NAME	PSNR	RI	GCE	VOI	METHOD
IN_0002A B	25.921	0.99	0.010	0.134	FCM
	21.018	0.983	0.015	0.192	K-MEANS
IN_0003A B	20.339	0.967	0.02	0.244	FCM
	18.963	0.956	0.018	0.315	K-MEANS
IN_0009A B	18.223	0.936	0.034	0.5239	FCM
	14.925	0.904	0.035	0.6622	K-MEANS
IN_00011 AB	18.818	0.89	0.046	0.833	FCM
	8.3639	0.62	0.124	2.3366	K-MEANS

Table IV and V give the idea to judge performance in terms of variation of statistical parameters like Peak Signal to Noise Ratio (PSNR in dB), Rand Index (RI), Global Consistency Error (GCE) and Variation of Information (VOI) [10].

Fig. 7, 8, 9 and 10 depicts the line graph comparison for average of above parameters respectively.

This section clearly shows that the area of FCM method is more precise and near to ground truth area than K-means tumor area. However, the time required by FCM is greater than K-means as it considers more iteration (in this case 100 iterations) but it is usually less than a minute so, can be neglected.

TABLE V AVERAGE OF VARIATION OF STATISTICAL PARAMETERS

AVERAGE	PSNR	RI	GCE	VOI
FCM	20.8253	0.94597	0.02795	0.433725
K-MEANS	15.8174	0.86655	0.0485	0.87645

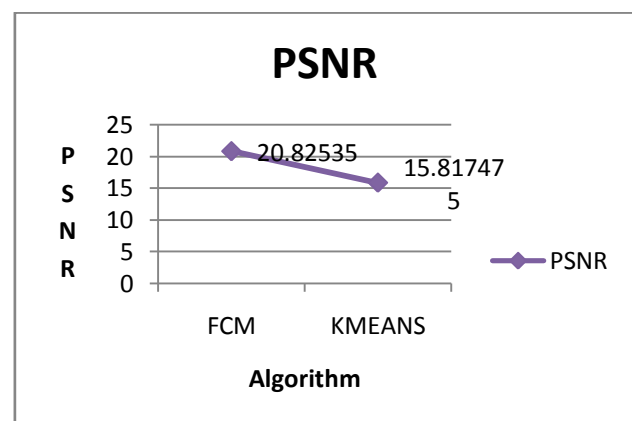


Fig.7. A graph of PSNR comparison

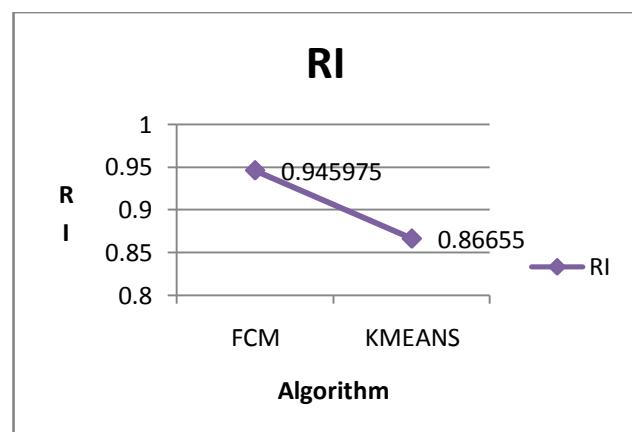


Fig.8. A line graph of Rand Index comparison

For better performance, ideally, PSNR and RI should be large whereas, GCE and VOI should be less. In the proposed method, FCM seems to satisfy all the points compare to K-means hence, proved that FCM gives optimum results compare to K-means.

Results reproducibility is also tested by repeating the segmentation 8 times on the same image by using both methods. FCM and K-means method avails reproducibility.



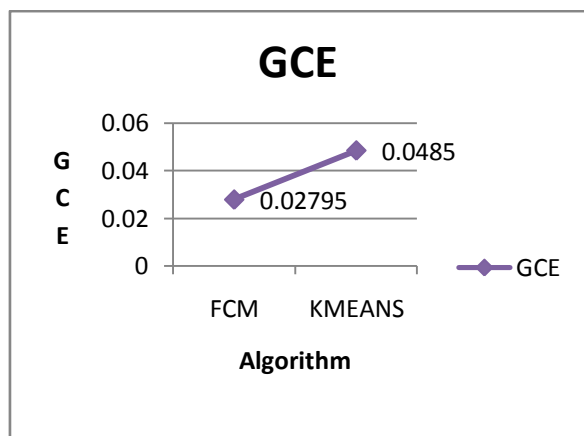


Fig.9. A line graph of Global consistency error comparison

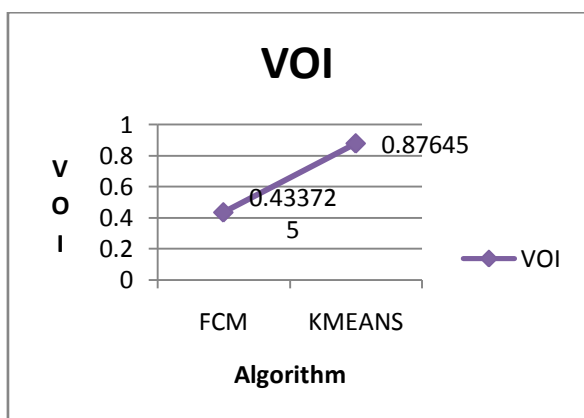


Fig.10. A line graph of variation of information comparison

## VI. CONCLUSION

In this paper an algorithm using Matlab GUI has been developed for the segmentation and detection of brain tumor from MRI brain scanned images based on various operations like pre-processing, Fuzzy C- means and K-means segmentation, feature extraction. The two algorithms K-means and FCM algorithm were successfully implemented. Comparison of these algorithms is done on the basis of time, tumor area and reproducibility, PSNR, RI, GCE, and VOI. The proposed method gives 98% accuracy in detection and 96% and 89% accuracy in segmentation using FCM and K-means respectively. The results obtained conclude that the efficiency of FCM is comparatively better than K-means algorithm for overlapped datasets. In future, this system can be implemented with some other algorithm which will give more accuracy and save more time.

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