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Brain Pathological Tissues Segmentation using IFCM and Comparison with FCM and K-means.

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ABSTRACT

Brain pathological tissues segmentation is very important because it provides anatomical information. Manual brain pathological tissue segmentation is a complex and time consuming process. So, Automatic segmentation process is required. In automatic segmentation method, Clustering approach is widely used in biomedical applications particularly for brain tumour, cyst and edema detection in abnormal MRI brain images. Fuzzy clustering using FCM algorithm provides segmentation efficiency. But, the major drawback of the FCM algorithm is the huge computational time required for convergence. The efficiency of FCM algorithm in terms of computational rate is improved by modifying the cluster centre and membership value updating criterion. In this paper, a fully automated 3 step segmentation process is proposed. First, the skull is stripped from the MRI images by generating a skull mask from the original brain image. Second, the skull stripped brain image is smoothed by using bilateral filter. Finally, an improved FCM algorithm is used to segment the pathological tissues. In the proposed method, the pathological tissues like tumour, cyst and edema are segmented. At last the convergence rate, correlation coefficient and similarity index are compared between the conventional Fuzzy C-means, K-means and Improved Fuzzy C-means algorithm.

Keywords: FCM, K-means, Improved FCM, MRI brain, Tumour, Cyst

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INTRODUCTION

Magnetic resonance (MR) imaging has a tremendous impact on the sophistication in the diagnosis of a brain pathological tissues. Although MR imaging has achieved remarkable advances in the information available from the vast array of pulse sequences and MR imaging techniques, the radiologist should still rely heavily on traditional criteria, such as location in the neuraxis and the age of the patient, for specific pathologic diagnoses. It is also clear that MR imaging has the most potential of any diagnostic method, including surgical biopsy, to allow a complete and accurate diagnosis and initial management strategy to be formulated for a brain tumour.

It has become generally recognized that MR would be the imaging study of choice in the evaluation of intracerebral tumours if cost and availability were not issues. Everyday tumour classification remains an inexact science, because of incomplete understanding of tumour histology, molecular genetics, and sometimes even clinical features. Current classifications thus are derived historically on the basis of suspected cell lineage, stage of cytogenesis (e.g., primitive or "-blastic", and differentiated or "-cytic"), and degree of dedifferentiation or anaplasia. Segmentation of MRI brain image in to different tissues (grey matter, white matter and cerebrospinal fluid) is complicated and challenging but its precise and exact segmentation is necessary for tumour detection. MRI image acquisition parameters can be adjusted for generating high contrast image with grey level for various cases of neuropathology.

Magnetic resonance imaging (MRI) is a well established non-invasive diagnostic medical imaging technique based on the nuclear magnetic resonance phenomenon. Segmentation of MRI brain image is still a challenging problem due to its complexity. The intensity of Brain MRI tissue is homogeneous and each tissue is connected. So, it is difficult to separate the adjacent tissue due to small intensity variation and smooth boundaries between tissues.

The diagnosis of many brain disorders involves accurate brain tissue segmentation. Manual segmentation of brain tissue is time consuming and very difficult even for medical experts [1]. So, there is a demand for automatic segmentation methods. Many automatic segmentation methods have been developed for the past decade based on different parameters of an image like gray level, colour and texture [2]. In medical images, segmentation is done mainly on the basis of the gray level of the pixels. Among available segmentation methods [3], thresholding, region growing and clustering methods are the standard methods based on pixels intensity. Among these, clustering method is frequently used. Clustering is a technique of grouping the data based on similarity metrics of probability density models. K-means clustering method [4] classifies the pixels in the image into a predefined number of clusters. In fuzzy clustering, a data item is given partial memberships in all the clusters within a range of membership values from zero to one. A cluster has a center of gravity which is basically the weighted average of the cluster.

The most popular clustering is Fuzzy C-means algorithm [5]. In order to overcome some of its limitations, i.e., convergence rate, we present an improved FCM algorithm. Convergence rate is the time period required for the system to reach the stabilized condition. The proposed algorithm is analysed with a set of skull stripped MRI brain images and found to be satisfactory. The MRI brain images are preprocessed by using morphological operators and thresholding techniques as explained in [6, 13].

This paper is organised as follows. Section 2 presents standard clustering methods. Modified FCM reported by many researchers are described in section 3. The proposed brain tumour detection using improved FCM technique is presented in section 4. The experimental results and discussions are given in section 5. The conclusions are summed up in section 6

STANDARD CLUSTERING METHODS

An Clustering is one of the most useful technique in MRI Segmentation, where it classifies pixels into classes, without knowing previous information or training. It classifies pixels with highest probability into the same class. Clustering technique training is done by using pixel features with properties of each class [7-9]. In this section a brief review of K-means and Fuzzy C-means algorithm are explained.

A. K-Means Algorithm

K-means clustering algorithm is the simplest unsupervised learning algorithm that can solve clustering problem. The procedure followed to classify a given set of data through a certain number of clusters are very simple.

The main is to define ‘K’ centers, one for each cluster. These clusters must be placed far away from each other. The next step is to take a point belonging to a given data set and associate it to the nearest center. When no point is pending, the first step is completed and early grouping is done. The second step is to recalculate ‘k’ new centroids as barycentre of the clusters resulting from the previous step. After having ‘K’ new centroids a new binding has to be done between the same data set points and the nearest new center. A loop has been generated. As a result of this loop, the k centers change their location step by step until centers do not move any more. Finally this algorithm aims at minimizing an objective function known as squared error function given by,

$$J(V) = \sum_{i=1}^c \sum_{j=1}^{c_i} \|x_i - v_j\|^2 \tag{1}$$

Where,

$\|x_i - v_j\|$ is the Euclidean distance between x_i and v_j

‘ C_i ’ is the number of data points in i^{th} cluster.

‘ C ’ is the number of cluster centers.

1) Algorithmic steps for K-means clustering:

Let $X = \{x_1, x_2, x_3, \dots, x_n\}$ be the set of data points and $V = \{v_1, v_2, v_3, \dots, v_c\}$ be the set of centers.

Step1: Randomly select ‘c’ cluster centers

Step2: Calculate the distance between each data point and cluster centers.

Step3: Assign the data point to the cluster center whose distance from the cluster center is minimum of all the cluster centers.

Step4: Recalculate the new cluster center using

$$v_i = \left(\frac{1}{C_i} \right) \sum_{j=1}^{c_i} x_j \tag{2}$$

Where ‘ C_i ’ represents the number of data points in i^{th} cluster.

Step5: Recalculate the distance between each data point and new obtained cluster centers.

Step6: If no data point was reassigned then stop, otherwise repeat from step 3.

K-means algorithm is fast, robust and easier to understand. It also gives better result when data set are well separated from each other. But, if there are 2 highly overlapping data then k-means will not be able to resolve that there are 2 clusters.

B. Fuzzy C-means Algorithm

Fuzzy FCM clustering is an unsupervised method for the data analysis. This algorithm assigns membership to each data point corresponding to each cluster centre on the basis of distance between the cluster center and the data point. The data point near to the cluster centre has more membership towards the particular center. Generally, the summation of membership of each data point should be equal to one. After each iteration, the membership and cluster centers are updated according to the formula

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

$$V_j = \frac{\left(\sum_{i=1}^n (\mu_{ij})^m x_i \right)}{\left(\sum_{i=1}^n (\mu_{ij})^m \right)}, \forall_j = 1, 2, \dots, c \quad (4)$$

Where,

'n' is the number of data points

'V_j' represents the jth cluster center

'm' is the fuzziness index $m \in [1, \infty]$

'c' represents the number of cluster center

'μ_{ij}' represents the membership of ith data to jth cluster center.

'd_{ij}' represents the Euclidean distance between ith data and jth cluster center.

'x_i' is the ith of d-dimensional measured data

'c_j' is the d-dimension center of the cluster

'|| * ||' is any norm expressing the similarity between any measured data and the center.

$d_{ij} = \|x_i - c_j\|$, $d_{ik} = \|x_i - c_k\|$

The main objective of fuzzy c-means algorithm is to minimize

$$J(U, V) = \sum_{i=1}^n \sum_{j=1}^c (\mu_{ij})^m \|x_i - v_j\|^2, 1 \leq m < \infty \quad (5)$$

Where,

$\|x_i - v_j\|$ is the Euclidean distance between ith data and jth cluster center.

1) Algorithmic steps for fuzzy C-means clustering:

Let $X = \{x_1, x_2, x_3, \dots, x_n\}$ be the set of data points and $V = \{v_1, v_2, v_3, \dots, v_c\}$ be the set of cluster centers.

Step1: Randomly select 'c' cluster centers

Step2: Calculate the fuzzy membership 'μ_{ij}' using the equation

$$\mu_{ij} = \frac{1}{\sum_{k=1}^c \left(\frac{d_{ij}}{d_{ik}} \right)^{\frac{2}{m-1}}}$$

Step3: Compute the fuzzy centers 'v_j' using

$$V_j = \frac{\left(\sum_{i=1}^n (\mu_{ij})^m x_i \right)}{\left(\sum_{i=1}^n (\mu_{ij})^m \right)}, \forall_j = 1, 2, \dots, c$$

Step4: Repeat step2 and step3 until the minimum 'J' value is achieved or $\|U^{(k+1)} - U^{(k)}\| < \beta$

Where,
 'k' is the iteration step
 'β' is the termination criterion between [0,1]
 'U=(μ_{ij})n*c' is the fuzzy membership matrix
 'J' is the objective function

The first loop of the algorithm calculates membership values for the data points in clusters and the second loop recalculates the cluster centers using these membership values. When the cluster center stabilizes the algorithm ends.

The FCM algorithm gives best result for overlapped data set and also gives better result than k-means algorithm. Here, the data point can belong to more than one cluster center. The FCM suffers from several constraints that affect the performance [10]. The main drawback is that the sum of membership value of a data point x_i in all the clusters must be one but the outlier points has more membership value. So, the algorithm has difficulty in handling outlier points. The next limitation is that due to the influence of all the data members, the cluster centers tend to move towards the center of all the data points [10].

MODIFIED FCM ALGORITHM

Many approaches have been made to modify the existing standard FCM algorithm to improve its performance. Each of the modified FCM algorithms proposes a new membership function for calculating the membership of data points in clusters. These new methods address the various limitations of the standard algorithm.

A. FCM with modified Distance function

Frank klawonn and Annette Keller proposed a modified FCM algorithm with new distance function which is based on dot product instead of the conventional Euclidean distance [11]. In this method they introduced a new membership function as given in equation (6).

$$\mu_{ik} = \frac{1}{\sum_{j=1}^c \left(\frac{d^2(v_i, x_k)}{d^2(v_j, x_k)} \right)^{\left(\frac{1}{m-1}\right)}} \tag{6}$$

Here is the membership of ith data point in kth cluster and c is the number of clusters. With this modified FCM membership function the fuzzy clustering algorithm can form clusters into their natural shapes.

B. Modified C-means for MRI segmentation

Lei jiang and Wenhui Yang presented a new approach for robust segmentation of MRI images that have been corrupted by intensity inhomogeneities and noise. The algorithm is formulated by modifying the objective function of the standard fuzzy C-means method to compensate for intensity inhomogeneities[12]. Here the membership function is given as (7)

$$\mu_{jk} = \frac{1}{\sum_{l=1}^c \left(\frac{\delta_{ik} + \gamma_k}{\delta_{jl} + \gamma_l} \right)^{\left(\frac{1}{m-1}\right)}} \tag{7}$$

Here, ‘ δ ’ is the distance and ‘ γ ’ denotes the influence on a pixel by the neighbouring membership values.

C. Adaptive Fuzzy clustering

The adaptive fuzzy clustering algorithm [10] is a modified version of standard FCM. The membership values in this method are calculated using (8)

$$\mu_{ij} = \frac{n * \left(\frac{1}{d_{ji}}\right)^{\frac{1}{m-1}}}{\sum_{k=1}^p \sum_{z=1}^n \left(\frac{1}{d_{kz}}\right)^{\frac{1}{m-1}}} \tag{8}$$

This algorithm is efficient in handling data with outlier points. In comparison with FCM algorithm it gives very low membership for outlier points [10]. Since the sum of distance of points in all the clusters (7) involves in membership calculation this method tends to produce very less membership values when the number of clusters and points increase.

PROPOSED METHOD

In our proposed method, the sum of memberships in a cluster center is considered as 0.5 instead of 1. Therefore for ‘ n ’ number of clusters, the sum of membership value becomes 0.5 n . In standard FCM, the membership of a data point in a cluster depends directly on the sum of distances of the point in other cluster centers (3). Instead, if we consider the sum of distances of data members in a cluster for the calculation of memberships in that cluster, it might improve the performance of the algorithm. The proposed membership function for i^{th} data point in j^{th} cluster is given by (9)

$$\mu_{ij} = \frac{0.5n * \left(\frac{1}{d_{ji}}\right)^{\frac{1}{m-1}}}{\sum_{i=1}^n \left(\frac{1}{d_{ji}}\right)^{\frac{1}{m-1}}} \tag{9}$$

The proposed method is composed of 3 major stages as shown in figure 1. In stage1, an initial preprocessing is done based on morphological operators and thresholding technique that we have proposed in our previous research papers [6, 13]. i.e., skull is removed and later a bilateral filter is applied to the skull stripped image in order to smoothen it. A bilateral filter is an edge-preserving and noise reducing filter. This preserves sharp edges by systematically looping through each pixel and adjusting weights to the adjacent pixels accordingly. The flowchart of the proposed IFCM algorithm is shown in figure 2.

Figure 1: Flowchart of proposed method

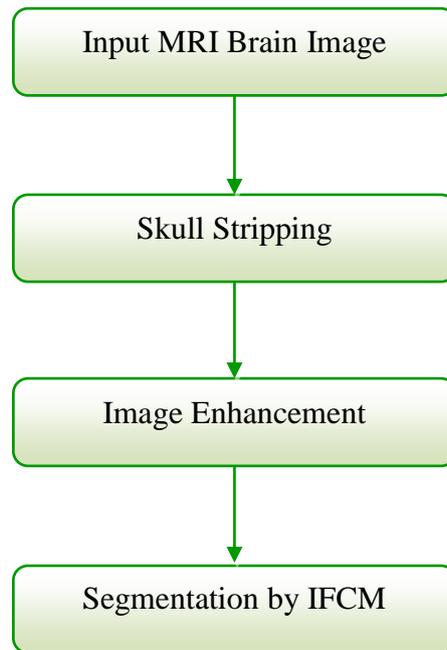


Figure 2: Flowchart of IFCM

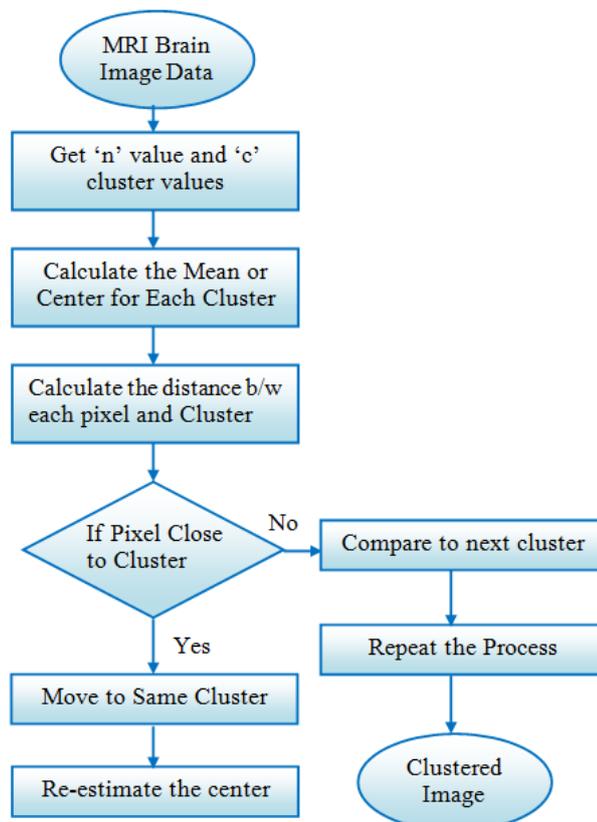


Figure 2: Flowchart of IFCM

The input MRI brain database and the skull stripped images are shown in Figure 3 and 4. The smoothed image after applying the bilater filter is as shown in figure 5 and 6. In stage 2, the segmentation is carried out on the skull stripped and filtered MRI brain image as shown in figure7 and 8.

Figure 3: Input MRI Normal and Abnormal Brain images

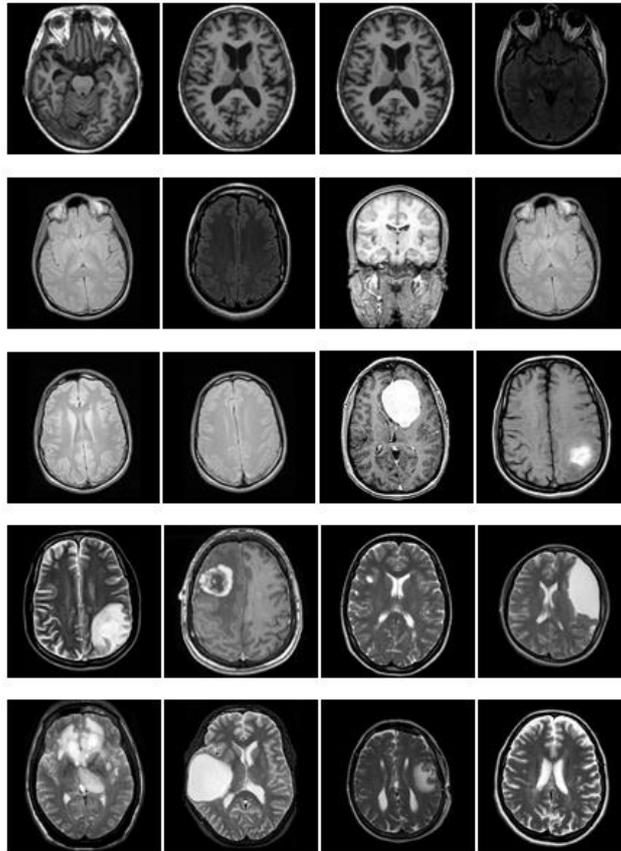


Figure 3: Input MRI Normal and Abnormal Brain images

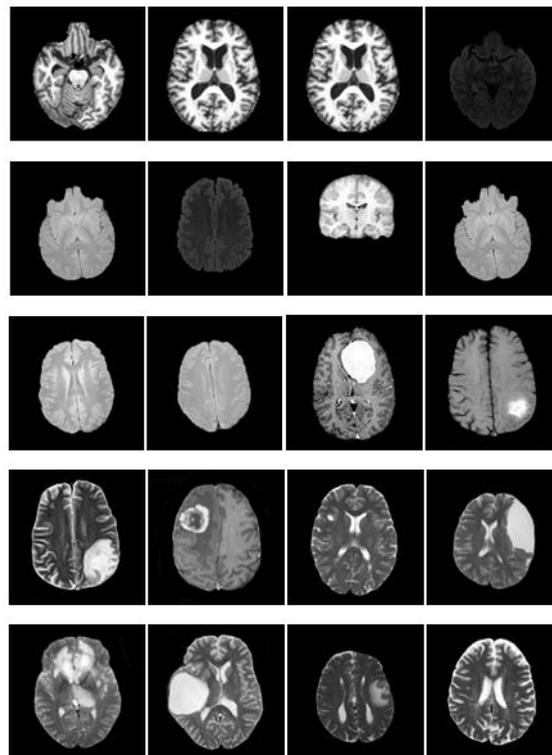


Figure 4: Skull Stripped MRI Normal and Abnormal Brain images

Figure 5: Filtered Normal Brain images

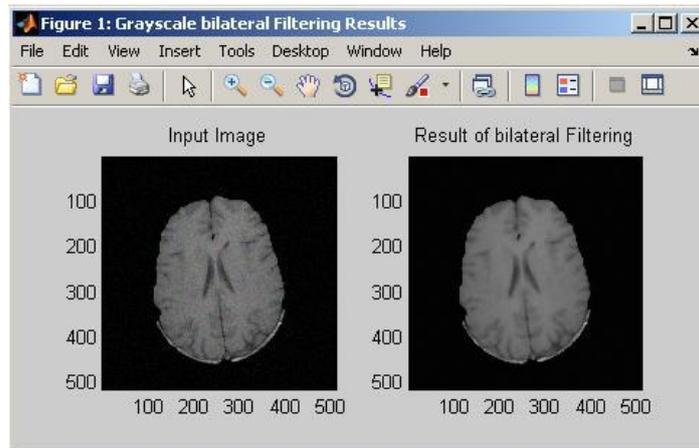


Figure 6: Filtered Abnormal Brain images

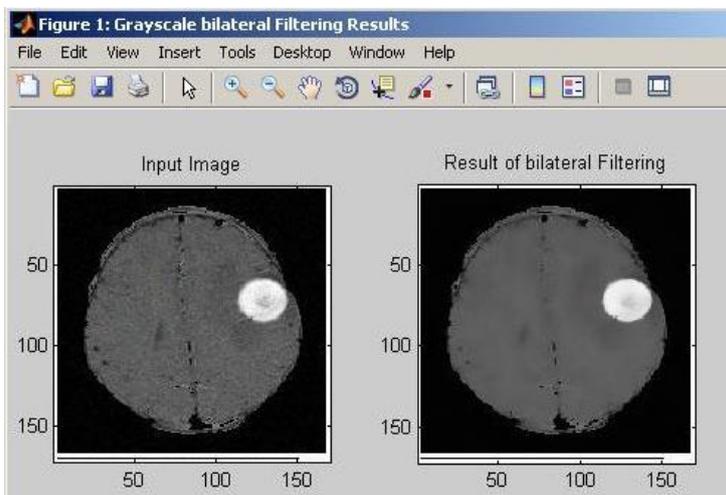


Figure 7: Segmentation process by IFCM of Brain image 1.

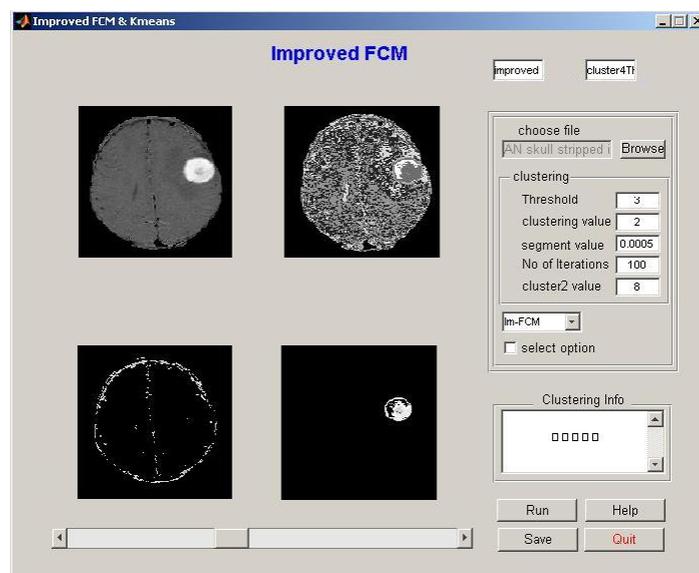


Figure 8: Segmentation process by IFCM of Brain image 2.

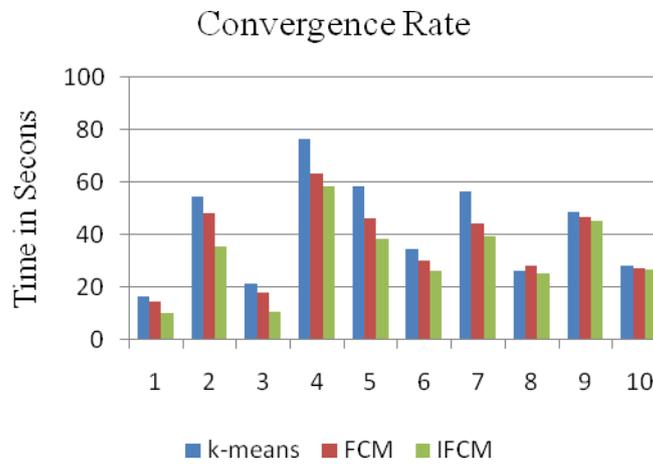
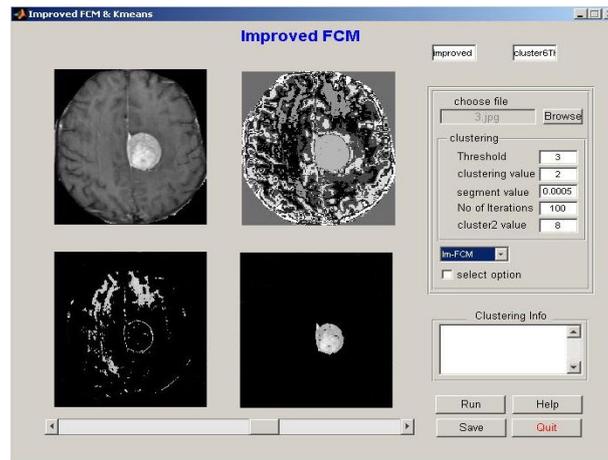


Figure 9: Comparison of Convergence Rate of 3 clustering methods

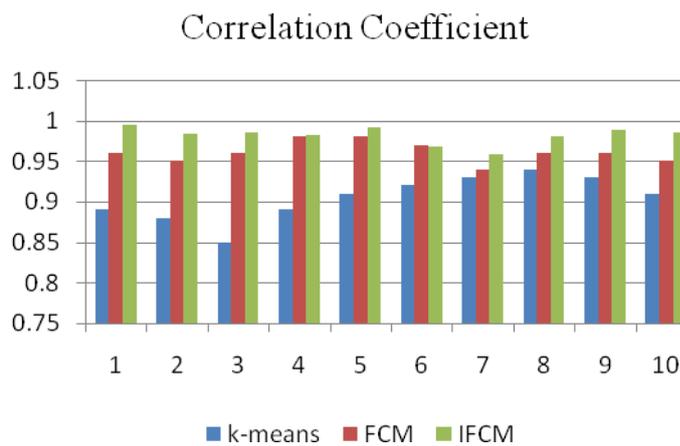


Figure 10: Comparison of Correlation Coefficient of 3 clustering methods

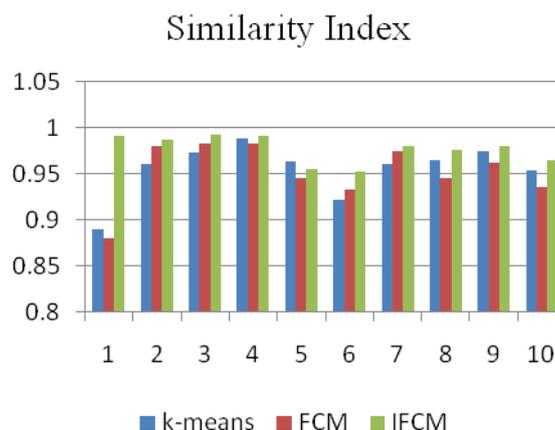
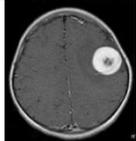
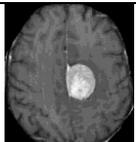
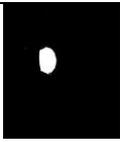
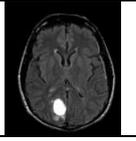
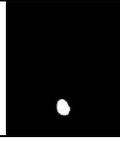
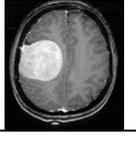
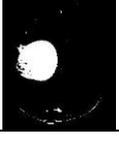


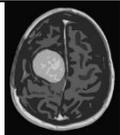
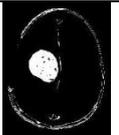
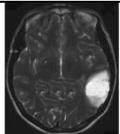
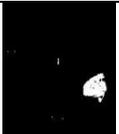
Figure 11: Comparison of Similarity Index of 3 clustering methods

RESULTS AND DISCUSSION

The MRI image dataset utilized in image segmentation technique is taken from the publicly available sources and collected from diagnostic centers. The input MRI brain dataset is shown in figure 3. This image dataset consists of 300 brain MRI images in which 200 brain images with tumor, cyst, edema and remaining 100 brain images without tumor. The brain images dataset are divided into two sets. Training dataset and Testing dataset The Training dataset is used to segment the brain tumor images and the testing dataset is used to analyze the performance of the proposed technique. Table 1 shows the extracted pathological tissues from the abnormal MRI brain image.

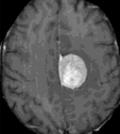
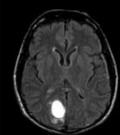
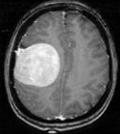
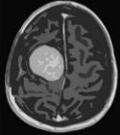
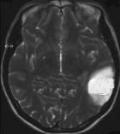
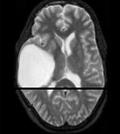
Table 1: Convergence rate comparison between standard clustering and proposed method

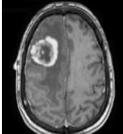
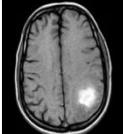
Input Image	K-means	FCM	IFCM
			
Convergence Rate:	16.45sec	14.44sec	10.22sec
			
Convergence Rate:	54.35 sec	48.11sec	35.40 sec
			
Convergence Rate:	21.18 sec	18.12 sec	10.44 sec
			

Convergence Rate:	76.35 sec	63.11sec	58.40 sec
			
Convergence Rate:	58.22 sec	46.11sec	38.20 sec
			
Convergence Rate:	34.44 sec	30.21sec	26.40 sec

The performance of the proposed algorithm is compared with the standard algorithms like K-mean and Fuzzy C-means. The proposed algorithm returns satisfactory Correlation coefficient and Similarity Index results comparing to k-means and FCM algorithm. The segmented pathological tissues and the convergence rate of the standard clustering methods and proposed IFCM method are tabulated in table 1. The comparison of convergence rate, correlation coefficient and similarity index of three clustering methods are shown in figures 9, 10 and 11 and tabulated in table 2.

Table 2: Quantitative performance of 3 clustering methods on MR Images

Images	Clustering Method	Convergence Rate (sec)	Correlation Coefficient	Similarity Index
	k-means	16.45	0.89	0.89
	FCM	14.44	0.88	0.96
	IFCM	10.22	0.991	0.995
	k-means	54.35	0.96	0.88
	FCM	48.11	0.98	0.95
	IFCM	35.40	0.986	0.983
	k-means	21.18	0.972	0.85
	FCM	18.12	0.983	0.96
	IFCM	10.44	0.992	0.985
	k-means	76.35	0.988	0.85
	FCM	63.11	0.982	0.98
	IFCM	58.40	0.991	0.982
	k-means	58.22	0.963	0.91
	FCM	46.11	0.945	0.98
	IFCM	38.20	0.955	0.990
	k-means	34.44	0.921	0.92
	FCM	30.21	0.932	0.97
	IFCM	26.40	0.952	0.968
	k-means	56.21	0.960	0.93
	FCM	44.23	0.974	0.94

	IFCM	39.22	0.980	0.959
	k-means	26.25	0.965	0.94
	FCM	28.23	0.945	0.96
	IFCM	25.02	0.975	0.981
	k-means	48.44	0.974	0.93
	FCM	46.43	0.962	0.96
	IFCM	45.21	0.979	0.988
	k-means	28.20	0.953	0.91
	FCM	27.21	0.935	0.95
	IFCM	26.52	0.965	0.986

CONCLUSION

The results show that the proposed method can successfully segment pathological tissues. The results also show that k-means, FCM and IFCM algorithm can successively segment pathological tissues provided that the parameters are properly selected. The visualization and detective valuations of the segmentation results show the success of the approach. From the comparison of all the standard clustering methods, the convergence rate of the proposed IFCM algorithm yields superior convergence rate than other methods as shown in table 1. The future work concentrates on extracting the features to classify these pathological tissues.

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