MR Brain Image Segmentation Based on Modified FCM Using Median Filter

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***Abstract*- In this paper we present both FCM and modified FCM and prove that modified FCM provides better results. Our main objective is to segment the MR craniopharyngioma type brain image using FCM & modified FCM technique and to perform a comparative study. Image segmentation is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super pixels).In fuzzy clustering, each point does not pertain to a given cluster, but has a degree of belonging to a certain cluster, as in fuzzy logic. The time required is large for convergence in Fuzzy C means. By improving cluster center and membership value updating criteria ie; by modified FCM technique this time can be minimized. The input images of Magnetic Resonance brain images can be used like Meningioma, Pineal tumor, Craniopharyngioma, and Ependymoma.**

***Keywords*: Image segmentation, Clustering, FCM, Modified FCM, Objective functions.**

I.INTRODUCTION

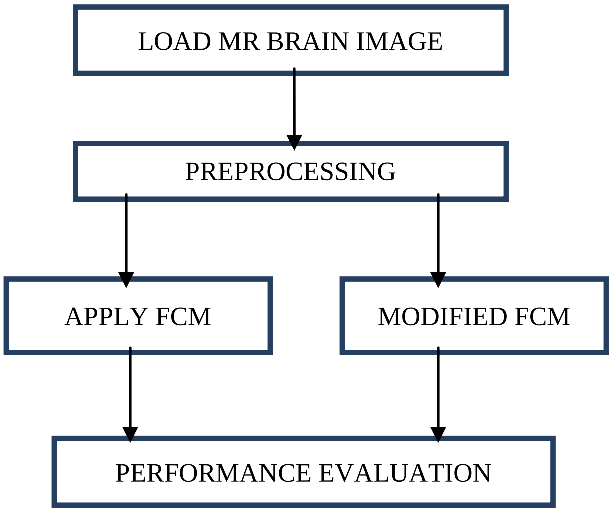
Image segmentation is the keystone of medical image processing quantitative analysis. The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze [1],[2]. More precisely, image segmentation is the process of assigning a label to every pixels in an image such that pixels with the same label share certain visual characteristics. Clustering algorithm can be categorized based on their cluster model. There is no objectively "correct" clustering algorithm, but as it was noted, "clustering is in the eye of the beholder" [3]. Clustering can be used to divide a digital image into distinct region for border detection or object recognition.

FCM is a class of algorithms for cluster analysis in which the allocation of data points to clusters. Fuzzy clustering is the process of dividing data elements into classes or clusters so that items in the same class are as similar as possible, and items in different classes are as dissimilar as possible. Depending on the nature of the data and the purpose for which clustering is being used, different measures of similarity may be used to place items into classes, where the similarity measure controls how the clusters are formed. Some examples of measures that can be used as in clustering include distance, connectivity, and intensity. In fuzzy clustering, every point has a degree of belonging to clusters, with changing degrees of membership [4] rather than belonging completely to just one cluster. Thus points on the edge of the cluster, maybe in the cluster to a lesser degree than points in the center of cluster. An overview and comparison of different fuzzy clustering algorithms are available [5]. Fuzzy c-means has been a very important tool for image processing on clustering objects in an image. In 70's, mathematicians introduced the spatial term into the FCM algorithm to improve the accuracy of clustering under noise [6].

Brain tumors include all tumors inside the humans skull or in the central spinal canal. They are created by an abnormal and uncontrolled cell division. Any brain tumour is inherently serious and life-threatening because of its invasive and infiltrative character in the limited space of the intra cranial cavity [7]. Its threat level depends on the combination of factors like types of tumor its location, its size and its state of development. Because the brain is well protected by the skull, the early detection of a brain tumor occurs only when diagnosis tools are directed at a intra cranial cavity. Imaging plays a central role in the diagnosis of brain tumor. High resolution technique especially MR imaging and computed tomography scans are usually used for diagnostic purposes.

Cluster center initialization method using silhouette method in 2005 improves efficiency of segmentation [8]. Kwon and Han proposed hierarchical FCM algorithm in 2010 which was based on template matching but it had disadvantage of need of a precise template [9]. Fast clustering algorithm based on random sampling was proposed by Cheng and Goldgof [10] in 1998 which afford a speed-up factor 2-3 times as compared to FCM algorithm. Siyal et al acquainted a new method on fuzzy c-means for segmentation in 1995 [11]. S.Murugavalli et al in 2007 described a high speed parallel fuzzy c-mean algorithm for brain tumor segmentation [12]. Kannan et al in 2005 described segmentation of MRI using unsupervised fuzzy c-mean algorithm [13]. Ruspini.E in 1970 described numerical methods for fuzzy clustering [14]. Dunn J.C, in 1973 described a fuzzy relative of the ISODATA process and its use in detecting compact, well separated clusters [15].

II.METHODOLOGY



A. *Load MR brain images*

The MR pineal tumor Brain image is collected from MRI center of size 256*256 & it is used. The brain tumor images are shown in Fig. 1,

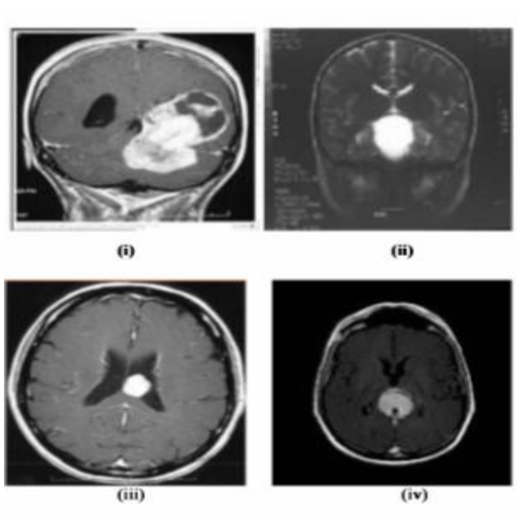


Fig. 1: (i)Meningioma (ii)Craniopharyngioma (iii)Ependymoma (iv)Pineal tumor

B. *Preprocessing*

The test image is preprocessed by using the median filter. The noise reduction is a typical pre-processing step to improve the results of later processing[16]. Median filtering is a common image preprocessing technique for removing salt and pepper noise. Because this filtering is less sensitive than linear techniques to extreme changes in pixel values, it can remove salt and pepper noise without significantly reducing the sharpness of an image.

In this paper, we use Median Filter to remove salt and pepper noise from the input image. To remove the Gaussian noise, the median filter is demonstrably better whilst preserving edges for a given fixed window size.

C. *FCM Technique*

Dunn introduced fuzzy c-means (FCM) c1ustering algorithm and further extended by Bezdek [15]. FCM is the c1ustering technique that permits one pixel to belong to more than one cluster. This algorithm divides collection of pixels into collection of clusters according to some criteria. Depending on the data and the application, similarity measures like distance, connectivity, and intensity may be used to distinguish classes. FCM algorithm is based on minimization of objective function given below [16],

$$J(U,c_1,c_2,c_3,..,c_c)=\Sigma^{c}_{i=1} j_i=\Sigma^{c}_{i=1} \Sigma^{n}_{j=1} \mu_{ij}^{2} d^{2}_{ij} \qquad (1)$$

Where, μ_{ij} is membership value of j^{th} input sample in i^{th} cluster center [16]. The membership values satisfy the following conditions,

$$0\leq\mu_{ij}\leq1 \qquad (2)$$

$$\Sigma_{i=1}^{c} \mu_{ij}=1 \qquad (3)$$

$$0\leq\Sigma_{j=1}^{n} x_j<n \qquad (4)$$

C_i is the centroid of cluster i; d_{ij} is the Euclidian distance which is measured between i^{th} centroid (C_i) and j^{th} data point is a weighting exponent. In many applications m = 2 is normally preferred. In center clustering m = 1 [16].

The above conditions imply the followings:

- The membership values of each sample belonging to a particular cluster should be between 0 and 1.
- Each sample must belong to at least one cluster and the sum of the membership values to each cluster should be 1.
- Each class must have at least one sample and all the samples cannot belong to a particular class.

Iterative optimization of the objective function given above is carried and fuzzy partitioning of data is done, with the update of membership ft_{ij} and the cluster centers by C_i,

$$\mu_{ij}=1/\sum^{c}_{k=1}(d_{ij}/d_{kj})^{2/(m-1)};\ c_i=\sum^{n}_{j=1}\mu_{ij}^{m}x_j/\sum^{n}_{j=1}\mu_{ij}^{m} \quad (5)$$

Algorithm for this is explained below,

1. FCM Algorithm:

This algorithm has following steps,

- Initiliaze U=[μij]' rnembership matrix.
- At k^{th} step, Calculate the center vectors C_i with μ_{ij}

$$c_i=\sum^{n}_{j=1}\mu_{ij}^{m}x_j/\sum^{n}_{j=1}\mu_{ij}^{m} \quad (6)$$

- Update membership matrix at k^{th} and $(k+l)^{th}$ step,

$$\mu_{ij}=1/\sum^{c}_{k=1}(d_{ij}/d_{kj})^{2/(m-1)} \quad (7)$$

where $d_{ij}=x_j-\mu_i$

- If $\|U(k+l) - U(k)\| <\varepsilon$ then STOP; otherwise return to step 2.

D. Modified FCM technique

Clustering technique can be seen as data compression technique. In this dimensionality of input is reduced to good extent. Here huge number of input sample's is converted to less number of representative clusters [4]. The quantization of the feature space is performed by masking the lower 'm' bits of the feature value. The quantized output will result in the common intensity values for more than one feature vector. In next step grouping of feature vector having same intensity values is done, this process is called aggregation. One representative vector from each group is taken and given as input to Fuzzy C Means algorithm. When c1ustering is done representative feature vector membership values are distributed identically to all members of quantization levels. As modified FCM uses reduced dataset convergence rate in improved as compared to normal FCM technique.

1. Modified FCM algorithm:

This technique includes similar steps as FCM except for the variation in the cluster updation and membership value updation criterions. The modified criterions are shown below,

$$c_i=\sum^{n}_{j=1}\mu_{ij}^{m}y_j/\sum^{n}_{j=1}\mu_{ij}^{m};\ \mu_{ij}=1/\sum^{c}_{k=1}(d_{ij}/d_{kj})^{2/(m-1)} \quad (8)$$

$$d_{ij}=y_j-c_i$$

y=reduced dataset

2. Performance parameters:

- *RI (The Rand index) :*

The Rand index (RI) counts the fraction of pairs of pixels whose labeling are logical between the computed segmentation and the ground truth averaging across multiple ground truth segmentations. Given a set of n elements and two partitions of S to compare, and, we define the following: a is the number of pairs of elements in S that are in the same set in X and in the same set in Y, b is the number of pairs of elements in S that are in different set in X and in different sets in Y.

c is the number of pairs of elements in S that are in the same set in X and in different sets in Y d is the number of pairs of elements in S that are in different set in X and in the same set in Y. The Rand index (RI) is,

$$RI=(a+b/a+b+c+d)=a+b/(n/2) \quad (9)$$

Where (a+b) as the number of agreements between X and Y and (c+d) as the number of dis agreements between X and Y. The Rand index has a value between 0 and 1, with 0 indicating that the two data clusters do not agree on any pair of points and 1 indicating that the data clusters are exactly the same [17],[18].

- *GCE*

The Global Consistency Error (GCE) measures the extent to which one segmentation can be viewed as a refinement of the other.

The formula for GCE is as follows,

$$GCE=(1/n)\min\{\Sigma_1 E(s1,s2,pi),\Sigma_1\, s2,s1,pi\} \quad (10)$$

Where, segmentation error measure takes two segmentations SI and S2 as input, and produces area valued output in the range [0::1] where zero signifies no error [16].

Here we can observe that RI is maximum for modified FCM approach as compared to FCM. And GCE is minimum for modified FCM [16],[19].

III. IMPLEMENTATION

Based on the Magnetic Resonance (MR) brain tumour images collected from MR center, experiments are conducted. We implement the experiments on intel core i5-3210M CPU @

2.50 GHz, 4GB RAM, x64 based processor and MAT LAB 7.7.0(R2008b).

IV. PERFORMANCE ANALYSIS/RESULT

Time required for the system to reach the stabilized condition is convergence rate (CPU sec). A comparative analysis is performed on the techniques based on the performance measures. For Eg; the clustered output for craniopharyngioma type image sample is shown in Fig. 2,

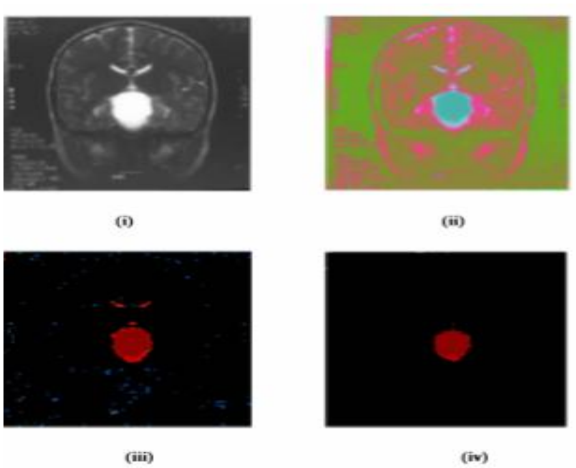


Fig.2

i)Original grayscale image.

ii)Color Space Translated Image

ii)Segmented Image using C-Means

iv)Segmented image using modified C--Means

A. CPU time comparison:

As compared to Fuzzy C- Means, Modified Fuzzy C-Means take less CPU time. The CPU time required for FCM and modified FCM technique is explained in table 1. Here for four types of abnormal images viz. Ependymoma, CNS lymphoma, Craniopharyngioma, pineal tumor CPU time is shown.

TABLE 1

CPU TIME COMPARISON

S.No	Abnormal image Type	Technique	Time(Sec)
1	Ependymoma	FCM	4.2419
		MFCM	1.5819
2	Meningioma	FCM	2.3744
		MFCM	1.2381
3	Craniopharyngioma	FCM	2.265
		MFCM	1.5523
4	Pineal tumour	FCM	2.8719
		MFCM	1.35

From time comparison we can say that modified FCM approach is somewhat fast as compared to traditional FCM approach. If we perform FCM and modified FCM technique for different number of clusters, then we can observe CPU time required go on increasing as number of clusters is increased.

TABLE II

PERFORMANCE TABLE

SN	Abnormal image type	Technique	RI	GCE
I	Ependymoma	FCM	0.5083	0.1871
		MFCM	0.6313	0.0949
II	Meningioma	FCM	0.5612	0.2381
		MFCM	0.7158	0.0858
III	Craniopharyngioma	FCM	0.7883	0.0721
		MFCM	0.8466	0.0162
IV	Pineal tumor	FCM	0.6933	0.1502
		MFCM	0.7568	0.0733

V. CONCLUSION

From the results obtained, it is explained that FCM and modified FCM can segment tumour based on parameters chosen properly. Thus we conclude that Modified FCM is good in terms of convergence rate as compared to FCM and also modified FCM is proved to be good in view of RI and GCE.

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