A Modified Fuzzy C-mean Algorithm for MRI Brain Images

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Abstract- Partitioning an image can be done with the process of image segmentation in the significant way. FCM (Fuzzy C-Means Clustering) is effective techniques to perform Image Segmentation. In fuzzy clustering, excellent mathematical tool to handle the uncertainty arising due to imprecision. The process of convergence in this technique is time consuming. To overcome, a Modified FCM technique is introduced to minimize convergence time by improving cluster center and membership value updating criteria. In this paper, both FCM and modified FCM have been presented to prove that the Modified FCM provides enhanced results. The main objective is to segment the MR craniopharyngioma type brain image using FCM & modified FCM technique and to perform a comparative study. However, other input of Magnetic Resonance brain images like Meningioma, Pineal tumor and Ependymoma can also be segmented.

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

I.INTRODUCTION

Image segmentation is the keystone of quantitative analysis in medical image processing. The purpose of segmentation is to simplify and/or change the representation of an image in a meaningful way which is easier to analyze [1] [2]. More precisely, image segmentation is the process of assigning a label to every pixel of an image such that the 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 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 completely belonging to a particular cluster. Thus points on the edge of the cluster, maybe in a lesser degree than points in the center. 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 both tumors inside the human skull as well as in the central spinal canal. They are created by an abnormal and uncontrolled cell division. Brain tumors are inherently serious and life-threatening because of its invasive and infiltrative character in the limited space of the intracranial 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 the intracranial cavity. Imaging plays a essential role in the diagnosis of brain tumor. High
resolution techniques, especially MR imaging and computed tomography scans are usually used for diagnostic purposes.


II. METHODOLOGY

![Block diagram of the methodology](image)

Fig 1. Block diagram of the methodology

The different MR Brain image are collected from MRI center of size 256*256 & it is used. The brain tumor images are shown in Fig 2.
Fig. 2 MR Brain Tumor Images – (i) Meningioma, (ii) Craniopharyngioma, (iii)Ependymoma, (iv)Pineal tumor

2.1 Preprocessing

Noise can be reduced by the preprocessing performed over the test image. The noise reduction is a usual pre-processing step which advances the results of post processing [16]. Median filtering is a most effective preprocessing method for eliminating salt and pepper noise. The salt and pepper noise can be removed without sinking the sharpness of an image.

In this paper, Median Filter is used to remove salt and pepper noise from the given input image. This can be used to eliminate Gaussian noise by preserving edges fixed window size.

2.2 FCM Technique

Dunn presented fuzzy c-means (FCM) clustering algorithm and advance it was extended by Bezdek [15]. In this method clustering technique that allows a pixel to belong multiple clusters. This algorithm splits collection of pixels into few clusters according meaningful criteria. So based on application, similarity of distance, intensity and connectivity may be used to differentiate classes. This algorithm is based on minimization of objective function given below [16],

\[
J(U; c_1, c_2, c_3, \ldots, c_c) = \sum_{k=1}^{c} \sum_{l=1}^{n} \mu_{kl}^2 d_{kl}^2
\]  

(1)

Where, \( \mu_{kl} \) is membership value of \( l \)th input sample in \( k \)th cluster center [16]. The membership values satisfy the following conditions,

\[
0 \leq \mu_{kl} \leq 1
\]  

(2)

\[
\sum_{k=1}^{c} \mu_{kl} = 1
\]  

(3)

\[
0 \leq \sum_{l=1}^{n} x_l \leq n
\]  

(4)
$C_k$ is the centroid of cluster $k$; $d_{kl}$ is the Euclidian distance which is measured between $k^{th}$ centroid ($C_k$) and $l^{th}$ data point is a weighting exponent. In many applications $M = 2$ is normally preferred. In center clustering [16].

The above conditions imply the followings:

1) The membership values of each sample belonging to a particular cluster should be between 0 and 1.
2) The sum of the membership values to every cluster should be 1 and each pixel must belong to at least one cluster.
3) 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 out and fuzzy partitioning of data gets completed, with the update of membership $\mu_{kl}$ and cluster centers by $C_k$,

$$\mu_{kl} = \frac{1}{\sum_{c=1}^{C} (d_{kl}/d_{ml})^{2/(M-1)}}$$

$$C_k = \frac{\sum_{l=1}^{n} \mu_{kl} m x_l}{\sum_{k=1}^{n} \mu_{kl} M}$$

(5)

Algorithm for this is explained below.

**FCM Algorithm:**

This algorithm has following steps,

1. Initialize $U=[\mu_{kl}]$ membership matrix.
2. At $m^{th}$ step, Calculate the center vectors $C_k$ with $\mu_{kl}$
   $$C_k = \frac{\sum_{l=1}^{n} \mu_{kl} m x_l}{\sum_{k=1}^{n} \mu_{kl} M}$$
   (6)
3. Update membership matrix at $m^{th}$ and $(m+1)^{th}$ step,
   $$\mu_{kl} = \frac{1}{\sum_{c=1}^{C} (d_{kl}/d_{ml})^{2/(M-1)}}$$
   (7)
   where $d_{kl}=x_l-C_k$

   If $||U(m+1) - U(m)|| \leq \varepsilon$ then STOP; otherwise return to step 2.

2.3 Modified FCM technique

Clustering method is a compression technique the size of the input is reduced to a good extent. Here huge number of input samples is converted to less number of representative clusters [4]. Masking the lower ‘m’ bits of the feature value is executed by the quantization of the feature space. The quantized output will result in the common intensity values for more than one feature vector. In the next step, feature vectors having same intensity values are grouped and this process is called aggregation. The Input to Fuzzy C-Means algorithm is given by one representative vector from each group is selected. When clustering gets over characteristic feature vector membership values are dispersed identically to all members of quantization levels. Convergence rate in enhanced for the modified FCM and it uses reduced dataset as compared with normal FCM technique.

**Modified FCM algorithm:**

This works similar to the FCM except the Variation in the cluster updation and membership value updation. The modified criterions are shown below,

$$C_k = \frac{\sum_{l=1}^{n} \mu_{kl} m y_l}{\sum_{l=1}^{n} \mu_{kl} m}; \mu_{kl} = \frac{1}{\sum_{c=1}^{C} (d_{kl}/d_{ml})^{2/(M-1)}}$$

$$D_{kl} = y_l-C_k$$

$$y = \text{reduced dataset}$$

$$\text{Reduced dataset} = \text{Input to FCM}$$
2.4 Performance parameters:

Rand index (RI):

The Rand index (RI) measures the segment of sets of pixels between the computed segmentation and the ground truth averaging. Given a set of $z$ elements and two partitions of $P$ to compare, and, we define the following: $a$ is the number of pairs of elements in $P$ that are in the same set in $X$ and in the same set in $Y$, $b$ is the number of pairs of elements in $P$ that are in different set in $X$ and in different sets in $Y$. $C$ is the number of pairs of elements in $P$ that are in the same set in $X$ and in different sets in $Y$. $D$ is the number of pairs of elements in $P$ that are in different set in $X$ and in the same set in $Y$. The Rand index (RI) is,

$$RI=(a+b)/a+b+c+d=a+b/(z/2)$$

Where, $(a+b)$ is the number of agreements between $X$ and $Y$ and $(c+d)$ is the number of disagreements 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 clusters and 1 indicating that the data clusters are exactly the same [17],[18].

Global Consistency Error (GCE)

The Global Consistency Error (GCE) evaluates the extent to which one segment can be viewed as an improvement of the other.

The formula for GCE is as follows,

$$GCE=\frac{1}{z}\min\{\sum_{p1,p2,pi}\Sigma_{s2,s1,pi}\}$$

Where, segmentation error measure takes two segmentations $P1$ and $P2$ as input, and produces area valued output in the range [0:1] where zero signifies no error [16].

Here it can be observed that RI has a higher value in modified FCM approach as compared to FCM. And GCE is minimum for modified FCM [16] [19].

III. IMPLEMENTATION

An experiment were conducted with the Magnetic Resonance (MR) brain tumor images collected from MR center and was implemented in Intel core i5-3210M CPU @ 2.50 GHz, 4GB RAM, x64 based processor using MATLAB 7.7.0(R2008b).

IV. PERFORMANCE ANALYSIS/RESULT

Time required for the system to reach the stabilized condition is the convergence rate. A comparative analysis was performed on the techniques based on the performance measures. The clustered output for craniopharyngioma image sample is shown in Fig. 3
Fig. 3 (i) Original grayscale image, (ii) Color Space Translated Image, (iii) Segmented Image using C-Means, (iv) Segmented image using modified C-Means

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. CPU time for abnormal images such as Ependymoma, CNS lymphoma, Craniopharyngioma, pineal tumor are shown.

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Abnormal Image Type</th>
<th>Technique</th>
<th>Rand Index (RI)</th>
<th>Global Consistency Error (GCE)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(i)</td>
<td>Ependymoma</td>
<td>FCM</td>
<td>0.495</td>
<td>0.1742</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>0.598</td>
<td>0.0852</td>
</tr>
<tr>
<td>(ii)</td>
<td>Meningioma</td>
<td>FCM</td>
<td>0.5421</td>
<td>0.2412</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>0.6984</td>
<td>0.0821</td>
</tr>
<tr>
<td>(iii)</td>
<td>Craniopharyngioma</td>
<td>FCM</td>
<td>0.6854</td>
<td>0.0652</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>0.7897</td>
<td>0.0148</td>
</tr>
<tr>
<td>(iv)</td>
<td>Pineal Tumor</td>
<td>FCM</td>
<td>0.7852</td>
<td>0.1485</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>0.7985</td>
<td>0.0685</td>
</tr>
</tbody>
</table>

If FCM and modified FCM technique for different number of clusters are performed, then it can be observed that CPU time required goes on increasing as number of clusters is increased.
<table>
<thead>
<tr>
<th>S. No.</th>
<th>Abnormal Image Type</th>
<th>Technique</th>
<th>Time (Sec)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(i)</td>
<td>Ependymoma</td>
<td>FCM</td>
<td>3.892</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>1.321</td>
</tr>
<tr>
<td>(ii)</td>
<td>Meningioma</td>
<td>FCM</td>
<td>2.124</td>
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<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>1.110</td>
</tr>
<tr>
<td>(iii)</td>
<td>Craniopharyngioma</td>
<td>FCM</td>
<td>1.985</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>1.214</td>
</tr>
<tr>
<td>(iv)</td>
<td>Pineal Tumor</td>
<td>FCM</td>
<td>2.742</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MFCM</td>
<td>1.21</td>
</tr>
</tbody>
</table>

V. CONCLUSION

From the results obtained, it is proved that FCM and modified FCM can segment tumor based on parameters chosen properly. Thus we conclude that Modified FCM is better in terms of convergence rate, Rand Index (RI), Global Consistency Error (GCE) as compared to FCM.

REFERENCES