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## MRI Brain Segmentation Using a Hybrid Artificial Bee Colony Algorithm with Fuzzy-C Mean Algorithm

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**Abstract:** In the field of medical image processing, image segmentation plays important role in extracting significant and reliable features in order to determine the tumor regions in the Magnetic Resonance Images (MRI). Where brain image segmentation is considered as an interesting and difficult issue in this field. In this study a new automatic and intelligent clustering approach is proposed for the segmentation of brain tumor using the hybridization of Fuzzy C-mean and Artificial Bee Colony algorithms (FCMABC), in order to enhance the ability of the FCM to segment the MRI brain image, extract the appropriate number of cluster centres (tumor region) and the number of abnormal cells (multiple sclerosis lesions) in each cluster using automatic and dynamic way. A comparative analysis was conducted between the proposed algorithm and traditional FCM. The experimental results showed the efficiency of the proposed FCMABC in improving the performance of traditional FCM in terms of the clustering accuracy. Moreover, the proposed algorithm is more robust and effective against noise, when compared with the traditional FCM.

**Key words:** Artificial bee colony algorithms, fuzzy C-means, automatic brain MRI segmentation and dynamic fuzzy clustering

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### INTRODUCTION

Now-a-days in the field of medical image processing MRI brain image segmentation has been conducted for several clinical applications with variety of difficulties (Alia *et al.*, 2011; Zantay and Aljahdali, 2010; Zhang *et al.*, 2008). Where in the MRI a dynamic segmentation process is very valuable for research and clinical work in the neurological pathology science. Therefore, in different tissue classes White Matter (WM), Gray Matter (GM) and Cerebro Spinal Fluid (CSF) of brain MRI accurate segmentation process is very important issue for the prognosis and diagnosis of certain diseases. Nevertheless, it remains a frequent problem. The main drawback of MRI segmentation is that MRI may be corrupted with a bias field smooth inhomogeneity (Heinonen *et al.*, 1998). Recently, a number of methods have been developed to overcome the complexity of the segmentation process such as boundary-based methods (Ashtari *et al.*, 1990; Atkins and Mackiewich, 1998) classification-based methods (Bezdek *et al.*, 1993; Dou *et al.*, 2007) and others (Beevi and Sathik, 2012; Clark *et al.*, 1997).

Moreover, the need for developing such algorithms to assist the segmentation and analysis processes of the medical images has become obvious with the increasing size and number of medical images (Pham *et al.*, 2000).

Image segmentation plays an important role in a vast number of biomedical imaging applications such as diagnosis (Taylor, 1995), computer integrated surgery (Ayache *et al.*, 1996; Grimson *et al.*, 1997), quantification of tissue volumes (Lawrie and Abukmeil, 1998) and treatment planning (Khoo *et al.*, 1997).

Segmentation process of the medical images is the essential and initial step in several medical image quantization and analysis approaches. Which is considered as important and challenging problem. Thus, the task of segmentation became extremely difficult due to the difficulty of medical images and the absence of the anatomical models that completely capture the potential deformations in each structure. The successful segmentation of medical images is one of the most significant tasks for various applications in the medical field (Beevi and Sathik, 2012).

FCM clustering is unsupervised algorithm and the most popular fuzzy clustering approach. FCM algorithm has been used in many image segmentation applications such as MRI clustering as in (Alia *et al.*, 2011), because FCM could retain more data than fragile clustering methods. For images with low levels of noise and noise-free images, the traditional FCM can obtain better results. But, in the segmentation process of noise-corrupted images, the traditional FCM have several drawbacks, such as vulnerability to initialization

sensitivity, getting stuck in the local minima and low convergence rate (Alomoush *et al.*, 2014).

According to previous studies, fuzzy-based segmentation methods are the most suitable and efficient methods to solve the MRI images segmentation problems, since the majority of the MRI images have indistinct boundaries between segmented clusters (regions). In the medical field applications, fuzzy clustering methods are the most widely used methods (Alia *et al.*, 2011; Balafar *et al.*, 2010; Hore *et al.*, 2009), that have shown great potency due to the ability of these methods to naturally handle such dataset traits (characteristics).

In real dataset the use of the clustering method is inappropriate, especially when there are no clear boundaries between the determined clusters (regions). Later, after introducing the fuzzy set concept (Zadeh, 1965), many researchers considered the combination between the principle and concept of fuzzy with clustering methods in order to solve data uncertainty problems (Ouaifel and Meshoul, 2012).

Clustering is an unsupervised learning technique that have been used for several applications in market segmentation, bioinformatics, machine learning and other fields. The goal of the fuzzy clustering techniques is to identify each element in each different cluster with different relationship degrees (Hashmi *et al.*, 2013).

Many researchers in the field of the medical image segmentation have triggered intense investigations to improve and enhance the performance of the traditional FCM algorithm. Generally, the reason behind the previous drawbacks is the disclosure of greedy search behaviour via the fuzzy C-mean clustering algorithm which just lead to cause trapping in the local optima (Karaboga and Ozturk, 2011). Subsequently, the selection of unsuitable initial cluster centres usually lead to undesired clustering results. Therefore; in order to solve these issues many researchers combined the traditional FCM algorithm with one of the metaheuristic search optimization algorithms which may lead to obtain the global optimal solution (Alomoush *et al.*, 2014; Kao *et al.*, 2008). Moreover, there is no proof that metaheuristic algorithms always yield the accurate solutions. But; they normally yield near-optimal or substantial solutions.

Recently, numerous metaheuristic algorithms have been developed and incorporated with FCM clustering algorithm to obtain the optimal cluster centres (Alomoush *et al.*, 2014). Where these metaheuristic search algorithms (such as harmony search, ant colony algorithm, genetic algorithm and tabu search) explore the whole search space to decide the possible and good solutions (Alsmadi *et al.*, 2011, 2012; Badawi *et al.*, 2013).

Despite the promising results of these algorithms, different metaheuristic algorithms must be established to successfully improve and enhance the accuracy of the clustering results (Alia *et al.*, 2011).

This study explores the ability of the hybrid Artificial Bee Colony (ABC) with FCM to solve the MRI images segmentation problems, where these problems are very difficult due to the complicated nature of the Magnetic Resonance Images.

## MATERIALS AND METHODS

**Fuzzy-C mean clustering algorithm:** Multiple feature spaces are used to any image, FCM clustering algorithm identifies and categorizes the image through grouping similar data elements into clusters (with different of relationship degrees) (Hung and Yang, 2001). The clustering process of the FCM is accomplished by an iterative process that has the capability to locally minimize the objective function as follow:

$$J_n = \sum_{j=1}^c \sum_{i=1}^n u_{ij}^m \|x_i - v_j\| \quad (1)$$

The cluster center  $C$  is denoted as  $\{V_i\}_{i=1}^c$  and  $m$  is any integer value more than 1 and denoted as  $m \in [1, \infty)$ ,  $\|\cdot\|$  denotes any inner-product norm refers to the similarity between data points  $x_i$  and the  $j$ -th cluster centres. The membership degree of  $x_i$  in the cluster  $j$  is represented as  $U_{ij}$ ,  $x_i$  is the  $i$ -th pattern of  $D$ -dimensional measured data, the cluster  $d$ -dimension center is denoted as  $v_j$ .

The pseudo-code of the FCM algorithm is described as the following:

- Step 1:** Initialize with  $c$  random preliminary cluster and their centers for each generation
- Step 2:** For each data point calculate the membership grade in each cluster
- Step 3:** For each generation, cluster centers are updated
- Step 4:** Steps 2 and 3 will be repeated until no more variation in the cluster centres, then, FCM clustering algorithm will be terminated

Fuzzy partitioning will be achieved by an iterative optimization process of the above objective function, as well as recalculating the membership  $U_{ij}$  and cluster center  $v_j$  using the following equations:

$$u_{ij} = \frac{1}{\sum_{k=1}^c \left( \frac{\|x_i - v_j\|}{\|x_i - v_k\|} \right)^{\frac{2}{m-1}}} \quad (2)$$

$$v_j = \frac{\sum_{i=1}^n u_{ij}^m X_i}{\sum_{i=1}^n u_{ij}^m} \quad (3)$$

When the cluster centers values are constant, the FCM algorithm will be terminated (Alia *et al.*, 2011; Alomoush *et al.*, 2014).

**Artificial Bee Colony (ABC):** Artificial Bee Colony (ABC) algorithm is a new and powerful population-based meta-heuristic algorithm inspired by the rummaging behaviour of bees, proposed recently by Karaboga. The ABC is used for solving the numerical optimization and unconstrained difficulties (Abraham *et al.*, 2012; Balasubramani and Marcus, 2013). Since ABC algorithm is easy to implement, highly flexible, simple in concept, has few setting parameters, many researchers have widely used ABC algorithms for various optimization problems, such as (Abraham *et al.*, 2012; Balasubramani and Marcus, 2013; Karaboga and Akay, 2009) and showed superior performance compared with other optimization algorithms.

An appropriate solution to solve the optimization problems can be obtained using the ABC algorithm which is performed using the location of the food source and the fitness of the identical solution using the amount of nectar of the food source (Balasubramani and Marcus, 2013; Tuba, 2012). Therefore, the available number of solutions will be equal to the employed number of bees. ABC algorithm is an iterative procedure which starts by linking every single employed bee with one food source which is randomly generated. Each employed bee discovers a food source in the neighborhood of its present food source and calculates its amount of nectar (fitness). If the new nectar content (fitness value) is better compared with currently linked food source, then employed bees travel to that new determine food source and giving up the old one, else retains the old food source. Subsequently, watching the movement of the employed bees, the information will be shared with onlooker, therefore, every onlooker bee travels to the food source and region according to the probability which is illustrated by Eq. 4:

$$P_i = \frac{fit_i}{\sum_{i=1}^{SN} fit_i} \quad (4)$$

The new exploited food source by onlooker bee is denoted as  $V_{ij}$  and  $k$  represents the solution in the neighborhood of  $i, j$  represents the dimension (magnitude) of the problem considered and  $r$  represents a random number between -1 to 1 (Eq. 5):

$$V_{ij} = X_{i,j} + r * (X_{i,j} - X_{k,j}) \quad (5)$$

where, the whole number of food sources is denoted as SN, fitness value is denoted as  $fit_i$  and updated by using Eq. 6:

$$fit_i = \begin{cases} \frac{1}{1+fit_i}, & \text{if } fit_i \geq 0 \\ 1+abs(f_i), & \text{if } f_i < 0 \end{cases} \quad (6)$$

Determine the deserted (abandoned) solution “Food source”, if exists and change it with a new solution “random solution”  $X_{ij}$  for the scout by using Eq. 7:

$$X_{ij} = min_j + rand(0,1) * (max_j - min_j) \quad (7)$$

Figure 1 shows the general structure of ABC algorithm (Hancer *et al.*, 2013).

The ABC algorithm pseudo code is given below (Ouadfel and Meshoul, 2012):

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```

Begin
Initialize the population of solutions
Evaluate the population
Cycle = 1
Repeat
Produce new solutions (food source position) for the employed bees
Apply the greedy selection process
Calculate the Pi (probability values)
Create the new solutions for the onlookers
Apply the greedy selection process for the onlookers between  $x_i$  and  $v_i$ 
Define the abandoned solution
Memorize the best food source position
Cycle = cycle+1
Terminate when cycle number reaching to the maximum cycle number
    
```

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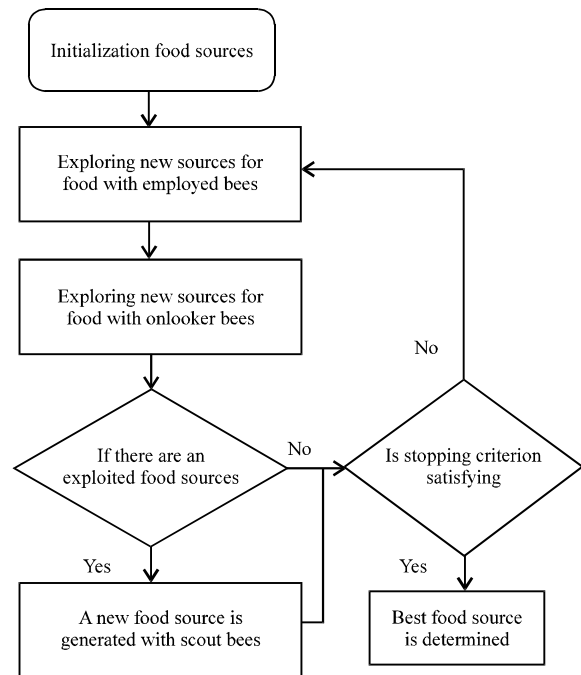


Fig. 1: General structure of ABC algorithm (Hancer *et al.*, 2013)

**Artificial Bee Colony Algorithm Based Fuzzy C-Mean Clustering (FCMABC):** The aim of the study is to develop a dynamic and automatic clustering technique in order to enhance the segmentation process of the MRI brain images and treat the drawbacks of the traditional FCM using the modified ABC algorithm to automatically determine the accurate location and number of the tumor cluster centres and the number of pixels (cells) in tumor cluster in the multiple sclerosis lesions (abnormal MRI images).

Figure 2 shows the steps of the segmentation process of the proposed FCMABC algorithm.

The following is the pseudo-code of the proposed FCMABC algorithm:

```

Begin
Step 1. Initialize with c random preliminary clusters and their centers for each generation
Step 2. For each data points calculate the membership grade in each cluster
Step 3. For each generation cluster centers are updated
Step 4. Steps 2 and 3 will be repeated until no more variation in the cluster centres, the FCM clustering algorithm will be terminated
Initialize the population of solutions
Evaluate the population
Cycle = 1
Repeat
Produce new solutions (food source position) for the employed bees
Apply the greedy selection process
Calculate the Pi (probability values)
if the Pi is not contained in the matrix(ci)
Matrix (ci) = Pi
Create the new solutions for the onlookers
Apply the greedy selection process for the onlookers between xi and vi
Define the abandoned solution
Memorize the best food source position
else
Cycle = cycle+1
Terminate when cycle number reaching to the Maximum Cycle Number
// to calculate the number of clusters
For i = 1 : n (all n image width)
For j = 1 : j (j image height)
if pixel(i,j).color equal white color (color of brain tumor)
if (if pixel(i-1,j-1).color not equal white color
number of cluster++
End if
End if
End for j
End for i
    
```

The differences between the traditional algorithms (FCM and ABC) and the proposed algorithm (FCMABC) are that the proposed algorithm has a matrix (ci), that speeds up the calculation of the probability value, also beside the objective function of the FCM the following rule for finding the tumor intensities is used, in order to increase the efficacy of the proposed algorithm and accurately extract the appropriate number of cluster centres (tumor region) and the number of abnormal cells (multiple sclerosis lesions) in each cluster using automatic and dynamic way.

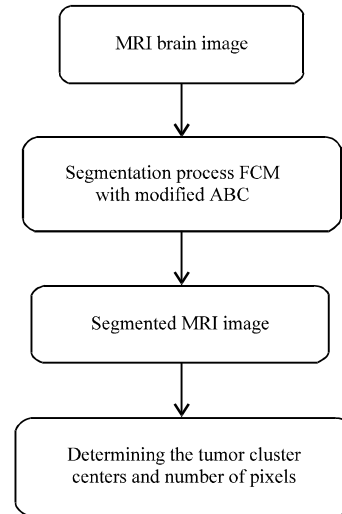


Fig. 2: Segmentation process of the FCMABC

If  $(\text{pixel}(i,j).B \leq 136 \text{ and } \text{pixel}(i,j).B \geq 109)$  and  $\text{pixel}(i,j).G < 135$  and  $\text{pixel}(i,j).G > 115$  and the sum of the RGB is not equal 393, 384, 411, 366, 309  
 $F(x) = (\text{pixel}(i,j)1, \text{pixel}(i,j)2, \dots, \text{pixel}(i,j)n)$

For further explanation about the above rule refer to (Alsmadi, 2014).

## RESULTS AND DISCUSSION

In this section, the performance of the proposed FCMABC algorithm was indicated using simulated and real MRI brain data which were collected from (BrainWeb, 2003; IBSR., 2005). In all experiments, the proposed algorithm FCMABC has run for 2500 cycles and the colony size is 50 bees.

**Experimental results based on simulated brain data:** A 3D simulated MRI brain volumes are used in this study with three parameter settings (BrainWeb, 2003) which are 20% intensity non-uniformity (RF), T1 modality, 3% noise and slice thickness equal to 1 mm. each volume contains 181 brain images with voxel size of  $1 \times 1 \times 1 \text{ mm}^3$  and all the images have a size of  $181 \times 217$ .

When FCMABC algorithm do the segmentation process, it segments the MRI brain images into number of clusters, where the segmentation process is achieved using the intensity values of the cluster pixels as a feature space.

The ground truth image will be used in order to compare against the output image (segmented image). Qualitative and quantitative judgment with other state-of-the-art techniques was conducted for the proposed FCMABC algorithm. The simulated data consists of 5

Table 1: FCMABC parameters evolution

ANI	FCMABC	NI	FCMABC
<b>Slice A110</b>		<b>Slice A40</b>	
Mean	0.6369122	Mean	0.6145072333333333
Median	0.05	Median	0.5
Std	0.261641166485705	Std	0.23927727987978
Best	0.05	Best	0.05
Worst	0.9107366	Worst	0.8435217
<b>Slice A99</b>		<b>Slice A64</b>	
Mean	0.6205837	Mean	0.6013697666666667
Median	0.05	Median	0.5
Std	0.245543987912553	Std	0.225133034744645
Best	0.05	Best	0.05
Worst	0.8617511	Worst	0.8041093
<b>Slice A40</b>		<b>Slice A102</b>	
Mean	0.6152455666666667	Mean	0.5847612333333333
Median	0.05	Median	0.05
Std	0.240047460585055	Std	0.205865530545224
Best	0.05	Best	0.05
Worst	0.8457367	Worst	0.7542837
<b>Slice A102</b>		<b>Slice A91</b>	
Mean	0.6099583333333333	Mean	0.6225187
Median	0.05	Median	0.05
Std	0.23447636696833	Std	0.247506262547032
Best	0.05	Best	0.05
Worst	0.829875	Worst	0.8675561
<b>Slice A103</b>		<b>Slice A51</b>	
Mean	0.6238596	Mean	0.6189627333333333
Median	0.05	Median	0.5
Std	0.248856987042759	Std	0.243888020752695
Best	0.05	Best	0.05
Worst	0.8715788	Worst	0.8568882

Table 2: Classification accuracy rate (MS), the obtained number of tumor clusters and cells in the abnormal MRI brain image using abnormal and normal MRI brain images by FCMABC

Normal MRI images	MS of FCMABC	No. of tumor clusters and cells	Abnormal MRI images	No. of tumor clusters	No. of tumor cells	MS of FCMABC
A-GA 40	0.74	0	A-GA 110	2	20	0.63
A-GA 64	0.55	0	A-GA 99	4	15	0.59
A-GA 102	0.60	0	A-GA 40	1	2	0.74
A-GA 91	0.55	0	A-GA 102	6	46	0.60
A-GA 51	0.66	0	A-GA 103	7	70	0.60

abnormal brain images (represented as ANI) and 5 normal brain images (represented as NI). Therefore, the median, mean and standard deviation, best and worst of the objective function for the proposed FCMABC algorithm are indicated in Table 1.

The obtained values of the mean, median, standard deviation, worst and best values illustrate the effectiveness of the proposed FCMABC using the normal and abnormal brain images. Therefore, regarding to the minimization problems all of the obtained results are near to the optimal value. Moreover, the proposed algorithm successfully determined the appropriate number of tumor clusters and cells in the abnormal images as shown in Table 2.

In this study, quantization index was used in order to evaluate the obtained results and the performance of the proposed FCMABC using the classification accuracy rate. The rate of classification accuracy will be calculated utilizing the similarity between the clustered image that obtained using the proposed method and ground truth

image that provided by BrainWeb (2003). Minkowski Score (MS) (Alia *et al.*, 2011) is the quantization index that used in this work. The MS was calculated using the following equation.

The Minkowski Score (MS) quantization index was used in this study in order to evaluate the performance and the obtained results of the proposed FCMABC algorithm using the classification accuracy rate. The following equation was used to calculate the MS.

$$MS(T,S) = \sqrt{\frac{n_{01} + n_{10}}{n_{11} + n_{10}}} \tag{8}$$

where, T represents the ground truth image partitioning matrix and S represents the segmented image partitioning matrix. The  $n_{11}$  denotes the pairs of elements in the same cluster in both T and S.

The  $n_{01}$  denotes the elements number of pair's in the same cluster in S only and the  $n_{10}$  denotes the number of pair's in T in the same cluster. The least value of the MS

is the best matching between the ground truth image and segmented image using FCMABC. The optimal value for MS is 0.

The obtained classification accuracy rate results show the capability of the proposed FCMABC algorithm in obtaining accurate segmentation results. Table 2 illustrates the number of tumor clusters and cells and the classification accuracy rate. The calculation of the classification accuracy rate was done based on the original normal (A40, A64, A102, A91 and A51), original abnormal (A110, A99, A40, A102 and A103) MRI images and their ground truth (GT40, GT64, GT99, GT102, GT103 and GT110) MRI images. Therefore, FCMABC accurately determines the appropriate number of tumor cells and clusters. For example, the number of tumor clusters and cells in the abnormal MRI image (A-GA103) are 7 and 70, respectively.

In order to measure the effectiveness of the proposed FCMABC algorithm a cluster validation experiments were conducted in this work. This experiments utilized some quality measurements and external criterion namely; F-measure, Rand measure, Confusion matrix measures and Jaccard index (Alsmadi, 2014). Therefore, the similarity between the original abnormal MRI image and its ground truth image are used in the validation clustering experiments. Where these experiments measure how the segmented image is comparable to the ground truth image. The validation experiments results show the ability and efficacy of the proposed FCMABC algorithm in obtaining more accurate segmentation results compared with traditional FCM algorithm regarding to the minimization problems as shown in Table 3.

Figure 3 and 4 shows the segmented abnormal MRI simulated brain images using the traditional FCM and the proposed FCMABC algorithm, respectively. Therefore, the proposed FCMABC algorithm successfully segmented the MRI image and determined the tumor pixels more efficiently than the traditional FCM algorithm. Thus, the proposed FCMABC algorithm improved and enhanced the ability of the traditional FCM to automatically extract the appropriate number of cluster centres (tumor region) and the number of abnormal cells (multiple sclerosis lesions) in each cluster using automatic and dynamic way.

**Real brain data experimental results:** In this section, a group of 3D real MRI brain images were used to evaluate the proposed FCMABC algorithm, 20 abnormal MRI brain images are included in this group with their corresponding ground truth images. These images were obtained from Internet brain segmentation repository (IBSR., 2005).

The images that were used have a size of 181\*217 and every image contains different tissue types depending on the brain image axial location. Figure 5 shows the segmented real abnormal MRI brain images using the FCM and the proposed FCMABC algorithm, respectively. The results obtained by the proposed FCMABC indicate the success of the algorithm in determining the tumor site clearly compared with the ground truth image. Therefore, the proposed FCMABC algorithm successfully segmented the MRI image and determined the tumor pixels more efficiently than the traditional FCM algorithm. Thus, the proposed FCMABC algorithm significantly improve and enhance the ability of the traditional FCM.

Table 3: Obtained results by the validation measures

Abnormal images and validation measures	FCM	FCMABC
<b>Slice A-GA 110</b>		
Rand measure	0.9107366	0.5
F-measure	0.903384	0.006241519
Jaccard index	0.8237925	0.00313053
Fowlkes-Mallows index	0.903708279193681	0.0396254990491556
<b>Slice A-GA 199</b>		
Rand measure	0.8617511	0.5
F-measure	0.8777192	0.00916118
Jaccard index	0.7820852	0.004601668
Fowlkes-Mallows index	0.881258823915253	0.0480777566607129
<b>Slice A-GA 40</b>		
Rand measure	0.8495303	0.5
F-measure	0.8550048	0.001346499
Jaccard index	0.7467324	0.0006737031
Fowlkes-Mallows index	0.86034423311025	0.0183597016178662
<b>Slice A-GA 102</b>		
Rand measure	0.829875	0.5
F-measure	0.8539198	0.02578875
Jaccard index	0.7450786	0.01306281
Fowlkes-Mallows index	0.86016953393443	0.0813501957546211
<b>Slice A-GA 103</b>		
Rand measure	0.8715788	0.5
F-measure	0.8811611	0.02723959
Jaccard index	0.7875674	0.01380786
Fowlkes-Mallows index	0.884437467949703	0.0836695381002054

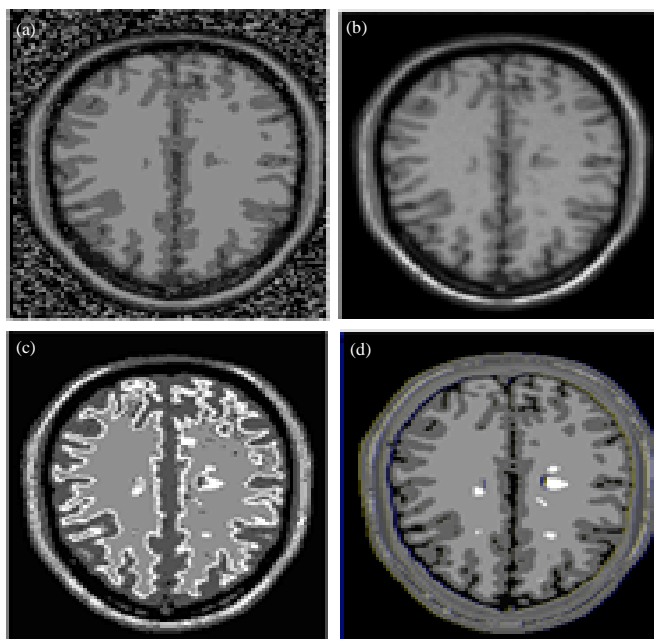


Fig. 3(a-d): Segmentation results of the FCM and FCMABC algorithms (based on simulated data) (BainWeb, 2003) (a) Original abnormal simulated MRI brain image (slice 103), (b) Segmented results by FCM, (c) Segmented results by FCMABC and (d) Ground truth abnormal MRI brain image (slice 103)

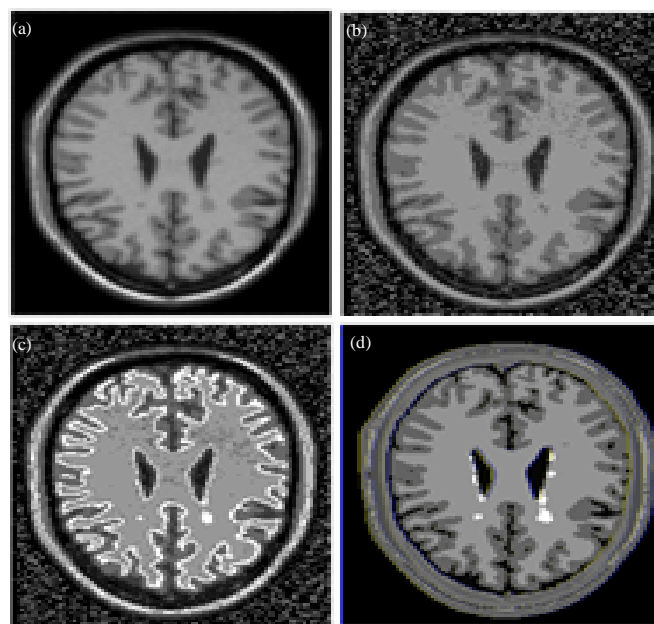


Fig. 4(a-d): Segmentation results of the FCM and FCMABC algorithms (based on simulated data) (BainWeb, 2003), (a) Original abnormal simulated MRI brain image (slice 99), (b) Segmented results by FCM, (c) Segmented results by FCMABC and (d) Ground truth abnormal MRI brain image (slice 99)



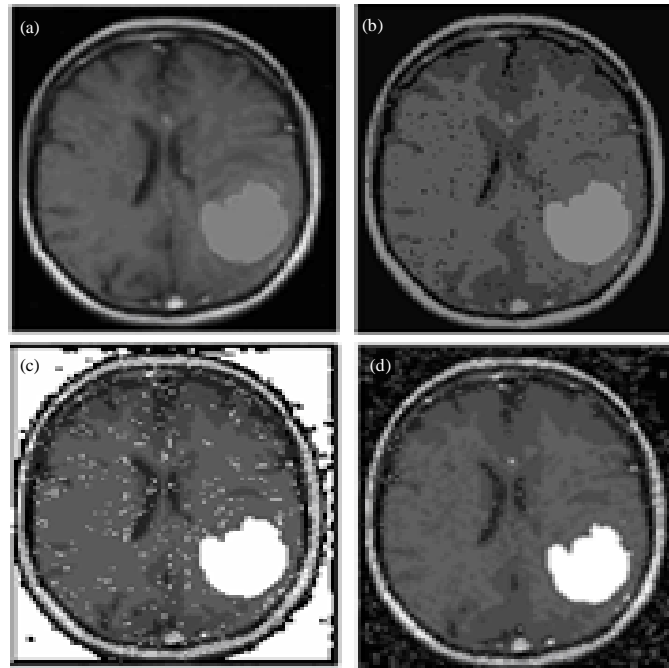


Fig. 5(a-d): Segmentation results of the FCM and FCMABC algorithms (based on real data) (IBSR., 2005), (a) Original abnormal real MRI brain image obtain from IBSR, (b) Segmented results by FCM, (c) Segmented results by FCMABC and (d) Ground truth abnormal real MRI brain image

**FCMABC execution time:** The execution time for finding the near-optimal number of the tumor clusters and cells for both real and simulated abnormal MRI brain images was calculated which was less than 1 min.

**Comparison with state-of art studies:** The results of the proposed algorithm were compared with the traditional FCM and DCHS algorithm in Alia *et al.* (2011), it can be inferred from the obtained results of the traditional FCM that the proposed FCMABC algorithm outperforms the traditional FCM in all cases (cluster validation experiments and experiments based on simulated and real data). The researchers in Alia *et al.* (2011) concentrated in their work on obtaining the near optimal number of clusters as well as the location of these cluster centers. Whilst; this research concentrates on automatically extracting the appropriate number of cluster centres (tumor region) and the number of abnormal cells (multiple sclerosis lesions) in each cluster using automatic and dynamic way.

Therefore, the proposed FCMABC algorithm successfully determined the appropriate number of tumor clusters and cells in the abnormal MRI images in an automatic and dynamic way.

## CONCLUSION

A novel segmentation based clustering algorithm were proposed in this study which is FCMABC based on the hybridization of FCM algorithm with modified ABC algorithm. Thus, the experimental results based on real and simulated MRI brain images show the effectiveness of the proposed FCMABC algorithm which has the ability to automatically segment the MRI brain images and effectively determine the appropriate number of tumor clusters and cells in the real and simulated abnormal MRI brain images without any prior information. Moreover, the proposed FCMABC has the capability to avoid the weaknesses of the fuzzy clustering algorithms, such as getting stuck in the local minima and low convergence rate. Due to the artefact (such as noise and outliers) and the high invariability of MRI brain images, finding the tumor intensities was the main limitation of this research.

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