

A HYBRID FIREFLY ALGORITHM WITH FUZZY-C MEAN ALGORITHM FOR MRI BRAIN SEGMENTATION

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ABSTRACT

Image processing is one of the essential tasks to extract suspicious region and robust features from the Magnetic Resonance Imaging (MRI). A numbers of the segmentation algorithms were developed in order to satisfy and increasing the accuracy of brain tumor detection. In the medical image processing brain image segmentation is considered as a complex and challenging part. Fuzzy c-means is unsupervised method that has been implemented for clustering of the MRI and different purposes such as recognition of the pattern of interest and image segmentation. However; fuzzy c-means algorithm still suffers many drawbacks, such as low convergence rate, getting stuck in the local minima and vulnerable to initialization sensitivity. Firefly algorithm is a new population-based optimization method that has been used successfully for solving many complex problems. This paper proposed a new dynamic and intelligent clustering method for brain tumor segmentation using the hybridization of Firefly Algorithm (FA) with Fuzzy C-Means algorithm (FCM). In order to automatically segment MRI brain images and improve the capability of the FCM to automatically elicit the proper number and location of cluster centres and the number of pixels in each cluster in the abnormal (multiple sclerosis lesions) MRI images. The experimental results proved the effectiveness of the proposed FAFCM in enhancing the performance of the traditional FCM clustering. Moreover; the superiority of the FAFCM with other state-of-the-art segmentation methods is shown qualitatively and quantitatively. Conclusion: A novel efficient and reliable clustering algorithm presented in this work, which is called FAFCM based on the hybridization of the firefly algorithm with fuzzy c-mean clustering algorithm. Automatically; the hybridized algorithm has the capability to cluster and segment MRI brain images.

Keywords: Dynamic Fuzzy Clustering, Firefly Algorithm, Fuzzy C-Means, Automatic Brain MRI Segmentation

1. INTRODUCTION

Nowadays; in the field of medical image processing research and clinical applications (computer-guided surgery, diagnosis of illnesses, tissue volume determination, treatment planning, functional brain mapping, therapy assessment and the anatomical structure studying) the automatic and dynamic MRI brain segmentation process is still a challenging issue and many researchers are working to resolve this issue (Alia *et al.*, 2011).

Generally, this domain deals with the changes in a specific areas in the brain, these areas are the Cerebrospinal Fluid (CSF), Gray Matter (GM) and White Matter (WM). Therefore; any Changes in these tissues volume can be used to characterize the diseases state and entities, such as the diseased tissues characterization (viable tumor, necrotic tissues and edema) (Alia *et al.*, 2011).

In the MRI brain image segmentation the main goal is partitioning such an image into multiple meaningful non-overlapping regions, where each segmented region shares some similar feature. So, this process involves

identifying the type of the tissue in each voxel or pixel in 3 dimensional or 2 dimensional datasets according to the previous knowledge and information available from MRI brain images (Alia *et al.*, 2011; Dou *et al.*, 2007).

Segmentation of brain images manually can be done, but is a tedious and time-consuming mission and relies on operator variability. So, developing an-automatic approaches is required to increase the volume of the objective brain segmentation (Alia *et al.*, 2011; Wang *et al.*, 2008).

Because of the complexity of the segmentation process automatic brain image segmentation requires several different approaches, where each approach utilizes diverse induction ways such as region-based methods (Adams and Bischof, 1994; Alia *et al.*, 2011; Chang and Li, 1994; Pohle and Toennies, 2001; Sijbers *et al.*, 1997), classification-based methods (Bezdek *et al.*, 1993; Dou *et al.*, 2007; Kapur *et al.*, 1996; Mokbel *et al.*, 2000; Szilagyi *et al.*, 2003; Van *et al.*, 1999a; 1999b; Wells *et al.*, 1996; Xiaohe *et al.*, 2008; Zhou and Rajapakse, 2008) boundary-based methods (Ashtari *et al.*, 1990; Atkins and Mackiewicz, 1998; Ji and Yan, 2002; McInerney and Terzopoulos, 1996) and others in (Beevi and Sathik, 2012; Clark *et al.*, 1997; 1998; Shen *et al.*, 2005; Sonka *et al.*, 1996; Cherfa *et al.*, 2007; Zanaty and Aljahdali, 2010; Zhou and Bai, 2007). This intricacy happens from the intrinsic nature, complicated structures of the MRI brain image (Alia *et al.*, 2011).

Based on the previous work, fuzzy clustering-based segmentation methods are of the most significant benefit for the MRI images segmentation, since most of the MRI brain images demonstrate indistinct borders between segmented regions. Fuzzy clustering techniques are the most used techniques in several applications in the medical fields (Alia *et al.*, 2011; Balafar *et al.*, 2010; Hore *et al.*, 2008), has shown great prospective as it can naturally deal with such dataset characteristics. In the last three decades, several studies relying on the FCM algorithm were suggested to overcome the errors in the segmentation process. Many of them were concentrated on enhancing the accuracy and performance of FCM in segmenting MRI brain images, to reduce the influences the artifacts of the MRI such as inhomogeneity sensitivity, noise and outliers (Alia *et al.*, 2011). For example, Pham and Prince (Pham, 1999) adapted the objective function of the traditional FCM by including the function of smooth membership and a factor to control the

exchange between them was set. Comparable method was developed by (Ahmed *et al.*, 2000). The authors adapted the fitness function of the FCM to recover for intensity inhomogeneity and to permit the pixel labelling to be affected by its direct neighborhood labels. Overtime, the authors in (Zhang and Chen, 2004) adapted the FCM algorithm fitness function by using the kernel-induced distance rather than the metric of the Euclidean distance.

However, the main drawback of these applied algorithms is calculating the neighborhood term for each phase of iteration, that takes a long time (very time-consuming) (Shen *et al.*, 2005). New methods relies on the image histogram representation were suggested in the literature such as (Cai *et al.*, 2007; Chen and Zhang, 2004; Chuang *et al.*, 2006; Liao *et al.*, 2008; Sijbers *et al.*, 1997; Szilagyi *et al.*, 2003; Liew and Hong, 2003) in order to solve time-consuming and decrease the computational demands of these algorithms. A level of gray scale of the obtained MRI image was used by these algorithms rather than the representation of the typical pixel level. One problem still not resolved which was inability these algorithms to developed a complete framework for automatic and dynamic brain segmentation to handle with the volume data of brain (Alia *et al.*, 2011). The operator has to enter the optimal number of cluster in each image, which makes the process semi-automatic and subjected to the operator variability and time-consuming.

The clustering process can be divided into hard and fuzzy clustering, depending on the process of dealing with uncertainty about the available data. Therefore; a hard clustering algorithm divided the dataset into distinct clusters (multiple meaningful non-overlapping regions) in which one object belongs to one cluster. Whereas; dataset of the fuzzy clustering can belong to multiple clusters (Sasa *et al.*, 2009).

This clustering process is unsuitable for real world dataset where there are no clear borders between the obtained clusters. Since the launch of the fuzzy set theory (Zadeh, 1965), researchers started to combine the concept and principle of fuzzy with clustering techniques to solve the problem of data uncertainty (Salima and Souham, 2012).

Clustering is a unsupervised learning mechanisms that have been applied for different applications in machine learning, market segmentation, bioinformatics and other various field. The main goal of the unsupervised fuzzy clustering mechanisms is to specify

each data element to all dissimilar clusters with different degrees of relationship (Hashmi *et al.*, 2013).

FCM algorithm is commonly used in the image segmentation clustering method (Hashmi *et al.*, 2013; MacQueen, 1967; Yancang *et al.*, 2010; Sasa *et al.*, 2009; Withey and Koles, 2008). FCM algorithm was selected as an alternative for the typical K-means algorithm to allow each element in the dataset to belong to more than one cluster. Despite of this improvement, the K-means algorithm still suffering from some drawbacks such as (low convergence rate and getting trapped in local minima).

Determining the number of the obtained clusters from the given images or dataset is the main challenge in the clustering domain (Alia *et al.*, 2011). In spite of the importance of development of the algorithms for the clustering process that can be automatically set the proper number of clusters without any pervious knowledge, a handful number of researchers conducted their work to resolve this problem. In the recent years many researchers used the Metaheuristic algorithm-based clustering technique as the first choice for this problem (Falkenauer, 1998), Metaheuristic algorithm-based clustering technique is applicable and feasible due to the problems of partitional clustering such as NP-hard nature (Falkenauer, 1998). In Chiong, (2009; Chiong *et al.*, 2009) authors strongly recommended that NP-hard problems can be solved using the Metaheuristic population- based algorithms in order to obtain suitable-optimal solutions and to reduce the calculation time compared with other algorithms. A fuzzy variable string length genetic point symmetry (Fuzzy-VGAPS) algorithm was proposed by (Saha and Bandyopadhyay, 2007; 2009; Das *et al.*, 2009a) used differential evolution algorithm for proposing fuzzy clustering, evolutionary-based algorithm was proposed by (Campello *et al.*, 2009) and other authors (Pakhira *et al.*, 2005; Maulik and Bandyopadhyay, 2003) proposed the Genetic Algorithm (GA) as a clustering method. Generally; these proposed algorithms applied an optimization process (such as particle Swarms and genetic algorithm optimization) as a clustering algorithm with fitness function used for cluster validity index. For further explanation refer to (Alia *et al.*, 2009; Das *et al.*, 2009b; Horta *et al.*, 2009; Hruschka *et al.*, 2006). Alia *et al.* (2011) in spite of the promising results that was obtained from these algorithms, a new metaheuristic algorithm must be developed

to significantly enhance and improve the accuracy of the segmentation results.

Alomoush *et al.* (2013) proposed a new firefly algorithm relies on fuzzy clustering algorithm. The proposed algorithm consists of 2 phases. Firstly; a near optimal value of predetermined clusters number are identified, then the output of the first phase will be used to initiate the FCM to perform the clustering segmentation process. The experimental results based on simulated and real MRI brain images shows a promising results compared with traditional FCM algorithm.

Alia *et al.* (2011) presented a new dynamic and automatic clustering algorithm for MRI brain image segmentation called DCHS based on hybridization between the Harmony Search with the FCM algorithm. The presented clustering algorithm DCHS has the capability to automatically cluster the obtain MRI images (dataset) without any previous knowledge. The presented algorithm DCHS was successfully able to overcome some of the disadvantages such as getting trapped in the local optima and the initialization sensitivity. Both of real and simulated brain MRI images are used to evaluate the proposed DCHS. The experimental results indicated that proposed DCHS accurately segmented the multiple tissue categories under serious noise environment and intensity distinctions.

2. FUZZY-C MEAN CLUSTERING ALGORITHM

Typically clustering algorithm is applied on a set of n objects or patterns $x = \{x_1, x_2, x_3, \dots, x_n\}$, each of them, $x_i \in \mathbb{R}^d$, is a feature vector containing d real-valued measurements depicting the features of the pattern represented using x_i (Alomoush *et al.*, 2013).

Fuzzy clustering algorithms divided into: Hard and fuzzy clustering. A hard clustering algorithm divide the dataset x into distinguished cluster $G_1, G_2, G_3, \dots, G_c$, (multiple meaningful non-overlapping regions) in which one object belongs to exactly one cluster (Alia *et al.*, 2011; Alomoush *et al.*, 2013) while in fuzzy clustering algorithms dataset x can be belong to more than on cluster. The output of the clustering is a fuzzy partition matrix (membership matrix) $U = [u_{ij}]_{(c,n)}$ and Equation 1, where $U_{ij} \in [0,1]$ denotes the fuzzy membership of the i th pattern to the j th fuzzy cluster:

$$M_{fcn} = \left\{ u \in R^{c \times n} \left\| \sum_{j=1}^c U_{ij}, 0 < \sum_{j=1}^n U_{ij} < n \right. \right. \quad (1)$$

and $U_{ij} \in [0,1]; 1 \leq j \leq c; 1 \leq i \leq n$

FCM algorithm is assumed as the most popular one among the fuzzy partitioning algorithms (Chattopadhyay *et al.*, 2011). FCM is an iterative process that has the ability to locally minimize the objective function as follow Equation 2:

$$J_m = \sum_{j=1}^c \sum_{i=1}^n u_{ij}^m \|x_i - v_j\| \quad (2)$$

The centroids of the clusters are represented as $\{v_j\}_{j=1}^c$ and $\|\cdot\|$ represents an inner-product norm from the data point x_i to the j th cluster centres, the fuzzy membership decides the amount of fuzziness of the classification results by the weighting exponent which is denoted as the parameter $m \in [1, \infty)$ the pseudo-code of the FCM algorithm is described as the following:

- Initiates with c random initial cluster centers for each iteration
- Calculate the membership matrix of each data point in each cluster
- Cluster centers are recalculated for each iteration
- Repeat steps 2 and 3 until no further change in the cluster centres the FCM algorithm will be terminated

The process of the FCM algorithm initiates with c random initial cluster centres for each iteration, FCM algorithm used the following Equation 3 to find the fuzzy membership for each data point in each cluster (Alia *et al.*, 2011; Alomoush *et al.*, 2013):

$$u_{ij} = \frac{1}{\sum_{k=1}^c \left(\frac{\|x_i - v_j\|}{\|x_i - v_k\|} \right)^{\frac{2}{m-1}}} \quad (3)$$

The cluster centers are recalculated based on the membership values using the following Equation 4:

$$v_j = \frac{\sum_{i=1}^n u_{ij}^m \cdot x_i}{\sum_{i=1}^n u_{ij}^m} \quad (4)$$

When the value of the cluster centres is constant the FCM algorithm will be terminated (Alia *et al.*, 2011; Alomoush *et al.*, 2013).

3. FIREFLY ALGORITHM (FA)

FA is a nature inspired multi-modal metaheuristic algorithm based on the firefly's flashing behaviour (Yang, 2010a). Firefly uses the flashing as a signal to attract other fireflies. A FA assumes three basic rules (Alomoush *et al.*, 2013; Chai-ead *et al.*, 2011; Yang, 2010b) which are described as follows:

- Every firefly will be attracted to other fireflies irrespective to their gender because they are unisexual
- They attract each other proportionally to their illumination intensity and reversely proportional to their search spaces, the brighter flashing firefly will attract the other less bright ones, the more the distance the less attractiveness, if no brighter firefly nearby they will move randomly
- The brightest firefly cannot be attracted and it will travel randomly

The cluster centres are the decision variables when FA is used to solve the clustering problems, then in an N-dimensional space there will be a correlation between the objective function and the value of all Euclidean distance (Alomoush *et al.*, 2013; Karaboga and Ozturk, 2011).

At the beginning and based on the objective function all of object (fireflies) will be randomly propagated in whole search distance (space). FA procedure consists of two phases: The first is the difference in the light intensity, thus, the light intensity is linked with the objective values (Alomoush *et al.*, 2013; Yang, 2008). Considering the maximization or minimization case problem, the firefly with either lower or higher light intensity will attract another individual with either lower or higher light intensity.

In a swarm containing a number of fireflies denoted by n and x_i represents the solution for any firefly (i) in the swarm, therefore; $f(x_i)$ is the fitness value for x and the brightness of the firefly I will determine the actual position i of the corresponding $f(x_i)$ (Alomoush *et al.*, 2013; Yang, 2008) Equation 5:

$$I_i = f(x_i) \quad 1 \leq i \leq n \quad (5)$$

The second phase is traveling to the direction of the attractive fireflies, the firefly attractiveness will

proportionate with light intensity gained by the neighbour fireflies (Alomoush *et al.*, 2013; Yang, 2008). The pseudo-code of the firefly algorithm is described as follows (Kwieceń and Filipowicz, 2012; Yang, 2008; 2009):

Begin

Initialize the parameters of the proposed algorithms:

- *Fireflies number (n).*
- *Maximum number of generations (Max-Generation, iterations,).*
- *β_0 α and γ*

Determine the objective function

$$F(x), x_i = (x_1, x_2, x_3, \dots, x_d)^T$$

Generate the initial population (n initial solutions)

of fireflies $x_i = (i = 1, 2, 3, \dots, n)$

The intensity of the light I_i at x_i will be determined using the objective function value $F(x)$.

Determine the absorption (assimilation) coefficient γ

While (m < MaxGeneration)

For i = 1: n // n number of all fireflies

For j = 1: n // n number of all fireflies

If ($I_j > I_i$)

Move firefly I towards j in d-dimension

End if

Get attractiveness, which differs with distance r through $\exp[-\gamma r]$

Calculate the new solutions and update light intensity

End for j

End for i

Rank the fireflies and find the current best

End while

Each member in the swarm has its own attractiveness denoted by β that will depend on distance (r_{ij}) between the fireflies i and j , the location of j is x_j , see the following Equation 6 and 7:

$$r_{ij} = \|x_i - x_j\| \tag{6}$$

$$\beta(r) = \beta_0 \exp\{-\gamma d(i,j)^2\} \tag{7}$$

β_0 is the attractiveness when r equals zero, γ denotes the coefficient of light absorption, assuming that firefly j illuminates light more than firefly i then i will move

toward j , the distance travelled will be calculated from the following Equation 8:

$$x_i(t+1) = x_i(t) + \beta_0 \exp\{-\gamma d^2\} (x_j - x_i) + \alpha(\text{rand} - 0.5) \tag{8}$$

Rand is a generator of random number distributed uniformly between 0 and 1. For further explanations refer to (Alomoush *et al.*, 2013; Kwieceń and Filipowicz, 2012; Yang, 2010a).

4. FIREFLY ALGORITHM BASED FUZZY C-MEAN CLUSTERING (FAFCM)

In this work the main contribution is a dynamic clustering method for tumor segmentation using the hybridization of modified FA with FCM. In order to automatically segment MRI brain images and improve the capability of the FCM to automatically elicit the proper number and location of the cluster centres and the number of tumor pixels in each cluster in the abnormal (multiple sclerosis lesions) MRI images.

In this section, the ability and performance of the firefly algorithm to determine the values of the near-optimal cluster centres in the initialization phase of the FCM will be demonstrated. Thus; the proposed clustering method consists of two phases:

- In order to determine the optimal cluster centers, firefly inspects the search space of the given dataset and then the values of the cluster centers will be obtained using the FA
- Starting the initialization of the Fuzzy C-Mean algorithm based on the evaluated results in the first phase in order to refine them and to overcome the drawbacks of Fuzzy C-Mean algorithm such as getting stuck in the local optimal and being susceptible to initialization sensitivity (Alomoush *et al.*, 2013) Equation 9:

$$A = \left(\begin{matrix} s_1 \{a_1, a_2, \dots, a_d\}, s_2 \{a_1, a_2, \dots, a_d\}, \\ s_3 \{a_1, a_2, \dots, a_d\} \end{matrix} \right) \tag{9}$$

The values of the near optimal cluster centres will be determined using firefly algorithm searching process. Where A represents the collection of the feasible array of each pixel, a_i denotes as the

numerical characteristic that describes a cluster centres and $a_i \in A$. Moreover; s_i represents each cluster centres and its define by the numerical feature $d \{a_1, a_2, \dots, a_d\}$. Consequently; each solution has an accurate size equals $(c*d)$, d defines the number of features that represents the given dataset and c denotes a pre-determined number of clusters. The parameter setting of the firefly algorithm (number of fireflies ($n = 110$), max iteration = 1000, $\beta = 1$ and $\gamma = 1$) was carefully selected based on preliminary experiments, then the examination step of initialization phase will start and the solutions in every cluster centres will be initialized randomly. The following is the pseudo-code of the modified FAFCM.

Begin

Starting the process of FCM algorithm:

1. *Initiates with c random initial cluster centers for each iteration*
 2. *Calculate the membership matrix of each data point in each cluster*
 3. *Cluster centers are recalculated for each iteration*
- Repeat steps 2 and 3 until no further change in the cluster centres the FCM algorithm will be terminated*

Set the parameters of the FA:

- *Fireflies number (n).*
- *Maximum number of generations (Max-Generation, iterations).*
- *β_0 α and γ*

Determine the objective function

$F(x), x_i = (x_1, x_2, x_3, \dots, x_d)^T$

Generate the initial population (n initial solutions) of fireflies

fireflies $x_i = (i = 1, 2, 3, \dots, n)$

The intensity of the light I_i at x_i will be determined using the objective function value $F(x)$.

Determine the absorption (assimilation) coefficient γ

While ($m < \text{MaxGeneration}$)

For $i = 1: n // n$ number of all fireflies

For $j = 1: n // n$ number of all fireflies

If ($I_j > I_i$),

Move firefly I towards j in d -dimension.

End if

else if $I_i <= I_j$ and firefly i is not the brightest and $m > 3$

matrix (i) = 0

End if

Get attractiveness, which differs with distance r through $\exp[-\gamma r]$.

Calculate the new solutions and update light intensity

End for j

End for i

best: Rank the fireflies and find the current best solution

End while

Post-process results (brighter firefly) and visualization.

To calculate the number of clusters

For $i = 1: n$ (all n image width)

For $j = 1: j$ (j image height)

if $\text{pixel}(i,j).color$ equal white color (color of brain tumor)

*if ($\text{if } \text{pixel}(i-1,j-1).color$ not equal white color
number of cluster++)*

End if

End if

End for j

End for i

5. OBJECTIVE FUNCTION

In the proposed algorithm the fitness function is used to indicate how good or bad a candidate solution is. The way of selecting the fitness function is a very significant matter in designing the proposed clustering algorithm, since the solution optimization and the performance of the algorithm count mainly on this fitness function (Alsmadi *et al.*, 2012; Sheta, 2006). Thus; the solutions will be ordered in ascending way after measuring their fitness function based on their fitness value. In the proposed clustering algorithm (a firefly (brighter one) that have minimum fitness value) for each iteration will has the ability to affect and influence in the movements of the other fireflies. Therefore; when comparing between two fireflies a and b , if b is brighter than firefly a , than firefly a will move toward firefly b . The proposed clustering algorithm was designed to enhance the performance of the traditional FCM in order to obtain more accurate segmentation process.

In order to update the solution with the newly generated $a' = (a'_1, a'_2, a'_3, \dots, a'_N)$ the objective function is calculated for every new firefly solution $f(a')$, if the objective function value of the new solution is better than the current solution, then the worst solution will be replaced by the new solution, otherwise the new solution will not be used. The pseudo-code to find the tumor intensities is as follows:

If ($\text{pixel}(i,j). B \leq 136$ 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.

$F(x) = (\text{pixel}(i,j)1, \text{pixel}(i,j)2, \dots, \text{pixel}(i,j)n)$.

In this work; the pseudo-code for finding the tumor intensities was carefully determined based on the

conformity between the ground truth images and the original images, this is due to the obviousness of the tumor in the ground truth images it was very helpful in determining the range of the colour values of the tumor in the original images.

If the value of blue colour is between 109 and 136 and the value of green colour is between 115 and 135 and the sum of the RGB is not equal to 393, 384, 411, 366 and 309. The obtained value will approximately belong to the pixels that contain the tumor in the brain. Thus; this work used the following linear Equation 10 to change the intensity of the pixels that contains a tumor to a specific intensity value (which is 9000) and to change the other pixels to another intensity value (which is zero).

$$f(i) = \begin{cases} 9000 & i \in \text{tumorpixels} \\ 0 & i \in \text{normalpixels} \end{cases} \quad (10)$$

The hybridization step between FA and FCM is introduced to enhance the quality of the FA clustering results. The FCM have the ability to modify the cluster centres values till reaching the minimum variance, therefore obtaining more specific clusters.

6. EXPERIMENTAL RESULTS

This section indicates the performance of the proposed FAFCM algorithm based on simulated and real MRI brain data obtained from (MBIC, 2014; IBSR, 2014).

6.1. Experimental Results Based on Simulated Brain Data

The experiments in this work were performed based on full 3D simulated MRI volumes with some parameter settings which are T1 modality, 3% noise, slice thickness equal to 1 mm and 20% intensity non-uniformity (RF) that were obtained from brainweb (MBIC, 2014). Every volume includes 181 brain images with voxel size of $1*1*1\text{mm}^3$ and image size is $181*217$ for the all images.

In this volume, in every image there is a different type of tissues according to the axial location of brain image.

During the automatic image segmentation process using FAFCM clustering algorithm the given image is segmented into regions, the intensity value of each pixel is used by the FAFCM as feature space to achieve the segmentation process.

3D real and simulated brain images are used to perform the segmentation algorithm. The simulated images (T1-Weighted MRI brain images (T1WI) are

obtained from brain-web Simulated Brain Database (SBD) repository (MBIC, 2014) and whereas the real data was obtained from the IBSR, center for Morphometric Analysis, Massachusetts General Hospital Repository (McInerney and Terzopoulos, 1996).

Moreover; the proposed FAFCM will be used to automatically segment the normal and abnormal (multiple sclerosis lesions) brain images and the number of tissue types will be not determined. For the validation proposes, the ground truth data will be compared against the obtained segmented image. Quantitative and qualitative comparison with other state-of-the-art methods was done for the proposed algorithm.

In order to improves the segmentation results and the effectiveness of the proposed method (FAFCM). The parameters setting (number of the used fireflies (n), γ , β , Max generation (M)) of FA was determined carefully based on preliminary experiment. **Table 1** illustrates the parameters settings that were used in the testing based on five scenarios to indicate the convergence behaviour of the FAFCM.

The Simulated Brain Database (consisting 5 normal brain images (denoted as NI) and 5 abnormal (multiple sclerosis lesions) images (denoted as ANI). According to experimental results in this work, the fifth scenario with the parameter settings ($n = 110$, $\gamma = 1$, $\beta = 1$ and $M = 1000$) obtained the best segmentation results (regarding to the minimum objective function). Therefore; the mean, median, standard deviation, worst and best of the objective function and the number of pixels that obtained Tumor (TP) for fifth scenario indicated in **table 2**.

The obtained mean, median, standard deviation, worst and best values show the good performance of the proposed algorithm FAFCM for both normal and abnormal (multiple sclerosis lesions) MRI brain images. Thus; all of obtained results are close to the optimal value regarding to the minimization problems. The obtained results shows the effectiveness of the proposed FAFCM in automatic determining the optimal number of tumor clusters and their tumorpixels in the abnormal (multiple sclerosis lesions) MRI brain images as shown in **table 3**.

In this work quantization index was used in order to evaluate the obtained results and the performance of the proposed FAFCM 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 the brianweb (MBIC, 2014). Minkowski Score (MS) (Alia *et al.*, 2011; Ben-Hur and

Guyon, 2003) is the quantization index that used in this work. The MS was calculated using the following Equation 11:

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

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

The n_{01} represents the elements number of pair's in the same cluster in S only and the n_{10} represents the number of pair's in T in the same cluster. The less value of the MS is the best matching between the segmented image using FAFCM and the ground truth image. The optimal value for MS is 0.

Moreover; the classification accuracy rate (MS) shows the ability of the FAFCM in obtaining good segmentation results. **Table 3** shows classification accuracy rate (MS), number of tumor cluster and number of tumorpixels. The classification accuracy rates were calculated using the original abnormal (A110, A99, A40, A102 and A103) and original normal (A40, A64, A102, A91 and A51) MRI brain images FAFCM and their ground truth (GT110, GT99, GT40, GT102, GT103 and GT64) MRI brain images. FAFCM is able to find the appropriate number of tumor clusters and number of tumorpixels. For example; the number of tumor clusters in the abnormal brain image A-GA110 is 2 and the number of tumorpixels in both clusters is 20.

In this work cluster validation was included to show the effectiveness of the proposed algorithm FAFCM based on some quality measurements, utilizing the external criterion which are Rand measure, F-measure, Jaccard index and Confusion matrix measures (CA, 2013). Therefore; the clustering results that were obtained from FAFCM using the original abnormal (multiple sclerosis lesions) MRI brain images are evaluated based on the similarity with the ground truth of the abnormal (multiple sclerosis lesions) MRI brain images. These cluster evaluation measurements measure how the clustered image (output of the original image) is close to the ground truth image.

The obtained result from the validation experiments indicates the efficacy and ability of the proposed algorithm FAFCM for segmentation of the MRI brain images. Regarding to the minimization problem the obtained results by the proposed algorithm FAFCM outperformed the obtained results of the FCM algorithm.

Table 5 illustrates the obtained results based on validation measures. **Figure 1 and 2** illustrates the clustered abnormal (multiple sclerosis lesions) images of the simulated brain images from (MBIC, 2014) using the FCM and the FAFCM algorithms respectively. In Figure 1 and 2, the success of the FAFCM in clustering and determining the tumor pixels is clear when compared with the FCM algorithm, due to the robust rule for finding the tumor intensities that was determined in this work based on the conformity between the ground truth images and the original images. Therefore; FA improve the capability of the FCM to automatically elicit the proper number and location of cluster centres and the number of tumorpixels in the abnormal (multiple sclerosis lesions) MRI brain images.

6.2. Experimental Results based on Real Brain Data

In this section; the experiments were performed based on group of full 3D real MRI brain images that were acquired from Internet brain segmentation repository (IBSR, 2014).

This group includes 20 abnormal MRI brain images with their matching ground truth images (experts' manual segmentations). The size of the used images is 181*217 and in every image there is a different type of tissues according to the axial location of brain image.

When real data is used in the experiment, the same fifth scenario with the parameter settings ($n = 110$, $\gamma = 1$, $\beta = 1$ and $M = 1000$) were used in order to obtain good segmentation results. **Figure 3** illustrates the clustered abnormal (multiple sclerosis lesions) real MRI brain images from (IBSR, 2014) using the FCM and the FAFCM algorithms respectively.

As shown in **Figure 3**, the number of tumor cluster is 1 and the number of tumorpixels is 1098. Therefore; the success of the FAFCM in clustering and determining the tumor pixels is clear when compared with the FCM algorithm, due to the robust rule for finding the tumor intensities that was determined in this work based on the conformity between the original images and the ground truth images.

7. FAFCM EXECUTION TIME

In order to find the near optimal number of the tumor clusters and the number of tumorpixels in the abnormal images for both of real and simulated MRI brain images obtained from (MBIC, 2014; IBSR, 2014). The execution time was calculated for both real and simulated data, which was almost in range of 5 to 7 min.

Table 1. Illustrates the parameters settings of the FAFCM

Scenarios	N	γ	β	M
1	10	0.1	0.90	1000
2	25	0.2	0.93	1000
3	50	0.6	0.95	1000
4	80	0.9	0.97	1000
5	110	1.0	1.00	1000

Table 2. FAFCM parameters evolution for the fifth scenario

ANI	Scenario 5	TP	NI	Scenario 5	TP
Slice A110	Mean	0.292538880000000	20	Slice A40	0.451457729833333
	Median	0.013740980000000		Slice A40	0.500000000000000
	Std	0.373361687911334		Slice A40	0.474799873806498
	Best	0.013440860000000		Slice A40	0.000587889500000
	Worst	0.850434800000000		Slice A40	0.853785300000000
Slice A99	Mean	0.289165794000000	22	Slice A64	0.463607099100000
	Median	0.008931230000000		Slice A64	0.500000000000000
	Std	0.374322430532823		Slice A64	0.481282194663380
	Best	0.008598452000000		Slice A64	0.000341997300000
	Worst	0.849967700000000		Slice A64	0.463607099100000
Slice A40	Mean	0.277830414033333	2	Slice A102	0.305475270800000
	Median	0.001175779000000		Slice A102	0.000610314300000
	Std	0.371923806063375		Slice A102	0.390426021481663
	Best	0.000563063100000		Slice A102	0.000471698100000
	Worst	0.831752400000000		Slice A102	0.915343800000000
Slice A102	Mean	0.308812123333333	46	Slice A91	0.287660195600000
	Median	0.026173540000000		Slice A91	0.000453617600000
	Std	0.375924582418690		Slice A91	0.378950246074600
	Best	0.025233130000000		Slice A91	0.000451569200000
	Worst	0.875029700000000		Slice A91	0.862075400000000
Slice A103	Mean	0.327028400000000	54	Slice A51	0.468961583633333
	Median	0.031727380000000		Slice A51	0.500000000000000
	Std	0.384253184762339		Slice A51	0.483858312284357
	Best	0.030525720000000		Slice A51	0.000723850900000
	Worst	0.918832100000000		Slice A51	0.906160900000000

Table 3. Illustrates the classification accuracy rate (MS) using abnormal and normal MRI brain images, the obtained number of tumor clusters and the number of tumorpixels in each abnormal MRI brain image by FAFCM

Abnormal	MS of FAFCM	N of tumor clusters	TP	Normal images	MS of FAFCM
A-GA 110	0.45	2	20	A-GA 40	0.47
A-GA 99	0.53	4	22	A-GA 64	0.58
A-GA 40	0.46	1	2	A-GA 102	0.51
A-GA 102	0.52	6	46	A-GA 91	0.51
A-GA 103	0.52	7	54	A-GA 51	0.51

Table 4. Indicates the classification accuracy rates of the FAFCM, DCHS and Fuzzy-VGAPS

Slice #	MS of FAFCM	MS of DCHS	MS of Fuzzy-VGAPS
1	0.45	0.39	0.58
2	0.53	0.50	0.58
3	0.46	0.47	0.71
4	0.45	0.47	0.67
5	0.45	0.47	0.62
6	0.45	0.47	0.71
7	0.58	0.48	0.70
8	0.51	0.49	0.71
9	0.51	0.49	0.68
10	0.51	0.74	0.65

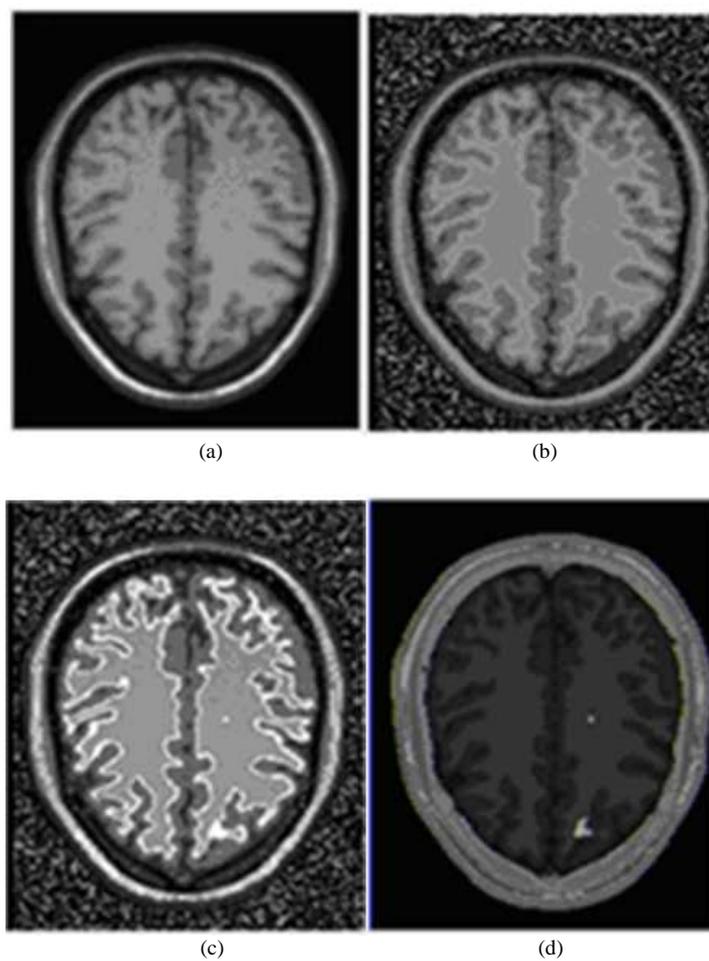
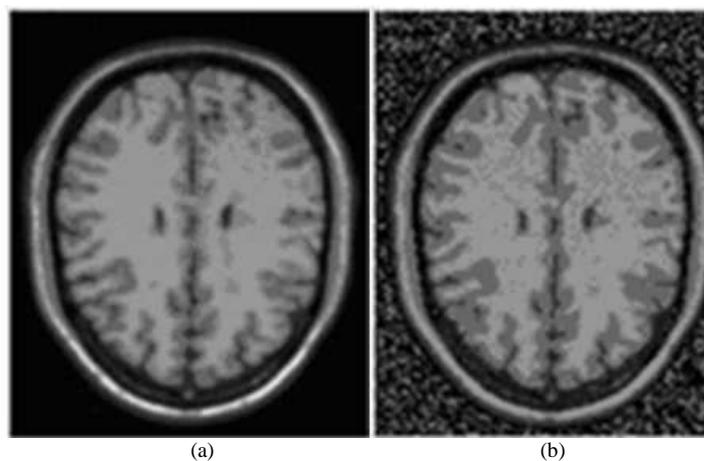


Fig. 1. Segmentation results of the FCM and FAFCM algorithms (based on simulated data) (MBIC, 2014). (a) The original abnormal simulated MRI brain image (slice 110). (b) Segmented result by FCM. (c) Segmented result by FAFCM. (d) The ground truth abnormal MRI brain image (slice 10)



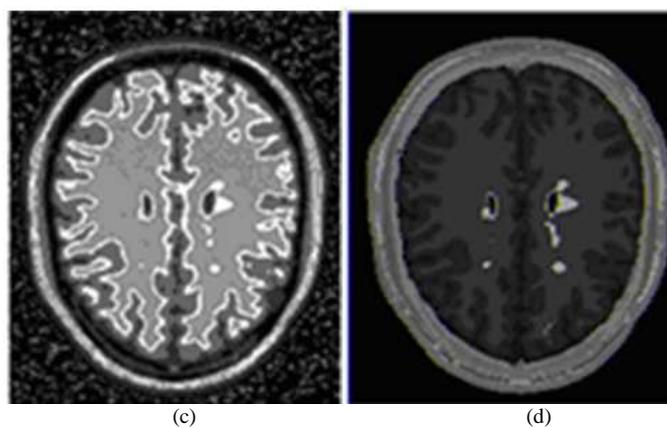


Fig. 2. Segmentation results of the FCM and FAFCM algorithms (based on simulated data) (MBIC, 2014). (a) The original abnormal simulated MRI brain image (slice 102). (b) Segmented result by FCM. (c) Segmented result by FAFCM. (d) The ground truth abnormal MRI brain image (slice 102)

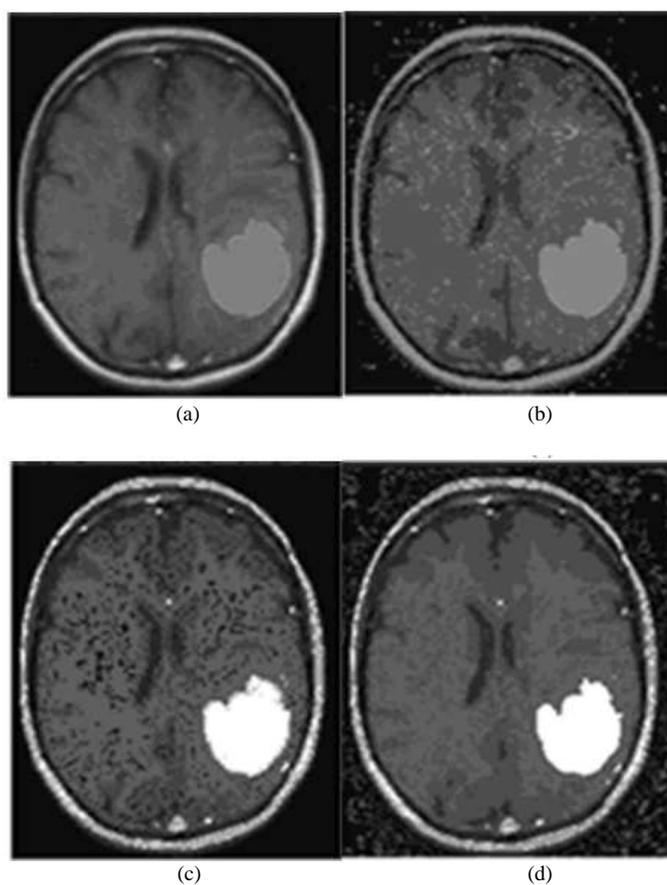


Fig. 3. Segmentation results of the FCM and FAFCM algorithms (based on real data) (IBSR, 2014). (a) The original abnormal real MRI brain image obtained from IBSR. (b) Segmented result by FCM. (c) Segmented result by FAFCM. (d) The ground truth abnormal real MRI brain image

Table 5. Illustrates the obtained results by the validation measures

Abnormal images	Validation Measures	FCM	FAFCM
Slice A-GA 110	Rand measure	0.84459100000000	0.5000000000000000
	F-measure	0.84454750000000	0.0128287400000000
	Jaccard index	0.73092350000000	0.0064557780000000
	Fowlkes-mallows index	0.84997912741131	0.0569987975504012
Slice A-GA 199	Rand measure	0.82857650000000	0.5000000000000000
	F-measure	0.84996770000000	0.0085984520000000
	Jaccard index	0.73908160000000	0.0043177890000000
	Fowlkes-mallows index	0.85535968532570	0.0465645443384328
Slice A-GA 40	Rand measure	0.85100690000000	0.5000000000000000
	F-measure	0.85460870000000	0.0010317260000000
	Jaccard index	0.74612810000000	0.0005161290000000
	Fowlkes-mallows index	0.85984670865748	0.0160685336951012
Slice A-GA 102	Rand measure	0.83664740000000	0.5000000000000000
	F-measure	0.84485920000000	0.0257198800000000
	Jaccard index	0.73139080000000	0.0130274700000000
	Fowlkes-mallows index	0.84939891254417	0.0812386183836495
Slice A-GA 103	Rand measure	0.92405220000000	0.5000000000000000
	F-measure	0.91883210000000	0.0305257200000000
	Jaccard index	0.84985150000000	0.0154994300000000
	Fowlkes-mallows index	0.91891483516315	0.0887227141635786

8. COMPARISON WITH STATE-OF ART STUDIES

In the comparison with the previous studies such as (Mokbel *et al.*, 2000) and alia, the authors focused in their researches on determining the number of clusters that brain has. While this research successfully determined the number of tumor clusters and the number of tumorpixels in the Abnormal MRI brain images with unclear tumors (recently happened). **Table 4** shows the same experimental results of the classification accuracy rates performed by DCHS in (Alia *et al.*, 2011) and fuzzy-VGAPS in (Saha and Bandyopadhyay, 2007) based on abnormal MRI brain Images, these results was described in “(Alia *et al.*, 2011).

DCHS algorithm is a clustering algorithm that has the ability to obtain the proper number of clusters with the proper correct centre values automatically, DCHS relies on the hybridization between Harmony Search (HS) with FCM in order to automatically segment the MRI brain images. Fuzzy-VGAPS algorithm is a clustering algorithm that has the ability to obtain the proper number of clusters with the proper correct centre values automatically, fuzzy-VGAPS relies on the combination between genetic algorithm and point symmetry-based index as an objective function.

Table 4 indicates the classification accuracy rates of the proposed algorithm FAFCM, DCHS and fuzzy-

VGAPS respectively. Based on the obtained results, it is clear that the classification accuracy rate of the proposed algorithm FAFCM based on 3, 4, 5, 6 and 10 is better than the obtained results by DCHS, while close results is obtained in the other rest MRI brain images 1, 2, 7, 8 and 9. Thus; the proposed FAFCM obtained much better and more accurate results in all images, when compared with the fuzzy-VGAPS.

These results were obtained because some tissues of the brain show equal levels of intensity in MRI images as in (Alia *et al.*, 2011) but in the ground images there are different intensity levels and this will affect the Matching test (MS).

9. CONCLUSION

A novel efficient and reliable clustering algorithm presented in this work, which is called FAFCM based on the hybridization of the firefly algorithm with fuzzy c-mean clustering algorithm. Automatically; the hybridized algorithm has the capability to cluster and segment MRI brain images. Therefore; the FAFCM successfully determined the types of the MRI brain images (normal or abnormal (multiple sclerosis lesions) image) and the number of the tumor clusters in the abnormal (multiple sclerosis lesions) brain image and the number of tumorpixels in the abnormal (multiple sclerosis lesions) image without any prior information. Moreover; FAFCM

has the ability to avoid the drawbacks of Fuzzy clustering, such as low convergence rate, getting stuck in the local minima and vulnerability to initialization sensitivity. Both of the simulated and real brain MRI images were used in this work. The experimental results shows the effectiveness of the FAFCM in clustering and segmenting both of simulated and real MRI images and obtaining more accuracy rate compared with other algorithms (such as DCHS and Fuzzy-VGAPS).

The most important limitation of this research is determining the robust rule for finding the tumor intensities due to the high invariability of MRI brain images and the artifacts such as outliers and Noise. The future work of this research is to develop such techniques, which are able to handle efficiently with the MRI invariability and artifacts such as outliers and noise. Moreover; use some methods to increase the robustness of the FAFCM algorithms such as image filters techniques.

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