

A Generalized Automatic Hybrid Fuzzy-Based GA-PSO Clustering Approach

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Received: November 2013

Revised: January 2014

Accepted: April 2014

ABSTRACT

The main contribution of the present research arises from developing the traditional methods in the area of segmentation of brain magnetic resonance imaging (MRI). Contemporary research is now developing techniques to solve the whole considerable problems in this field, such as the fuzzy local information c-mean (FLICM) approach that incorporate the local spatial and the gray level information. It should be noted that the present approach is robust against noise, although the high computational complexity is not truly ignored. A novel approach in segmentation of brain MRI has been investigated and presented through the proposed research. Because of so many noises embedded in the acquiring procedure, like eddy currents, the segmentation of the brain MR is now tangibly taken into account as a difficult task. Fuzzy-based clustering algorithm is one of the solutions in the same way. But, it is so sensitive to change through noise and other imaging artifacts. The idea of combining the genetic algorithm (GA) and particle swarm optimization (PSO) for the purpose of generalizing the FLICM is the ultimate goal in the present investigation, since the computational complexity could actually be reduced. The experiments with a number of simulated images as well as the clinical MRI data illustrate that the proposed approach is applicable and effective.

KEYWORD: Fuzzy-Based Clustering, Genetic Algorithm, PSO, FLICM.

1. INTRODUCTION

The ultimate goal of image segmentation algorithms is to illustrate automatically the anatomical structures in case of medical issues. The whole segmentation algorithms are so important to use in the area of medicine for the purpose of diagnosing and locating the damage. It should be noted that brain tissues consist of three areas including white matter, gray matter and cerebrospinal Fluid, as well. Fuzzy-based clustering algorithm could be taken into account as one of the solutions, which is realized for this case. It is obvious that one of the methods in case of data management is taken as data classification under similar properties within a set of clusters. It is essential to note that the main issue is the non-supervised classification of a set of unlabeled patterns within the meaningful groups. In this case, it is necessary to locate the patterns with the highest similarity within a cluster. In the mean time, various criterions are used to measure the similarities, dependent on the nature of the data. Based upon the matter, the K-means clustering approach is one of the most popular methods [1]. This is in line with the minimization of the total square error between the patterns and the center of closest cluster that can be

found. It is shown that the shape of clusters is not adjusted with the distribution and type of data. In addition, the clustering is not done properly, provided that there could be some data in the almost equal distance from the center of the clusters.

In order to solve these problems, various algorithms such as the fuzzy c-mean (FCM) are suggested, which are able to find clustering in various forms of the data [2]. Derivatives and other developments to improve the FCM clustering results are presented in component with the impact of neighborhood, as a regulator [3]-[6]. The main problem of these algorithms is their dependence, in case of the accuracy, on the number and the initial location of clusters centers. Some of these evolutionary algorithms could solve errors with the procedure of merge and split of cluster as well as the displacement of the centers of clusters though the evolutionary algorithms. It is apparent that algorithms could be divided into data, coding into strings or bits [7].

In this regard, Krinidis and Chatzis presented the fuzzy-based local information c-mean (FLICM) algorithm [8]. This can do the clustering images, while other algorithms, such as FCM and others, have truly

failed. The FLICM algorithm guarantees the stability against the noise, but the high computational complexity is the disadvantage point in case of the present algorithm.

The proposed approach is robust against the noise and more speed, where the low computational complexity utilizing the combination of GA and PSO approaches are acquired within the benefits and capabilities of fuzzy-based clustering. Additional calculations have been made to find the cluster center and determine the distance of other data from the cluster center. The reset of the paper is organized as follows: Preliminary theory is given in Section 2. The proposed automatic hybrid fuzzy-based GA-PSO clustering approach is given in Section 3. Experimental results are presented in Section 4 and finally the research concludes in Section 5.

2. PRELIMINARY THEORY

A. Fuzzy C-Means (FCM) Algorithm

The fuzzy C-mean (FCM) algorithm is a known traditional method in the area of clustering. This assigns pixels to each category through fuzzy memberships. Let $X=(x_1, x_2, \dots, x_N)$ denotes an image under N pixels to be partitioned into c clusters, as long as x_i represents multispectral (features) data. The present algorithm is an iterative optimization method that minimizes the cost function given by the following

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

where u_{ij} denotes the membership of pixel x_j in the i^{th} cluster. The present cost function needs to be minimized, while pixels that are close to the center of their clusters, are assigned to high membership values. It causes that the low membership values are assigned to pixels with data far from the center. The membership function denotes the probability that a pixel is belonging to a specific cluster. In the FCM algorithm, it should be noted that the probability is solely dependent on the distance between the pixels with respect to each individual cluster center in the features. The membership functions and cluster centers could be updated as follows: v_i is taken as the i^{th} cluster center, $\|\cdot\|$ is taken as a norm metric and m is to be constant. In fact, the parameter m deals with the fuzziness of the resulting partition.

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

And

$$v_i = \frac{\sum_{j=1}^N u_{ij}^m x_j}{\sum_{j=1}^N u_{ij}^m} \quad (3)$$

By supposing the initial guess for each one of cluster centers, the FCM algorithm converges to a solution for

v_i illustrating the local minimum or a saddle point of the cost function. In this regard, the convergence can be eliminated through comparing the changes in the membership function or the cluster center at two successive iteration steps.

B. Fuzzy Logic Information C-means (FLICM) Algorithm

Stelios Krinidis and Vassilios Chatzis introduced the novel fuzzy factor defined as:

$$G_{ki} = \sum_{\substack{j \in N_i \\ i \neq j}} \frac{1}{d_{ij+1}} (1 - u_{kj})^m \|x_j - v_k\|^2 \quad (4)$$

where the i^{th} pixel is taken as the center of the local window, k is taken as the reference cluster and the j^{th} pixel belongs to the set of the neighbors that falling into a window around the i^{th} pixel (N_i). In the same way, d_{ij} is taken as the spatial Euclidean distance between pixels i and j , u_{kj} is taken as the degree of membership of the j^{th} pixel in the k^{th} cluster. Furthermore, m is taken as the weighting exponent on each fuzzy membership and finally v_k is taken as the prototype of the cluster center.

By assuming G_{kj} , the FLICM clustering algorithm could be presented. It incorporates of the local spatial and gray level information into its objective function by the following

$$J_m = \sum_{i=1}^N \sum_{k=1}^c [u_{ki}^m \|x_i - v_k\|^2 + G_{ki}] \quad (5)$$

The two necessary conditions in case of J_m for being at its local minimal extreme, with respect to u_{kj} and v_k is now obtained as follows:

$$u_{ki} = \frac{1}{\sum_{j=1}^c \left(\frac{\|x_i - v_k\|^2 + G_{ki}}{\|x_i - v_j\|^2 + G_{ji}} \right)^{\frac{1}{m-1}}} \quad (6)$$

And

$$v_k = \frac{\sum_{i=1}^N u_{ki}^m x_i}{\sum_{i=1}^N u_{ki}^m} \quad (7)$$

C. Genetic Algorithm (GA)

GA algorithms that are efficient, adaptive and robust are taken into account as an optimization method, utilizing random choice as a tool to guide the search in so large, complex and multimodal spaces [10]. In the GA algorithms, the parameters are encoded in string-like structures titled chromosomes. A GA algorithm starts firstly under a population of chromosomes that could be initialized either randomly or through a knowledge-based system. Thereafter, each one of chromosomes is decoded, where its fitness value could be computed. Then, the genetic operators, selection, crossover and finally mutation are all applied, probabilistically, after a new population could be created. The fitness values of

the chromosomes are recomputed in the present procedure, where the results proceed in an iterative manner, till a termination criterion could be gained after the best chromosome is found as the solution to the problem concerned. It is shown that due to its effectiveness, GA algorithm has been widely realized in the area of clustering [9].

D. The Particle Swarm Optimization (PSO)

Particle swarm optimization (PSO) is originally presented by Kennedy [12]-[13]. It is first intended to simulate social behavior as a representation of the movement in case of organisms in the bird flock or fish school. The present PSO algorithm optimizes by having a population of candidate solutions. Population includes particles and their moving in the search-space in accordance with simple mathematical formulate over the particle's position and velocity. It should be noted that each particle's movement could be influenced by its local best known position, since is guided toward the best known positions in the present search-space that are updated as better positions, found by other particles. This is expected to note that the swarm should move toward the best solutions. Particle positions and their movements are obtained in a iterative manner through

$$\begin{cases} v_i(t+1) = wv_i(t) + C_1 \text{rand}_1(\text{pbest}_i(t) - x_i(t)) + \\ C_2 \text{rand}_2(\text{gbest}(t) - x_i(t)) \\ x_i(t+1) = x_i(t) + v_i(t+1) \end{cases} \quad (8)$$

where $x_i(t)$ denotes the particle's position at time t and $v_i(t)$ denotes particle's velocity at time t . The parameter titled "pbest $_i$ " is taken as the best known position of i^{th} particle, where "gbest" is taken as the swarm's best known position. The parameters w , C_1 and C_2 are chosen through the practitioner to control the behavior and efficacy of the PSO algorithm [14]. figure 1 illustrates a brief view of the PSO realization by

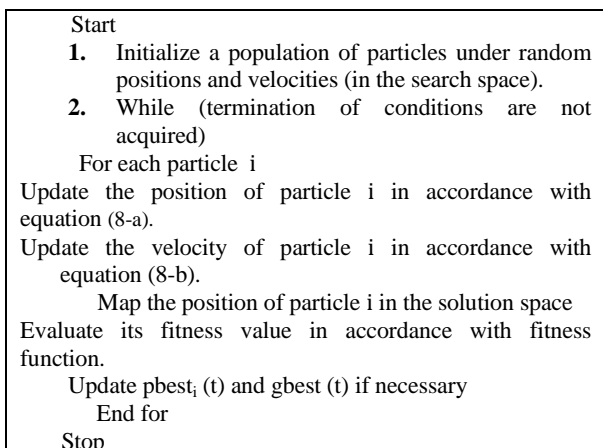


Fig .1. A brief view of the PSO realization

3. THE PROPOSED AUTOMATIC HYBRID FUZZY-BASED GA-PSO CLUSTERING APPROACH

The proposed automatic hybrid fuzzy-based GA-PSO clustering approach is now discussed. In the followings, the cost function in case of the FLICM algorithm is used, reversely, as the fitness function of Genetic algorithm. . In such cases, the PSO relations are used for the selection operator. The steps of algorithm are given as follows:

- **Encoding:**

A chromosome encodes K -cluster centers using $H \times K$ real numbers, where H is taken as the number of dimensions. For initializing a chromosome, K -cluster centers are randomly chosen from the data set. This is iterated P times for a population size of P . In this research, in order to speed up the clustering process, gray level values of the pixels, as the dimensions are assumed.

- **Fitness Computation:**

The cluster centers, encoded in the chromosome, are extracted. Thereafter, each data point is assigned to the cluster of the closest center and all ties are resolved arbitrarily. The new centers of each one of clusters are computed as the mean of the points, which are assigned to that cluster. The new centers replace the centers, originally, that are encoded in the chromosome. Finally, the clustering metric J is computed as given in Eq. (5) and the fitness of the chromosome is also defined by

$$f = \frac{1}{J+1} \quad (9)$$

Maximization off indicates the minimization of J .

- **Genetic Operators:**

In selection stage of genetic algorithm, population selects based on equation (8). Single-point crossover with a fixed probability of 0.6 is used. Each chromosome undergoes mutation with a fixed probability 0.03. The process continues for a maximum number of iterations, 200, after the best output string is chosen as the solution to the clustering problem. Figure 2 shows the framework of GA PSO clustering approach.

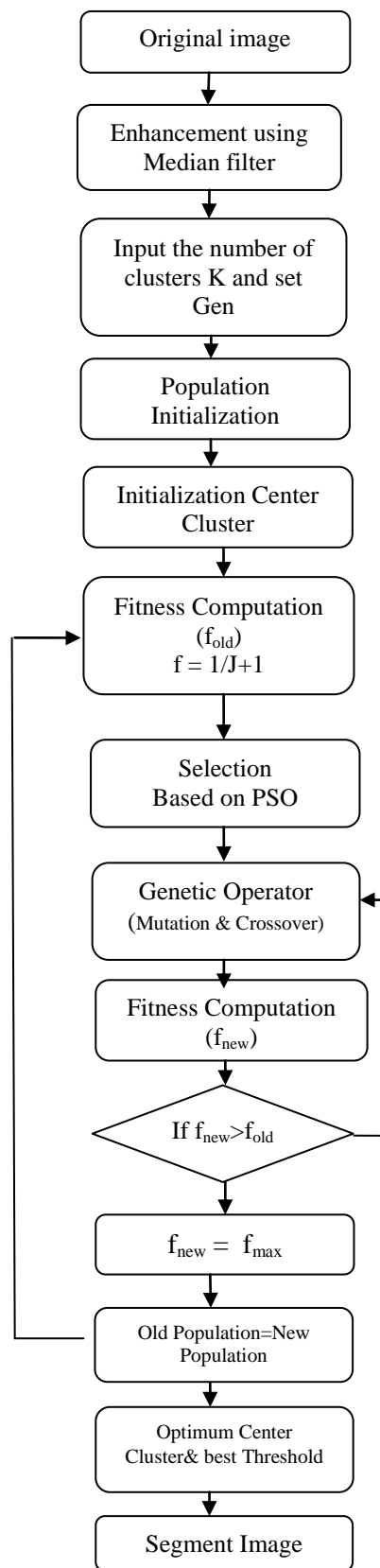


Fig. 2. Flowchart of GA PSO_ based segmentation

4. EXPERIMENTAL RESULTS

Regarding the experimental results, the three clustering algorithms are applied to the real image eight, at first [15] (see Fig. 3(a)). Then, it is contaminated with salt& pepper 30% (see Fig. 3(b)). In this case, the clustering results are shown (see Fig. 3(c)-3(e)).

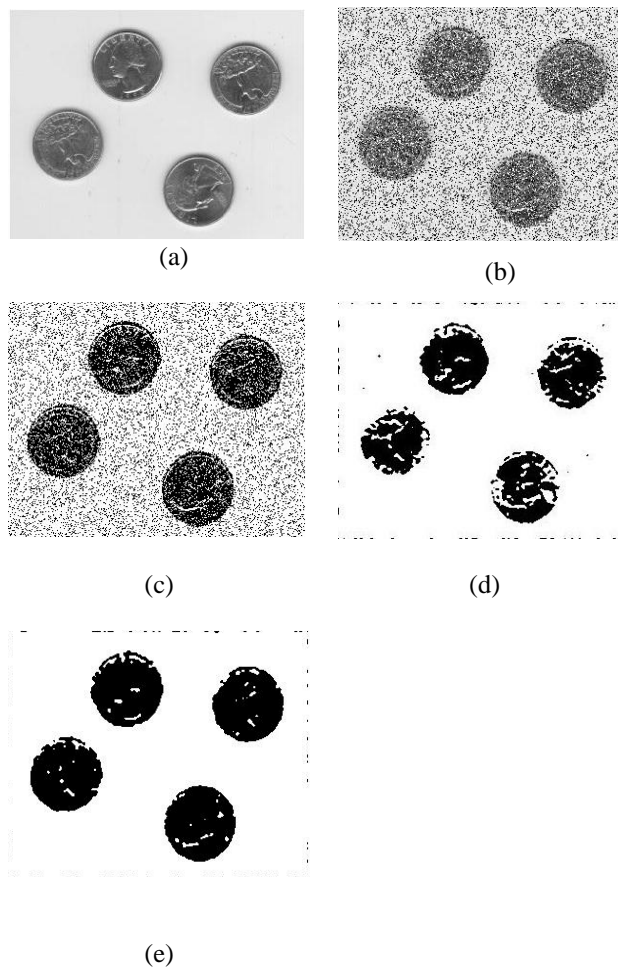


Fig. 3. Clustering result on eight image (a) Original image, (b) the same image with salt & pepper noise 30% (c) FCM (d) GA-FLICM, and (e) GAPSO-FLICM

In this section, the application of the GAPSO-FLICM segmentation on real T1 brain MR images is described. A simulated image is employed for comparing with the GA-FLICM and FCM algorithms. The Simulated image is taken as a T1-weighted phantom. There are many advantages to use the digital phantoms rather than real image including prior knowledge of the true tissue types for the purpose of controlling over image parameters such as mean intensity values, noise and intensity in homogeneity. The simulated MR images are gained from the brain imaging center at the Montreal Neurological Institute, McGill University

[11]. Afterwards, Fig. 4 displays the simulating image and the segmentation results.

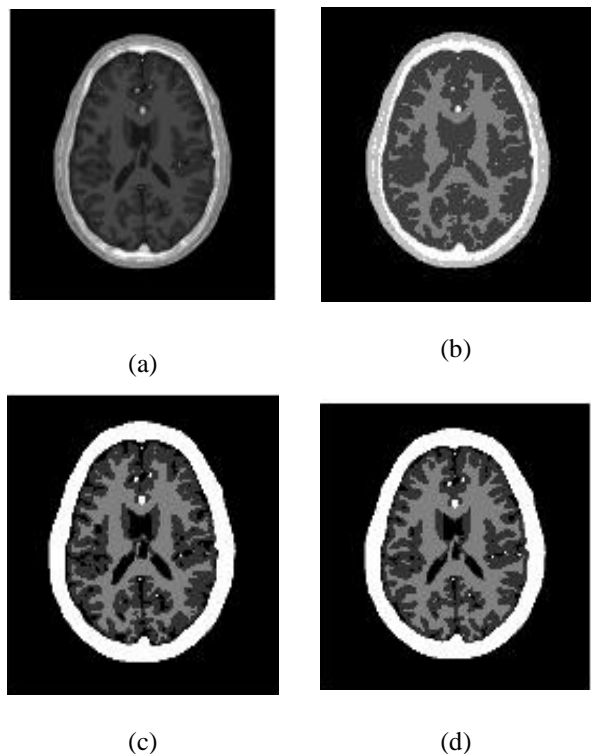


Fig. 4. Comparison of segmentation results on simulated T1 MR Image
(a) Original image, (b) FCM, (c) GA-FLICM, and (d) GAPSO-FLICM

The Segmentation Accuracy (SA) to evaluate the differences among algorithms is used by

$$SA = \frac{\text{number of classified pixels}}{\text{total number of pixels}} \times 100\% \quad (10)$$

Table 1 tabulates the SA, which can explain the performance of those algorithms under different noise level. Columns are without noise. The FCM, GA-FLICM and GAPSO-FLICM are resulted as 89.2% and 98.6%, respectively. In addition, the GAPSO-FLICM is more robust for noise. The real MRI image is taken as T1-weighted MR images of human brains in the axial plane on a GE 1.5T scanner in the Navy General Hospital of PLA with image matrix size of 256 X 256 pixels, FOV of 20 cm, TR of 400 ms, and TE of 25 ms. Figure 5 illustrates the clinical T1 MR Imaging and the segmentation results.

Table 1. Segmentation accuracy (SA) of different methods

SA	Salt & Pepper Noise		
	none	10%	15%
FCM	89.2	85.4	79.3
GA-FLICM	98.6	96.2	91.5
GAPSO-FLICM	98.8	96.3	91.5

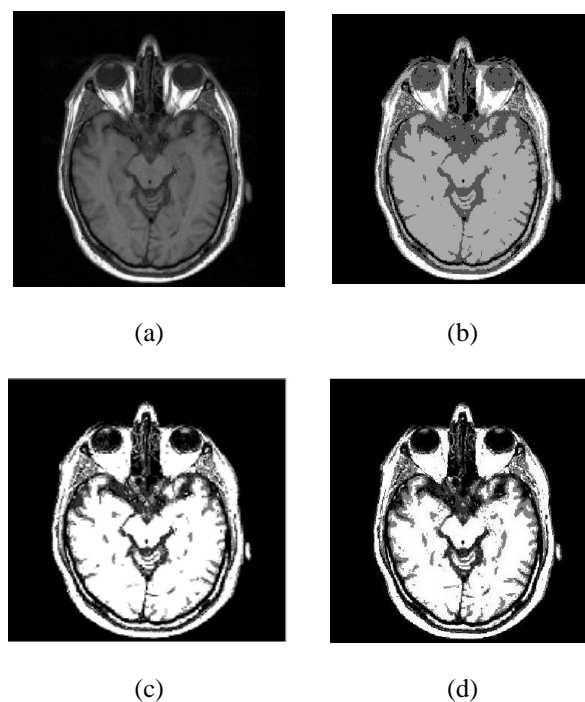


Fig. 5. Comparison of segmentation results on Real T1 MR Image
(a) Original image, (b) FCM, (c) GA-FLICM, and (d) GAPSO-FLICM

As it can be seen, the results in case of the standard FCM is not nearly appropriate, since both GA-FLICM and GAPSO-FLICM approaches are acceptable. Next, the computational complexity of algorithms is put into comparison. Figure 6 illustrates the average computational cost for each of the three algorithms compared above. The methods in the figure are presented in computational time descending order. It is shown that the proposed approach is faster with respect to the FLICM approach. The whole of experiments are carried out on a Pentium IV CPU 3GHz under Windows XP Professional. Due to the fact that the gray level value of the pixels is 256 gray levels, the number of gray levels is generally much smaller than the size of the image. Thus, the execution time is significantly reduced.

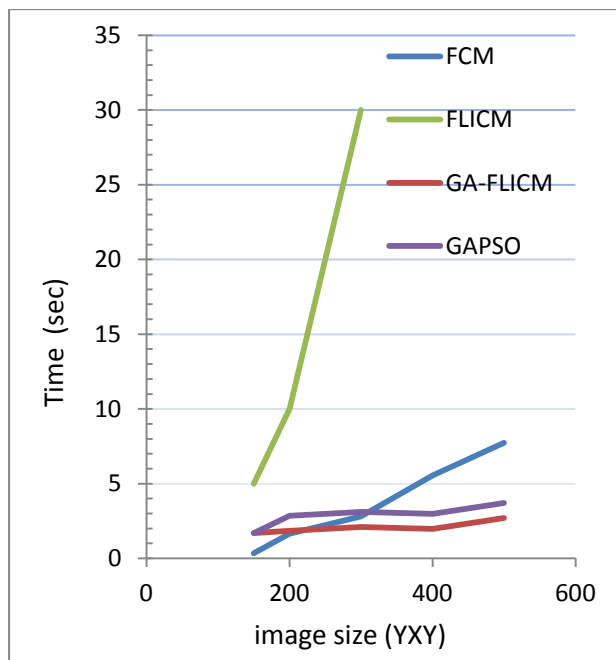


Fig. 6. Computational cost (in seconds) in case of the four clustering algorithms

In another example, the application of the GA-FLICM segmentation on real T1 brain MR images is now described. A virtual simulated image is also employed in order to compare with the FLICM and the FCM algorithms. The simulated image is taken as a T1-weighted phantom [11]-[15]. Figure 7 illustrates the simulating image and the segmentation results, as well. The Segmentation Accuracy (SA) is used to evaluate the differences among algorithms. Table 2 tabulates the SA, which can explain the performance of those algorithms with different noise levels. The FCM, FLICM and GA-FLICM approaches are resulted as 89.2%, 96.2% and 98.6%, respectively, while the GA-FLICM is more robust as is obvious.

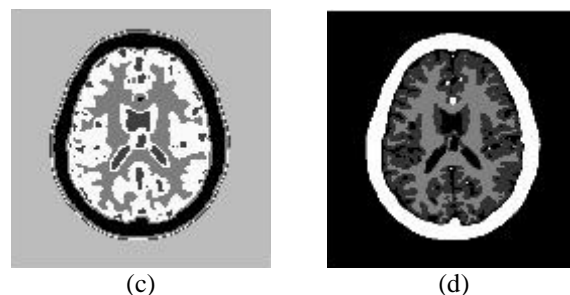
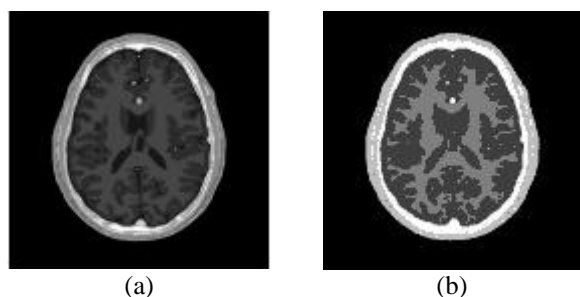


Fig. 7. Comparison of segmentation results on simulated T1 MR Image (a) Original image, (b) FCM, (c) FLICM, and (d) GA-FLICM

Table 2. Segmentation accuracy-SA of different approaches

SA	Salt& Pepper Noise		
	none	10%	15%
FCM	89.2	85.4	79.3
FLICM	96.2	96.1	89.3
GA-FLICM	98.6	96.2	91.5

Figure 8 shows the clinical T1 MR imaging. As it can be seen, the standard FCM is not well resulted, while both GA-FLICM and FLICM are appropriate. Figure 9 illustrates the average computational cost for each of the three algorithms compared above. The approaches in the figure are presented in computational time descending order. It is obvious that the proposed approach is faster than the FLICM approach.

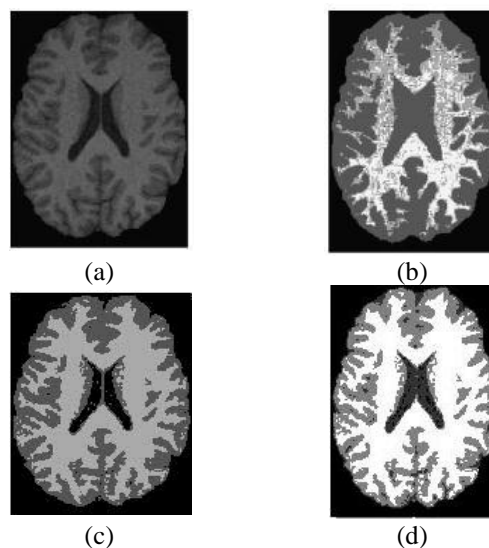


Fig. 8. Comparison of segmentation results on Real T1 MR Image (a) Original image, (b) FCM, (c) FLICM, and (d) GA-FLICM

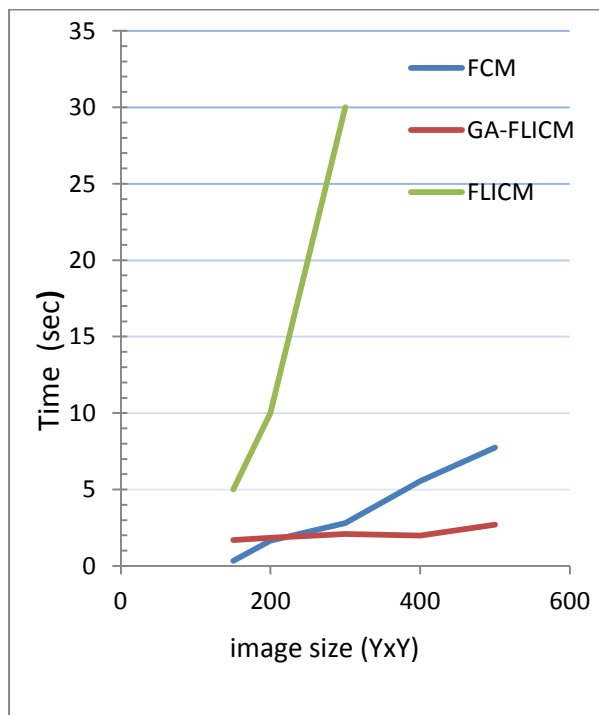


Fig. 9. Computational cost (in seconds) in case of the four clustering algorithms

5. CONCLUSION

An effective approach for automatic tissue classification is proposed. This has been applied to the segmentation of MR brain structures with noise. The present results are evaluated by using cluster validity function. Preliminary results are shown that not only the effect of the noise in segmentation is considerably less than the new one, but also the execution time is significantly reduced.

6. ACKNOWLEDGMENTS

Authors express all the best wishes to the Islamic Azad University (IAU), South Tehran Branch, Tehran, Iran. The key idea of the present research has been found and investigated by IAU, Electrical Engineering Department.

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