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Genetic Algorithm-Based Anisotropic Diffusion Filter and Clustering Algorithms for Thyroid Tumor Detection

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Abstract

Medical imaging is a technique that has been used for diagnosis and treatment of a large number of diseases. Therefore it has become necessary to conduct a good image processing to extract the finest desired result and information. In this study, genetic algorithm (GA)-based clustering technique (K-means and Fuzzy C Means (FCM)) were used to segment thyroid Computed Tomography (CT) images to an extraction thyroid tumor. Traditional GA, K-means and FCM algorithms were applied separately on the original images and on the enhanced image with Anisotropic Diffusion Filter (ADF). The resulting cluster centers from K-means and FCM were used as the initial population in GA for the implementation of GAK-Mean and GAFCM. Jaccard index was used to study resemblance, dissimilarity, distance between two sets of images, and effect of ADF on enhancing the CT images. The results showed that ADF increases the segmentation accuracy, where the value of Jaccard index of similarity between the ground truth image and segmented image was increased for all segmentation algorithms, in particular for FCM and GAFCM where similarity percent was up to 88%.

Keywords: Anisotropic Diffusion Filter, Genetic Algorithm, Clustering algorithms (K-means, FCM, GAFCM, GK-Means).

الخوارزمية الجينية المعتمدة على مرشح الانتشار متباين الخواص والخوارزميات التجميعية للكشف عن اورم الغدة الدرقية

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الخلاصة

تستخدم الصور الطبية كتقنيات للمساعدة في التشخيص المبكر وعلاج GAK-Mean ومجموعة من الأمراض ، لذلك أصبح من الضروري إجراء معالجة أولية على الصور الناتجة عن تقنيات التصوير الطبي لاستخراج أفضل النتائج. في هذه الدراسة ، تم استخدام الخوارزمية الجينية (GA) المستندة إلى تقنيات GAK-Mean و -Mean ، (Fuzzy C-mean (FCM)) لتجزئة صور الأشعة المقطعية (CT) لاستخراج ورم الغدة الدرقية . تم تطبيق خوارزميات GA و K-mean و FCM التقليدية بشكل منفصل على الصور الأصلية ومرة أخرى على الصورة المحسنة باستخدام مرشح الانتشار متباين الخواص (ADF). مراكز الكتلة الناتجة من K-mean و FCM كمجموعة أولية في GA لتطبيق كل من GAK-Mean و GAFCM. ولتقييم أداء

الخوارزميات تم استخدام فهرس جاكا رد (Jacquard Index) لدراسة التشابه والاختلاف والمسافة بين مجموعتين من الصور وتأثير ADF على تحسين الصور المقطعية أظهرت النتائج أن مرشح الانتشار متباين الخواص يزيد من قدرة التجزئة ، حيث يتم تقسيم الصور باستخدام GAK-Mean و GAFCM بشكل أفضل مقارنة بخوارزميات GA و FCM و K-Means التقليدية المطبقة على الصور غير المرشحة .

Introduction

Thyroid gland is a small butterfly-like endocrine gland located in front of the neck and surrounds the trachea. It helps to adjust the metabolism by excreting thyroid hormones which are carried by the blood to all tissues of the body where they regulate energy utilization. Any decrease or increase in the amount of these hormones cause thyroid disorders. Physicians usually diagnose thyroid disturbance by the estimation of thyroid gland size [1]. Thyroid nodules are solid lumps inside the thyroid gland that provide it with a clear appearance through the neck [2].

Medical imaging has been widely used for thyroid tumor detection through the use of technologies such as ultrasound, computed tomography (CT), and magnetic resonance imaging (MRI) [3, 4]. Researchers focused on medical imaging as it plays a significant role in early diagnosis of many diseases [5]. CT is one of the common tools for early diagnosis of thyroid cancer. Thyroid image information (e.g. pixel intensity) is very important to distinguish the normal from abnormal thyroid tissues. The intensity in normal tissues is smooth and homogeneous, while in the benign or malignant tumors it is heterogeneous [3]. Image processing techniques were firstly used to improve the medical image for additional processing. In this study, ADF was used to smoothen inhomogeneities and remove the noise from an image. Image segmentation is a method of analyzing and partitioning the image to extract parts of interest and display image information in an easy and simple way [5]. Image segmentation is considered to be a significant process because it is the first task of any automatic image grasp process, and all next steps, such as classification, feature extraction, detection, and recognition, closely depend on its results [6].

The region-based segmentation methods (K-mean and FCM) have been successfully applied to cluster medical images to extract any organ. FCM has been significantly used for CT image segmentation; it is obtained by a simple modification in the k-mean method [7]. The K-means and FCM algorithms have been widely used because of their effective theory, simple algorithms, quick grouping and effective treatment of large data sets. The traditional GA is sensitive to the initial cluster centers so that the clustering results from GA are affected by the isolated pixels. For this reason, the initial cluster centers of GA use K-means or FCM algorithms to improve the GA algorithm and hence to minimize the effect of isolated pixels [8]. The resultant class levels, derived by K-Mean or FCM, are employed as the input of the GA algorithm. The proposed algorithms (GAK-Mean and GAFCM) can be compared with the traditional algorithms [9].

Jaccard index or Jaccard similarity coefficient is used to measure the similarity between original images and segmented image; it is defined as the intersection of the images divided by the union of them [10].

Over recent years, a great number of studies related to AD filtering were conducted, starting with that of Perona and Malik [11]. Chourmouzios and Maria examined the best choice parameters of ADF, such as the conductance function, the gradient threshold and the number of iterative processes [12]. Surya Prasath proposed a method to denoise noisy images by such multiscale AD with effectively merging the inter-scale details. The results indicated a perfect denoising with edge protection on a set of images.[13]. van Marlen discussed the theory of several linear and nonlinear DF algorithms and tested them on some test problems [14]. Nair et al. introduced and proposed a robust and efficient algorithm for anisotropic diffusion smoothing of images [15]. Sunanda and Sourav studied MRI images that are segmented with genetic algorithm based fuzzy C-means algorithm. They conclude that the used method provided best performance [9]. Dennis et al. used Jaccard index to assess segmentation quality, where a 3D segmentation approach was proposed by combining the discriminative power of convolutional neural networks (CNNs) [16]. Dang et al. (2019) proposed three blood vessels segmentation methods where the accuracy was proven by Jaccard metrics [17]. Halil et al. proposed an effective method for skin lesion segmentation by combining a deep convolutional neural network. The method obtained good results according to several metrics of accuracy such as Jaccard index [18].

Materials and Proposed Method

The following flowchart explains the strategies used in this study to detect and extract tumors from thyroid CT images (Figure-1).

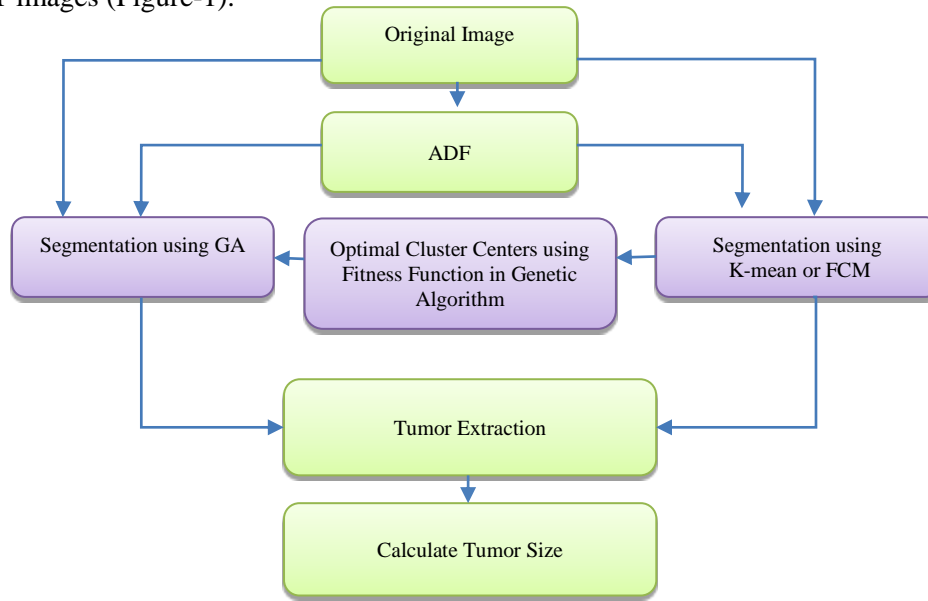


Figure 1-A diagram of the strategies used in the present study.

It is worth to mention that the X-ray computed tomography (CT) images adopted in this study were supplied by:

1. Abu Ghareeb hospital \ Department of radiology (image size 512x512 pixels and 5mm slice thickness).
2. X-Ray institute (Image size 256 x 256 pixels and 5mm slice thickness).
3. Figure-2 shows some of CT images for patients with thyroid cancer of different modalities.

Thyroid Tumor

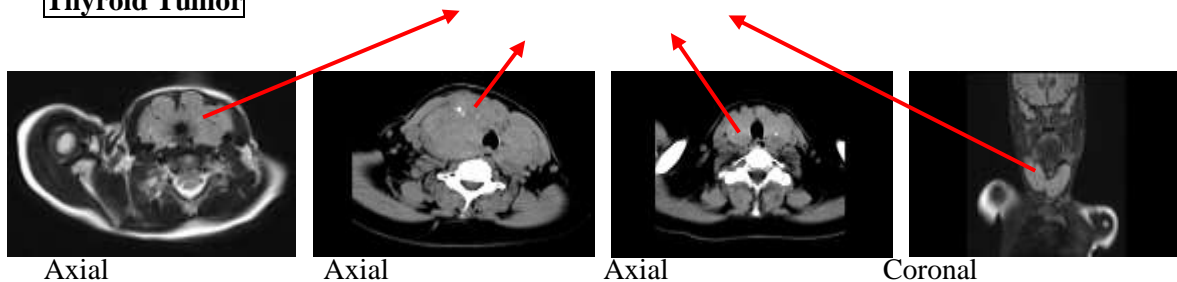


Figure 2-The four adopted images: the red arrows refer to the abnormalities (thyroid cancer) in the images.

Anisotropic Diffusion Filter (ADF)

The process of diffusion described by Fick’s first law is a physical process which equalizes the concentration difference. If the concentration replaces the image intensity and the inhomogeneities of small concentration can be modeled as the noise, the diffusion filter can be used to smoothen the inhomogeneities of the image and adjust the image by solving equation 1 (the partial differential equation for noise removing) [19] :

$$\frac{\partial I}{\partial t} = \text{div} (D \cdot \nabla I) \dots\dots\dots (1)$$

where ($\frac{\partial I}{\partial t}$) is the change of intensity as a function of time and D is the diffusion tensor . The diffusion is isotropic if D of image is homogenous. In this case, the filter constantly minimizes the noise of image but it also blurs the edges, which is it difficult to identify [19].

The traditional model (equation 1) of diffusion function is being changed with the new one, $D = d(|\nabla I|)$, in which the original image is smoothened while maintaining the intensity of the edges constant. The anisotropic equation $d(|\nabla I|)$ is called the diffusion coefficient [11] that needs to accept the following conditions to achieve the above properties [19]:

$$\begin{cases} d \rightarrow 0 \text{ for } |\nabla I| \rightarrow \infty, \\ d \rightarrow 1 \text{ for } |\nabla I| \rightarrow 0. \end{cases} \dots\dots\dots (2)$$

The following equations are proposed by Perona and Malik for $d(|\nabla I|)$ [19, 11]:

$$d(|\nabla I|) = \frac{1}{1 + \left(\frac{|\nabla I|}{k}\right)^2}, \dots\dots\dots (3)$$

$$d(|\nabla I|) = e^{-\left(\frac{|\nabla I|}{k}\right)^2}, \dots\dots\dots (4)$$

When the anisotropic diffusion is performed, the diffusion coefficient in equation (3) is favored to recognize the edges of high-contrast from the edges of low-contrast, while the wide area is favored over the smaller regions in equation (4) [20, 11].

$$\begin{cases} \frac{\partial I}{\partial t} = \text{div}(d(|\nabla I|) \cdot \nabla I), \\ I(x, y, 0) = g(x, y). \end{cases} \dots\dots\dots (5)$$

The partial differential equation which is used to enhance the image is [19]:

The parameter (k) controls the diffusion magnitude. The low k value means that the low-intensity gradients are stopping the diffusion over the edges, while the large k leads the diffusion to skip the small intensity barriers, and hence decreasing the effect of intensity on anisotropic diffusion. The ideal range of k is between 20 and 100 [19]. The number of the iterations is another control parameter over the filtered images with ADF to smoothen the homogeneity of image regions, with keeping the edges [11].

Clustering Methods

The conventional methods in clustering analysis are the unsupervised segmentation algorithms, such as k-mean and fuzzy c-mean, where an automatic algorithm separates the given dataset (CT image) into two or more clusters. The procedure involves grouping the data of similar features into one cluster and the data points of dissimilar characteristics into another cluster [21-22].

1. K-Means Clustering Algorithm

K-mean algorithm is built on the cluster centers selection. Optimum cluster centers are chosen to achieve the best result. Minimum Euclidean distance between pixels and cluster center is used to assign each pixel to the nearest cluster [23]. The process continues until the mean vectors in two consecutive iterations are equals [24].

The objective function used in this algorithm is [21]:

$$J(v) = \sum_{i=1}^C \sum_{j=1}^{C_i} \left(\|x_i - v_j\| \right)^2, \dots\dots\dots (6)$$

where $\|x_i - v_j\|$ is the Euclidean distance from the pixel (x_i) to the cluster center (v_j), C is the number of cluster centers, and C_i is the number of pixels in each cluster [21].

2. Fuzzy C-Mean (FCM) Clustering Algorithm.

FCM is a method developed by Dunn in 1973 and improved in 1981 by Bezdek. It is an algorithm used to clustering data of unities information into two or many clusters and employed in pattern recognition [25]. It is based on minimizing the objective functions difference in two sequences (J_q^{t+1} and J_q^t) [26, 27]:

$$\|J_q^{t+1} - J_q^t\| \leq \epsilon \quad \dots\dots\dots (7)$$

$$J_q = \sum_{i=1}^n \sum_{j=1}^2 U_{ij}^m d(x_i, c_j) \quad m \in [1, \infty] \quad \dots\dots\dots (8)$$

$$d(x_i, c_j) = \|x_i - c_j\| \quad \dots\dots\dots (9)$$

$$U_{ij} = \frac{1}{\sum_{k=1}^2 (d(x_i, c_j) / d(x_i, c_k))^{2/(m-1)}} \quad \dots\dots\dots (10)$$

$$C_j = \frac{\sum_{i=1}^N U_{ij}^m x_j}{\sum_{i=1}^N U_{ij}^m} \quad \dots\dots\dots (11)$$

where $d(x_i, c_j)$ is the Euclidean distance between cluster center and each pixel, U_{ij} is a membership of each pixel x_i to cluster with center c_j .

The object function is optimized by a continual update of the (u_i) and (c_j) until the difference between two iterations becomes less than the threshold (ϵ)[26, 27].

Genetic Algorithm

Genetic algorithms (GA) are defined as models of natural evolutionary systems and they have been used in science and engineering for solving practical computational problems as adaptive algorithms [28, 29]. Genetic algorithm was inspired from the Darwinian theory of evolution by the concept of “survival of the fittest”. It is of a stochastic analysis type, which depends on the selection of crossover and mutation operators. Genetic algorithm is composed of a population of a bit (0 or 1) represented as a chromosome. Each chromosome is a solution of a fitness function, which plays an important factor in the optimization function. The crossover and the mutation operators are used to produce new chromosomes from the old ones, where the new populations are generated at each iteration until the best solutions are found, due to the genetic algorithm nature. Fit individuals are used to reproduce the next generation by replacing some or all chromosomes in the old generation. The cycle continues until the optimum function value reaches the element of higher fitness [30, 31], where the fitness is a key to success and meaningful for GA applications [29].

A simple GA consists of the following steps [28, 32, 33]:

1. Input data (image or data).
2. Population of N chromosomes is generated with a random way.
3. Calculate fitness function for each chromosome in population.
4. Select the subset of greater fitness feature.
5. Crossover and mutation should be done between the fittest individuals.
6. The current population should take the value of the new generation.
7. When the new generation does not reach the highest accuracy of classification, go to step 3. In order to calculate the new fitness value.
8. Repeat steps (3-7) until reaching the desired accuracy.
9. Extract the correct chromosomes.

Genetic Algorithm Based Clustering (GAFCM, GAK-Mean)

The GA-based clustering method was proposed, where each chromosome in the population encodes a suitable partition of the image and the quality of the chromosome is calculated by using a fitness

function. The clustering technique using GAFCM or GAK-mean can be described by the following steps [26].

1. Population initialization

Real numbers of pixel intensity in thyroid images represent the population chromosomes of GA. Each chromosome has several variables (genes) that represent cluster centroids and they are taken randomly between 0 and 1 (lower and upper bound values, respectively) from all possible values of intensity in the CT images [26].

2. Fitness computation

The factor that indicates the degree of quality of a solution is the fitness of a chromosome. In this study, the fitness of a chromosome is calculated as follows:

1. Executing an objective function of clustering algorithms (K-mean or FCM) to minimize the sum of intra-cluster differences and find the membership of each pixel of the clusters, so the optimum cluster centers' values are used for the initial GA.
2. The resultant centers from the clustering algorithms encoded in the chromosome are replaced by the respective clusters' mean points [34].
3. Maximizing the fitness function via the objective of GA, then calculating the fitness function (Fit) using equation 12. Make sure that D_c value has increased and E and E_c values have decreased to satisfy the objective [26].

$$\begin{aligned}
 \text{Fit} &= \frac{D_c}{E + E_c} \\
 \text{Where } E_c &= ||F^{t+1} - F^t|| \\
 D_c &= \max_{i,j=1} ||c_i - c_j|| \\
 E &= G_{ij} - u_{ij}
 \end{aligned}
 \dots\dots\dots (12)$$

where E_c is the variation between two sequent objective functions that resulted from FCM, the value of which must be reduced. D_c is Euclidean distance through cluster centers, E is the matrix of the error. G_{ij} is the reference matrix (2xN). One dimensional binary image represents the first row of the reference matrix, while the second row is the complement of the first [26].

4. Selection

The Roulette wheel strategy was utilized for the population strings, where each chromosome had a number relative to its own fitness value [26, 35].

5. Crossover and Mutation

The genetic operators, crossover and mutation, were used for the creation of the new chromosomes. For the crossover, the cluster centers were investigated in order to be divided, which means that the crossover points are only performed through two cluster centers to select the best. The mutation role was to restore the missing or the unexplored genetic material into the population to prevent the early convergence of GA to a suboptimal ending [26]. The mutation is of three types; the first type includes the probability of a replaced valid location in the chromosome, the second includes the valid positions that were randomly generated and now removed and replaced by '#', while third type includes the invalid position which was randomly chosen and now changed with a random point of the data set. One of the three types of mutations was applied on selected chromosomes [35].

Jaccard distance

Jaccard index measures the resemblance, dissimilarity, and distance between two data sets. It is defined as the intersection divided by the summation of the sets of data [36].

$$I(A, B) = |A \cap B| / |A \cup B| = |A \cap B| / (|A| + |B| - |A \cap B|) \quad , \quad 0 \leq I(A, B) \leq 1$$

where A & B are two sets of data. Jaccard similarity coefficient is expressed as [25]:

$$I(x, y) = \sum \text{imin}(x_i, y_i) / \sum \text{imax}(x_i, y_i) \dots\dots\dots (13)$$

where, $x(x_1, x_2, \dots, x_n)$ and $y(y_1, y_2, \dots)$ are two vectors and $y_i \geq 0$.

Jaccard distance is the variation between the expected and observed images. It is complementary to the coefficient of Jaccard and is obtained by subtracting the coefficient from one, as follows [25]:

$$dI(x, y) = 1 - I(x, y) \dots\dots\dots (14)$$

Jaccard coefficient is the parameter used to detect the similarity between the segmented image and the original image. Jaccard index will always give a value between 0 (no similarity) and 1 (identical sets); if x and y are empty then its range is $0 \leq I(x, y) \leq 1$ and $I(X, Y) = 1$. The values of Jaccard distance lie between 0 and 1, where the best value is 1 and the worst is 0 [25].

Results and Discussion

1. In the first stage of the study, the anisotropic diffusion filter (ADF) technique was directly applied to smoothen the image regions and retain the edges. The results of applying ADF on four images are shown in fig.3. The anisotropic diffusion tools were applied with success as a sufficient preprocessing step to remove noise and significantly improve the visual quality of the image, while preserving the boundaries of objects without enhancement.

2. To evaluate the quality of ADF, the differences between the original image and the filtered image can be determined by several parameters such as variance and signal-to-noise ratio (SNR). Table-1 shows that the SNR value of the filtered images was increased while the value of variance of the filtered images was decreased. A good filter is that which reduces the variance while increasing SNR [19].

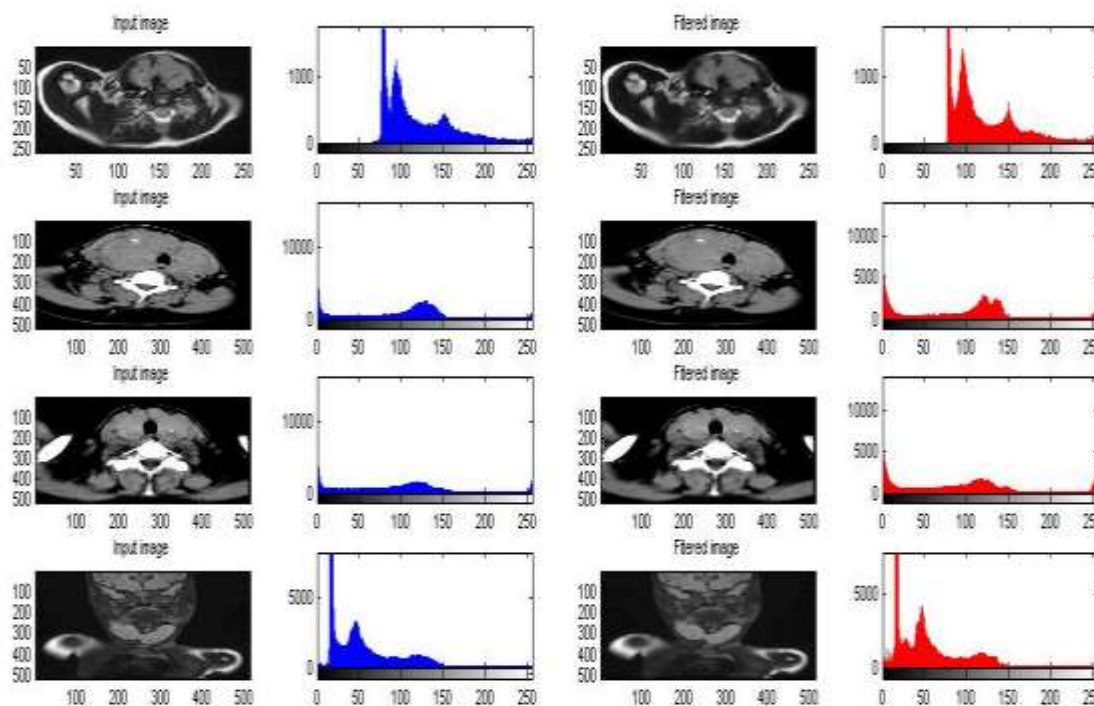


Figure 3-Implementing ADF on four images. The 1st and 2nd columns show the original images and their histograms, whereas the 3rd and 4th columns show the filtered images and their histograms, respectively.

Table 1-Variance and SNR of the original and filtered images.

Image no.	Original Image		Filtered image	
	SNR	Variance	SNR	Variance
1	8.9135	1613.1	9.2587	1489.5
2	-1.1235	4503.3	-1.0388	4415.1
3	-1.5515	5618.4	-1.4846	5529.2
4	1.1977	1725.7	1.3398	1661.1

3. The segmentation algorithms GA, KM, FCM, GAK-Meam, and GAFCM were applied independently on the filtered and non-filtered (original) images to extract the tumor and determine the effect of the filter on the segmentation by computing the tumor size and comparing the Jaccard distance between the original and the segmented images. Morphological operation was employed to extract the tumor from the segmented image. The results of applying the algorithms on one sample of images are shown in Figures-(4 and 5). The segmentation ability of all algorithms is measured by computing and comparing tumor size and jaccard distance values (Table-2).

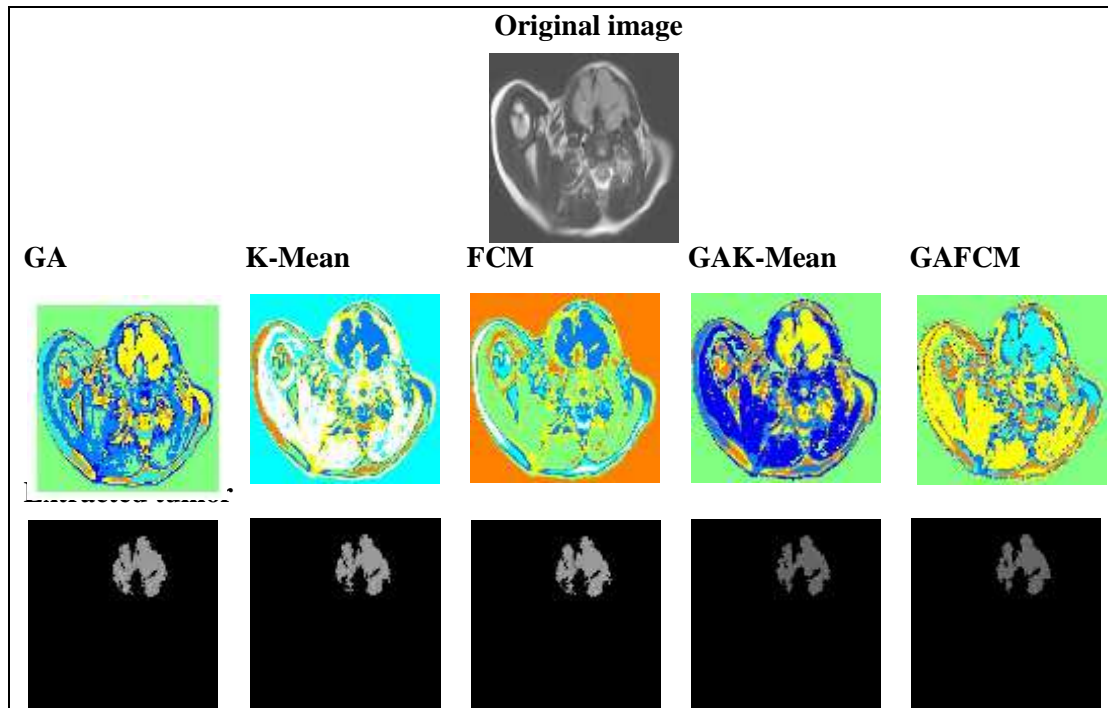


Figure 4-The five segmentation algorithms applied to the original CT image of the thyroid cancer to extract the tumor.

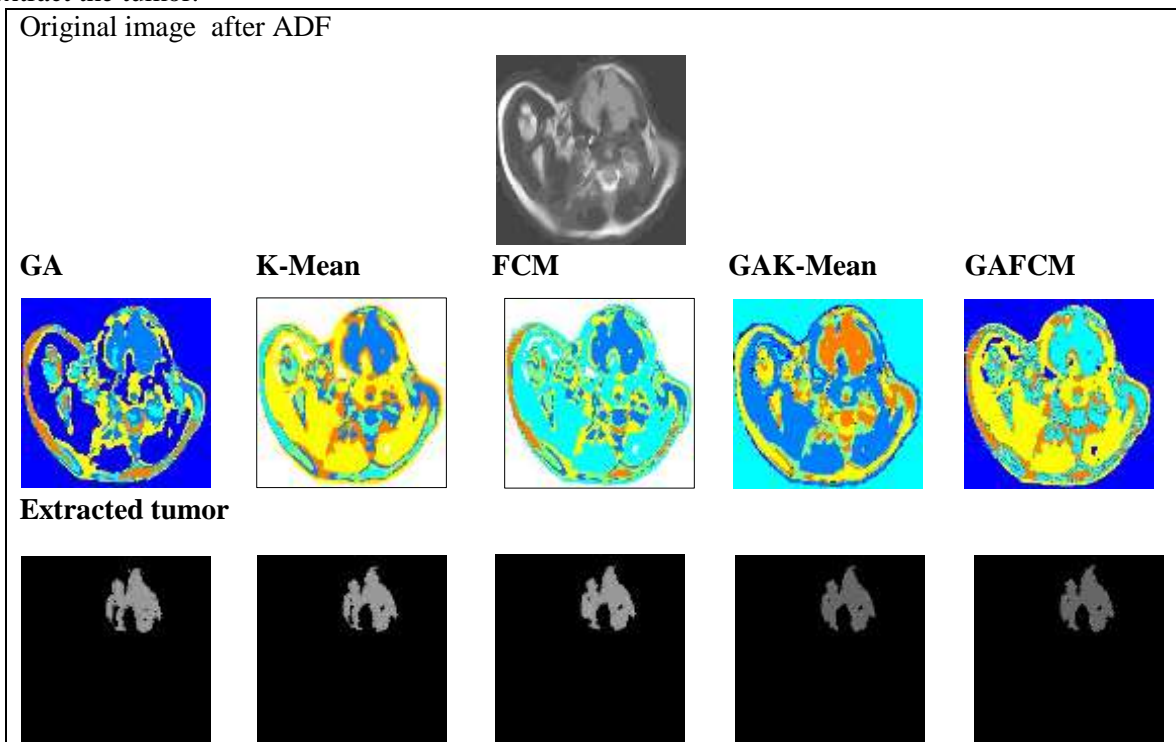


Figure 5-The five segmentation algorithms applied to the CT image of the thyroid cancer, filtered with ADF to extract the tumor.

Table-2 shows the results of calculating tumor size and Jaccard distance. It is obvious from the results that both FCM and GAFCM methods showed an overall percent similarity of 88% for the filtered image as compared to 84% for the original image. While, K-mean and GAK-mean methods showed a percent similarity of 87% (in both methods) for the filtered image as compared to 85% and 84%, respectively, for the original image. This indicates that the proposed FCM and GAFCM methods have better segmentation. In addition, the comparison of tumor size clearly demonstrates the effect of ADF on the image, where tumor size for the filtered image was increased in all methods.

Table-2 Tumor size and Jaccard distance for all segmentation algorithms of filtered and non filtered images

image	Segmentation Method	Tumor Area (Pixel)	Jaccard Index	Percent Similarity
Non Filter image	GA	3289	0.8631	86%
	K-Mean	3075	0.8483	85%
	FCM	3105	0.8389	84%
	GAK-Mean	2892	0.8389	84%
	GAFCM	2941	0.8432	84%
Filter image with ADF	GA	3499	0.8811	88%
	K-Mean	3357	0.8657	87%
	FCM	3452	0.8794	88%
	GAK-Mean	3463	0.8735	87%
	GAFCM	3527	0.8775	88%

Conclusions

Unsupervised segmentation is an important clustering technique where two-dimension data of images are grouped into clusters, so that the pixels of similar features are in the same cluster. K-mean and FCM algorithms were effective and easy techniques, but they may give suboptimal results, depending on the initial selection of the cluster center. While, GA-based clustering is an optimization technique that depends on the evolution and genetics laws and, hence, it is expected to bring out a result of optimal clustering which is better than that obtained by K-Mean and FCM methods. However, this method might take a longer time. Jaccard Index was applied in this study to assess the performance of these methods. It is obvious from the results that ADF increased the segmentation accuracy, where Jaccard index increased with the enhancement of the image, reaching to the value of 1 which indicates that the original image matched the segmented image.

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