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A naive Fuzzy Clustering Method for Pixel Segmentation by using Differential Evolution

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Abstract—Breast Cancer is one of the major causes of cancer deaths in women. An evolutionary-fuzzy clustering algorithm for automatically grouping the pixels of an image into different homogeneous regions. The fuzzy clustering task in the intensity space of an image is formulated as an optimization problem. An improved variant of the differential evolution (DE) algorithm has been used to determine the number of naturally occurring clusters in the image as well as to refine the cluster centers. We report extensive performance comparison among the new method, a recently developed genetic- fuzzy clustering technique and the classical fuzzy c-means algorithm over a test suite comprising ordinary grayscale images and remote sensing satellite images. Such comparisons reveal, in a statistically meaningful way, the superiority of the proposed technique in terms of speed, accuracy and robustness and also determining tissues from breast cancer images by comparing the results of the algorithm with the radiologist's manual markings.

Keywords- Fuzzy clustering, Differential evolution, Image segmentation, Genetic algorithms.

1. Introduction

Image Segmentation of medical images is a pre processing step in radiotherapy planning. Computed tomography (CT) and Magnetic resonance imaging (MRI) are the two widely used radiographic techniques, produce sequences of images representing 2D sections of a 3D anatomical structure of interest[1]. Such medical imaging techniques are useful in diagnosis, clinical studies and treatment planning. Structures of interest in medical images can be found by segmentation of medical images. Clustering is an unsupervised classification technique that aims at grouping of homogeneous elements into meaningful k clusters where the value of k is a priory in most of the clustering algorithms for example k-means, fuzzy k-means, etc.,[2].

Image segmentation may be defined as the process of dividing an image into disjoint homogeneous regions. These homogeneous regions usually contain similar objects of interest or part of them. The extent of homogeneity of the segmented regions can be measured using some image property (e.g., pixel intensity [1]). Segmentation forms a fundamental step towards several complex computer vision and image analysis applications including digital mammography, remote sensing and land cover study. Segmentation of non-trivial images is one of the most difficult tasks in image processing. Segmentation accuracy determines the eventual success or failures of computerized image analysis procedures.

Clustering can be defined as the optimal partitioning of a given set of n data points into c subgroups, such that data points belonging to the same group are as similar to each other as possible whereas data points from two different groups share the maximum difference. Image segmentation can be treated as a clustering problem where the features describing each pixel correspond to a pattern, and each image region (i.e., segment) corresponds to a cluster [1]. Therefore, many clustering algorithms have widely been used to solve the segmentation problem (e.g., k- means [2], FCM [3], ISODATA [4] and Snob [5]).

Clustering algorithms can be hierarchical or partitional [1]. Within each of the types, there exists a wealth of subtypes and different algorithms for finding the clusters. In hierarchical clustering, the output is a tree showing a sequence of clustering with each cluster being a partition of the dataset [7]. Hierarchical algorithms can be agglomerative (bottom-up) or divisive (top-down). Agglomerative algorithms begin with each element as a separate cluster and merge them in successively larger clusters. Divisive algorithms begin with the whole set and proceed to divide it into successively smaller clusters. Hierarchical algorithms have two basic advantages [6]. Firstly, the number of classes need not be specified a priori and secondly, they are independent of the initial conditions. However, the main drawback of hierarchical clustering techniques is they are static, i.e., data points assigned to a cluster cannot move to another cluster. In addition to that, they may fail to separate overlapping clusters due to lack of information about the global shape or size of the clusters.

Clustering can also be performed in two different modes: crisp (or hard) and fuzzy (or soft). In crisp clustering, the clusters are disjoint and non-overlapping in nature. Any pattern may belong to one and only one class in this case. In case of fuzzy clustering, a pattern may belong to all the classes with a certain fuzzy membership grade [1]. Popular crisp clustering approaches do not consider overlapping of classes that occur in many practical image segmentation problems. For example, in remote sensing satellite images, a pixel corresponds to an area of the land space, which may not necessarily belong to a single type of land cover. This in turn indicates that the pixels in a satellite image can be associated with a large amount of imprecision and uncertainty. Therefore, application of the principles of fuzzy set theory appears to be natural and appropriate in such domains.

Finding an optimal number of clusters in a large dataset has always remained a challenging task. Several researchers have investigated the problem but the outcome is still un satisfactory [10]. Works on automatic clustering with evolutionary strategies (ES) [9], evolutionary programming (EP) [13] and genetic algorithm (GA) [8] have been reported in Refs. [11].

Recently, researchers working in this area have started taking some interest on two promising approaches to numerical optimization, namely the particle swarm optimization (PSO) [5] and the differential evolution (DE) [8].

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The proposed an image segmentation algorithm based on the PSO. The algorithm finds the centroids of a user-specified number of used a crisp criterion function for evaluating the partitions on the image data. Only in 2005, the same authors came up with another automatic hard clustering scheme. The algorithm starts by partitioning the dataset into a relatively large number of clusters to reduce the effect of the initialization. Using binary PSO, an optimal number of clusters is selected. Finally, the centroids of the chosen clusters are refined through the k-means algorithm. The authors applied the algorithm for segmentation of natural, synthetic and multi-spectral images. Omran et al. also devised a non-automatic crisp clustering scheme based on DE and illustrated the application of the algorithm to image segmentation problems.

2. The fuzzy clustering problem

The pattern is a physical or abstract structure of objects. It is distinguished from others by a collective set of attributes called features, which together represent a pattern [4].

Let $P = \{P1, P2, \dots, Pn\}$ be a set of n patterns or data points, each having d features.

These patterns can also be represented by a profile data matrix

Xn _ d having n d-dimensional row vectors. The ith row vector xi characterises the ith object from the set P and each element xi, j in Xi corresponds to the jth real value feature

(j = 1, 2, ..., d) of the ith pattern (i = 1, 2, ..., n).

Given such an Xn-d, a partitional clustering algorithm tries to find a partition $C = \{C1, C2, ..., Cc\}$ such that the similarity of the patterns in the same cluster Ci is maximum and patterns from different clusters differ as far as possible. The partitions should maintain the following properties:

(1) Each cluster should have at least one pattern assigned i.e.,

Ci not equal to empty set and belongs to $\{1, 2, \ldots, c\}$.

(2) Two different clusters should have no pattern in common i.e.,

Ci intersection Cj = Empty, for all I not equal to j and i, j belongs to $\{1, 2, ..., c\}$.

(3) ESach pattern should definitely be attached to a cluster i.e., Ci = P.

2.1. The fuzzy c-means algorithm

In the classical fuzzy c-means algorithm, a within cluster sum function Jm is minimized to evolve the proper cluster centers:

$$J_m = \sum_{j=1}^n \sum_{i=1}^c (u_{ij})^m \|\vec{X}_j - \vec{V}_i\|^2$$

where Vi is the ith cluster center, X j is the jth d-dimensional data

vector and $\|.\|$ is an inner product-induced norm in d dimensions. Given c classes, we can determine their cluster centers Vi for i = 1 toc by means of the following expression:

$$\vec{V}_{i} = \frac{\sum_{j=1}^{n} (u_{ij})^{m} \vec{X}_{j}}{\sum_{j=1}^{n} (u_{ij})^{m}}$$

Here m (m > 1) is any real number that influences the membership grade. Now differentiating the performance criterion with respect to Vi (treating uij as constant) and with respect to uij (treating Vi as constant) and setting them to zero the following relation can be obtained:

$$u_{ij} = \frac{\|\vec{X}_j - \vec{V}_i\|^{2/1-m}}{\sum_{k=1}^{c} \|\vec{X}_j - \vec{V}_k\|^{2/1-m}}$$

2.2. Cluster validity indices in the fuzzy environment

The quality of a partition provided by some clustering algorithm, it is necessary to have a well-defined statistical– mathematical function, called a cluster validity index, evaluated on the final clustering solutions. In what follows we describe the three well-known validity indices used in the experimental results reported in this paper.

2.2.1. Beni index

This index, due to Beni is given by:

$$XB_m = \frac{\sum_{i=1}^{c} \sum_{j=1}^{n} u_{ij}^2 \|\vec{X}_j - \vec{V}_i\|^2}{n \times \min_{i \neq j} \|\vec{V}_i - \vec{V}_j\|^2}$$

The optimal number of clusters can be obtained by minimizing the index value.

2.2.2. The PS measure

The PS measure rests upon the concept of a point symmetry distance, which was shown to be very effective for clustering by Chou and co-workers [6]. The point symmetry distance is defined as follows. Given N patterns described by feature vectors Xk, where $k = \{1, 2, ..., n\}$ and a reference vector V (e.g., a cluster center), the "point symmetry distance" between a pattern X j and

the reference vector V is defined as

$$d_{s}(\vec{X}_{j}, \vec{V}) = \min_{\substack{k = 1, 2, ..., n \\ \text{and } k \neq j}} \left\{ \frac{\|(\vec{X}_{j} - \vec{V}) + (\vec{X}_{k} - \vec{V})\|}{(\|\vec{X}_{j} - \vec{V}\| + \|\vec{X}_{k} - \vec{V}\|)} \right\}$$

A clustering validity index based on the point symmetry measure as

$$PS(c) = \frac{1}{c} \sum_{i=1}^{c} \left[\frac{1}{n_i} \sum_{j \in C_i} \frac{d_s(\vec{X}_j, \vec{V}_i) \times d_e(\vec{X}_j, \vec{V}_i)}{\min_{\substack{m, n = 1, 2, ..., c \\ and m \neq n}} \left\{ d_e(\vec{V}_m, \vec{V}_n) \right\} \right]$$

where de is the Euclidean distance between two points in the d dimensional feature space, Ni is the number of data points belonging to cluster Ci. The cluster centers Vi 0s are calculated as per above equation and while computing the point symmetry distance ds also We will calculate. We keep in mind that the vectors X j and Xk belong to the same class Ci. Finally, the smallest PS(c) indicates a valid optimal partition with the optimal cluster number c.

3. DE-based automatic fuzzy clustering

3.1. The DE algorithm and its modification

The DE is a population-based global optimization algorithm that uses a floating-point (real-coded) representation. The ith

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individual (parameter vector or image) of the population at generation (time-step) t is a D-dimensional vector containing a set of D optimization parameters:

$$\overline{Z}_{i}(t) = [Z_{i,1}(t), Z_{i,2}(t), \dots, Z_{i,D}(t)]$$

Now in each generation (or one iteration of the algorithm) to change the population members Zi(t), a donor vector Yi(t) is created. It is the method of creating this donor vector which demarcates between the various DE schemes. In one of the earliest variants of DE, now called DE/rand/1 scheme, to create Yi(t) for each ith member, three other parameter vectors

(say the r1, r2, and r3th vectors (say the r1, r2, and r3th vectors such that r1, r2, r3 2 [1,NP] and r1not equal to r2 not equal to r3) are chosen at random from the current population. Next the difference of any two of the three vectors is multiplied by a scalar number F and the scaled difference is added to the third one, whence we obtain the donor vector Yi(t). The process for the jth component of the ith vector may be expressed as

Next a crossover operation takes place to increase the potential diversity of the population. The DE family uses two kinds of crossover schemes, namely 'exponential' and 'binomial' [10]. To save space, we here briefly describe the binomial crossover, which is also employed by the modified DE algorithm. The binomial crossover is performed on each of the D variables whenever a randomly picked number between 0 and 1 is within the Cr value. In this case the number of parameters inherited from the mutant has a (nearly) binomial distribution. Thus for each target vector Zi(t), a trial vector Ri(t) is created in the following fashion:

$$\begin{array}{ll} R_{i,j}(t) = & Y_{i,j}(t) & \text{if } \operatorname{rand}_j(0,1) \leq \operatorname{Cr} \operatorname{or} j = m(i) \\ & Z_{i,j}(t) & \text{if } \operatorname{rand}_j(0,1) > \operatorname{Cr} \operatorname{or} j \neq m(i) \end{array}$$

To keep the population size constant over subsequent generations, the next step of the algorithm calls for 'selection' in order to determine which one between the target vector and trial vector will survive in the next generation i.e., at time t = t + 1. If the trial vector yields a better value of the fitness function, it replaces its target vector in the next generation;

otherwise the parent is retained in the population

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$$Z_i(t+1) = \overline{R}_i(t) \quad \text{if} \quad f(\overline{R}_i(t)) \ge f(\overline{Z}_i(t)) \\ = \overline{Z}_i(t) \quad \text{if} \quad f(\overline{R}_i(t)) < f(\overline{Z}_i(t))$$

where f(.) is the function to be maximized. To improve the convergence properties of DE we have tuned its parameters in two different ways here. In classical DE the difference vector (Xi(t)- X j(t)) is scaled by a constant factor 'F'.

Table 1	
Algorithm	parameters

4

FVGA		AFDE		
Parameter	Value	Parameter	Value	
Pop_size	20	Pop_size	10*dim	
Crossover probability, Pc	0.6	Rmax	1.5	
Mutation probability, Pm	0.05	R _{min}	0.5	
K _{ma x}	10	Kmax	10	
K _{min}	2	Kmin	2	

* signifies the multiplication (into) symbol, i.e. the Pop_size is 10 times dimension.

The usual choice for this control parameter is a number between 0.4 and 1. We propose to vary this scale factor in a random manner in the range (0.5, 1) by using the relation

F = 0.5(1+rand(0,1))

But at the later stages of the optimizing process, if Cr be decreased, more components of the parent vector are then

inherited by the offspring. Such a tuning of Cr helps to explore the search space exhaustively at the beginning, but adjust the movements of trial solutions finely during the later stages of search, so that they can explore the interior of a relatively small space in which the suspected global optimum lies. The time-variation of Cr may be expressed in the form of the following equation,

$$Cr = Cr_{max} - (Cr_{max} - Cr_{min}) \times \frac{iter}{MAXITER}$$

where Crmax and Crmin are the maximum and minimum values of crossover rate Cr, iter is the current iteration number and MAXIT is the maximum number of allowable iterations.

3.2. Cluster representation

In the proposed method, for n data points, each d-dimensional, and for a user-specified maximum number of clusters Cmax, a image is a vector of real numbers of dimension Cmax + Cmax _ d. The first Cmax entries are positive floating-point numbers in (0, 1), each of which controls whether the corresponding cluster is to be activated (i.e., to be really used for classifying the data) or not. The remaining entries are reserved for Cmax cluster centers, each d-dimensional. \vec{x} (A)





Activation ThreshholdCluster CentroidsThe cluster center is active (i.e., selected for classification) ifflagi,j = 1 and inactive if flagi,j = 0. Each flag is set or resetaccording to the value of the activation threshold Ti,j. Notethat these flags are latent information associated with thecluster centers and do not take part in the DE-type mutation ofthe breast images.



Fig.1. (a) The original MRI image(Breast Image). (b) Segmentation by FVGA (c = 5). (c) Segmentation by AFDE (c = 5). (d) Segmentation with FCM (provided with c = 5).

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3.3. The pseudo-code of the proposed algorithm

The sample pseudo-code for the complete algorithm for dynamic clustering is given below:

Step 1: Assign each image to contain c randomly

selected cluster centers and c (randomly chosen) activation thresholds between 0 and 1.

Step 2: Find out the active cluster centers in each image by evaluating the activation thresholds and set or reset the corresponding flag.

Step 3: For t = 1 to tmax do

(i) For each data vector Xp, calculate its Euclidean distance

D(Xp,Vi, j) from all active cluster centers Vi; j of a parameter vector Zi (i = 1, 2, ..., NP).

(ii) Assign Xp to cluster center Vi, j such that

 $D(Xp,Vi, j) = min \text{ for all } b \text{ belongs to } \{1, 2, ..., c\} \{d(Xp, Vi, b)\}$ (iii) Check if the number of data points belonging to any cluster center is less than two. Then, update the cluster centers of the

DE vector using the concept of average. (iv) Now perform mutation on each population member Zi(t) of DE using to form the corresponding donor vectors Yi(t). Then exchange body parts of the donor with the target vector Zi(t) according to [1] to form the trial vectors Ri(t).

(v) Locate the active cluster centers of the trial vectors thus formed, by applying rule and set or reset the associated flags correspondingly.

(vi) Repeat steps (i), (ii) and (iii) for each trial vector.

(vii) Evaluate fitness of both the target and trial vectors. Use only the active cluster centers in both the vectors (that is the ones with the flag set to 1). Replace the target vector Zi(t) with the trial vector Ri(t) only if the latter yields a higher value of the fitness function.

Step 4: Report as the final solution the cluster centers and the partition obtained by the best image (the one yielding the lowest value of the objective function) at time t = tmax

4. Experimental setup and results

4.1. The FVGA algorithm

We compared AFDE with the FVGA (fuzzy variable string genetic algorithm) based clustering technique [8] in the

present work. The FVGA-clustering algorithm tries to determine appropriate number of clusters present in a dataset and the corresponding best partition. Here the images (or strings) encode the cluster centers as a sequence of real numbers. For example, if the number of clusters is three, then the string will contain these three cluster centers in any arbitrary order. Each string can have a certain maximum length, which is equal to the maximum possible number of clusters Cmax that may be present in the data. Out of this total maximum number of positions in the string, only some are used to store the cluster centers. The other positions remain do not care (represented by '#' symbol). The value of c is assumed to lie in the range [Cmin, Cmax], where Cmin is chosen to be 2, unless specified otherwise. Note that the choice of Cmax should not exceed the number of data patterns present in the dataset.

The fuzzy set describes total number of clusters and compare which cluster images are related to another clusters. Each evolution shows which type of damage will be placed at particular pixels.

Special Issue of ICACSSE 2014 - Held on October 10, 2014 in St.Ann's College of Engineering & Technology, Chirala, Andhra Pradesh 4.2. The simulation strategy

We have selected a test suite of six grayscale images among which 'clouds', 'MRI image of brain', 'the pepper image' and 'robot' come in 256 pixels _ 256 pixels, while 'the IRS (Indian remote sensing satellite) image of Mumbai (a mega city of India)' and 'the Science Magazine' image are of size 512 512. The IRS image of Mumbai was obtained using the LISS-II sensor. It is available in five bands, viz. blue, green, red and near infrared.. All the images have been clustered in their intensity space using only pixel intensities as features. The parameter setup is given in Table 1.

4.3. Results

Fig. 1 show the four original images and their segmented

Counter parts obtained using AFDE, FVGA and the classical FCM. The FCM algorithm cannot handle an unknown number of clusters and has, therefore, in each case been fed with the number of classes yielded by the better between the AFDE and the FVGA. The segmented portions of an image have been marked with the grey level intensity of the respective cluster centers. Table contains the mean and standard deviations of the number of classes obtained by the two automatic clustering algorithms. In three of the four cases, AFDE yields a better segmentation that FVGA does.

4.4. Discussions on the results

In this study, the proposed AFDE has been compared with one state-of-the-art GA based automatic clustering algorithm and the classical FCM algorithm. To make the performance evaluation/comparison meaningful and effective, we have used variety of test images containing real life images, medical images as well as remote sensing satellite images. Regardless of the shape of the original population [2]. From Table 1 we see that for all the test cases, the mean clustering accuracy of FNDE is significantly better than that of the second best competitor i.e., the FVGA as judged by the Beni index. In three out of these four cases (MRI breast image and the pepper image) the difference of the means is extremely significant. However, the PBMF and PS indices calculated over the final clustering results. This is perhaps due to the fact that different validity indices judge the cohesiveness and separation between the clusters in different fashions (over the same dataset).

For example, one place is linked with another place by using different connectors.. In addition, the predominance of one category of pixels in the southern part of the image conforms to the ground truth; this part is known to be heavily industrialized, and hence the majority of the pixels in this region should belong to the same class of concrete. The Arabian Sea has come out as a combination of pixels of two different classes. The seawater is found to be decomposed into two classes, turbid water 1 and turbid water 2, based on the difference of their reflectance properties. It can be further observed that the AFDE consumes lesser computational time on average than the FVGA for six images and the one possible reason of this may be the use of less complicated variation operators (like differential mutation) in DE as compared to the operators used for GA.

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Original Image	Output Images of FVGE in different independent runs		FVGE		
Q	10/15	14/30	11/20	13/20	14/20
	6/10	7/10	18/30.	11/20	11/30
	12/20	17/30	15/40	12/30	
	12/20	16/30	19/30	10/30	
	10/20	19/40	25/50	5/15	

Fig.2. Segmentation by FVGE

5. Conclusion

This paper has presented a naïve differential evolution-based strategy for fuzzy clustering of images and presented a differential evolution-based algorithm for fuzzy clustering of breast cancer images An important feature of the proposed algorithms that it is able to find the optimal number of clusters automatically (that is, the number of clusters does not have to known in advance). Experimental results show that our approach outperforms the state-of-the-art FVGA strategy and the classic FCM over a variety of image datasets. Future research may focus on employing other improved cluster validity indices to form the fitness function and a multi-objective DE. Besides the pixel intensity alone, it may be interesting to take into account other features related to texture, shape and color for the segmentation task by AFDE.

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