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Automatic Tissue Segmentation in Medical Images using Differential Evolution

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Abstract: Segmentation of medical images is a challenging task and preprocessing step in medical diagnosis. Evolutionary algorithms such as Genetic Algorithms (GA) have been found to be effective in medical image segmentation. Almost all GAs are semiautomatic, requires either some parameters or domain knowledge such as number of segments, shape, texture etc. Differential Evolution (DE) is a simple and robust evolutionary algorithm and Automatic Clustering using Differential Evolution (ACDE) is a variant of DE. There is no study in medical image segmentation using ACDE. This study is made an attempt to extract the shape of the tissues in medical images automatically using ACDE. The performance of the ACDE algorithm in determining shape of breast cancer, lung tissues has been studied using different ultrasound images. The experimental results are compared with the regions identified by the radiologist and have demonstrated that the ACDE can extract shape of the tissues automatically (without domain knowledge) and helpful in operation surgery and radiology to cure diseases like breast cancer.

Key word: Segmentation, genetic algorithms, differential evolution, automatic clustering, ultra sound image

INTRODUCTION

Clustering is a process of grouping similar elements used for image segmentation. Medical Image segmentation is a challenging task and a preprocessing step in medical diagnosis, planning of surgical operations and in radiation treatments. Breast Cancer is one of the major causes of cancer deaths in women (Sheshadri and Kandaswamy, 2006). Breast Cancer and Lung cancer can be determined from ultrasound and x-rays. Segmentation of such images is helpful for the early detection of cancer and effective treatment.

Many segmentation methods are proposed for medical-image data are either direct applications or extensions of approaches from computer vision. Image-segmentation algorithms can be classified in many ways (Haralick and Shapiro, 1985; Sarkar and Boyer, 1993; Zucker, 1976; Zhang *et al.*, 2008) have presented a number of image classification methods. Three broad classes of segmented algorithms are manual, semiautomatic and automatic. Reviews of algorithms from each class can be found in the studies of Clarke *et al.* (1995) and Suetens *et al.* (1993). In order to overcome the limitations of the traditional clustering algorithms many

heuristic optimization algorithms such as Genetic algorithms (Kharrousheh *et al.*, 2011), Particle Swarm Optimization (PSO) (Saadi *et al.*, 2010), Differential Evolution algorithms are proposed. Tlelo-Cuautle *et al.* (2010) have studied the significance of evolutionary algorithms in parameter optimization. Genetic Algorithms are found to be effective in image segmentation (Maulik, 2009; Mahi and Izabatene, 2011). Almost all GAs are semiautomatic and requires either some parameters in advance or domain knowledge such as number of segments, shape, texture etc. Differential Evolution is a recent simple evolutionary algorithm for optimization (Adeyemo and Otieno, 2009). DE shares many features of the Genetic Algorithms. DE has won the third place in the International contest on Evolutionary Computation (Peng and Wang, 2010). DE is a very fast and robust algorithm and performs well on synthetic, natural and multi-spectral satellite images when compared with the other evolutionary population-based algorithms like Genetic Algorithm (GA) and PSO etc. (Das *et al.*, 2009; Liu and Li, 2011). Automatic Clustering using Differential Evolution (ACDE), is a variant of DE. ACDE is a DE/rand/1/Either-or algorithm and determines the nearly optimal clusters automatically (Das *et al.*, 2008). There is

no research found in medical image segmentation using ACDE. This study is made an attempt to extract the shape of the tissues in medical images automatically using ACDE. The performance of the ACDE in extracting shapes of tissues has been studied using 5 breast cancer images and two lung images. The experimental results have shown that ACDE can determine the appropriate shapes by pixel intensity.

DIFFERENTIAL EVOLUTION SCHEME

Differential Evolution (DE) is the stochastic, population-based optimization algorithm (Price *et al.*, 2005). It was developed to optimize real (float) parameters of a real valued function. DE Algorithms can be used in search of the global optimum, when objective function is non-differentiable, non-continuous, non-linear, noisy, flat, multi-dimensional, with many local minima. DE also can be used when a problem is difficult or impossible to solve analytically and the parameters are real (float) variables.

The difference between GA and DE is, GA relies on uniform crossover and DE uses a non uniform crossover (Otieno and Adeyemo, 2010). The parameter vector \bar{x} is called an individual (or chromosome, or genome). The objective function is also called the fitness function. Figure 1 presents that the general scheme is the same for all EAs:

- Initialization - creation of a population of individuals
- Mutation (and migration in multi-population versions)-random change of the vector \bar{x} components (genes). It can be a single-point mutation, inversion, translocation, deletion, etc
- Recombination (crossover)-merging the genetic information of two or more parent individuals for producing one or more descendants
- Selection-choice of the best individuals for the next cycle
- One cycle in the above scheme is called a generation. The solution is found if some stopping criterion is met

Procedure

Input: Randomly initialized position and velocity of the particles: $x_i(0)$.

Output: Position of the approximate global optima.

Begin:

```

Initialize population;
Evaluate fitness of each chromosome;
For i = 0 to max-iteration do
Begin
    Create Difference-Offspring from randomly selected 3 parent
    chromosomes;
    Evaluate fitness;
    If an offspring is better than its parent
    Then replace the parent by offspring in the next generation;
    End If;
End For;

```

End.

New offsprings are created using two main DE operators known as crossover and mutation.

AUTOMATIC CLUSTERING USING DIFFERENTIAL EVOLUTION

The classical DE (Price *et al.*, 2005), is a population-based global optimization algorithm that uses a floating-point real-coded) representation.

Generation of F and Cr: The *i*th individual vector (chromosome) of the population at time-step generation *t* has *d* components (dimensions), i.e.:

$$\bar{z}_i(t) = [Z_{i,1}(t), Z_{i,2}(t), \dots, Z_{i,d}(t)]$$

For each individual vector $Z_{i,i}(t)$ that belongs to the current population, DE randomly samples three other individuals, i.e., $Z_i(t)$, $Z_j(t)$ and $Z_m(t)$, from the same generation (for distinct *k*, *i*, *j* and *m*). It then calculates the (component wise) difference of $Z_i(t)$ and $Z_j(t)$, scales it by a scalar *F* (usually [0, 1]) and creates a trial offspring $U_i(t+1)$ by adding the result to $Z_m(t)$. Thus, for the *n*th component of each vector:

$$U_{k,n}(t+1) = \begin{cases} Z_{m,n} + F(Z_{i,n}(t) - Z_{j,n}(t)), & \text{if } \text{rand}_n(0, 1) < Cr \\ Z_{k,n}(t), & \text{otherwise} \end{cases}$$

Cr [0, 1] is a scalar parameter of the algorithm, called the crossover rate. If the new offspring yields a better value of the objective function, it replaces its parent in the

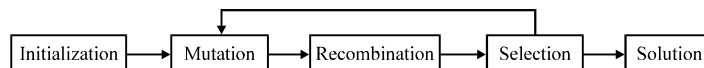


Fig. 1: General evolutionary algorithm scheme

next generation; otherwise, the parent is retained in the population, i.e.:

$$\bar{Z}_i(t+1) = \begin{cases} \bar{U}_i(t+1), & \text{if } f(\bar{U}_i(t+1)) > f(\bar{Z}_i(t)) \\ \bar{Z}_i(t), & \text{if } \bar{U}_i(t+1) \leq (\bar{Z}_i(t)) \end{cases}$$

where, $f(\bullet)$ is the objective function to be maximized. To improve the convergence properties of DE, we have tuned its parameters in two different ways here. In the original DE, the difference vector $(Z_i(t)-Z_j(t))$ is scaled by a constant factor F . 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:

$$F = 0.5 \times (1 + r \text{ and } (0, 1))$$

where, r and $(0, 1)$ is a uniformly distributed random number within the range $[0, 1]$. The mean value of the scale factor is 0.75.

Pseudo code of the ACDE: The pseudo code for the complete ACDE algorithm is given here.

Step 1: Initialize each chromosome to contain K number of randomly selected cluster centers and K (randomly chosen) activation thresholds in $[0, 1]$.

Step 2: Find out the active cluster centers in each chromosome.

Step 3: For $t = 1$ to t_{\max} do

- For each data vector X_p , calculate its distance metric $d(X_p, m_{i,j})$ from all active cluster centers of the i th chromosome V_i
- Assign X_p to that particular cluster center $m_{i,j}$

Where:

$$d(\bar{X}_p, \bar{m}_{i,j}) = \min \forall b \in \{1, 2, \dots, K\} \{d(\bar{X}_p, \bar{m}_{i,b})\}$$

- Check if the number of data points that belong to any cluster center $m_{i,j}$ is less than 2. If so, update the cluster centers of the chromosome using the concept of average described earlier
- Change the population members according to the DE algorithm outlined in the above equations. Use the

fitness of the chromosomes to guide the evolution of the population

Step 4: Report as the final solution the cluster centers and the partition obtained by the globally best chromosome (one yielding the highest value of the fitness function) at time $t = t_{\max}$.

We have used CS measure as the fitness function. Chou *et al.* (2004) have proposed the CS measure for evaluating the validity of a clustering scheme. The centroid of a cluster is computed by averaging the elements that belong to the same cluster using:

$$\bar{m}_i = \frac{1}{N_i} \sum_{x_j \in C_i} \bar{X}_j$$

$$CS = \frac{\sum_{i=1}^k \left[\frac{1}{N} \sum_{x_i \in C_i} \max \{d(\bar{X}_i, \bar{X}_q)\} \right]}{\sum_{i=1}^k \left[\min_{j \neq i, j \neq 1} \{d(\bar{m}_i, \bar{m}_j)\} \right]}$$

where, $d(\bar{X}_i, \bar{X}_j)$ is the distance between X_i and X_j i.e., the difference of two pixel intensities and $d(\bar{m}_i, \bar{m}_j)$ is the distance between two cluster centroids. CS measure is a function of the ratio of the sum of within-cluster distance to between-cluster distance. The cluster configuration that minimizes CS is taken as the optimal number of clusters, k .

EXPERIMENTAL RESULTS

The performance of ACDE has been studied using ultrasound breast cancer tissue images. The extracted shapes of tissues are compared with shape specified by a radiologist and with the chain optimization (Rahnamayan and Mohamad, 2010). The ultrasound images are taken from (Rahnamayan and Mohamad, 2010). The Fig. 2 shows the sample of original ultrasound images, tissue segmentation (green) as specified by the radiologist and the corresponding tissue segmentation (red) results of Chain optimization (Rahnamayan and Mohamad, 2010).

As the ACDE results different clusters in different independent runs, the Table 1 shows different segmented regions for a given medical image. The experimental results demonstrated that the extracted shape of tissues is insensitive to the number of clusters.

Canny edge detection method is applied to the clustering solutions of ACDE to identify the segments and the segmented regions for sample images are included

Table 1: Original Images and corresponding output images of ACDE


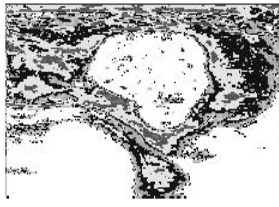
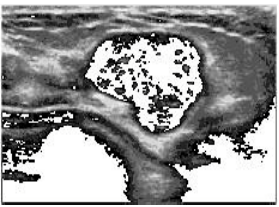
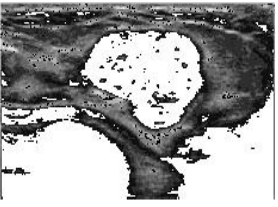
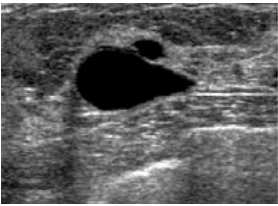
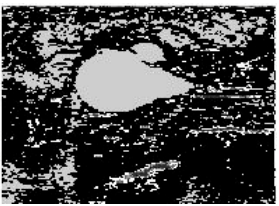
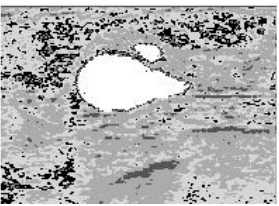
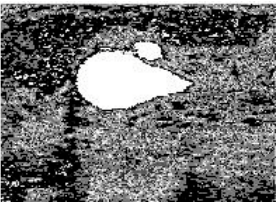

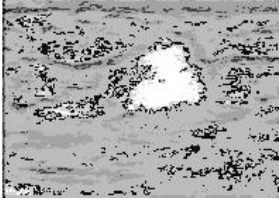
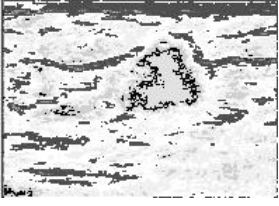
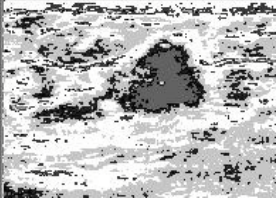

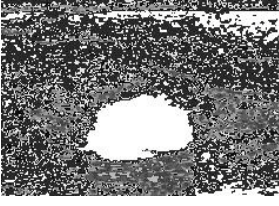
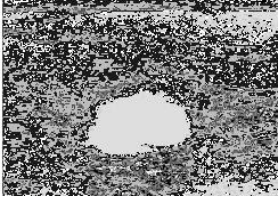




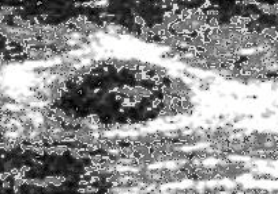

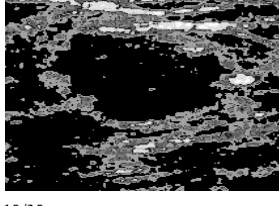
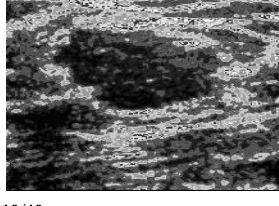
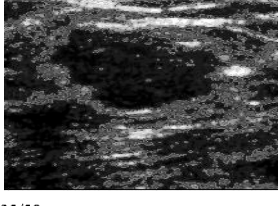
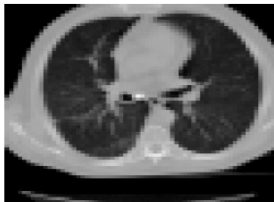
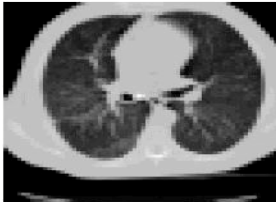

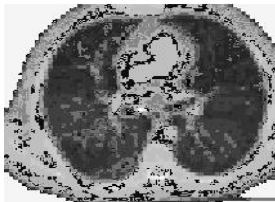
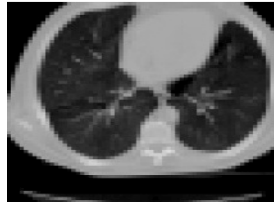

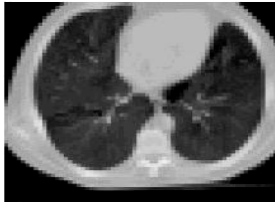
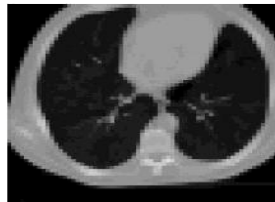
Original image	Output images of ACDE in different independent runs		
			
	10/15	14/30	11/20
			
	6/10	7/10	18/30
			
	12/20	17/30	15/40
			
	12/20	16/30	19/30
			
	17/30	19/35	21/45
			
	10/20	19/40	25/50

Table 1: Continued

Original image	Output images of ACDE in different independent runs		
			
	29/45	23/50	24/50
			
	14/25	30/40	29/45

*Segments determined out of total given segments

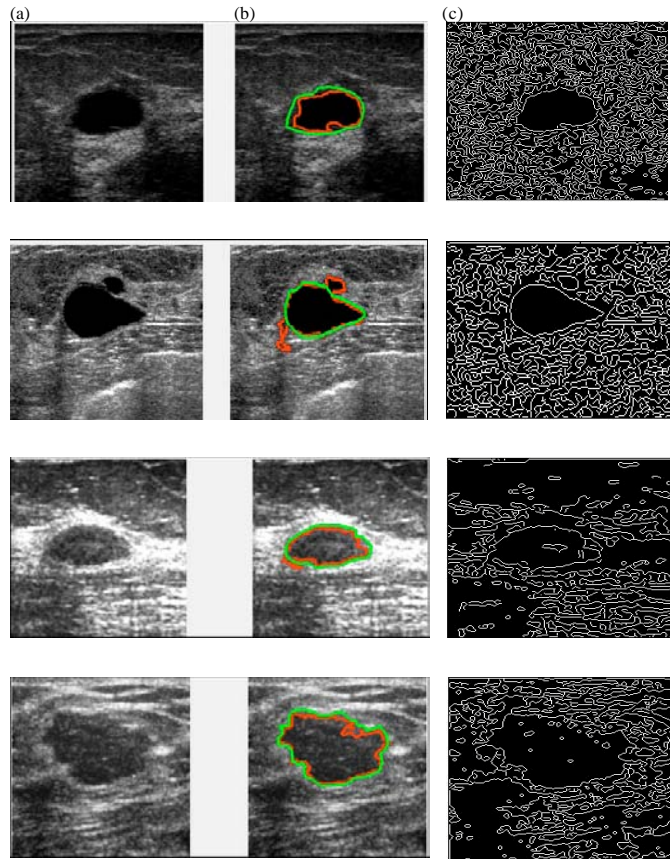


Fig. 2(a-c): (a) Four test ultrasound breast cancer images, (b) The green segmentation has been performed by a radiologist and the red one by the chain optimization (5) and (c) Segmented regions from ACDE

in the Fig. 2. The resultant segments of ACDE are compared with the chain optimization and with the segments identified by radiologists. The results of ACDE demonstrated that the ACDE can determine the shape of the tissues as specified by the radiologist.

CONCLUSION

Almost all existing clustering algorithms for medical image segmentation require domain knowledge and some parameters in advance. ACDE is the automatic clustering using differential evolution on real valued data sets. Here, we have applied the ACDE on medical images and the experimental results have proved that ACDE accurately identifies the shape of the tissues in medical images and is insensitive to the number of clusters. The results are helpful in medical diagnosis, radiology. Determining shapes of tissues from the medical images using multi objective optimization is our future endeavor.

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