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A Real-Valued Quantum Genetic Niching clustering Algorithm and its Application to Color Image Segmentation

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***Abstract*—This paper proposes a novel genetic clustering algorithm, called a real-valued quantum genetic niching clustering algorithm (RQGN), which is based on the concept and principles of quantum computing, such as the qubits and superposition of states. Our algorithm can automatically clustering a data set into clusters without the need to know the number of clusters in advance. A dynamic identification of the niches is performed at each generation to automatically evolve the optimal number of clusters as well as the cluster centers of the data set. After getting the niches of the population, a Q-gate with adaptive selection of the angle for every niches is introduced as a variation operator to drive individuals toward better solutions. The experimental results show that RQGN algorithm has high performance, effectiveness and flexibility.**

Keywords-quantum genetic algorithm; dynamic niching; quantum rotation; image segmentation

I. INTRODUCTION

Image segmentation is a first and key step for image analysis and pattern recognition. It is a process of partitioning an image into different regions that are homogeneous or “similar” in some image characteristics. Many segmentation algorithms have been proposed in the literature [1]. Generally, they may be broadly divided into three categories: edge-based [2], region-based [3], and clustering-based [4]. In computer vision, clustering algorithm has been used extensively to image segmentation due to its clustering validity and simplicity of implementation. It is a pixels clustering process of dividing pixels into clusters so that pixels in the same cluster are as similar as possible and those in different clusters are as dissimilar as possible. However, the implementations of the traditional clustering algorithms often encounter two unavoidable difficulties of deciding the cluster number and obtaining the initial cluster centers. In order to overcome these problems, stochastic clustering algorithms based on simple Genetic Algorithm (GA) have been proposed [5]. All these algorithms are characterized by the representation of the individual, the evaluation function, genetic operators, etc. To have a good performance, all these components should be designed properly. In this paper, the representation and genetic operators are investigated to represent the individual effectively to explore the search space with small number of individuals and to exploit the global solution within a short time, respectively. For these purpose, some concepts of quantum computing are adopted in the proposed algorithm.

Quantum mechanical computers were proposed in the early 1980s [6] and the description of quantum mechanical computers was formalized in the late 1980s' [7]. In this paper, a novel clustering algorithm based on a real-valued quantum genetic niching (RQGN) is presented. Within the RQGN, a dynamic niching is developed to preserve the diversity of the population. A simpler representation with real-coded is adopted, whereby each individual represents a single cluster center. All the niches presented in the population at each generation are automatically and explicitly identified. Then, the application of Q-gate with adaptive selection of the angle is limited to individuals belonging to the same niche.

The rest of this paper is organized as follows. Section II provides the objective function of the clustering problem used in the algorithm. The real-valued genetic quantum niching method is presented in Section III. Experimental results are given in Section IV. Finally, conclusions are drawn in Section V.

II. THE OBJECTIVE FUNCTION

Let $\mathbf{X} = \{\mathbf{x}_1, \mathbf{x}_2, \cdots, \mathbf{x}_n\}$ be a finite subset of a N-dimensional space, K be the number of clusters. Our clustering goal is to find $\mathbf{c}_i$ to maximize the total similarity measure $J_s(\mathbf{c})$ with

$$J_s(\mathbf{c}) = \sum_{i=1}^{K}\sum_{j=1}^{n}\left(\exp\left(-\frac{\left\|\mathbf{x}_j - \mathbf{c}_i\right\|^2}{\beta}\right)\right)^{\gamma} \tag{1}$$

where $\mathbf{c} = (\mathbf{c}_1, \mathbf{c}_2, \cdots, \mathbf{c}_K)$ and β can be defined by

$$\beta = \frac{\sum_{j=1}^{n}\left\|\mathbf{x}_j - \bar{\mathbf{x}}\right\|^2}{n}, \text{ where } \bar{\mathbf{x}} = \frac{\sum_{j=1}^{n}\mathbf{x}_j}{n} \tag{2}$$

According to the analysis of γ in ref. [8], we know that γ can determine the location of peaks in $J_s(\mathbf{c})$. Let $\tilde{J}_s(\mathbf{x}_k)$ be the total similarity of $\mathbf{x}_k$ to all data points with

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$$\tilde{J}_s(\mathbf{x}_k) = \sum_{j=1}^{n} \left(\exp - \frac{\|\mathbf{x}_j - \mathbf{x}_k\|^2}{\beta} \right)^{\gamma}, \quad k = 1, 2, \cdots, n \tag{3}$$

This function can be seen closely related to the density shape of the data points in the neighborhood of $\mathbf{x}_k$. A large value for $\tilde{J}_s(\mathbf{x}_k)$ means that $\mathbf{x}_k$ is close to some cluster centers and has many data points around it. A good estimation of γ can give a good estimation of the peak of $\tilde{J}_s(\mathbf{x}_k)$. The CCA algorithm [8] is used to estimate γ. After getting the estimation of γ, $\tilde{J}_s(\mathbf{x}_k)$ becomes a multimodal function, and the number of peaks is equal to the number of clusters.

III. THE REAL-VALUED QUANTUM GENETIC NICHING CLUSTERING ALGORITHM

In traditional GA, a population of individuals evolves according to the transition operators. At each generation, the individuals are selected and create offspring. At the end of the evolution process, the population consists of a single fittest individual, representing the best solution found. However, there are many cases that the desired solution is not necessarily the best one, but rather a collection of best. In order to deal with this class of problem, niching has been suggested as a viable mean to simultaneously evolve subpopulations exploiting different niches. In this section, RQGN is proposed and the flowchart is provided in Fig. 1.

A. Chromosome Representation and Initialization

In quantum computation, the smallest unit of information is called a qubit. A qubit may be in the "1" state, in the "0" state, or in any superposition of the two. It can be represented as

$$\left|\Psi\right\rangle = \alpha\left|0\right\rangle + \beta\left|1\right\rangle \tag{4}$$

where $|\alpha|^2 + |\beta|^2 = 1$. In order to make the representation more effective, the following representation is used

$$\left|\Psi\right\rangle = \alpha\left|x^l\right\rangle + \beta\left|x^u\right\rangle \tag{5}$$

Where x^l and x^u are the lower and the upper bound of $\mathbf{x}$, respectively. Obviously, a qubit may be in the x^l state, in the x^u state, or in any superposition of the two. Then the chromosome can be represented by qubit as follow

$$\mathbf{q}^{\mathrm{i}} = \begin{bmatrix} \alpha_{1,1}^i & \alpha_{1,2}^i & \cdots & \alpha_{k,1}^i & \alpha_{k,2}^i \\ \beta_{1,1}^i & \beta_{1,2}^i & \cdots & \beta_{k,1}^i & \beta_{k,2}^i \end{bmatrix} \tag{6}$$

Here k is the dimension of $\mathbf{x}$. For any qubit $\left[\alpha_{i,k}^t, \beta_{i,k}^t\right]^T$, $k = 1,2$, we generate a random number $r_{i,k} \in [0,1]$. If $r_{i,k} < \left|\alpha_{i,k}^t\right|^2$, the qubit will be found in x^l state, otherwise, the qubit will be in x^u state. Therefore, the qubit chromosome collapses into $\left[x^i, x^j\right]$, where $\{i, j\} \in \{l, u\}$.

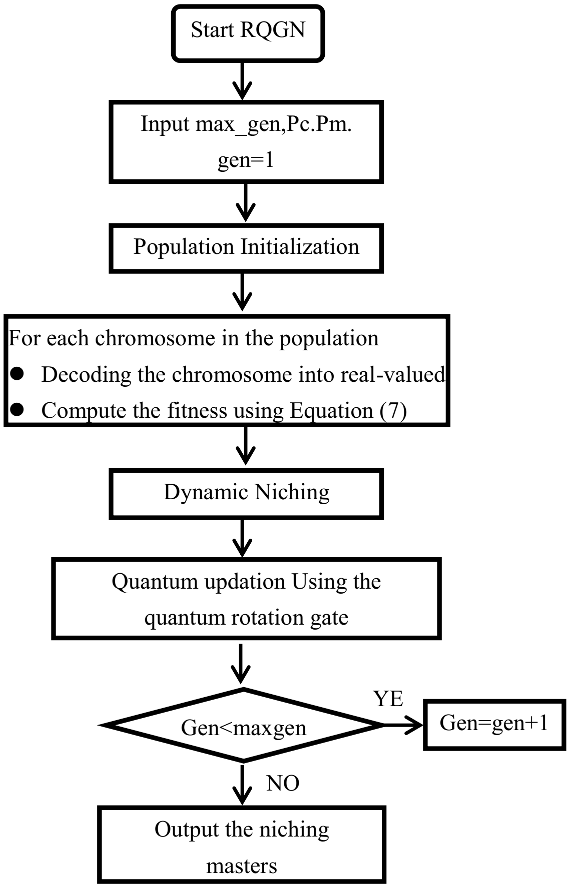

Figure 1. Flowchart of the RQGN algorithm

And each dimension of the chromosome will be one of the four states $\{[x^l \ , x^l],[x^l, x^u],[x^u \ , x^l],[x^u \ , x^u]\}$

In order to decoding the chromosome into real value, a decoding rule is introduced in Table I. Here, $\Delta x_i = (x^u - x^l)/4$ and r is a random number between 0 and 1. If the chromosome is $[x^l \ , x^l]$, the x_i will take a small value inclining to the lower bound. If the chromosome is $[x^u \ , x^u]$, the x_i will take a small value inclining to the upper bound. Through this decoding criterion, the chromosome can be transformed into a real-valued chromosome.

An initial population of size P for RQGN algorithm is usually chosen at random. Here, $\alpha_{i,j}^0$ and $\beta_{i,j}^0$, $i = 1,2,\cdots,P$ and $j = 1,2$, are initialized with $1/\sqrt{2}$.

TABLE I. DECODING RULES OF THE CHROMOSOME

Qubit	***Decoding***
$[x^l\ ,x^l]$	$x_i = x^l + r\dfrac{\Delta x_i}{4}$
$[x^l,x^u]$	$x_i = x^l + (1+r)\dfrac{\Delta x_i}{4}$
$[x^u\ ,x^l]$	$x_i = x^u - (1+r)\dfrac{\Delta x_i}{4}$
$[x^u\ ,x^u]$	$x_i = x^u - r\dfrac{\Delta x_i}{4}$

B. *Fitness Function*

The fitness function of the chromosome, f, is defined as the objective function introduced in section II

$$f(\mathbf{c}) = \tilde{J}_s(\mathbf{c}) = \sum_{j=1}^{n}\left(\exp - \frac{\left\|\mathbf{x}_j - \mathbf{c}\right\|^2}{\beta}\right)^{\gamma}, \quad j = 1,2,\cdots,n \tag{7}$$

where $\mathbf{x}_j$, $j = 1,2,\cdots,n$ are all data points in the data set to be clustered.

C. *Dynamic Niching*

In order to preserve the population diversity which prevents GA being trapped by a single local optimum, several methods have been developed [10]-[11]. For these algorithms, each individual in the population shares its fitness with all the individuals located at a distance smaller than the niche radius, no matter for the niche, to which they belong. Therefore, it is not guaranteed that the methods would provide as many subpopulations as the number of peaks. In order to overcome this drawback, a dynamic niching method is proposed and is presented in Table II.

After the dynamic identification of the niche master candidates of the population Pop_t, the individuals belonging to the same master candidate can be defined as a subset $S_t^i \neq \varnothing$ in Pop_t which have a distance from the master candidate less than the niche radius and do not belong to other niches. If the number of the individuals in S_t^i is larger than 1, then this subset is assumed as an actual niche; otherwise, the single individual in the subset is considered as an isolated individual and all the isolated individuals form the subset S_t^*. Then, the population Pop_t is partitioned into $v(t)$ groups, say S_t^1, S_t^2, $\cdots$, $S_t^{v(t)}$, and a number of isolated individuals

$$Pop_t = \bigcup_{i\in\{1,2,\cdots,v(t)\}} S_t^i \cup S_t^* \tag{8}$$

where S_t^* represents the set of all the isolated individuals.

TABLE II. THE DYNAMIC NICHING ALGORITHM

```
Input: $Pop_t$ the real-valued population at generation $t$
       $P$ population size
       $\sigma$ the niche radius.
The niche master candidates identification.
Sort the current population according to their fitness
$v(t) = 0$ (the number of niches at generation $t$ )
$u(t) = 0$ (the number of niche master candidates)
For $i = 1$ to $P$ do
    If the $i$ th individual is not marked then
        $u(t) = u(t) + 1$
        $N(u(t)) = 1$ (number of individuals in the $u(t)$ th niche candidate)
        For $j = i + 1$ to $P$ do
            If $d(i, j) < \sigma$ ) and ( $u(t)$ th individual not marked)
                insert the $j$ th individual into the $u(t)$ th niche masters candidate
                $N(u(t)) = N(u(t)) + 1$
            End If
        End For
        If ( $N(u(t)) > 1$ ) then
            $v(t) = v(t) + 1$
            mark the $i$ th individual as the niche master of the $v(t)$ th niche
        End If
    End If
End For
```

In order to make the qubit chromosomes effectively converge to the fitter states, we put forward an adaptive rotation angles computing method, which is defined as

$$\theta_{k,i}^{t,q} = sign\{\alpha_{k,i}^{t,q} \cdot \beta_{k,i}^{t,q}\} \cdot \frac{M_i^{t,q} - c_i^{t,q}}{x_i^u - x_i^i} \times 0.05\pi \tag{9}$$

where $\mathbf{M}^{t,q}$ is the master of the q th niche, $\mathbf{c}_l^t$ is the individual in the q th niche, $f(\mathbf{M}^{t,q})$ and $f(\mathbf{c}_l^t)$ are the fitness of $\mathbf{M}^{t,q}$ and $\mathbf{c}_l^t$, respectively. $sign(\cdot)$ is described as

$$sign(\cdot) = \begin{cases} +1 & if \quad \alpha_{k,i}^t \beta_{k,i}^t > 0 \\ -1 & if \quad \alpha_{k,i}^t \beta_{k,i}^t < 0 \\ \pm 1 \quad if \quad \alpha_{k,i}^t = 0 & and \quad M_i^t - c_{l,i}^t < 0 \\ \pm 1 \quad if \quad \beta_{k,i}^t = 0 & and \quad M_i^t - c_{l,i}^t > 0 \\ 0 & otherwise \end{cases} \tag{10}$$

For the individuals in the isolated individual set S_t^*, the rotation angle is defined as

$$\theta_{k,i} = \begin{cases} 0 & if \quad f(\mathbf{c}_l) = f(\mathbf{c}_{best}^t) \\ 0.02\pi & otherwise \end{cases} \tag{11}$$

where $\mathbf{c}_{best}^t$ is the best individual at generation t.

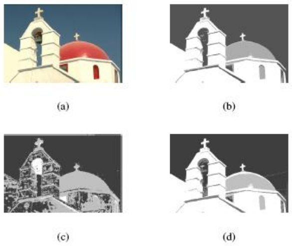

Figure 2. The image Church (a) original image, and the rests are segmentation results obtained by (b) FCM, (c) EM, and (d) RQGN

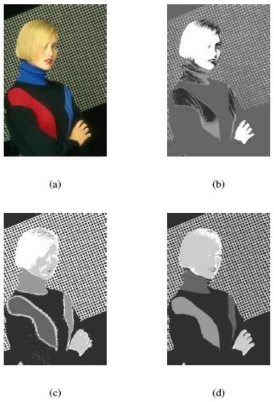

Figure 3. The image Church (a) original image, and the rests are segmentation results obtained by (b) FCM, (c) EM, and (d) RQGN

IV. EXPERIMENT RESULTS

In order to validate the proposed algorithm, we have performed a set of experiments with images taken from the Berkeley segmentation dataset [12] and the segmentation result obtained through the grouping of the pixels. For the purpose of comparison, we have also executed two popular partitioning techniques Fuzzy C-means [13] and Expectation Maximization [14] on the test images with K is set as the actual number of clusters present in the image.

The segmentation results for the four images are shown in Figures~2-3. Generally, as shown in figures, the proposed RQGN approach produces better segmentation results as compared to the Fuzzy C-means and the EM. The segmented regions of the resultant images produced by the RQGN approach are more homogeneous. For example, notice for the image Church, the RQGN approach gives better segmentation result than the Fuzzy C-means and the EM by producing more homogeneous flag and line behind the church as depicted in Fig. 2. As for the image Girl, the RQGN approach outperforms other approaches by classifying the blue and red part of the shirt as single cluster while the FCM and EM can not classify them correctly.

V. CONCLUSIONS

In this paper, an automatic clustering algorithm based on real-valued quantum genetic niching clustering algorithm (RQGN) has been developed for clustering problem with unknown cluster number. As the number of clusters is not known a priori in most practical circumstance, RQGN clustering algorithm can be used more widely. In the new algorithm, each chromosome is encoded a center of a cluster by a real-valued qubit. The dynamic niching is accomplished without assuming any a priori knowledge on the number of niches. And an adaptive selection of the rotation angle used by the quantum rotation gate is introduced. The application of RQGN for color image segmentation demonstrates that the the proposed method is able to automatically segment the image into several classes. All the experiment results have shown that our algorithm is effective.

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