

# QUANTUM-INSPIRED EVOLUTIONARY ALGORITHM AND DIFFERENTIAL EVOLUTION USED IN THE ADAPTATION OF SEGMENTATION PARAMETERS

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## ABSTRACT

The key step in object-based image interpretation is segmentation. Frequently the relationship between the segmentation parameter values and the corresponding segmentation outcome is not obvious, and the definition of suitable parameter values is usually a time consuming, trial and error process. In (Costa et al., 2008), a supervised, semi-automatic method for the adaptation of segmentation parameters was proposed. Initially a human operator delineates polygons enclosing a representative set of target image objects. The manually drawn polygons are then used as reference segments by a Genetic Algorithm (GA), which searches the segmentation parameter space for values that produce segments as similar as possible to the reference. Although GA based methods have been successfully applied in many optimization problems, they are characterized by a high computational load, and do not guarantee that optimal values are found. Alternatives to the basic GA model have been proposed in order to accelerate convergence, preventing at the same time convergence to local maxima. In this work two of such alternatives have been investigated: Quantum-Inspired Evolutionary Algorithm (QIEA) (Abs da Cruz, 2007) and Differential Evolution (DE) (Storn and Price, 1997). Those two models were employed in the method proposed in (Costa et al., 2008), substituting the conventional GA originally used. Experiments showed that both models converge significantly faster than the original GA. Additionally, for an equivalent computational load, dissimilarity among the reference segments and the ones generated with the parameter values found by applying QIEA and DE was in average respectively 44% and 50% lower, when compared to the results obtained with the original GA.

## 1. INTRODUCTION

*Segmentation* is the key step in object-based interpretation of remote sensing image data (Blaschke and Strobl, 2001). The basic elements of the interpretation process are created at this step. Regarded as *segments*, those elements represent geographical regions that will be later classified through the use of rules, which take into account the segments' particular morphological, spectral or topological attributes, among other data. The quality of the segmentation outcome is, therefore, a determining factor for interpretation performance.

Most segmentation algorithms have explicit parameters that can be used to tune them, considering the characteristics of the particular type of images to be processed or of the particular classes of objects expected to be found. In most cases, however, the relationship between the parameter values and the corresponding segmentation outcome is not obvious, and the definition of appropriate values is usually done through a time consuming, trial and error process.

Automatic adaptation of segmentation parameters involves two main issues: the selection of an objective function that expresses adequately the quality of the segmentation (Bhanu et al. 1995); and the choice of the optimization method for the search of parameter values that maximize the objective function. Generally, though, the relationship among the parameter values and the segmentation quality measure cannot be formulated analytically, and calculus based optimization methods can't be used.

A Genetic Algorithm (GA) is an optimization technique that does not require an explicit model of the underlying process (Davis 1990), and that can work with virtually any objective function. GAs, however, do not guarantee that optimal values are found and are characterized by a high computational cost. If one considers the use of a GA for the adaptation of

segmentation parameters, its high processing load becomes a critical issue, since segmentation is also usually a demanding process in terms of computational resources.

Aiming at increasing convergence speed and at hindering convergence to local maxima, alternatives to the conventional GA model, such as Quantum-Inspired Evolutionary Algorithm (QIEA) (Abs da Cruz, 2007) and Differential Evolution (DE) (Storn and Price, 1997), have been proposed.

In (Costa et al., 2008) a method for the adaptation of segmentation parameters based on a conventional GA was introduced. Initially a human operator delineates a set of reference segments. Then the GA searches the segmentation parameter space for values that will produce segments similar to the references. The segmentation procedure used was the region growing algorithm proposed in (Baatz and Schäpe, 2000).

In this work the two alternative evolutionary computational techniques – QIEA and DE – were employed in the method proposed in (Costa et al., 2008), substituting the GA originally used. The performance of the two new variants of the method was assessed through a set of experiments and compared to that of the original implementation.

The subsequent text is organized in the following way. It begins with an introduction on the evolutionary computation techniques mentioned in this paper. Next, a succinct overview of the method proposed in (Costa et al., 2008) is presented. The succeeding section reports on the experimental investigation carried out within this work. The final section contains conclusions and suggestions of future research directions.

## 2. EVOLUTIONARY COMPUTATION

In this section a brief introduction on the evolutionary computational techniques used in this work is given. Initially the conventional GA model used in (Costa et al., 2008) is described, subsequently the QIEA and DE models are presented.

### 2.1. Conventional Genetic Algorithms

A Genetic Algorithm is a computational search technique, inspired on natural selection and genetic reproduction, to find approximate solutions to optimization problems. GAs implement adaptive, parallel search processes suited for complex optimization problems – problems that are hard to be mathematically formulated or characterized by a large search space.

An *individual*, in evolutionary computing terms, stands for potential solution for a given problem, its relevant characteristics with respect to the problem are called *genes*, and its *fitness value* is a measure of its capacity to solve the problem. An individual's fitness value is determined through a *fitness function*, which indicates numerically how good an individual is as a solution to the problem. A *population* is a set of individuals in a particular *generation*.

GAs implement an evolutionary process to search for solutions that maximize or minimize a fitness function. This search is performed iteratively, over generations of individuals. The process starts with the creation of an *initial population*. The gene values of the individuals in the initial population are generated randomly. Then the best fittest individuals are selected and new individuals are created through a process called *reproduction*, in which information encoded into the genes of the fittest individuals are exchanged or randomly changed by procedures denoted as *genetic operators*, such as *crossover* or *mutation*. Furthermore, a number of the best individuals from one generation can be kept in the next generation. The evolutionary process stops after a fixed number of generations, and the fittest individual of the final population is taken as the final solution.

A more comprehensive and detailed description of genetic algorithms can be found in (Michalewicz, 1996).

### 2.2. Quantum-Inspired Evolutionary Algorithm (QIEA-R)

Quantum-Inspired Evolutionary Algorithm using Real Representation (QIEA-R) is an evolutionary computation technique inspired in concepts of quantum physics, namely the *uncertainty principle* and the *observer effect*. In practical terms, this model keeps knowledge of the most promising regions of the search space, and uses it to speed up convergence.

QIEA-R deals with two distinct populations of individuals: a population of *conventional individuals* with *conventional genes*, structurally similar to those of a conventional GA; and a population of *quantum individuals*, characterized by *quantum genes*. While conventional genes usually store information encoded into a single value, represented by a scalar variable, quantum genes represent a probability density function.

The general idea is that individuals of a conventional population are created through *observations* of the quantum individuals, and that the effect of performing observations is the alteration of the information stored in the quantum individuals' genes.

In the model proposed in (Abs da Cruz, 2007), which was used in the experiments presented in this work, the quantum genes' probability density function is a square pulse function. The information stored in the genes are the center ( $\mu$ ) and the width ( $\sigma$ ) of the pulse.

In the beginning of the evolutionary process a population of identical quantum individuals is created. Then a fixed number of observations is made, each observation generating a different conventional individual.

To obtain a real, conventional gene value from a quantum gene, a random real number  $r$ , in the interval  $[0, 1]$  is generated. The conventional gene value  $y$  is then given by:

$$y = F_{ij}^{-1}(r), \quad (3)$$

where  $F_{ij}^{-1}$  is the inverse of the cumulative distribution function  $F_{ij}$  associated to the probability distribution function  $f_{ij}$  (Equation 4), whose parameters are stored in the quantum gene. The indexes  $j$  and  $i$  identify the  $j^{\text{th}}$  quantum gene of the  $i^{\text{th}}$  quantum individual.

$$F_{ij}(x) = \int f_{ij}(x) dx \quad (4)$$

A fitness value – determined through the fitness function – is assigned to each conventional individual generated. After the conventional population has been created, a reproduction phase starts, in which new conventional individuals are created from the fittest individuals of the conventional population. Moreover, the fittest individuals created in the reproduction phase substitute the worst evaluated individuals in the conventional population.

The quantum individuals' genes are then updated in such a way as to map the most promising regions of the search space – by shifting the respective probability density functions towards the (conventional) gene values of the better evaluated conventional individuals. New observations are realized, and the process is repeated until a certain number of generations of conventional individuals have been created. During this process, the probability density functions for the correspondent quantum genes of the quantum individuals tend to converge to the same function, and this function tend to a unit impulse function. The best conventional individual at the last generation is taken as the final solution.

A detailed description of QIEA-R can be found in (Abs da Cruz, 2007).

### 2.3. Differential Evolution (DE)

Differential Evolution (DE) is regarded as a perfected version of genetic algorithms for rapid numerical optimization. DE has a lower tendency to converge to local maxima with respect to the conventional GA model, because it simulates a simultaneous search in different areas of solution space. Moreover, it evolves populations with smaller number of individuals, and have a lower computation cost. DE individuals' genes are represented by real numbers.

The evolution process starts with the creation of an initial population, containing individuals with randomly generated gene values. After the fitness values are calculated through the

fitness function, each individual from the population is selected in sequence. Once an individual is selected, the following procedure is executed. Initially, three other individuals are selected randomly. The differences of the gene values of the two first individuals are multiplied by a random, real value  $r$  in the interval  $[0, 1]$ . Then, the gene values of the third individual are added to the result of the last operation, and a new individual is created by performing a uniform crossover between the newly calculated gene values and the individual originally selected. The new individual's fitness is calculated and compared to that of the original individual, and the fittest of the two individuals will be moved to the next generation. A new population results from the execution of the above procedure for all individuals of a population, and this is repeated for a number of generations. The gene values of the best individual of the last generation are taken as the solution to the problem.

A detailed description of DE can be found in (Storn and Price, 1997).

### 3. GENETIC ADAPTATION OF SEGMENTATION PARAMETERS

The method proposed in (Costa et al, 2008) uses a conventional GA for the adjustment of segmentation parameters. It evolves a population of individuals whose genes correspond to segmentation parameters.

Although the proposed adaptation method can be applied to any segmentation procedure, the experiments reported in (Costa et al, 2008) were limited to the region growing algorithm proposed in (Batz and Schäpe, 2000). The parameters subjected to adaptation were the scale parameter ( $s$ ), the spectral band weights ( $w_e$ ), the color weight ( $w_{cor}$ ), and the compactness weight ( $w_{compact}$ ).

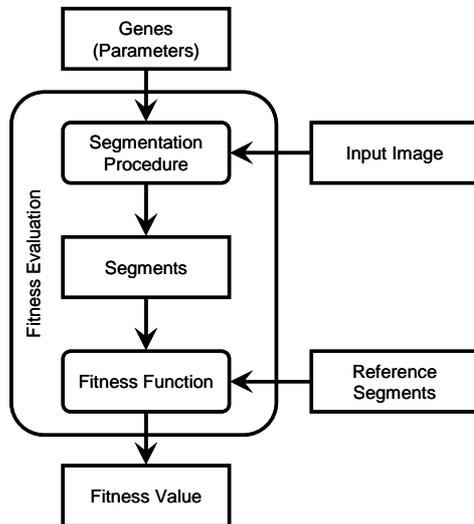


Figure 1: Fitness evaluation procedure

The fitness of each individual is calculated by comparing the segmentation produced through the use of its respective parameter values with a manually created reference segmentation (Fig. 1).

In mathematical terms, given a set of segments  $S$ , a set of parameter values  $P$  and the objective function  $F(S, P)$ , the task of the GA consists in searching for the parameter vector  $P_{opt}$ , for which the value of  $F$  is minimum:

$$P_{opt} = \arg_p (\min[F(S, P)]) \quad (1)$$

The fitness function is defined as follows. Let  $S_i$  denote the set of pixels belonging to the  $i^{th}$  segment of the set  $S$ . Let  $O_i(P)$  denote the set of pixels belonging to the segment with the largest intersection with  $S_i$  among the segments produced by using  $P$  as parameter values of the segmentation algorithm. The fitness function is then given by the equation below, in which ‘-’ represents the set difference operator, ‘#( )’ is the cardinality function, and  $n$  is the number of segments in the set  $S$ .

$$F(S, P) = \frac{1}{n} \sum_{i=1}^n \frac{\#(S_i - O(P)_i) + \#(O(P)_i - S_i)}{\#(S_i)} \quad (2)$$

Figure 2 shows graphically the components of the proposed fitness function. The region with the solid contour represents a referent segment  $S$ , and the region with the dashed contour represents  $O(P)$ . A perfect match between the reference segmentation and the output segmentation corresponds to  $F=0$ .

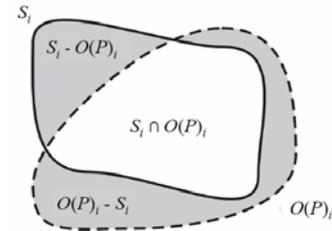


Figure 2: Graphical representation of the fitness function

It is important to point out that  $S$  does not need to represent a complete segmentation of the input image – where every pixel of the image would belong to a segment in  $S$ . Actually if  $S$  represents a complete segmentation, we would be looking for the best set of parameters, considering all different objects on an image. This means that the adapted parameters would work equally well for all object classes represented on the image, eventually including natural and man-made objects. However, objects from different classes have different morphological and spectral characteristics, and, for most segmentation algorithms, the ideal segmentation parameters for a specific object class would be different than the optimum parameters for any other class. In this sense the segmentation parameters can specialize segmentation algorithms with respect to a particular object class.

### 4. EXPERIMENTS

The experiments implemented in this work followed the same design as the second set of experiments described in (Costa et al. 2008). The only methodological difference was that the Genetic Algorithm used in that work was substituted in turn by two other evolutionary computation techniques, namely QIEA-R and DE. Furthermore, the same images and reference segments were used.

The objective of the experiments was to compare the performance obtained by using each of the three evolutionary techniques described in Section 2 as the search technique in the parameter adaptation method proposed in (Costa et al. 2008),

both in terms of segmentation quality and of computational load.

#### 4.1. Input data

The images used in the experiments were produced by different sensors, over areas with different land covers. Image 1 (Figure 3) was extracted from an aerial photograph taken over a residential area in the City of Rio de Janeiro. The other two images are satellite images obtained from public resources on the Internet. Image 2 (figure 4) shows the parking area of bus company, also situated in Rio de Janeiro, and image 3 (figure 5) shows storage tanks of an industrial plant in the City of Duque de Caxias, in Rio de Janeiro State. The three images have 400x400 pixels, RGB format with 24 bits (8 per band).

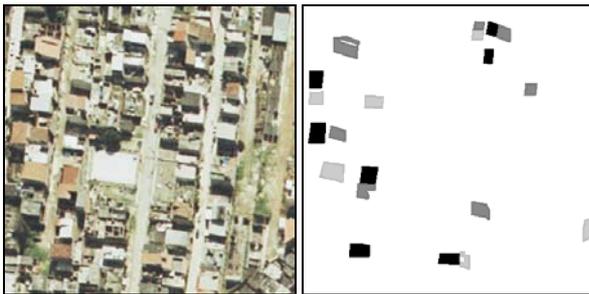


Figure 3: Image 1 and respective reference segments

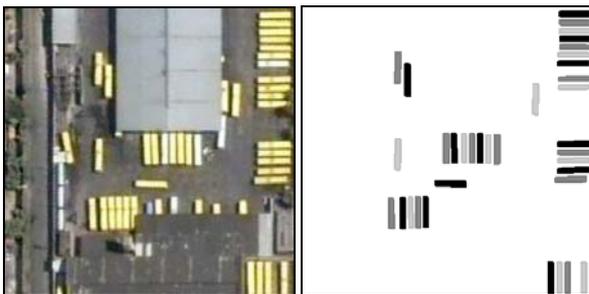


Figure 4: Image 2 and respective reference segments

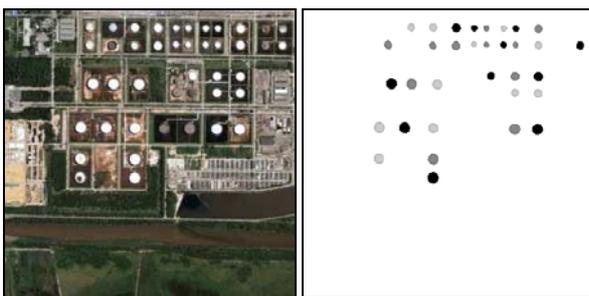


Figure 5: Image 3 and respective reference segments

The reference segments were manually drawn by a photo-interpreter, delimiting different image objects for each input image: respectively, roof tops of ceramic material; buses; and storage tanks. For each image the delimited segments were organized in three groups (A, B and C), each group containing approximately the same number of segments. The segments were assigned to the groups randomly. In the figures 3, 4 and 5, the segments in each group are identified by different shades of gray (group A: black; group B: dark gray; group C: light gray).

#### 4.2. Experimental procedure

Segments representing only one class of objects (roofs, busses, tanks) were considered in each experiment. One of the segment groups (A, B or C) was selected to serve as the reference for the parameter evolution. The selected group was regarded as the *training set*. Three experiments were performed for each image, using different groups of segments for the training set.

For both evolutionary techniques – QIEA-R and DE – the population size was set as 10 individuals, and in each execution of the respective algorithms a total of 1805 individual fitness evaluations were performed – the exact same number of evaluations made by the conventional GA in the experiments reported in (Costa et al. 2008).

#### 4.3. Results

Table 1 shows the best results obtained for 3 executions of each evolutionary technique for each experiment. The column *image* indicates the image used in the experiment. The column *group* shows the segment group used as the training set. The column *fitness* contains the fitness values calculated for the fittest individuals obtained with each evolutionary technique, using as reference segments the different training sets. The best fitness value in each experiment is shown in bold style.

exp	image	group	Fitness		
			GA	QIEA-R	DE
1	1	A	0.21	<b>0.18</b>	0.20
2	1	B	0.28	0.19	<b>0.18</b>
3	1	C	0.19	0.18	<b>0.16</b>
4	2	A	0.48	<b>0.11</b>	0.13
5	2	B	0.51	0.14	<b>0.13</b>
6	2	C	0.45	<b>0.09</b>	0.09
7	3	A	0.38	<b>0.19</b>	0.21
8	3	B	0.26	<b>0.14</b>	0.28
9	3	C	0.39	<b>0.18</b>	0.19

Table 1: Comparative results

In all experiments the best solutions were found with either QIEA-R or DE.

Figures 6 to 8 allow a visual inspection of the results obtained respectively in experiments 1, 4 and 7, in which the QIEA-R evolutionary algorithm was used. Those images were produced from the complete segmentation of respective input images, but contain only the segments with largest intersection with the reference segments. A large similarity can be perceived among the manually drawn segments and those produced by the segmentation procedure with the parameters found through the adaptation method.

Figure 9 shows a graph in which the fitness values of the best individuals, in consecutive generations of the evolution process for experiment 3, are plotted. The graph is exemplary for a behavior noticed in the majority of the experiments: in less than 40 generations (less than 400 individual evaluations), both QIEA-R and DE found solutions that were equal or better than the ones found using the conventional GA. This means that similar results were obtained with approximately 20% of the computational load required by the conventional GA.

Furthermore, for an equivalent load, dissimilarity among the reference and the corresponding segments – largest intersecting segments – generated with the parameter values found with

QIEA and DE was, in average, respectively 44% and 50% lower than that achieved with the conventional GA.

In most experiments the solutions found by using the AEIQ-R technique were the best ones. When that was not the case – experiments 2, 3 and 5, the fitness values of the best solutions were very similar to the ones found with AEIQ-R.

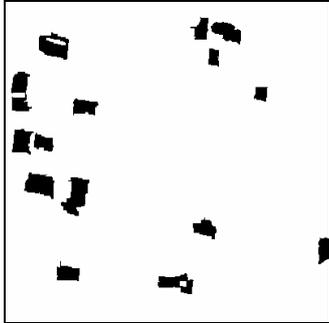


Figure 6: Segmentation result of experiment 3

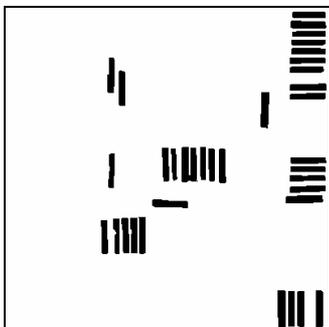


Figure 7: Segmentation result of experiment 6

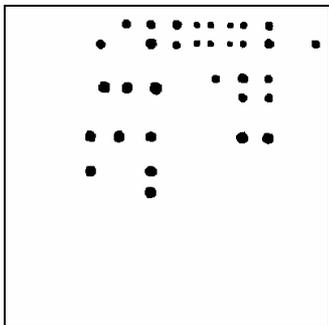


Figure 8: Segmentation result of experiment 9

## 5. CONCLUSIONS

In this work two alternative evolutionary computational techniques – QIEA and DE – were employed in the method for the adaptation of segmentation parameters proposed in (Costa et al, 2008), substituting the conventional GA originally used.

Experiments demonstrated that the use of the alternative techniques resulted in significantly higher convergence rates and lower computational costs – the performance of the genetic adaptation method has showed a notable improvement when the two alternative techniques were used as the method's search technique.

Further investigation of the method is under way, considering different segmentation procedures and different fitness functions.

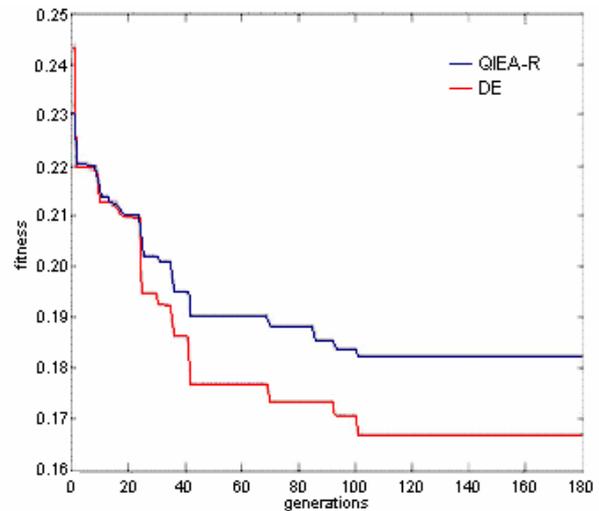


Figure 9: QIEA-R and DE evolution for experiment 3

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