TWO-POPULATION GENETIC ALGORITHM
An Approach to Improve the Population Diversity

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Abstract: Genetic Algorithms (GAs) are a technique that has given good results to those problems that require a search through a complex space of possible solutions. A key point of GAs is the necessity of maintaining the diversity in the population. Without this diversity, the population converges and the search prematurely stops, not being able to reach the optimal solution. This is a very common situation in GAs. This paper proposes a modification in traditional GAs to overcome this problem, avoiding the loose of diversity in the population. This modification allows an exhaustive search that will provide more than one valid solution in the same execution of the algorithm.

1 INTRODUCTION

Based on natural evolution, Evolutionary Computation (EC) tools have shown to be very efficient techniques when solving different problems. One of these techniques, Genetic Algorithms (GAs), is used mainly for the optimization of a set of parameters (Fogel, 2006).

All of the EC techniques are based on the same principles: an initial random population is made to evolve by means of genetic operators (crossover and mutation) inspired in Biology.

This evolution is done until a stop criterion is fulfilled like maximum number of generations, a MSE threshold or the convergence of the population.

But, if the population has a low diversity, i.e. the population is very homogeneous, resulting in having many individuals very similar, or identical. This leads to having the crossover operator very inefficient, because it builds new solutions that explore areas of the search space that have already been explored by other solutions. Therefore, only the mutation operator can introduce new diversity in the population. This all leads to a big loss of efficiency in the whole algorithm, and it is a very common problem in GAs (Zaharie, 2003).

Another problem due to the lack of diversity appears when problems with multiple valid solutions (or solutions with a very similar fitness) are trying to be solved (multimodal problems). In these cases a traditional GA will try to keep in the populations values corresponding only to one of these solutions.

2 EVOLUTIONARY APPROACHES TO INCREASE DIVERSITY

As already stated, the diversity lack leads to an efficiency and efficacy loss. Even this diversity lack is very common on later stages of the evolution, its appearance on the early generations is a very important problem that affects the whole search. To avoid this problem, different strategies have been proposed, most of them based on heuristics.

First, some of the approaches try to solve this problem by means of the dynamic variation of crossover and mutation rates (Ursem, 2002). A diversity measure is needed to control this problem, which allows changing dynamically the mutation and crossover rates.

New crossover algorithms have also been proposed to solve this problem. Some of them are BLX (Blend Crossover), SBX (Simulated Binary Crossover), PCS (Parent Centric Crossover), CIXL2 (Confidence Interval Based Crossover using L2 Norm), UNDX (Unimodal Normally Crossover) or fuzzy recombination (Lozano, Herrera and Cano, 2008).

Different approaches in replacement algorithms have also been proposed to avoid diversity loss. En example of this is Crowding algorithm. This

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algorithm began as a deterministic approach, but also a probabilistic version has been published, in which individuals compete in a probabilistic tournament (Mengshoel and Goldberg, 2008).

Species-based are also used when the problem requires an in-depth search over the solution space. In this case, the solution to the lack of diversity is simulated adding new populations, but the problem remains within each of these populations (Nicholson and White, 2008).

The main inconvenience of the techniques previously described (replacement and crossover operators) lies in the fact that they add new parameters that should be configured according the process of execution of GA. This process may be disturbed by the interactions among those parameters (Bäck, Eiben and van der Vaart, 2002).

3 TWO-POPULATION GENETIC ALGORITHM

In this work a novel approach is presented to preserve the genetic diversity. It tries to keep the diversity stable by means of the use of a new population that works as repository information. This repository will allow the GA to be able to create solutions all over the search space. In this way, the population diversity does not reduce over the time.

3.1 General Structure

The lack of diversity of the genetic population is the key feature which will lead to improving efficacy and efficiency. To do this, a new population is added to the traditional GA. This population is called *genetic pool*, and it forces a homogeneous search through the search space.

This genetic pool divides the search space into sub-regions (see Fig. 1), because each individual has its own fenced range for gene variation, i.e., each gene of each individual can take values only inside a limited rank. Therefore, each individual of the genetic pool represents a sub-region of the search space, and the whole search space is divided into all of the individuals of this genetic pool.

Depending on both type and complexity of the problem that it is intended to solve, the user has to set the number of sub-regions that require into the search space. It should be borne in mind that a traditional GA performs its search only one sub-region (the whole of the search space).

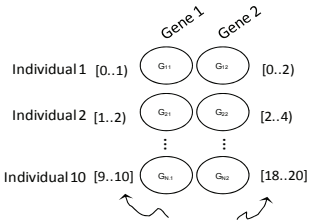


Figure 1: Sample of Genetic Pool configuration.

The secondary population works as a classical population, i.e., no additional rank restrictions are introduced in this population (each individual's genes can take values all over the search space). Its only variation refers to the application of crossover and mutation operators, which operate between both populations (explained below).

This secondary population contains the solutions to the problem, whereas the genetic pool acts as a support, keeping the search space homogeneously explored and a diverse population.

3.1.1 Genetic Pool

The main objective of the genetic pool is to allow the GA to explore the whole search space with a homogeneous search. As each individual in the genetic pool represents a sub-region of the global search space, it has the same structure or gene sequence than when using a traditional GA.

But these individuals need some extra information (see Fig. 2). First, in a traditional GA population these genes can take any valid values, but in the genetic pool the genes can take values only in a restricted range (different for each individual). The total range values are divided into the same number of parts than individuals in genetic pool, so that a sub-range of values is allowed to each individual. Those values that a given gene may have will remain within its range for the whole of the performance of the proposed GA. Therefore, if the genetic pool has a size of N individuals, the whole search space is partitioned into N parts of the same size, each of them represented by an individual of the genetic pool.

In addition of this partition, every individual in the genetic pool knows which of its genes are part of the best solution found up to then, i.e., genes that belong to the best individual in the secondary population. This flag is used to avoid the modification of those genes that are the best solution to the problem.

Also, each gene in each individual in the genetic pool has a value that indicates the relative increment

that would be applied to the gene during a mutation operation (the I value). This mutation operator is described below.

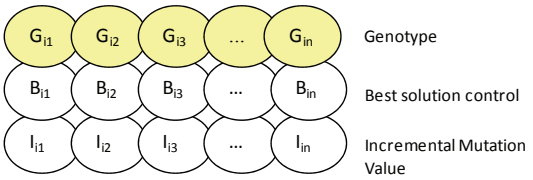


Figure 2: Genetic Pool individual.

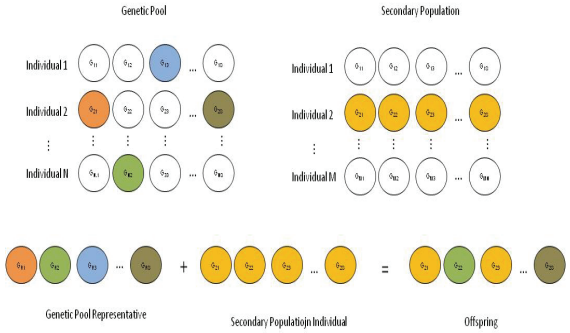


Figure 3: Crossover operation.

An important thing to bear in mind is that these individuals do not represent global solutions to the problem. Therefore, their fitness value is useless and no computational time is wasted in this task.

3.1.2 Secondary Population

The individuals in the secondary population are similar than those of a traditional GA population, i.e., they can adopt values throughout the whole of the solutions area. In this way, they offer global solutions to the problem, which is something that none of the individuals of the genetic pool is able to do due to the range restriction. Therefore, this population contains the solutions to the problem and performs an evolution similar to a classical GA population, with some differences in the genetic operators (crossover and mutation).

3.2 Genetic Operators

3.2.1 Crossover

The crossover operator has been modified in order to operate between individuals in the secondary population (using complete solutions to the problem) and the genetic pool. This operator now recombines genetic material from two parents, each of them from each population.

First, an individual is randomly chosen from the secondary population. Therefore, there is no need to have this population organized attending to the fitness value of its individuals.

The Representative is also built from the genetic pool. This representative is assembled by randomly choosing the genes from the individuals of the genetic pool (see Fig. 3).

These two individuals (the randomly chosen from the secondary population and the representative from the genetic pool) will be the parents in the crossover operation. A uniform crossover is performed between these two parents. As a result of this crossover, only one individual is generated after the random selection of every one of its genes from both ancestors.

A non destructive replacement algorithm has been used in order to insert this new individual into the secondary population. This insertion is performed when the fitness of the offspring is better that the fitness of the selected parent from the secondary population. Therefore, if the new individual represents the new best solution, the genes of the representative individual in the genetic pool (Boolean values B_{ij} at Fig. 2) are consequently marked in the corresponding individuals of the genetic pool.

3.2.2 Mutation

The mutation operator only modifies individuals in the genetic pool. First of all, a random individual is chosen from the genetic pool. A gene is chosen from that individual and the specified increment value associated to that gene is applied to it (the value I in Fig. 2). The selected gene must not have the mark of belonging to the best solution in the secondary population, i.e., it should not have the Bi value marked.

When the addition of current gene value plus the increment exceeds the upper end of the sub-range in which the gene may vary, this gene becomes the lower value of the sub-range. Furthermore, if this happens, the incremental value that is going to be applied to subsequent mutations of that gene is also reduced. This is done in order to perform a more exhaustive search in all of the values that a gene may adopt as the evolution process goes on.

4 EXPERIMENTS

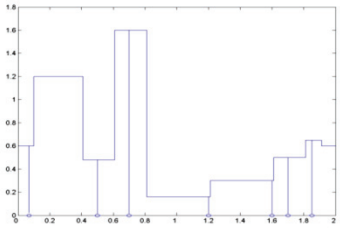
In this section different experiments will show the performance of the proposed system. A comparison with traditional GAs is done in order to measure the

goodness of applying this modification to the GA.

Different problems have been solved with this system. First of all, some *synthetic* problems will be used to assess the approach functioning. They will allow to test whether the system proposed is able to provide several valid solutions in the same run, and, therefore if the population does not converge to a single individual. The performance of the algorithm proposed and the ability of finding different solutions is studied with these problems, in comparison with results obtained with traditional GAs.

The preliminary tests tried to establish the level of convergence and exhaustive search of the new algorithm compared to the classic GA.

Among different test trials, the discrete function represented in Fig. 4 was used to prove the proposed system. This function takes values within the interval [0..2] where several narrow local minimums with value 0 have been added.



x	f(x)
0.07	0.08
0.5	0.01
0.7	0.001
1.2	0.05
1.6	0.08
1.7	0.02
1.85	0.005

Local Minimums

Figure 4: Test function.

Parallel executions of classical GA and the proposed GA will be done until one of them reach a threshold error, in this concrete case establish when mse<0.05. Once the algorithm reach the threshold the number of solutions kept in the solution is annotated.

The main objective of this synthetic function is to find out how the search space is explored in-depth.

Each individual will codify five times the same function, so five simultaneous runs will be performed. It will allow to graphically checking the minimum achieved and increase the complexity of the individuals. To avoid possible constructive blocks that make simpler the resolution of the problem the fitness function will be the following one:

Fitness = $f(G_1) + f(2\text{-}G_2) + f(G_3) + f(2\text{-}G_4) + f(G_5)$

5 RESULTS

The Fig. 5 presents the results with the test function represented in Fig 4. This graph shows the average number of solutions kept inside the population respect to the population size (number of individuals). Different genetic pool sizes were taken, from 1 to 50 individuals, and the secondary population size also changed between 2 and 50 individuals. The population size in the classical GA has also been changed with sizes between 2 and 50. For each configuration 50 runs were performed and the mean values annotated.

This figure shows that the behaviour of the two-population GA is better to the traditional GA. Even the efficiency of the classical GA improves with bigger populations, it does not reach the results achieved by the two-population GA. More precisely, the average number of solutions in the population of the two-population GA was 5.5048 (over 7 possible different solutions), while the average number in the traditional GA was only 0.5216 (with a maximum in 0.92).

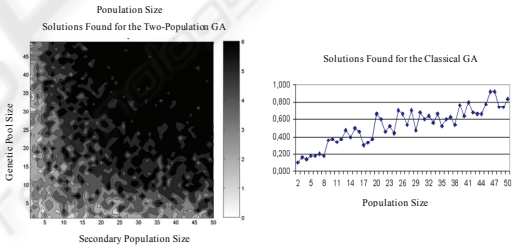


Figure 5: Population sizes and solutions found.

6 CONCLUSIONS

Several conclusions can be drawn from the results obtained with the use of the system proposal. The most important one is that it was able to keep the population diversity over the execution of the algorithm, the start point of this work. In the problems presented, this behaviour allowed to keep a number of solutions in the population greater than the classical GA. So, the approach seems a promising line where interesting results can be finding.

In the proposed system the number of regions on the genetic pool is fixed in advance. It would be good to investigate different ways to allow it to change dynamically. So, new operators (like region gathering, division) would be interesting to explore.

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