Simulating Gender Separation with Genetic Algorithms

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Abstract

Gender separation is a largely encountered in the natural systems that allows the preservation of the genetic diversity in a species. In this paper, we want to analyse the mechanism by which this reproduction mode may have evolved and the way it influences the evolution of a population toward an optimal individual.

1 INTRODUCTION

It is a known fact that gender separation is a powerful biological tool that helps preserving the genetic diversity in a population by preventing organisms from self-duplicating. It has also been shown that allogen reproducing organisms have a greater capacity to quickly adapt to difficult environments and to resist hostile exterior factor like disease (Hamilton, Axelrod, and Tanese, 1990).

The gender separation and sexual reproduction have been of interest in the study and application of genetic algorithms (GAs), since they are an important feature of the living organisms. Some research has followed the direction of sexual reproduction and the impact on the biodiversity (Todd and Miller, 1997; Todd, 1997).

In another direction, sexual reproduction can also be viewed as a factor for developing the communication through the emergence of complex mating signals (Werner and Todd, 1997; Noble, 1999).

Gender can also be seen as a factor for developing the collaboration between the individuals in a population (Hemelrijk, 1999), and can be a component for multi-optimization algorithms (Allenson, 1992).

In this paper, we try to model the way gender separation has occurred in nature in the first place and how it became such a wide-spread feature in our ecosystem. Our hypothesis is that the reproduction constraints related to the sexual reproduction alone cannot explain the survival and spreading of this reproduction mode in nature. Thus, the individuals that initially developed mating schemes that aim to preserve the genetic diversity in a population can eventually lead to the emergence of two distinct subpopulations that reproduce in general with each other.

Section 2 presents a model in which the distribution of gender types in a given population evolves along with the rest of the genotype. Section 3 examines the fitness of the individuals that evolve following various reproduction modes. Section 4 studies the influence of the population size on the performance of each of the models.

2 EVOLVING THE REPRODUCTION MODE

In this section present a simulation model based on several gender types that can evolve through genetic operations along with the rest of the chromosome.

2.1 MODEL DESCRIPTION

The first experiment that we introduce in our paper concerns the evolution of various gender types through natural selection. We start from the assumption that the initial population is composed in an equal way of individuals presenting various reproduction constraints, that we classify as gender types. In the mating process, some of them require specifically a partner of different gender in order to reproduce, while others can mate with a partner of any gender. Part of them can even self-duplicate.

The gender type is inherited by the offspring from the parents in a random fashion with no particular prefer-

ence. The goal of the experiment is to analyse the composition of the population as it evolves toward individuals of higher fitness through the mechanism of natural selection. Thus, the gender distribution in the final population is determined by two factors: the probability of occurrence of each gender type in the next generation based on the reproduction constraints, and the gender inherited by the fittest individuals in a given generation, which are more likely to be chosen for reproduction.

In our model, we have four types of individuals: male (M), female (F), self-fertilizing (S-F), and hermaphrodite (H). The gender of the individual is assigned by random in the initial population with no preference for any of the four types. This parameter is inherited by the offspring and thus evolves by natural selection.

Each of the four gender types has a different constraint in the mating process. The self-fertilizing individuals can mate with any individual regardless of their gender, including themselves. The hermaphrodite individuals can mate with any individual other than themselves. The males and females can mate an individual of any gender type different from their own. Thus, we suppose that in the initial conditions of gender separation, a male or a female could mate with either a female, or with a hermaphrodite individual presenting the features of both gender types.

The male - female mating constraints can lead the algorithm to a deadlock in the case where the population becomes exclusively composed of one of these two gender types, such that the reproduction is not possible anymore. We prevent these situations by introducing the possibility of spontaneous sex change from male to female or the reverse in the situation where an individual has made a number of unsuccessful mating attempts equal to the least of 25 and the quarter of the population size.

The offspring inherits the gender type of the parents randomly, with an equal probability assigned to each parent. Let us denote by n_{0M}, n_{0F}, n_{0S}, and n_{0H} the number of male, female, self-fertilizing, and hermaphrodite individuals respectively in a given generation. We can compute the expected number of occurrences of each gender type n_{1M}, n_{1F}, n_{1S-F}, and n_{1H} in the next generation considering exclusively the mating scheme we have described and ignoring the mechanism of natural selection. Let $n_{0M} + n_{0F} + n_{0S-F} + n_{0H} = n$, the size of the population.

The general reproduction scheme that we have used consists in selecting two parents for reproduction by

crossover, and producing exactly two children by this operation. Since the gender type is randomly inherited by the offspring, we expect the children to have the same gender distribution as the parents. For example, from a male and a hermaphrodite we expect to produce again a male and a hermaphrodite, only with a different genetic code.

The male and female individuals can be found in the next generation either if they are selected as the first parent, or if the first parent has a different gender than their own and they are selected as a second parent. The probability that a random individual from the initial population is a male is equal to n_{0M}/n, and the probability of the contrary event is $(n - n_{0M})/n$. Considering that we select $n/2$ individuals as the first parent and the same number as the second parent, we can compute the expected number of occurrences of the male gender type in the next generation as

$$n_{1M} = \frac{n}{2}\frac{n_{0M}}{n} + \frac{n}{2}\frac{(n - n_{0M})}{n}\frac{n_{0M}}{n}$$
$$= n_{0M}\frac{2n - n_{0M}}{2n} < n_{0M}$$

The same computation can be done for female individuals.

$$n_{1F} = \frac{n}{2}\frac{n_{0F}}{n} + \frac{n}{2}\frac{(n - n_{0F})}{n}\frac{n_{0F}}{n}$$
$$= n_{0F}\frac{2n - n_{0F}}{2n} < n_{0F}$$

We can find a hermaphrodite in the new generation if a hermaphrodite was chosen as a first parent, or if the second parent is a hermaphrodite and not identical to the first one. We have

$$n_{1H} = \frac{n}{2}\frac{n_{0H}}{n} + \frac{n}{2}\frac{n - n_{0H}}{n}\frac{n_{0H}}{n} + \frac{n}{2}\frac{n_{0H}}{n}\frac{n_{0H} - 1}{n}$$
$$= n_{0H}\frac{2n - 1}{2n} < n_{0H}$$

In this formula, the first term of the sum corresponds to the event that the first parent is hermaphrodite. The second term corresponds to the event that the first parent is not a hermaphrodite, but the second parent is, in which case they cannot be the same individual. The third term corresponds to the event that the both parents are hermaphrodites and different individuals.

The number of self-fertilizing individuals should remain stable, since they can constitute any of the parents, regardless of what the other parent is.

$$n_{1S-F} = 2\frac{n}{2}\frac{n_{0S-F}}{n} = n_{0S-F}$$

As the sum of these numbers is inferior to n, we should scale them correspondingly with a factor greater than 1. This would most probably modify the expected number of hermaphrodite individuals in the new generation such that $n_{1H} \geq n_{0H}$. The result is that the number of self-fertilizing and hermaphrodite individuals are expected to increase, while the two others may converge to 0.

2.2 EXPERIMENTAL CONDITIONS

This section presents the fitness functions that the GA must optimize and the parameter settings that we have used for the experiment.

Fitness Functions

We have chosen three classes of problems: the set of 10 standard test functions, an NP-complete problem and several deceptive functions. Each class presents a special challenge for the GA.

Standard functions This class contains 10 standard minimization functions used in many cases to experiment with GAs (Whitley et al., 1996).

Deceptive problems This class of problems is based on the phenomenon of deception (Whitley, 1990; Deb and Goldberg, 1994) and contains problems that are known to be difficult for GAs. For this reason, they are a frequent choice as test functions in the study of GAs (Goldberg, Deb and Horn, 1992; Kingdon and Dekker, 1995; Mohan, 1998). Their difficulty comes from the fact that the optimal individual is isolated from other individuals of high performance, and there are one or more suboptimal individuals that are easier to reach by hill-climbing.

We have chosen 8 deception problems that consist in concatenating a number of 3-bit functions as shown in Table 1. For these problems, the optimal individual is represented by a string of 3 bits whose closest neighbors display the lowest performance. We have conducted our experiences with individuals composed of 100 strings of 3 bits, so the optimal individual should have a performance of 3000.

Hamiltonian circuit (HC) Given a graph, does there exist a circuit that passes once and only once through each vertex? This problem is known to be NP-complete (Brassard and Bratley, 1994).

We have performed our experiences with 10 HC problems with graphs of 9 to 150 vertices and up to 3000 edges. The direct representation of a HC problem for

Table 1: Deception functions

	000	001	010	011	100	101	110	111
decep1	28	26	22	0	14	0	0	30
decep2	28	26	22	14	14	26	22	30
decep3	22	0	28	26	0	30	14	0
decep4	0	14	30	0	26	28	0	22
decep5	22	14	28	26	22	30	14	26
decep6	26	14	30	22	26	28	14	22
decep7	22	14	28	26	14	30	24	14
decep8	14	22	30	14	24	28	14	26

the GAs can be difficult. De Jong and Spears (1989) suggest to transform the HC instances into SAT instances, whose genetic representation is easier.

SAT (Boolean satisfiability) Given a Boolean expression depending on some variables, does there exist an assignment to those variables such that the expression evaluates as true?

A detailed description of the reduction of a HC instance into a SAT instance can be found in (Brassard and Bratley, 1994) or (Vrajitoru, 1999). For any given graph, a Boolean variable corresponds to each edge, and is given the true value if the edge belongs to the HC. Thus, if we represent each variable as a gene, the size of an individual is equal to the number of edges in the graph.

To evaluate a Boolean expression to more than true or false, we have used fuzzy logic measures, also proposed by De Jong and Spears (1989). The 'and' operation is evaluated to the average of the terms, while the 'or' operation returns the maximum of the terms. Thus, the fitness function takes values between 0 and 1, and the optimal individual has a fitness of 1.

2.3 PARAMETER SETTINGS

We have performed for each problem 100 runs of the GA, half of which without mutation, and half with a mutation rate of 0.01. The crossover rate is equal to 1 in all the cases. Each generation contains 50 individuals and the number of generations is limited to 500. We have used the fitness proportionate or roulette wheel selection (Goldberg, 1989), and a variant of the elitist reproduction called monotone: the worst individual in the new generation is replaced by the ancient best individual, if and only if the new generation contains nothing better than it (Vrajitoru, 1999).

Table 2: Gender convergence in 500 generations

	M/F	H	S-F
Standard	9	438	553
Deception	6	370	424
HC	11	973	1116
Total	26	1781	2093
%	0.67	45.67	53.66

We have used a crossover operator called *combined balanced* that combines four variations of crossover in each generation : the 1-point (Holland, 1975), 2-point (De Jong, 1975), uniform (Syswerda, 1989), and dissociated (Vrajitoru, 1999). For each operation, one of the four crossover forms is used by a random choice giving each of them equal chances.

2.4   SIMULATION RESULTS

The parameter that interests us in this first experiment is the composition of the population in the last generation. The simulation has shown that the distribution of the gender types in the population converges to one of the four types very fast.

To illustrate this fact, Figure 1 shows the evolution of the gender types in 30 generations, computed over 80 runs on 4 HC problems of various difficulty. The measure that we have plotted is the average number of occurrences of each type in the population according to the generation number.

From this figure we can see that the male and female gender types have completely disappeared after 30 generations. In 77 out of 80 runs, the population is already completely composed of one of the two remaining gender types. In the conditions of our experiment, the gender converges much more rapidly than the rest of the genetic material.

A second set of results shows that after 500 generations, the population is composed completely of one gender type in all the cases. Table 2 shows the distribution of each gender type in the last generation for each class of problems. We can remark that although the general distribution of gender types follows the tendency that we have also observed in Figure 1, the number of resulting populations that are composed of male/female individuals is not equal to the expected number (0).

This fact is due to the influence of the natural selection mechanism. Thus, the best individuals are more likely to be chosen for mating, and their gender type will be transmitted to a greater number of the new individuals than expected from the mating constraints.

This factor can explain the mechanism by which a genetic feature that restrains the potential number of individuals with which a given individual can mate, has survived and currently dominates an important part of our natural system. We can entail that the first organisms developing only one gender type also presented some adaptation to their environment that made them stronger and allowed the feature to survive and spread.
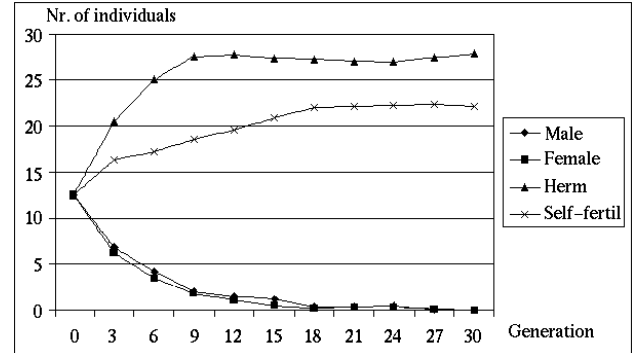

Figure 1: Gender evolution in 30 generations

3   COMPARING THE REPRODUCTION MODES

In this section we compare several reproduction schemes based on the gender types previously described. We are interested in the influence of the self-fertilization and of the gender separation on the performance of the GAs.

3.1   REPRODUCTION SCHEMES

We propose four reproduction schemes that we compare using the average performance over 100 runs on each test problem.

The first reproduction scheme is the usual one based on the fitness-proportionate selection. In this case, all the individuals are self-fertilizing, and thus the process of mating doesn't require any special operation. We denote this scheme by *simple*.

The second scheme is the one presented in the previous section, where the gender types belong to any of the four categories. They are assigned randomly in the initial population and evolve through generations. We denote this scheme by *mixed*.

The last two schemes, denoted by *gender* and

Table 3: Results on the standard test functions

Problem	Simple	Mixed	Gender	Herm
F1	0.192	0.177	0.155	0.182
F2	0.449	0.31	0.59	0.365
F3	11.85	11.84	11.97	11.83
F4	2.894	3.053	2.751	3.013
F5	5.14	6.208	4.765	3.943
F6	3.205	3.407	3.228	3.475
F7	616.627	620.549	616.096	596.507
F8	2.115	2.306	2.429	2.237
F9	0.125	0.132	0.13	0.138
F10	1.456	1.725	1.357	1.622

Table 4: Results on deception problems

Problem	Simple	Mixed	Gender	Herm
d1	2684.36	2697.44	2699.16	2689.32
d2	2851.22	2929.4	2853.84	2857.02
d3	2494.2	2502.12	2504.92	2503.88
d4	2504.94	2498.54	2501.22	2500.7
d5	2767.86	2771.5	2767.1	2772.42
d6	2764.82	2765.42	2769.24	2768.92
d7	2650.18	2652.48	2653.22	2651.22
d8	2665.78	2667.86	2666.9	2668.4

Table 5: Results on HC problems

Problem	Simple	Mixed	Gender	Herm
hc9	0.968	0.97	0.972	0.97
hc10	0.966	0.966	0.966	0.964
hc11	0.965	0.963	0.964	0.965
hc12	0.963	0.962	0.962	0.962
hc13	0.96	0.96	0.961	0.962
hc14	0.959	0.959	0.962	0.961
hc15	0.959	0.959	0.96	0.96
hc20	0.958	0.958	0.958	0.957
hc25	0.953	0.952	0.953	0.953
hc30	0.944	0.943	0.943	0.944
hc50	0.937	0.937	0.937	0.937
hc60	0.94	0.938	0.938	0.939
hc70	0.939	0.939	0.939	0.939
hc80	0.94	0.94	0.94	0.94
hc90	0.94	0.94	0.94	0.942
hc100	0.94	0.939	0.939	0.94
hc110	0.942	0.941	0.94	0.942
hc120	0.938	0.938	0.939	0.94
hc130	0.939	0.939	0.939	0.937
hc140	0.935	0.935	0.936	0.937
hc150	0.941	0.94	0.935	0.938

herm, are based on populations completely formed of male/female and hermaphrodite individuals respectively. For both of them, an individual cannot self-duplicate. For the first one, the mating choice is limited to about half of the population.

3.2 EXPERIMENTAL RESULTS

Table 3 presents the average performance over 100 runs in 500 generations achieved by each reproduction scheme on the set of standard function. Each problem in this class is a minimization problem, so that the smaller results are the best ones.

Table 4 presents the results under the same conditions on the deception problems. This class contains optimization problems, where the maximal performance is equal to 3000.

Table 5 shows the results of the reproduction schemes on the HC problems. The maximal performance in this case is equal to 1.

From these tables we can notice that the best average performance is obtained almost in all the cases by either the two-gender or the hermaphrodite populations.

The mixed scheme, where the gender type evolves by genetic operations, is almost never the best one. We can deduce that avoiding self-fertilization can improve the performance of GAs.

Table 6 summarizes the results presented in the previous tables, by counting the number of times each scheme presents the best average performance for each class of problems (the columns marked by μ). We have also considered the number of problems where each scheme presented the best result for the optimal run out of 100 (the columns marked by *opt*). This table emphasizes the conclusions we have made based on the previous tables, and shows that the best reproduction scheme for the GAs is the hermaphrodite. This means that for the size of the population we have considered, it is better to allow a wider mating choice for each individual, while avoiding the self-duplication.

From this second set of experiments, we can deduce that given the success of gender separation in our natural system, this factor must contribute to the capacity of survival and of adaptation of the individuals to their environment in other ways than just providing a means of preserving the genetic diversity.

One of the possible advantages of gender separation is the development of complex communication sys-

Table 6: Summary of results

	standard		deception		HC		Total
	μ	opt	μ	opt	μ	opt	
Simple	3	3	1	3	7	5	22
Mixed	1	2	1	2	2	3	11
Gender	4	1	4	3	4	3	19
Herm	2	4	2	0	8	10	26

Table 7: Results on HC problems

Population size	Simple	Gender	Herm
50	0.961	0.962	0.963
60	0.968	0.969	0.968
70	0.970	0.971	0.970
80	0.972	0.972	0.972
90	0.973	0.973	0.973
100	0.973	0.974	0.974

tems that are enhances by the necessities of finding a mate. A second factor could be the fact that the biological differences between the two genders has given way to the raise of a social structure for some of the more evolved organisms and to the distribution of the survival tasks. This phenomenon has evolved into the complex social systems of the human beings, and is also a positive factor for developing the intelligence and for preserving the experience accumulated through generations. These hypothesis constitute the subject of a future research.

4 THE ROLE OF THE POPULATION SIZE

The previous experiences have shown that in the given conditions, the gender separation can be slowing down the search for the optimal individual. This is probably due to the fact that during the crossover operation, a given individual can only mate with half of the individuals in the population. Thus, the best individuals that were found so far may not be available in the process because they are of the same gender as the first parent selected for reproduction.

In the natural habitat, the populations are in general much larger than the experimental size for the GAs. When the population size increases and if there is a balanced distribution of the two genders in the population, it is possible for an individual to find an individual of high fitness among the opposite sex.

Our hypothesis is that the mating restriction inherent to the gender separation presents a significant disadvantage only in the conditions where the population size is small. In the following experiences we will analyze the impact of the population size on the model with gender separation and on the model where the individuals are hermaphrodite but cannot mate with themselves.

We have performed experiences with a HC problem based on a graph with 150 vertices. This problem presents an interesting challenge because the size of the individual is around 3000 genes according to the number of edges in the graph.

Table 7 shows the performance of the simple self-fertilizing model, of the model with gender separation, and of the model with hermaphrodite individual that cannot reproduce with themselves. From this table, we can see that in general, for a difficult problem, avoiding the self-fertilization can help the GA in finding fitter individuals.

Figure 2 shows the evolution of the performance of the two models that avoid self-fertilization (gender separation and hermaphrodite) in 500 generations as the population size increases. The measure that we have considered is the average fitness based on 10 experiences in the same conditions. From this figure we can remark that the difference between the performance of the models decreases as the population size increases. A second remark is that in a given number of generations, both models can find individuals of better fitness when the population is larger.
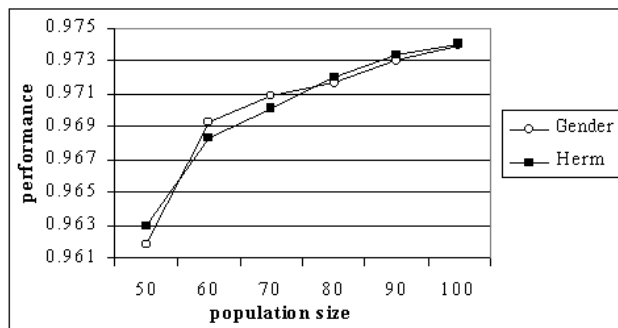

Figure 2: Comparing performance of the models according to the population size

To emphasize the effect of the population size on the performance of the models that we are interested in, Figure 3 shows the evolution of the absolute difference between the average performance of the gender separated model and that of the hermaphrodite model. We can clearly see that as the population size increases,

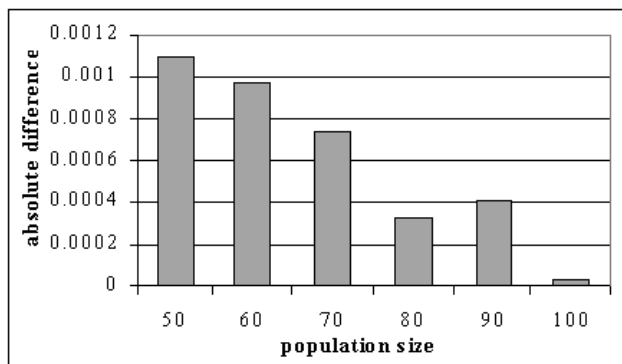the difference between the average performance of the two models is dramatically reduced.

Figure 3: Absolute difference between the models according to the population size.

The experiments introduced in this section have shown that although the hermaphrodite model can present an advantage over the model with gender separation, as suggested by the previous experiences, this advantage seem to disappear as the population size increases.

This phenomenon can explain the large occurrence of gender separation in nature, where the size of the populations is much higher than in our simulations. We can also observe a disadvantage of gender separation for some of the endangered species, where the population size is too small. For some of these species, like the Panda bears, finding a mate can be a real challenge because of the small number of available individuals in a given geographical area.

5 CONCLUSIONS

In this paper, we have used the GAs to analyse some of the aspects related to a phenomenon that is largely encountered in the natural system, the gender separation.

Section 2 has introduced a model in which the gender type evolves through the genetic operations as the individuals try to adapt to a specific problem. From these experiments we can deduce that the first individuals that developed this feature must have presented some adaptation advantages over the others to allow this feature to survive.

Section 3 compares the quality of the individuals that evolve through various reproduction modes, some of which are based on gender separation. The results presented in this section suggest that for small size populations, gender separation can slow down the rate by which the individuals can adapt to a problem.

To continue the idea from the second experiment, Section 4 examines the influence of the population size on the performance of each of the models. These last results suggest that the difference between the models concerning the fitness of the evolved individuals becomes insignificant as the population size increases. Moreover, for a larger size of the population, avoiding the self-duplication can be an advantage.

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