Simulating Gender Separation and Mating Constraints for Genetic Algorithms

Dana Vrajitoru
Intelligent Systems Laboratory
Indiana University South Bend
Department of Computer and Information Sciences
danav@cs.iusb.edu

TR-20050520-1

May 20, 2005

Abstract

This report presents a model for simulating various reproduction modes and types restrictions from nature with the genetic algorithms. We consider three reproduction modes, which are self-fertilizing, hermaphrodite excluding self fertilization, and with two differentiated gender types (male and female). We start with a model in which the reproduction mode evolves along with the rest of the genotype. Next, we compare the performance of the reproduction modes we have introduced and study the influence of the population size on their performance. Finally, we introduce some mating restrictions similar to the natural geographical and social limitations and study their influence on the performance of each reproduction mode.

1 Introduction

In this report, we introduce a simulation of the phenomenon of gender separation using the genetic algorithms (GAs). The purpose of this simulation is to study some of the mechanisms by which this natural feature has become dominant in our ecosystem and the ways it is connected to the evolution and the potential for adaptation of the species. Our hypothesis is that the mating schemes developed by individuals of high fitness, i.e. those highly adapted to their environment, have become dominant in the population as a consequence of natural selection. This research is a continuation of (Vrajitoru, 2002).

The study of the sexual reproduction and of the mating schemes has been an interest of research in GAs and evolutionary computation (Sumida et al., 1990; Miller and Todd, 1995; Ventrella, 1996; Hemelrijk, 1999; Noble, 1999; Rejeb and

AbuElhaija, 2000), especially in relation to the development of communication systems and of biodiversity.

The phenomenon of natural selection of the living beings combined with the preservation of the genetic diversity are among the most powerful adaptation schemes by which many species have survived and evolved into more intelligent ones. In this context, sexual reproduction is the most important mechanism for insuring the genetic diversity of a population and increasing the potential for adaptation of a species to hostile environments. Many studies have demonstrated the importance of preserving the biodiversity (Naeem et al., 1994; Martinez, 1996), some of them in particular for the genetic algorithms (Schaffer and Eshelman, 1991).

Looking at the history of this feature, the original unicellular organisms achieved reproduction by simple division. Subsequently evolution introduced an exchange of genetic information with another individual during the process of cellular division. Later, multicellular organisms came to reproduce through specialized organs that can either be male or female. We can classify these organisms in three major categories according to their mating mechanism.

The first type, called self-fertilizing, is manifest in many plants and consists of individuals that present both male and female features simultaneously, thus being capable of producing offspring without any exterior contribution. The offspring are practically genetic clones of the parent.

The second category contains organisms that present both male and female organs, but that have developed a mechanism to prevent the self-fertilization. For example, some plants develop the male and female organs at different moments in time, while some hermaphrodite species of fish can change their sex at particular stages of their life.

The third category includes all the other multicellular species, in particular the majority of the animals, for which each individual develops only one of the two possible reproductive organs and thus can only mate with individuals of a different gender. This represents in general about half of the population, although for some species an imbalance in the distribution of the two genders can be observed.

Sexual reproduction with completely separate male and female organisms has proven to provide several advantages in nature. The most obvious one is that by preserving the biodiversity it contributes to the strength of the species, to its resistance to diseases, and to its adaptability to novel conditions. Some studies have also shown that sexual differentiation is instrumental in developing communication within a population. Furthermore, we can remark that all the mammals and most vertebrate species have adopted this reproduction mode. This suggests that this reproductive mode may be instrumental in evolving more intelligent organisms, according to the human criteria of defining intelligence.

It has been observed that, in environments free of viruses like the polar or desert regions, and where life is sparse, self-fertilizing organisms are more widespread than in well populated areas (Hamilton et al., 1990). These authors relate their findings to the presence or absence of viruses in those regions and conclude that the existence of two gender types in a species provides it with better chances to adapt to new situations and harsher environments.

Moreover, the gender differentiation has compelled the organisms to develop sophisticated mating schemes, which enhance the natural selection of the best individuals for reproduction (Werner and Todd, 1997). Recruiting an individual of another gender for mating purposes requires among other things a complex communication system whose development may have contributed to evolving language and social structure, both of which are closely related to the intelligence of a species.

Other interesting research concerning gender approaches the problem of multi-optimization (Allenson, 1992). In this context, sexual selection can be regarded as a cooperation between two individuals or even two genetic operators to solve a symbiotic problem (Sanchez-Velazco and Bullinaria, 2003).

In this report we explore several of the reproductive models and their impact on the performance of the genetic algorithms.

The first phenomenon that we study in this report is the mechanism by which gender separation has occurred in nature. For this, we start with a population following a balanced distribution of all the reproduction modes and evolve the gene representing this feature along with the rest of the genetic code. This experiment follows the hypothesis that the original conditions for the separation of the two genders in nature may have involved a mixed population. Thus, initially these individuals were competing with hermaphrodite organisms for survival and dominance within the same species.

The second experiment focuses on a simple comparison of these reproductive modes with respect to the global performance of the population. For this part of the study we explore the question: if two species have the exact same genetic code except for the reproductive mode, how different are their adaptation to the environment and chances for survival?

In the third part of the report we introduce a new variation in the comparison of the reproduction modes. We introduce mating restrictions simulating natural conditions such as geographical and social limitations of the mating choices for any given individual. We then compare the influence of this factor on the performance of the species with the influence of the reproduction mode itself.

The remainder of the report is structured as follows. Section 2 presents our gender evolution model and the general context of our experiment. Section 3 compares the three reproduction modes using three classes of problems: a set of standard functions, several deception problems, and the problem of Hamiltonian circuits in a graph. Section 4 introduces the mating restrictions and studies their influence on the performance of the population, followed by a summary and conclusions.

2 Evolving the Reproduction Mode

In this section we present a simulation model in which the population is initially composed of an equal number of several gender types that can evolve through genetic operations along with the rest of the chromosome. In our experiments, the population always converges to one or two (male/female) gender types, and we are interested in the probability of convergence to each type.

2.1 Model Description

In our model, we have four types of individuals: male (M), female (F), self-fertilizing (SF) and hermaphrodite (H). The gender of the individual is assigned at random in the initial population, and is also inherited by the children from their parents. Thus, the reproduction mode of the individuals selected for reproduction will be inherited by the new generation.

A self-fertilizing individual will mate any individual, including itself. The hermaphrodite individuals can mate any individual other than themselves. The males and females can mate an individual of the opposite sex or any of the two other kinds. It is obvious that in this model, if the population is composed entirely of male or female individuals, the mating search will not succeed no matter what first parent we start with. The distribution between males and females being probabilistically balanced by the design of our algorithm, this situation is extremely unlikely, but not impossible. We prevent such deadlocks by a spontaneous sex change from male to female or the other way around after a number of 25 attempts, or when we have tested 25% of the population and could not find the second parent. Since this situation can only happen after the population has already converged to the male/female model, this precaution does not introduce any bias in the results.

The children inherit the gender type of their parents randomly, with an equal probability attributed to each parent. To keep a fair balance between male and female individuals, when one or two of the parents are of either of these types, then one or two or the children will be either a male or a female, according to a random choice. Thus, the child of a hermaphrodite and a male could be a female with a probability of 25%.

Let us denote by n_{0M}, n_{0F}, n_{0SF}, 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 in the next generation, denoted by n_{1M}, n_{1F}, n_{1SF}, and n_{1H}, considering the mating scheme we have described, first by ignoring the roulette wheel selection. Let $n_{0M} + n_{0F} + n_{0SF} + n_{0H} = n$ be the size of the population. To simplify the computation, let n_{0MF} and n_{1MF} be the number of individuals that are either males or females in the old and new generation respectively, $n_{iMF} = n_{iM} + n_{iF}, i = 0, 1$.

For the male/female individuals, their type can be found in the next generation in either of these situations: if a male or female are chosen as the first parent, or if an individual of any other type is chosen as the first parent and it is matched by a male-female individual. The probability that one chosen individual is a male or female is equal to n_{0MF}/n, the number of such individuals divided by the size of the population.

$$\begin{aligned} n_{1MF} = \frac{n}{2}\left(2\left(\frac{n_{0M}}{n}\frac{n_{0F}}{n-n_{0M}} + \frac{n_{0F}}{n}\frac{n_{0M}}{n-n_{0F}}\right) + \right. \\ \left. + \frac{n_{0M}}{n}\frac{n-n_{0MF}}{n-n_{0M}} + \frac{n_{0F}}{n}\frac{n-n_{0MF}}{n-n_{0F}} + \frac{n_{0H}}{n}\frac{n_{0MF}}{n-1} + \frac{n_{0SF}}{n}\frac{n_{0MF}}{n}\right) \end{aligned} \tag{1}$$

To simplify Equation 1, let us consider that the number of males and of females is about the same and let if be $m_0 = n_{0MF}/2$. If we also note that $n_{0H} + n_{0SF} = n - 2m_0$, then we have that

$$\begin{aligned} n_{1MF} &= m_0\left(\frac{2m_0}{n-m_0} + \frac{n-2m_0}{n-m_0} + \frac{n_{0H}}{n-1} + \frac{n_{0SF}}{n}\right) = \\ &= m_0\left(\frac{n}{n-m_0} + \frac{n-2m_0}{n-1} + \frac{n_{0SF}}{n(n-1)}\right) \\ &= m_0\left(\frac{2n^2 + 2m_0^2 - 3nm_0^2 - n}{(n-1)(n-m_0)} - \frac{n_{0SF}}{n(n-1)}\right) \end{aligned} \tag{2}$$

By ignoring the last term in Equation 2 since it's a small negative quantity, let us see how the expected number of male and female individuals compares to the previous one which is $2m_0$. We will try to prove that the expected number in the new generation is lower than their number in the previous one. This is equivalent to proving that

$$\begin{gathered} \frac{2n^2 + 2m_0^2 - 3nm_0^2 - n}{(n-1)(n-m_0)} \leq 2 \Leftrightarrow \\ 2n^2 + 2m_0^2 - 3nm_0^2 - n \leq 2n^2 - 2n - 2nm_0 + 2m_0 \Leftrightarrow \\ (m_0 - 1)(2m_0 - n) \leq 0 \end{gathered} \tag{3}$$

In Equation 3, we can assume that $m_0 \geq 1$, otherwise $n_{1MF} = 0$. What remains to verify is that $2m_0 \leq n$. If we remember that we have made the assumption that $n_{0MF} = 2m_0$, this means that if either the number of hermaphrodite or of self-fertilizing individuals in the population is not 0, then the population of male/female individuals will decrease from each generation to the next.

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. The probability of the second case requires a complex computation because in the case where the first parent is a male, a hermaphrodite individual will be chosen from the entire population except for the male individuals, which increases their chances. Their expected number is

$$n_{1H} = \frac{n}{2}\left(\frac{n_{0H}}{n} + \frac{n_{0SF}}{n}\frac{n_{0H}}{n} + \frac{n_{0M}}{n}\frac{n_{0H}}{n-n_{0M}} + \frac{n_{0F}}{n}\frac{n_{0H}}{n-n_{0F}} + \frac{n_{0H}}{n}\frac{n_{0H}-1}{n-1}\right) \tag{4}$$

To simplify Equation 4 we will make the same assumption as for Equation 1. Then we can rewrite Equation 4 the following way:

$$n_{1H} = \frac{n_{0H}}{2}\left(1 + \frac{n-2m_0}{n-1} + \frac{2m_0}{n-m_0} - \frac{n+n_{0SF}}{n(n-1)}\right) \tag{5}$$

Considering that the last factor in the previous equation is a negligeable quantity, if $m_0 \geq 1$, we can say that

$$n_{1H} \geq \frac{n_{0H}}{2}\left(1 + \frac{n}{n-1}\right) \geq n_{0H} \tag{6}$$

We can interpret Equations 5 and 6 to indicate that as long as the number of male/female individuals is not negligible, the number of self-fertilizing individuals is expected to increase. Then if the number of male/female individuals is close to 0, the expected number of hermaphrodite individuals will slowly decrease in favor of the self-fertilizing ones.

The number of self-fertilizing individuals is computed similar to the hermaphrodite individuals, except that there is no restriction for the parents not to be the same individual. The equation is:

$$n_{1SF} = \frac{n}{2}\left(\frac{n_{0SF}}{n} + \frac{n_{0SF}}{n}\frac{n_{0SF}}{n} + \frac{n_{0M}}{n}\frac{n_{0SF}}{n-n_{0M}} + \frac{n_{0F}}{n}\frac{n_{0SF}}{n-n_{0F}} + \frac{n_{0H}}{n}\frac{n_{0SF}}{n-1}\right) \tag{7}$$

By making the same assumption as for Equation 4, we can rewrite Equation 7 this way:

$$\begin{aligned} n_{1SF} &= \frac{n_{0SF}}{2}\left(1 + \frac{n_{0SF}}{n} + \frac{n_{0H}}{n-1} + \frac{2m_0}{n-m_0}\right) = \\ &= n_{0SF} + \frac{n_{0SF}}{2}\left(\frac{m_0^2}{n(n-m_0)} + \frac{n_{0H}}{n(n-1)}\right) \end{aligned} \tag{8}$$

Equation 8 tells us that as long as the population is not entirely composed of self-fertilizing individuals, their number is expected to increase. It is also notable that the increment of the number of self-fertilizing individuals depends more on the male/female individuals than on the hermaphrodite ones. This means that as long as the population contains some male/female individuals, the number of self-fertilizing individuals will grow at a fast rate. When the population contains only hermaphrodite and self-fertilizing individuals, their numbers will evolve a lot slower.

Using Equations 1 to 8, we have plotted the expected numbers of individuals of each of the four types for a population size of 50 over 500 generations, starting from an equal number of individuals of each type (12.5). Figure 1 shows the results of this simulation.

In this figure we can see that the number of self-fertilizing individuals is continuously growing until it almost dominates the population. The number of hermaphrodite individuals starts by growing while the number of male/female individuals is still large enough, then it starts to decrease, but at a slower rate

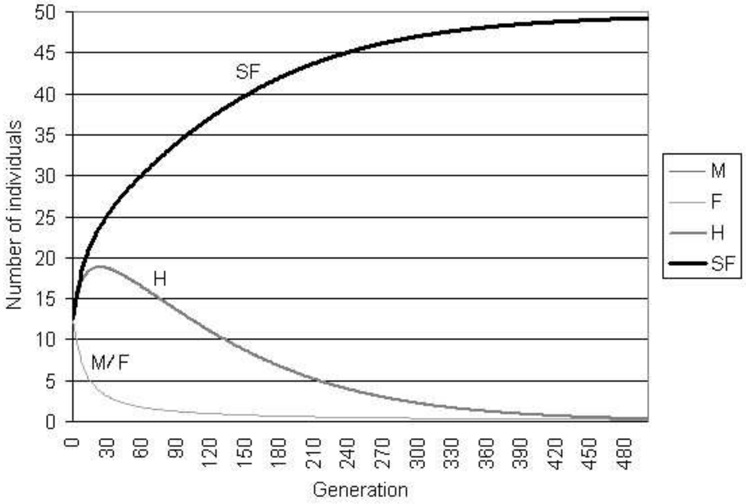

Figure 1: Theoretical evolution of the number of individuals of each gender type for a population of size 50 in 500 generations

than the male/female individuals. The number of male/female individuals becomes less than 1 in generation number 117, while the number of hermaphrodites becomes less than 1 only in generation number 380. Our experiences with a genetic algorithm have shown that the population converges to one gender type a lot faster than in the theoretical case, in general after less than 50 generations.

Note that these computations are done without taking the roulette wheel into consideration. Roulette wheel selection of the parents for crossover will favor the individuals of high fitness and increase the expected number of individuals with their corresponding reproduction type in the new generation.

2.2 Parameter Settings

In this section we introducethe test functions and other parameters that we have used for the genetic algorithm in our simulation.

2.3 Test Functions

We have chosen three classes of problems to test our model: a set of ten standard test functions, several deceptive functions, and one NP-complete problem. Each class of problems presents a special challenge for the GAs, and a combination of them can give us a better idea of the mechanisms in the model that we try to simulate.

Standard functions set

We started our experiments with a set of ten standard functions used in many cases to test GAs (Whitley et al., 1996). The goal is to find values of the variables x_i that minimize each of the functions in Equation 9.

$$
\begin{aligned}
F1: &\quad f(x_i|i=1,3) &&= \sum_{i=1}^{3} x_i^2,\ x_i \in [-5.12, 5.11] \\
F2: &\quad f(x_i|i=1,2) &&= 100(x_1^2 - x_2)^2 + (1-x_1)^2,\ x_i \in [-2.048, 2.047] \\
F3: &\quad f(x_i|i=1,5) &&= sum_{i=1}^{5} \lfloor x_i \rfloor,\ x_i \in [-5.12, 5.11] \\
F4: &\quad f(x_i|i=1,30) &&= \left[\sum_{i=1}^{30} i \cdot x_i^2 \right] + Gauss(0,1),\ x_i \in [-1.28, 1.27] \\
F5: &\quad f(x_i|i=1,2) &&= \left[0.002 + \sum_{j=1}^{25} \frac{1}{j + \sum_{i=1}^{2} (x_i - a_{ij})} \right]^{-1},\ x_i \in [-65.536, 65.535] \\
F6: &\quad f(x_i|i=1,N) &&= 10N + \left[\sum_{i=1}^{N} \left(x_i^2 - 10\cos(2\pi k_i) \right) \right],\ x_i \in [-5.12, 5.11] \\
F7: &\quad f(x_i|i=1,N) &&= \sum_{i=1}^{N} -x_i^2 \sin(\sqrt{|x_i|}),\ x_i \in [-512, 511] \\
F8: &\quad f(x_i|i=1,N) &&= 1 + \sum_{i=1}^{N} \frac{x_i^2}{4000} - \prod_{i=1}^{N} \cos\left(\frac{x_i}{\sqrt{i}} \right),\ x_i \in [-512, 511] \\
F9: &\quad f(x_i|i=1,2) &&= 0.5 + \frac{\sin^2 \sqrt{x_1^2 + x_2^2}}{[1.0 + 0.0001(x_1^2 + x_2^2)]},\ x_i \in [-100, 100] \\
F10: &\quad f(x_i|i=1,2) &&= (x_1^2 + x_2^2)^{0.25} \lfloor \sin^2 \left(50(x_1^2 + x_2^2)^{0.1} \right) + 1.0 \rfloor,\ x_i \in [-100, 100]
\end{aligned}
\tag{9}
$$

For each function, we have chosen the genetic representation of the variables xi such that the optimal individual is neither fully composed of 0 values, nor of 1 values to avoid any bias of the genetic operators. The size of an individual is usually ten times the number of variables involved in the description of its function, meaning that ten genes are used to encode each variable.

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 et al., 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 eight deception problems that consist of concatenating a given 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 experiments with individuals composed of 100 3-bit strings, making the fitness of the optimal individual 3000.

To illustrate the concept of deceptive functions, Figure 2 shows a graph of the function decep1 where the eight possible 3-bit combinations are grouped according to the Hamming distance between them. In this graph, the combinations that are different by just one bit are connected with a line. The fitness value associated with each combination is placed under the vertex. Thus, there is a connection between the combinations 001 and 101 since one is obtained from the other by mutating the first bit.

From this figure we can notice that the two combinations of highest fitness are 000 and 111, the latter being the optimal one. All of the closest neighbors to 111 have a fitness of 0, while the closest neighbors to 000 are assigned positive fitness values which make the suboptimal solution 000 much easier to reach.

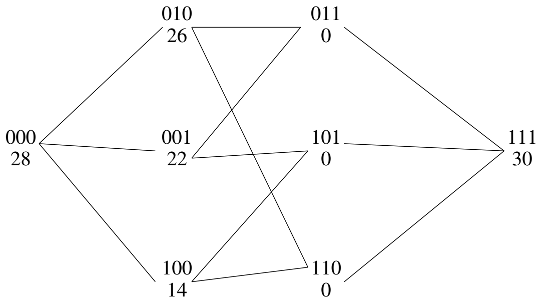

Figure 2: Graph of 3-bit combinations with associated fitness values for the function *decep1*. The edges represent Hamming distances of 1 bit.

Hamiltonian circuit (HC)

Given an oriented 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 experiments with ten HC problems having graphs of 9 to 150 vertices and up to 3000 edges. The direct representation of a HC problem for the GAs is difficult. De Jong and Spears (1989) suggest transforming the HC instances into instances of the satisfiability (SAT) problem, described bellow, 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 value of the expression becomes true?

Table 1: Fitness associated with each 3-bit combination for the 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

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 circuit. The SAT expression represents the fact that, for each vertex, one and only one of the entering edges and of the exiting edges must belong to the circuit. This translates into an 'xor' clause binding all the edges entering each vertex and a similar one for the edges exiting each vertex. The entire expression is built by combining all the clauses with the 'and' operator.

For example, let us consider the graph in Figure 3. The conversion of the HC instance for this graph into a SAT instance would result in Equation 10, in which a Boolean variable with the same name as edge is true if the edge belongs to the Hamiltonian circuit. The symbols '⊗' and '∧' represent the Boolean 'xor' and 'and' operators.

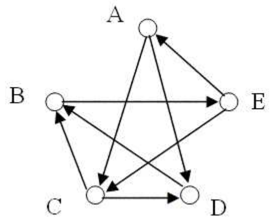

Figure 3: The graph for which Equation 10 represents the instance of SAT corresponding to its HC instance

$$\begin{array}{ll} out & (AC \otimes AD) \wedge BE \wedge (CB \otimes CD) \wedge DB \wedge (EA \otimes EC) \wedge \\ in & EA \wedge (CB \otimes DB) \wedge (AC \otimes EC) \wedge (AD \otimes AD) \wedge BE \end{array} \tag{10}$$

This SAT expression can be satisfied by the following truth assignment: AC, CD, DB, BE, and BA being true, and all of the other variables being false. This solution also represents a Hamiltonian circuit in the graph if considered as a sequence of edges.

The genetic representation of SAT is straightforward. Each variable is mapped onto a binary gene, where the 0 / 1 values can be interpreted as false/true. In the classical evaluation of a Boolean expression, an individual can only be evaluated to the true / false values. Thus, as long as an individual does not represent an exact solution for the expression, it is evaluated to 0. This makes it difficult for the GA to improve the individual performance, because it cannot decide whether an individual is far from, or close to, the optimal solution. To evaluate an expression to more than true or false, we used fuzzy logic measures, also proposed by De Jong and Spears (1989) . Specifically, the 'and' operation is evaluated to the average of the terms, while the 'or' operation returns the maximum of the terms.

2.4 The Crossover Operator

We have used the combined balanced crossover operator (Vrajitoru, 2004). This operator utilizes four variations of crossover to build every new generation: 1-point, 2-point, uniform and dissociated. For each operation, one of the four crossover forms is chosen randomly, each of them having an equal probability to be selected. We will briefly describe the functionality of these operators.

Let L be the length of the individual, where the genes are numbered from 0 to $L-1$.

The 1-point crossover (Holland, 1975) cuts each parent at a random cross site between 1 and $L-1$, and swaps the resulting right hand sides of the parents. In particular, if the cross site is equal to $L-1$, no exchange of information occurs between the parents.

The n-point crossover (De Jong, 1975) is equivalent to n independent 1-point crossovers applied in sequence to the same parents. It cuts the parents in n points and exchanges every other resulting part from the parents. For our experiments, we have chosen $n = 2$.

The uniform crossover (Syswerda, 1989) swaps each of the parent genes with a probability $p_{swap} < 0.5$ independently of any other gene. We have chosen $p_{swap} = 0.5$ for our research, which means that approximately $L/2$ of the parent genes will be randomly exchanged. This operator is interesting because it eliminates the location bias in the genetic representation of the solutions to the problem.

The dissociated crossover (Vrajitoru, 1999) splits each parent in two at a different cross site, and swaps the resulting right hand sides of the parents by applying logical conjunction and disjunction respectively on the parent genes for determining the values between the cross sites.

2.5 Experiment Description

In this experiment we start with a population composed of equal numbers of each gender type and run the GA for 500 generations. The gender type is inherited by the children from the parents as we described in Section 3.1. Gender type evolves along with the rest of the genotype. Our primary interest is in the composition of the population at the conclusion of the evolutionary simulation.

We performed 150 runs of the GA for each problem with a different initial population. 50 of the trials were with a mutation rate of 0 (no mutation), 50 of them with a mutation rate of 0.0005, and 50 of them with a mutation rate of 0.01. The crossover rate is equal to 1 in all the cases. We performed each experiment with an initial population size of 50.

To have a baseline for estimating the impact of the fitness-proportionate selection on the gender evolution, we have performed a simulation in the same conditions as our experiments (population of size 50, 500 generations, 50 trials) with a fictious population for which the fitness function was constant (equal to 1). This gives us an idea of what the expected gender evolution is if we only consider the probabilities derived from the mating constraints.

Figure 4 shows the result of this simulation in the first 215 generations, since the population had completely converged at that point in all of the 50 trials. The generation number actual total convergence generation is number 212, but the generation at which the number of male/female individuals have become 0 is 109.

If we compare this figure with Figure 1, we notice that in this second case, the convergence was less smooth and the population also took longer to converge, but the general outline of the evolution of the number of individuals of each gender type is similar. The difference between the two simulations is that Figure 1 presented only a computation of the sequences of expected numbers of individuals based on the probabilities introduced in Section 2.1. The expected number of individuals of each gender is a real number in that case. The later simulation presented in Figure 4 is a more practical one in which individuals are selected randomly regardless of their fitness, but the mating constraints are the same as in the case of a real population. The number of individuals of each gender in this case must be an integer number.

The results of our experiments with the three types of problems are shown Tables 2 and 3. We display the percentage of simulations for which the population has converged to each of the gender types, for each class of problems, and for population sizes of 50 and 100 respectively. These results are compared with the convergence number for each gender type in the simulation presented in Figure 4, denoted in the table by constant fitness. In our experiments, the population has always converged to one particular gender type in 500 generations, and often a lot sooner than that.

We note that although the general distribution of gender types confirms the previous computations, the number of male/female composed populations is not equal to the expected number (0). Also, the number of hermaphrodite individuals is higher than the expected one. These discrepancies are due to the

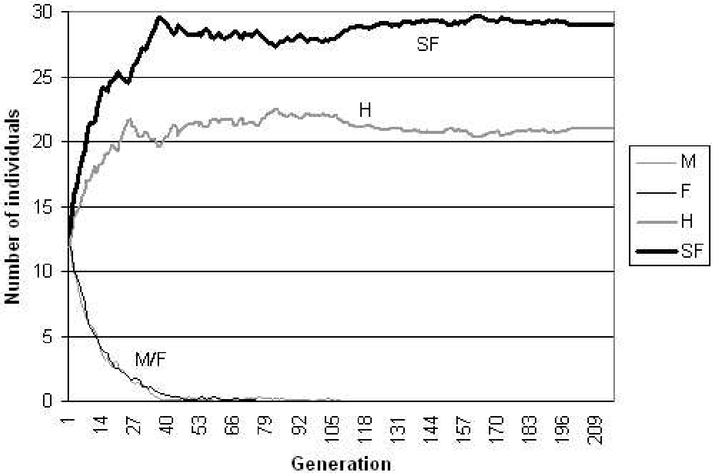

Figure 4: Simulation of gender evolution with a population size of 50 in 500 generations (215 shown), constant fitness

influence of the fitness-proportionate selection and also suggest that the mating constraints that preserve the bio-diversity of the population by preventing the self-fertilization (or cloning) show a better performance than the simple reproduction scheme, which is why their numbers are higher than expected. This phenomenon is accentuated for the populations of smaller size. For the larger populations, the results are closer to the probabilistic expectations and this is most likely due to the probabilistic law of big numbers.

3 Comparing the Reproduction Modes

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

Here we compare four reproduction schemes that we compare using the average performance over 100 runs on each test problem. Half of these tests were conducted without mutation and half with a mutation rate of 0.01. The population sizes were 50 and 100.

The first reproduction scheme is 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

Table 2: Gender convergence in 500 generations, population size of 50

	M/F	H	S-F	
	Constant fitness	0	42%	58%
$p_m = 0$	Standard	1.00%	45.80%	53.20%
	Deception	0.50%	47.00%	52.50%
	HC	0.57%	46.29%	53.14%
	Average	0.69%	46.36%	52.95%
$p_m = 0.0005$	Standard	0.00%	42.67%	57.33%
	Deception	0.00%	46.34%	53.66%
	HC	0.00%	47.90%	52.10%
	Average	0.00%	45.64%	54.36%
$p_m = 0.01$	Standard	1.00%	45.80%	53.20%
	Deception	0.50%	48.00%	51.50%
	HC	0.48%	46.38%	53.14%
	Average	0.66%	46.73%	52.61%
Global	Average	0.68%	46.54%	52.78%

Table 3: Gender convergence in 500 generations, population size of 100

	M/F	H	S-F	
	Constant fitness	0%	40%	60%
$p_m = 0$	Standard	0.20%	48.19%	51.61%
	Deception	0.00%	46.02%	53.98%
	HC	0.00%	41.65%	58.35%
	Average	0.07%	45.29%	54.65%
$p_m = 0.0005$	Standard	0.20%	46.37%	53.41%
	Deception	0.00%	37.73%	62.27%
	HC	0.00%	44.97%	55.03%
	Average	0.07%	43.02%	56.9%
$p_m = 0.01$	Standard	0.20%	47.15%	52.65%
	Deception	0.00%	42.00%	58.00%
	HC	0.00%	43.86%	56.14%
	Average	0.07%	44.34%	55.59%
Global	Average	0.07%	44.22%	55.71%

by *mixed*.

The last two schemes, denoted by *hetero* and *herm*, are based on populations completely formed of male/female and hermaphrodite individuals respectively. For both of them, an individual cannot be mated with itself. For hetero, the mating choice is limited to about half of the population.

We have based our evaluation on the best fitness value achieved in the terminal generation. To evaluate each reproduction type on each problem, we have chosen two measures: the average performance over the 100 runs and the best performance from the same 100 runs. This gives us an estimation of the average and best case performance of each model. These measures provide a classification of our schemes in which we only consider the top first and second positions.

We have defined the score of each crossover operator as the number of occurrences it has on the top first and top second positions for each of the average and best case performance. For a global classification of the models, we compute the total number of points in each case as a weighted sum of these four numbers, where the top second positions receive half the weight of the top first positions.

3.2 Experimental Results

Table 4 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 smaller results are better. Table 5 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 6 shows the results of the reproduction schemes on the HC problems. The maximal performance in this case is equal to 1.

We have compared the results using a T-Test with a confidence of 95%. In each table, we have displayed the best results that are significantly better than the next one in bold. The best results for each class of problems that are not significantly better than the average are displayed only in bold.

From these tables we observe that the best average performance is obtained in almost all cases by either the hetero or the hermaphrodite populations. The mixed scheme, where gender type evolves, is almost never the best one. This suggests that avoiding self-fertilization can improve the performance of GAs.

Tables 7, 8, and 9 show the same results for a population size of 100, rounded to 2 or 3 decimals. These represent an average over 150 trial with mutation rates of 0, 0.01, and 0.0005. Just as before, we have compared the best and second best results with a T-test with a confidence of 95% and marked in italics the best results that showed a significant difference with the next ones. We notice that just as before, very few of these results can be considered significantly better than the previous ones.

These tables also suggest that for larger populations, the gender-separated mating type, that we have denoted by “hetero”, performs better than the others

Table 4: Average fitness in 500 generations, standard test functions, population size of 50

Problem	Simple	Mixed	Hetero	Herm	Best
F1	0.136	0.119	0.104	0.122	hetero
F2	0.307	0.212	0.398	0.249	mixed
F3	1.687	1.68	*1.667*	1.673	hetero
F4	2.433	2.516	2.315	2.463	hetero
F5	3.645	5.074	4.87	4.283	simple
F6	2.636	2.843	2.639	2.822	simple
F7	95.993	110.867	97.407	87.523	herm
F8	1.64	1.846	1.865	1.749	simple
F9	0.091	0.1	0.093	0.1	simple
F10	1.239	1.396	1.119	1.302	hetero

Table 5: Average fitness in 500 generations, deception problems, population size of 50

Problem	Simple	Mixed	Hetero	Herm	Best
d1	2720.51	2730.41	2729.75	2725.16	mixed
d2	2875.99	2926.21	2877.45	2876.83	mixed
d3	2548.84	2558.95	2560.35	2563.56	herm
d4	2562.77	2554.69	2553.65	2554.93	simple
d5	2782.01	2783.45	2781.81	2785.69	herm
d6	2780.37	2780.64	2782.03	2782.28	herm
d7	2682.13	2686.25	2683.99	2684.99	mixed
d8	2687.71	2688.39	2688.64	2690.07	herm

Table 6: Average fitness in 500 generations, HC problems, population size of 50

Problem	Simple	Mixed	Hetero	Herm	Best
hc50	0.946	0.946	0.946	0.945	hetero
hc60	0.946	0.945	0.944	0.945	simple
hc70	0.944	0.944	0.944	0.944	hetero
hc80	0.943	0.944	0.944	0.943	hetero
hc90	0.943	0.943	0.944	0.945	herm
hc100	0.943	0.943	0.943	0.943	mixed
hc110	0.945	0.944	0.944	0.945	simple
hc120	0.943	0.943	0.944	0.944	herm
hc130	0.943	0.943	0.943	0.942	simple
hc140	0.94	0.941	0.942	0.942	herm
hc150	0.946	0.946	0.942	0.945	simple

more often than for small populations. This confirms some empirical observations from nature where small populations that reproduce with two separated sexes have more difficulties than hermaphrodite species under the same conditions, but for large populations, this reproduction type is quite successful.

Table 10 summarizes the results presented in the previous tables, by counting the number of times that each scheme results in the best average performance for each class of problem (the columns marked by average) for the two values we have chosen for the population size. This table suggests that the gender-separated model performs better than the others, especially for the larger population size, which reinforces the hypothesis that it is the better fitness that has made this mating type successful in nature, and not the probabilistic expectations.

4 Population Size and Mating Limitations

In this section we introduce a new experiment designed to simulate geographically or socially restricted mating options. We also explore the influence of the population size on the performance of each of our models. For this set of experiments we have chosen a mutation rate of 0.0005 and a number of generations equal to 1000. We have found this mutation rate and population size more suitable for the particular problem (HC) that we have chosen for these experiments.

4.1 The Population Size

The previous experiments have shown that, in the given conditions, the separation of genders may be inhibiting the search for the optimal individual. This is

Table 7: Average fitness in 500 generations, standard test functions, population size of 100

Function	Simple	Mixed	Hetero	Herm	Best
F1	0.001	0.001	0.001	*0.001*	hetero
F2	0.003	0.003	0.003	0.002	hetero
F3	0.3	0.313	0.387	0.353	simple
F4	1.496	1.405	1.504	1.424	mixed
F5	0.729	1.242	0.393	0.854	mixed
F6	0.829	0.8	0.729	0.876	hetero
F7	8.463	9.567	1.357	3.252	hetero
F8	0.338	0.363	0.328	0.358	hetero
F9	0.012	0.012	0.011	0.012	hetero
F10	0.47	0.469	0.467	0.459	herma

Table 8: Average fitness in 500 generations, deception problems, population size of 100

Problem	Simple	Mixed	Hetero	Herm	Best
d1	2782.61	2781.79	2717.29	2785.27	hetero
d2	2936.25	2943.2	2929.81	2943.13	mixed
d3	2526.47	2531.55	2440.65	2521.63	mixed
d4	2525.67	2530.32	2442.67	2527.96	mixed
d5	2745.28	2746.77	2713.41	2745.84	mixed
d6	2743.72	2744.59	2711.75	2745.96	hetero
d7	2656.05	2658.49	2595.72	2658.61	hetero
d8	2666.36	2663.76	2631.01	2665.67	simple

Table 9: Average fitness in 500 generations, HC problems, population size of 100

Problem	Simple	Mixed	Hetero	Herm	Best
hc50	0.941	0.937	0.943	0.942	herm
hc60	0.937	0.931	0.937	0.937	simple
hc70	0.934	0.93	*0.934*	0.935	hetero
hc80	0.935	0.931	0.934	0.935	hetero
hc90	0.939	0.937	0.939	0.939	hetero
hc100	0.94	0.939	0.94	0.94	hetero
hc110	0.946	0.945	0.946	0.946	herma
hc120	*0.95*	0.948	0.95	0.95	simple
hc130	0.95	0.949	0.95	0.95	simple
hc140	0.952	0.95	0.952	0.952	herm
hc150	0.961	0.959	0.961	0.961	hetero

Table 10: Number of problems for which each model has been the best on average and for the optimal run

	standard		deception		HC		Total
pop size	50	100	50	100	50	100	
Simple	4	1	1	1	4	3	14
Mixed	1	2	3	4	1	0	11
Hetero	4	5	0	3	3	5	20
Herm	1	2	4	0	3	3	13

Table 11: Average fitness in 1000 generations with no mating restrictions

Population size	Simple	Hetero	Herm	Best
50	0.966	0.966	0.967	Herm
60	0.970	0.971	0.971	Herm
70	0.973	0.973	0.973	Hetero
80	0.974	0.974	0.974	Hetero
90	0.975	0.975	0.975	Simple
100	0.975	0.975	0.975	Simple

probably due to the fact that a given individual can only mate with half of the individuals in the population. Thus, the best individuals found so far may not be available for mating because they are of the same gender as the first parent selected for reproduction.

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

Our hypothesis is that the mating restriction inherent to the gender separation presents a significant disadvantage only in the situation where the population size is small. In the following experiments we analyze the impact of population size on the gender separation model and on the hermaphrodite, non self-mating, model.

We performed these experiments using 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, based on the number of edges in the graph.

Table 11 shows the performance of simple self-fertilization, gender separation, and hermaphrodite model with avoidance of the self-reproduction. The best result on each row is displayed in bold. 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. This table also shows that in this case there is no significant difference between the three models we have considered.

4.2 Mating Restrictions

In the previous section we have seen that the difference between a heterosexual and a hermaphrodite population decreases with the population size, and that for a sufficiently large number of individuals, the difference is insignificant. In nature the populations are, in general, very large compared to these simulations, but the mating process is limited by geographical constraints for most species. Thus, an individual can only mate another individual that is within a reasonable distance from its spatial location.

Moreover, for humans, these limitations are also of a social nature. Thus, an individual will generally look for a mate with common social, cultural, often religious, or ethnic background. This also reduces the number of potential candidates for reproduction. In simulation, this background can be translated to a degree of adaptation to the problem, or to similarity in the fitness value of the individual.

In the following experiment we simulate mating limitations by imposing a geographical distance (range) within which the potential mate can be found. We compute the performance of each reproduction type depending on the population size and on the mating restrictions.

In this model, for each crossover operation the first parent is chosen at random with a probability proportionate to its fitness. Next, the second parent is chosen within a given distance from the first individual.

Since the population is sorted in ascending order by fitness, the mating range has two effects. First, it simulates a geographical limitation, and second, it insures that the mating process will choose parents of similar performance. The latter constraint simulates social mating limitations.

We performed our experiments with a fixed range of 10 and 25 individuals, followed by a range equal to 10% and 25% of the population. We have tested the influence of this factor on the performance of each of the three reproduction schemes: common asexual, hermaphrodite avoiding the self-reproduction, and with gender separation. The population size varies between 50 and 100.

Tables 12 and 13 show the results obtained by each of these schemes for a fixed mating radius and for a radius representing a percentage of the population respectively. Each entry represents the average over 50 trials of the best fitness in the last generation. The best result in each situation is displayed in bold. The number of generations is limited to 1000, and the mutation rate is 0.0005. For this experiment we have chosen a graph with 150 nodes and 3136 edges representing the number of genes in each individual. The results are displayed in order of the population size.

The first observation that we can make based on these results is that a small population radius has a beneficial effect on the performance of the algorithm. This can be explained by noting that the individuals in a given range around the first parent possesses a fitness that is closer to it than outside this radius. Thus, if the first parent is already selected based on its fitness, it is likely to be one of the individuals of high performance and the mating radius enforces this first choice. The result is a fitness-based selection that favors the best individuals more than the simple fitness-proportionate one.

The second observation is that for a relatively small population, the hermaphrodite model produced better results than the gender-separated one. However, when the population size increases, the difference between the two models becomes insignificant. Moreover, both of the schemes that avoid the self-reproduction, show better results than the simple model.

A second set of experiments explored the model in the case where the population is not sorted. We would expect these restrictions to lead the algorithm to less fit solutions, since this is a weaker fitness-based selection. In this case

Table 12: Average fitness in 1000 generations with a fix mating radius of 10 and 25, sorted population

	Mating radius					
	10			25		
Population size	Simple	Hetero	Herm	Simple	Hetero	Herm
50	0.963	0.964	0.966	0.961	0.961	0.962
60	0.970	0.970	0.970	0.968	0.968	0.968
70	0.973	0.973	0.974	0.971	0.971	0.972
80	0.975	0.975	0.976	0.974	0.973	0.973
90	0.976	0.977	0.977	0.975	0.975	0.975
100	0.977	0.977	0.977	0.976	0.976	0.976

Table 13: Average fitness in 1000 generations with a mating radius of 10% and 25% of the population, sorted population

	Mating radius					
	10%			25%		
Population size	Simple	Hetero	Herm	Simple	Hetero	Herm
50	0.962	0.964	0.966	0.963	0.965	0.967
60	0.969	0.970	0.971	0.969	0.971	0.972
70	0.973	0.974	0.974	0.972	0.974	0.974
80	0.975	0.976	0.976	0.974	0.975	0.976
90	0.976	0.977	0.977	0.975	0.977	0.977
100	0.977	0.978	0.977	0.976	0.977	0.977

Table 14: Average fitness in 1000 generations with a mating radius of 10 and 25, unsorted population

	Mating radius					
	10			25		
Population size	Simple	Hetero	Herm	Simple	Hetero	Herm
50	0.962	0.962	0.962	0.962	0.962	0.963
60	0.964	0.963	0.964	0.964	0.964	0.963
70	0.964	0.964	0.964	0.964	0.964	0.964
80	0.965	0.964	0.964	0.965	0.964	0.964
90	0.965	0.964	0.965	0.965	0.965	0.965
100	0.966	0.964	0.965	0.966	0.965	0.965

the first parent is chosen by fitness-proportionate selection, while the second one is chosen proportional to fitness within a given radius around the first. If the population is not sorted according to the fitness values, this means that the second parent will be chosen within a sample of the original population, and that the best individuals for reproduction may not be available in the close neighborhood of the first parent.

In this second experiment, we also note that individuals resulting from one crossover operation are placed by the algorithm next to each other in the population, so the geographical closeness also means some sort of genealogical link between the parents selected for crossover. Thus, individuals that are close to each other in the population are more likely to have some common ancestors.

Tables 14 and 4.2 show the same experiment performed for a population that is not sorted. The best result in each experiment is displayed in bold.

These tables indicate that the performance in each situation where the population is not sorted hass deteriorated as compared to a sorted population. The mating restriction to a given radius has the effect of enhancing the fitness-proportionate selection in the case of a sorted population and of reducing it for an unsorted population.

In this experiment we note that for smaller populations, the hermaphrodite mating scheme seems to perform better than the others, while for larger populations it's the simple reproduction form with no gender definition that is better than the others, although the difference in performance between all the results obtained by various mating schemes are not significant.

For a visual comparison of these various mating schemes and restrictions, we have plotted the performance of a population of 50 and 100 individuals respectively with a mating restricted to 10 individuals as shown in Figures 5 and 6. The horizontal marks represent, respectively, the sorted population with a mating radius of 10, the unsorted population with the same mating radius, and the original model with no mating restrictions, in which case the sorted or

Table 15: Average fitness in 1000 generations with a mating radius of 10% and 25% of the population, unsorted population

	Mating radius					
	10%			25%		
Population size	Simple	Hetero	Herm	Simple	Hetero	Herm
50	0.962	0.960	0.963	0.967	0.967	0.969
60	0.963	0.963	0.963	0.967	0.970	0.968
70	0.963	0.963	0.964	0.969	0.971	0.970
80	0.964	0.964	0.965	0.968	0.969	0.969
90	0.965	0.964	0.965	0.971	0.968	0.968
100	0.966	0.965	0.965	0.970	0.969	0.968

unsorted populations should perform about the same. The noticeable difference between these categories indicate that sorting the population and the restricting the mating choices to a radius have a much larger influence on the performance of the algorithm than the choice between the three mating schemes.

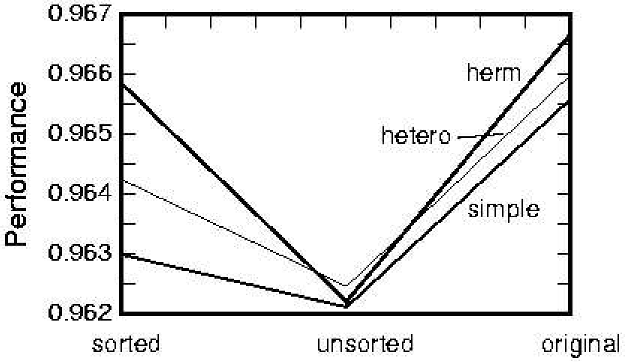

Figure 5: Average fitness for the 3 mating schemes for a population of size 50

Sorting the population could relate to two biological phenomena. A sorted population is comparable to the process by which some specialized species of animals and plants are artificially created through a supervised mating. This enhances the specific features of that plant or animal that are interesting to the human cultivator, such as the color of the flowers or the resistance to disease or parasites.

On the other hand, the mating restrictions in an unsorted population resembles the situation encountered by endangered species like the panda bear, for which limitations in the geographical availability of other individuals for mating can deteriorate the genetic material and increase the frequency of genetic

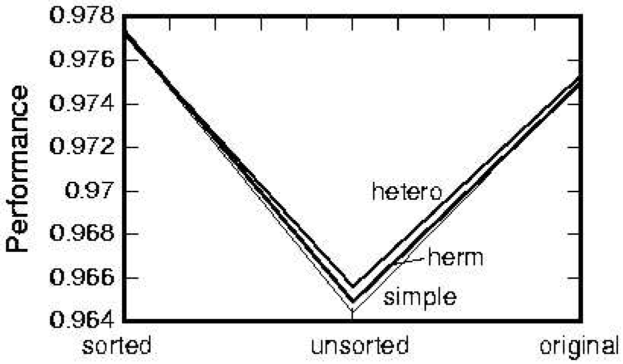

Figure 6: Average fitness for the 3 mating schemes for a population of size 100

diseases.

5 Conclusions

In this report we have introduced several models simulating a variety of mating schemes related to gender separation. We have also explored the influence of social factors such as the size of the population and mating restrictions on the potential population adaptation.

We simulated several reproduction models including hermaphrodite and separate genders competing for dominance in the same population. Our experiments show that the particular features associated with individuals of high fitness tend to become dominant in the population and can override the simple probabilistic expectations, as seen in Section 2. This could have been a contributing mechanism through which gender separation initially occurred in nature.

Section 3 compared the general performance of parallel populations that have the same genetic representation, but different reproduction modes. From our experiences we can infer that hermaphrodite populations have a better chance of finding good solutions and that encouraging the biodiversity by preventing of self-reproduction (or cloning) is benefic to performance.

Finally, in Section 4we studied the influences of social factors like population size and geographical or social mating restrictions on the performance of the population. From our experiments we observe that these factors have a much larger impact on the quality of the evolved solutions than the reproduction type itself. Moreover, the differences in the average fitness between the populations with various mating schemes decrease with the population size such that for large enough populations, the reproduction mode becomes insignificant.

References

Allenson, R. (1992). Genetic algorithms with gender for multi-function optimisation. Technical Report EPCC-SS92-01, Edinburgh Parallel Computing Centre, Edinburgh, Scotland.

Brassard, G. and Bratley, P. (1994). *Fundamentals of Algorithmics*. Prentice-Hall.

De Jong, K. (1975). *An Analysis of the Behaviour of a Class of Genetic Adaptive Systems*. PhD thesis, University of Michigan.

De Jong, K. and Spears, M. (1989). Using genetic algorithms to solve NP-complete problems. In *Proceedings of the International Conference on Genetic Algorithms*, pages 124–132, Fairfax (VA). George Mason University.

Deb, K. and Goldberg, D. E. (1994). Sufficient conditions for arbitrary binary functions. *Annals of Mathematics and Artificial Intelligence*, 10:385–408.

Goldberg, D. E., Deb, K., and Horn, J. (1992). Massive multimodality, deception and genetic algorithms. In Manner, R. and Manderick, B., editors, *Proceedings of Parallel Problem Solving from Nature II*, pages 37–46.

Hamilton, W., Axelrod, R., and Tanese, R. (1990). Sexual reproduction as an adaptation to resist parasites. *Proceedings of the National Academy of Sciences*, 87:3566–3573.

Hemelrijk, C. (1999). Effects of cohesiveness on intersexual dominance relationships and spatial structure among group-living virtual entities. In *Proceeding of the European Conference on Artificial Life V*, pages 524–534. Springer Verlag.

Holland, J. H. (1975). *Adaptation in Natural and Artificial Systems*. University of Michigan Press, Ann Arbor.

Kingdon, J. and Dekker, L. (1995). The shape of space. In *Proceedings of the Conference on Genetic Algorithms in Engineering Systems: Innovations and Applications (GALESIA '95)*, pages 543–548, London (UK). IEE.

Martinez, N. (1996). *Biodiversity: A Biology of Numbers and Difference*, chapter Defining and measuring functional aspects of biodiversity, pages 114–148. Blackwell Scientific, Oxford, UK.

Sanchez-Velazco, J. and Bullinaria, J. (2003). Sexual selection with competitive/co-operative operators for genetic algorithms. In *IASTED International Conference on Neural Networks and Computational Intelligence (NCI 2003)*. ACTA Press.

Miller, G. and Todd, P. (1995). The role of mate choice in biocomputation: Sexual selection as a process of search, optimization, and diversification. In Banzhaf, W. and Eeckman, F., editors, *Evolution and biocomputation: Computational models of evolution*, pages 169–204, Berlin. Springer-Verlag.

Mohan, C. K. (1998). Selective crossover: Towards fitter offspring. In *Proceedings of the Symposium on Applied Computing (SAC'98)*, Atlanta (GA).

Naeem, S., Thompson, L., Lawlor, S., Lawton, J., and Woodfin, R. (1994). Declining biodiversity can alter the performance of ecosystems. *Nature*, (386):734–737.

Noble, J. (1999). Sexual signalling in an artificial population: When does the handicap principle work? In Floreano, D., Mondada, F., and Nicoud, J.-D., editors, *Proceeding of the European Conference on Artificial Life V*, pages 644–653. Springer Verlag.

Rejeb, J. and AbuElhaija, M. (2000). New gender genetic algorithm for solving graph partitioning problems. In *43rd IEEE Midwest Symposium on Circuits and Systems*, volume 1, pages 444–446. IEEE.

Schaffer, J. D. and Eshelman, L. (1991). On crossover as an evolutionary viable startegy. In Belew, R. and Booker, L., editors, *Proceedings of the Fourth International Conference on Genetic Algorithms*, pages 61–68, San Mateo (CA). Morgan Kaufmann Publishers.

Sumida, B., Huston, A., McNamara, J., and Hamilton, W. (1990). Genetic algorithms and evolution. *Journal of Theoretical Biology*, (147):59–84.

Syswerda, G. (1989). Uniform crossover in genetic algorithms. In Schaffer, J. D., editor, *Proceedings of the International Conference on Genetic Algorithms*, San Mateo (CA). Morgan Kaufmann Publishers.

Ventrella, J. (1996). Sexual swimmers: Emergent morphology and locomotion without a fitness function. In *Proceedings of the Fourth International Conference on Simulation of Adaptive Behavior*, pages 484–496. Bradford Books.

Vrajitoru, D. (1999). Genetic programming operators applied to genetic algorithms. In *Proceedings of the Genetic and Evolutionary Computation Conference*, pages 686–693, Orlando (FL). Morgan Kaufmann Publishers.

Vrajitoru, D. (2002). Simulating gender separation with genetic algorithms. In *Proceedings of the Genetic and Evolutionary Computation Conference*, pages 634–641. Morgan Kaufmann Publishers.

Vrajitoru, D. (2004). Intra and extra-generation schemes for combining crossover operators. In *The Midwest Artificial Intelligence and Cognitive Science Conference*.

Werner, G. and Todd, P. (1997). Too many love songs: Sexual selection and the evolution of communication. In Husbands, P. and Harvey, I., editors, *The Fourth European Conference on Artificial Life*, Cambridge (MA). MIT Press/Bradford Books.

Whitley, D. (1990). Fundamental principles of deception in genetic algorithms. *Foundations of Genetic Algorithms*, pages 221–241.

Whitley, D., Mathias, K., Rana, S., and Dzubera, J. (1996). Evaluating evolutionary algorithms. *Artificial Intelligence*, 85:245–276.