

# A Genetic Algorithm with Feminine Selection

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## Abstract.

This paper describes a selection approach for evolutionary algorithms – called *feminine selection* – that is inspired in the fact that in some animal species the female actively select their reproduction partners. In these species, the males exhibit their attributes, sometimes fighting with other males, and the female chooses the one she considers the best. To implement this approach, the algorithm adopts a sexual reproduction mechanism, that among other properties precludes the reproduction between two identical genomes, avoiding premature convergence. The proposed algorithm was implemented and its results compared with those of the standard Goldberg algorithm.

**Keywords:** Genetic Algorithms

This paper is not under review or accepted for publication in another conference or journal.

## 1 Introduction

Genetic algorithms are a family of computational models that share with other models in the field of Evolutionary Computing the inspiration in the natural evolution: over many generations, natural populations evolve according to the principles of natural selection and “survival of the fittest”. These principles were first clearly stated by Charles Darwin in the *Origin of the Species*. Genetic algorithms encode a possible solutions for a problem in the form of a “population” of simple chromosome-like data structures and apply recombination operators to these structures in order to generate “descendants” that are joined in new populations. If the solutions are properly encoded, each new generation contains “better adapted” chromosomes, optimizing the solution. The basic principles of genetic algorithms were established by Holland [7] and since than many variations have been proposed [6].

This paper describes a new selection mechanism for genetic algorithms, called “feminine selection”. This mechanism is based on the natural *sexual selection*, that is, the choice of a mate based on a preference for certain characteristics. To apply this selection mechanism, the population is divided into female and male groups.

The paper is organized as follows. In Section 2, the biological motivation of the algorithm is presented. In Section 3, the proposed algorithm is formally defined highlighting its difference with respect to the classical Holland’s algorithm. In Section 4, the obtained results and the comparison with the classical algorithm are shown. In Section 5, some related work is presented and compared with the proposed approach. Finally, in Section 6, some conclusion and future work are presented.

## 2 Sexual Selection

Besides the usual competition among individuals, the main natural evolution mechanism described by Darwin, evolutionary biology research also study other mechanisms, in particular sexual selection ([14], [10], [9], [8],[4]). In some species, the mating selection does not depend on individual competition but mainly on the choice of the reproduction partner by an individual, usually a female. The criteria used by the females to do the selection vary from direct genetic benefits for the descendants, as indicated by the physical characteristics of the possible male partner, e.g., size of the body ([9], [2]), certain type of ornaments [14], color or bird song, to indirect benefits, as indicated by some male abilities, such as nest building, or territory ownership [2], that could facilitate the development of the descendants.

In any way, the female tries to choose the most adequate partner, from her point of view. In some species, as the *Uta stansburiana* lizard, the female can even select the sex of the descendants according to the male characteristics, in order to have female descendants with small males and male descendants with big males [2]. In other species, as the *Hirundo rustica* [14], some types of ornaments are associated with good characteristics for reproduction, such as a good immunological system. This sexual criteria represent an important aspect of natural selection.

## 3 Genetic Algorithm with Feminine Selection

The proposed algorithm introduces some modification with respect to the standard algorithm as presented in [5]. Its formal definition is presented as algorithm 1. The steps that differ from the traditional implementations are the following:

**Creation of the initial population** The creation of the initial population is similar to the traditional algorithms with binary representation, where, usually, each individual is assigned a random string of zeros and ones of a fixed length, but in the proposed algorithm each individual has one specific gene, associated with the lowest order bit, that is not related to the representation of the problem solution and determines the sex of the individual. Therefore chromosomes are of two types:

**Female** when the lowest order bit is equal to zero.

**Male** when the lowest order bit is equal to one.

Once the initial population is created, it is separated in females and males. Due to the random generation of the individual, the size of each sub-population should be approximately equal.

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**Algorithm 1** Feminine Selection Algorithm

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```
BEGIN
Read(ConfigurationParameters)
Pop ← MakeInicialPopulation
[PopMales, PopFemale] ← DividePop(Pop)
for  $i = 2$  to GenerationNumber do
  ContPop ← 0
  NewPop ←  $\emptyset$ 
  while ContPop < PopulationSize do
    SelectedFemale ← SelectFemale(PopFemale)
    SelectedMaleGroup ← SelectMales(PopMales)
    for all  $male_i \in$  SelectedMaleGroup do
      ProjectedDescendants ←
        ProjectDescendants( $male_i$ , SelectedFemale)
      Fitness[ $male_i$ ] =  $\sum$  Fitness(ProjectedDescendants)
    end for
    SelectedMale ←
      max(Fitness[ $male_i$ ],
         $1 \leq i \leq$  Size(SelectedMaleGroup))
    Descendants ←
      Crossover(Mutation(SelectedMale),
        Mutation(SelectedFemale))
    NewPop ← (NewPop  $\cup$  Descendants)
  end while
  Pop ← NewPop
  [PopMales, PopFemale] ← DividePop(Pop)
end for
END
```

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**Feminine selection** The parent selection mechanism used to choose the individuals that will form the “mating pool” is where the proposed algorithm most differ from the standard versions. In the traditional algorithms (e.g., [5],[1], [17]), the individuals are randomly selected to join the mating pool, with highly fit individuals being more likely to be selected more than once and unfit individuals being more likely not to be selected at all. The selection is done one by one, in the case the roulette wheel selection method is used, or by random groups (typically of two individuals), in the case the tournament selection method is adopted (Whitley [17] presents a good survey of tournament methods and a comparative study of them). Once the mating pool is full, individuals are randomly extracted and mated. Their descendants form the new population.

Standard selection methods do not make any distinction among the individuals, in particular it is frequent that the same individual mates with itself if it has a high fitness value with the respect to the rest of the population. This may cause a loss of diversity and premature convergence.

Another aspect of standard selection methods is that the competition between individual only takes into account the individual fitness and not the prospective fitness of the descendants, as is the case in some species with sexual selection. The proposed algorithms tries to capture this type of selection, analogous to a female search for “good genes”, as measured by the possible fitness of prospective descendants.

The selection method includes the following steps:

1. One female is selected using a traditional method (in the case of the implemented algorithm, see Section 4, the roulette wheel method). This models a female ready for mating.
2. Next, a group of males is selected, also using a traditional method. This group models the set of males attracted by the ready for mat-

ing female.

3. The female chooses one of the males to mate, the one that has the most “compatible” genes with respect to the female genome. This choice is done through a problem dependent *attraction* function, that differently from the fitness function, receives two chromosomes as input and returns the degree of compatibility between them.

The attraction function used in the implemented version of the algorithm (see Section 4) simply performs a simulated reproduction that generate prospective descendants representing the female expectations about each male. The combined fitness of the male and its prospective descendants is used to rank the male inside the group. In a population of  $N$  individual, if the size of the male group is  $m$  and the number of prospective descendants per male is  $p$ , the adopted attraction function implies  $\frac{1}{2}mpN$  extra calls to the fitness function. This overhead should be compensated by the convergence speedup.

In problem domains where a “complementarity” aspect can be devised on chromosomes, the attraction function could be defined independently from the fitness function, improving the efficiency of the algorithm.

After the selection, the female and the chosen male mate, i.e., the crossover operator is applied to their chromosomes, descendant chromosomes are generated and, after the application of the mutation operator, these are added to the new population. The crossover and mutation operators are the same as in the standard algorithms.

## 4 Examples

The proposed algorithm was implemented and its results were compared with those of the traditional algorithm presented in [5], implemented with the use of the SAG *shell* [13]. In the tests, both algorithms were used to optimize the following functions:

$$z = \frac{\sin(\sqrt{x^2 + y^2} + eps)}{\sqrt{x^2 + y^2} + eps} \quad (1)$$

$$z = \text{Humps}(x, y) = \left( \frac{1}{(x-0.3)^2 + 0.01} + \frac{1}{(x-0.9)^2 + 0.04} - 6 \right) \cdot \left( \frac{1}{(y-0.3)^2 + 0.01} + \frac{1}{(y-0.9)^2 + 0.04} - 6 \right) \quad (2)$$

$$z = [2e^{-x} \cdot \sin(x) + 2e^{-y} \cdot \sin(y)]^2 \quad (3)$$

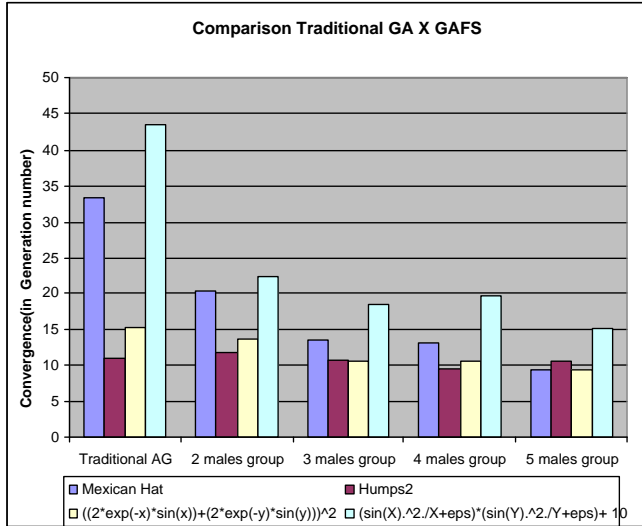
$$z = \frac{\sin(x^2)}{x + eps} \cdot \frac{\sin(y^2)}{y + eps} + 10 \quad (4)$$

The interval of values in which the functions were evaluated are:  $[-1, 1]$  for function 1,  $[0, 3]$  for function 2,  $[-2, 2]$  for function 3 and  $[1, 6]$  for function 4.

The choice of function optimization instead of other benchmarks, such as the traveling salesman problem, is due to the facility in comparing the results with other optimization methods and also because it is easy to modify the function to be optimized without changing the chromosome structure. The adopted efficiency measure was the convergence time, i.e., the mean number of generations needed to find the optimal (known) result. The mean was taken over 100 executions of the algorithms. The rare cases of premature convergence to a sub-optimal result were not taken into account. The results are shown in figure 1. The size of the male varied from 2 to 5. The parameters used in the experiments, both in the traditional implementation and in the feminine selection one, are show in table 1.

Crossover probability	0.9994
Mutation probability	0.0006
Chromosome size	32 bits
Population size	50 individuals

**Table 1.** Genetic Algorithms Parameters



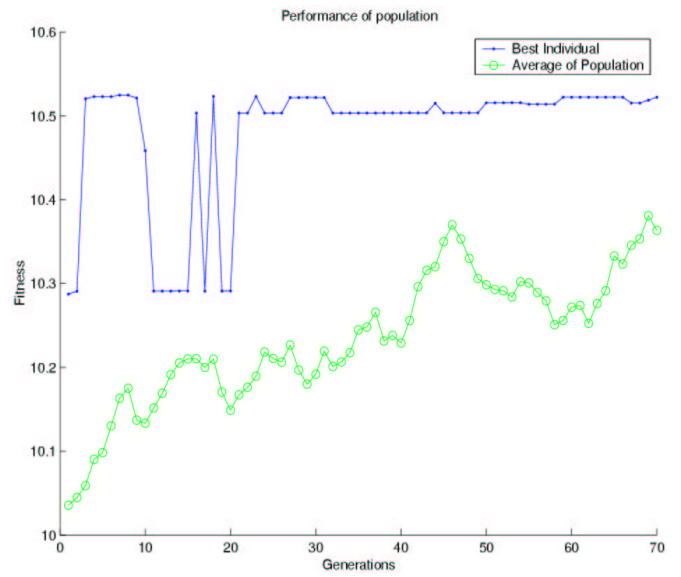
**Figure 1.** Test results

It can be seen that the performance of the proposed algorithm varies according to the size of the male group. The optimal size depends on the problem, but clearly very small groups reduce the female choice, what reduces the convergence speed. As the size of the male group grows, the performance of the algorithm is improved but only up to certain optimal size. After this optimal size any increase in the number of males in the group has a negative effect on the performance.

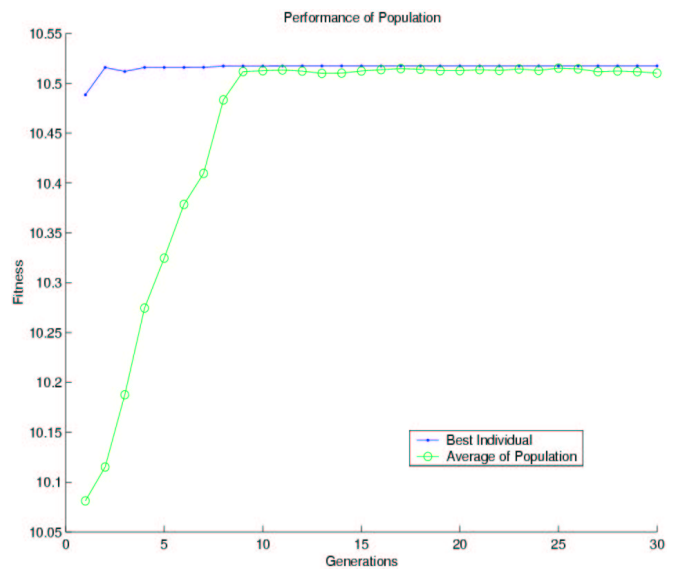
Algorithm	Number of males	Time (seconds)
Traditional		0.1250
Feminine selection	2	0.1095
Feminine selection	3	0.1980
Feminine selection	4	0.2618
Feminine selection	5	0.3374

**Table 2.** Execution Time per Generation (Mexican Hat function)

The mean time per generation obtained for the Mexican hat function is presented in table 2. It can be seen that the evaluation of the fitness function on the prospective descendants introduces an overhead on the execution time of the feminine selection algorithm, but this overhead is compensated by the faster convergence. Figures 2 and 3 show the results of one typical run of the traditional and feminine selection algorithms respectively. The results correspond to function 4.



**Figure 2.** Traditional Algorithm Convergence (function 4)



**Figure 3.** Feminine Selection Algorithm Convergence (function 4)

In the tests, it was also observed that, as expected, because of the random character of the crossover and mutation operators, the number of females and males are maintained approximately the same.

## 5 Related Work

In biology, the idea of female selection is not new, it was already noticed by the author of the *The Origin of Species*, Charles Darwin. He observed two kind behaviors with respect to the sexual selection: the competition among males and the female choice [11]. Although

the two kinds of sexual selections have been proposed at the same time, initially only the male competition had been accepted by biologists. Only recently, the female selection has been rediscovered as object of research among biologist and computer scientist, interested in constructing computational models for the evolutionary processes.

The traditional versions of selection algorithms do not take sexual selection into account and chromosomes are usually of one single type, without any representation for different sexes. Recombination strategies generally aim to avoid reproduction between individuals that are too different. Goldberg [5], for instance, has proposed a fitness function, called *sharing* function, that measures the similarity between chromosomes in order to avoid the emergence of subspecies inside a given population. He also proved that sexual differentiation improves local and global adaptability.

Eshelman [3] proposed an “incest prevention” mechanism, in which two individuals, randomly chosen to reproduce, are actually used for reproduction only if their Hamming distance is superior to a given threshold value. He also proposed to make the initial threshold value equal to the mean distance among the elements of the population and to decrease its value as the population converges. In Eshelman’s mechanism there is no sexual differentiation, it only avoids the reproduction among individuals that are too similar.

Miller and Todd [11] proposed a selection method called *directional mate preferences* and compared it with a traditional genetic algorithm implementation. In this method, instead of using a simple similarity measure, the individuals that differ with respect to a particular phenotypical characteristic are preferred to reproduce. Although this method uses a kind of sexual selection, the chromosomes do not represent it explicitly.

Velazco and Bullinaria [16, 15] proposed a genetic algorithm with sexual reproduction. In their models there is an explicit distinction between individuals of different sexes. They also introduce the concept of *cooperation* between members of a pair formed by two individuals of different sexes, with the goal of optimizing the survival chances of the next generation. This concept takes into account parameters such as age and fertility. The model applies a different selection strategy depending on the sex: males are selected directly by the fitness function, but females are selected also by an evaluation of the possible descendants, considering parameters such as the age and fertility of the selected male. Differently from the proposed approach, in this model the male is selected first and the female is selected according to the male characteristics. In the proposed method, the female is the first to be selected and then a group of males is selected according to traditional strategies. Among this group, one male is selected taking into account the characteristics of the possible descendants that it could generate with the selected female.

The experiments made by Velazco and Bullinaria suggest that sexual selection improves genetic algorithms with respect to both, the number of generations necessary to convergence and the quality of the obtained solutions.

## 6 Conclusion

A new approach to optimize convergence in evolutionary algorithms, called *feminine selection*, was introduced. This approach divides the population into female and male groups and modifies the selection operator in such a way that each mating pair is the result of the choice of a highly fit female among a group of also highly fit males, based on an *attraction* function.

A formal algorithm describing the proposed approach was defined and implemented. The implementation was tested and compared with

a traditional genetic algorithm implementation, showing promising results.

Future work includes applying the approach to other problems, e.g., problems involving combinatorial optimization such as the traveling salesman problems and production scheduling problems, and extending the approach to other evolutionary computational techniques, in particular genetic programming [12], where we intend to apply the proposed algorithm to the automatic generation of code.

## Acknowledgment

The authors express their thanks to the Brazilian research support agency “Fundação Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (Capes)” (project number 400/02) for the partial support of this work.

## REFERENCES

- [1] Tobias Bickel and Lothar Thiele, ‘A comparison of selection schemes used in evolutionary algorithms’, *Evolutionary Computation*, **4**(4), 361–394, (1996).
- [2] Ryan Calsbeek and Barry Sinervo, ‘Uncoupling direct and indirect components of female choice in the wild’, in *Proceedings of The National Academy of Sciences Of The USA*, ed., Mary Jane West-Eberhard, volume 99 (23), pp. 14897 – 14902. The National Academy of Sciences Of The USA, (november 2002).
- [3] Larry J. Eshelman and David Schaffer, ‘Preventing premature convergence in genetic algorithms by preventing incest’, in *Proceedings of The Fourth International Conference on Genetic Algorithms*, eds., Rick Belew and Lashon Booker, pp. 115–122, San Mateo, CA, (1991). Morgan Kaufman.
- [4] V. A. Geodakian, ‘Evolutionary role of sex chromosomes: A new concept’, *Journal of Mathematical Sciences*, **93**(4), 521–530, (February 1999).
- [5] David E. Goldberg, *Genetic Algorithms in Search, Optimization and Machine Learning*, Addison Wesley, 1. edn., 1989.
- [6] D.E. Goldberg, ‘Genetic and evolutionary algorithms come to age’, *Communications of ACM*, **37**(3), 113–119, (March 1994).
- [7] J.H. Holland, *Adaptation in Natural and Artificial Systems*, University of Michigan Press, Ann Arbor, 1975.
- [8] Vikram K. Iyengar and Thomas Eisner, ‘Female choice increases offspring fitness in an arctiid moth (*utetheisa ornatrix*)’, in *Proceedings of The National Academy of Sciences Of The USA*, volume 96 (26), pp. 15013 – 15016. The National Academy of Sciences Of The USA, (December 1999). Contributed by Thomas Eisner, November 5, 1999.
- [9] Vikram K. Iyengar and Thomas Eisner, ‘Heritability of body mass, a sexually selected trait, in an arctiid moth (*utetheisa ornatrix*)’, in *Proceedings of The National Academy of Sciences Of The USA*, volume 96, pp. 9169 – 9171. The National Academy of Sciences Of The USA, (August 1999). Contributed by Thomas Eisner, June 3, 1999.
- [10] M. Kirkpatrick and N. H. Barton, ‘The strength of indirect selection on female mating preferences’, in *Proceedings of The National Academy of Sciences Of The USA*, volume 94, pp. 1282–1286. The National Academy of Sciences Of The USA, (1997). Communicated by George Williams, State University of New York, Stony Brook, NY, December 9, 1996 (received for review July 25, 1996).
- [11] Geoffrey F. Miller and Peter M. Todd, ‘Evolutionary wanderlust: Sexual selection with directional mate preferences’, in *Proceedings of The Second International Conference on Simulation of Adaptive Behaviour*, eds., J. A. Meyer, H.L. Roitblat, and S. W. Wilson, volume 2 of *From Animals to Animats*, pp. 21–30, Cambridge, MA, (1993). MIT Press/Bradford Books.
- [12] Riccardo Poli and William B. Langdon, ‘On the search properties of different crossover operators in genetic programming’, in *Genetic Programming 1998: Proceedings of the Third Annual Conference*, eds., John R. Koza, Wolfgang Banzhaf, Kumar Chellapilla, Kalyanmoy Deb, Marco Dorigo, David B. Fogel, Max H. Garzon, David E. Goldberg, Hitoshi Iba, and Rick Riolo, pp. 293–301, University of Wisconsin, Madison, Wisconsin, USA, (1998). Morgan Kaufmann.

- [13] Adriana Postal, Daniele Chrusciak, Luciano Lopes da Costa, Salette Vinhote Sambugaro, and Josué Pereira de Castro, 'Sag - uma shell para algoritmos genéticos', in *Anais do XII Seminário Regional de Informática da Universidade Regional Integrada do Alto Uruguai e das Missões*, ed., Maria Augusta Silveira Netto Nunes, pp. 155 – 170, Santo Ângelo - RS, (Novembro 2002). Departamento de Engenharias e Ciência da Computação - URI - Campus de Santo Ângelo, EDIURI.
- [14] Nicola Saino, Anna Maria Bolzern, and Anders Pape Moller, 'Immunocompetence, ornamentation, and viability of male barn swallows (*hirundo rustica*)', in *Proceedings of The National Academy of Sciences Of The USA*, volume 94, pp. 549 – 552. The National Academy Of Sciences Of The USA, (1997). Communicated by Gordon H. Orians, University of Washington, Seattle, WA, November 4, 1996 (received for review June 20, 1996).
- [15] Jose Sánchez-Velazco and John A. Bullinaria, 'Gendered selection strategies in genetic algorithms for optimization', in *Proceedings of the UK Workshop on Computational Intelligence: UKCI-2003*, eds., J. M. Rossiter and T. P. Martin, pp. 217–223, Bristol, UK, (2003). University of Bristol, University of Bristol.
- [16] Jose Sánchez-Velazco and John A. Bullinaria, 'Sexual selection with competitive/co-operative operators for genetic algorithms', *Neural Networks and Computational Intelligence*, 191–196, (2003).
- [17] Darrel Whitley, 'A genetic algorithm tutorial', *Statistics and Computing*, **4**, 65–85, (1994).