TOWARDS A DAWKINS' GENETIC ALGORITHM: TRANSFORMING AN INTERACTIVE EVOLUTIONARY ALGORITHM INTO A GENETIC ALGORITHM

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Abstract*: This paper addresses the transformation of an interactive evolutionary algorithm - the biomorphs model introduced by Dawkins in his book "The Blind Watchmaker" - in a genetic algorithm. One of the critical steps was the substitution of the evaluation made by a human by a fitness function. In addition we studied two experimental situations: (i) biomorphs populations with only mutation and (ii) populations including a crossover operator. In both cases, significant evolutionary differences are observed, classifying individuals in different classes according to their genotypic frequencies. Finally, in order to assess whether there is an influence of computer "hardware" in the simulated evolution, experiments were performed on a conventional computer and using a supercomputer. Surprisingly the results obtained allow us to conclude that the type of computer used has no significant effect on evolutionary computation experiments, as long as evolution is the result of Darwinian natural selection.*

Keywords*: interactive evolutionary algorithm, Dawkins' biomorph program, artificial life, evolutionary computing on supercomputers*

ACM Classification Keywords*: I.6 Simulation and Modeling*

Introduction

One of the most popular evolutionary models in Artificial Life was introduced in 1986 by Richard Dawkins [Dawkins, 1986] in the book entitled "The Blind Watchmaker". The model introduced by Dawkins mimics the evolution of individuals termed as *biomorphs* and is inspired by the principle of continuity of 'germ plasm' introduced in 1893 by Weismann. The aim of the model was the simulation of the Darwin's principle of natural selection [Lahoz-Beltra, 2008] in individuals with asexual reproduction [Lahoz-Beltra, 2004]. Therefore, the mutation is the only source of variability and the mechanism for evolution is the familiar principle of cumulative selection. In the Dawkins' original model is the researcher - playing the role of a "blind watchmaker" - who selects in accordance with their own criteria (e.g. the largest, smaller, beautiful etc.) the optimum biomorph in every generation. One of the goals of the present paper was to overcome these limitations, transforming the algorithm introduced by

Dawkins, thus an interactive evolutionary algorithm, in a genetic algorithm (GA) [Guil Lopez, 2000]. Interactive evolutionary algorithms use human evaluation as a fitness function [Milani, 2004], e.g. aesthetic selection based on biomorph attractiveness, being Darwinian selection the result of human preferences. In this paper we substitute the evaluation made by a human by a fitness function. Also we studied the role of genetic crossover in evolution, building an evolutionary algorithm (EA without crossover) and a genetic algorithm (GA including crossover). Therefore, from a biological point of view, the genetic algorithm simulates a population of biomorphs with sexual reproduction whereas the evolutionary algorithm emulates a population of biomorphs with asexual reproduction. Simulation experiments with EAs and GAs were performed on a personal computer and a supercomputer SGI-Cray ORIGIN 2000 in order to figure out whether the evolution of a population of biomorphs depends on the type of hardware, i.e. the 'test tube', where the evolution experiments were conducted. The experiments described in this paper are part of the work done during several years of work [Guil Lopez, 2000] about *bio-inspired evolutionary algorithms* [Lahoz-Beltra, 2008; Perales-Gravan et al., 2013; Thai Dam and Lahoz-Beltra, 2014]. At present we continue working on this long term research project.

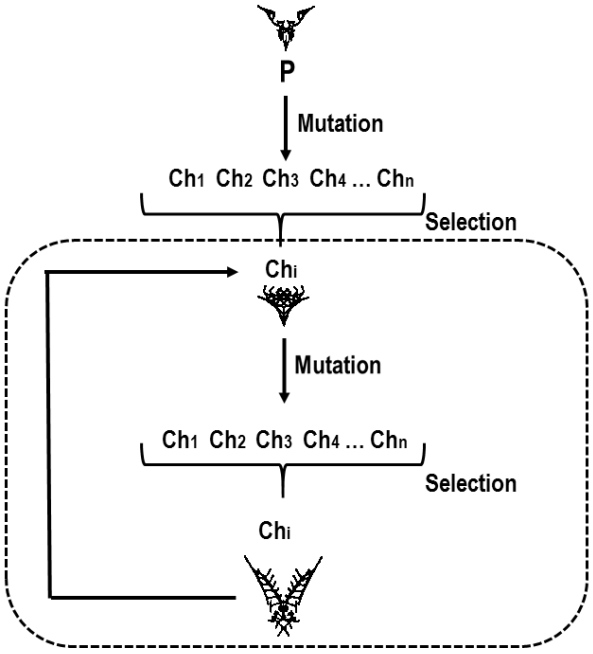


Figure 1. Dawkins' original algorithm [Dawkins, 1986]. A parental individual (P) will produce an offspring of n 'children' (Ch). The children are similar to P, except for the value of a gene which has changed by mutation. A human selects according to their judgment the 'best biomorph' (Chi) which will produce a new offspring of n children. This loop is repeated again and again until we decide to conclude the evolutionary cycle.

From the Dawkins' algorithm to a Dawkins genetic algorithm

In the original model introduced by Dawkins (Figure 1) an individual or biomorph is represented by a one-dimensional array or vector which simulates a chromosome. A position on chromosome simulates a gene, being chromosomes constituted by eight genes {$gene_1$, $gene_2$,…, $gene_8$} whose values are positive integers, i.e. $gene_i \in \mathbb{Z}^+$. The genes values codify for the biomorph shape or phenotype as defined in Table 1. From a genetic point of view the phenotypic expression of a character can be the result of the sum of several genes, e.g. branching length ***L*** (gene 3 + gene 4), denominating these genes as polymers factors or cumulative factors. In other cases some genes multiply their effects as it occurs again with the branching length ***L*** (gene 3 * gene 4). The model also includes epistasis, thus the interaction of genes affecting the same character, modifying as a consequence the Mendelian segregation (Mendel's genetic laws). For instance, in the present model the genes encoding branches angles, i.e. genes 6 and 7, have an effect on the character "branching length" that is encoded by genes 3, 4 and 5. Figure 1 shows the recursive algorithm introduced by Dawkins. In this paper we studied populations without crossover or asexual reproduction (Figure 2) and populations with crossover or sexual reproduction (Figure 3), but substituting in both cases the human selection by a selection operator. The aim of the *selection operator* is the Darwinian selection of biomorphs from which the next generation will be obtained. The fitness of each individual was calculated as follows.

Table 1. Biomorph's chromosome or genotype ($gene_1$, $gene_2$,…, $gene_8$)

Gene 1: Number of offspring individuals
Gene 2: Number iterations to draw a biomorph
Genes 3 and 4: Numbers encoding for the length of the branches
Gene 5: Length of a branch ***L*** is defined according to the following algorithm

$$L = \begin{cases} \text{Gene 3 + Gene 4} & \text{, if Gene 5 is an even number} \\ \text{Gene 3 * Gene 4} & \text{, if Gene 5 is an odd number} \end{cases}$$

Gene 6: Angle of the first branching
Gene 7: Angle between the second and first branching
Gene 8: Length of the body

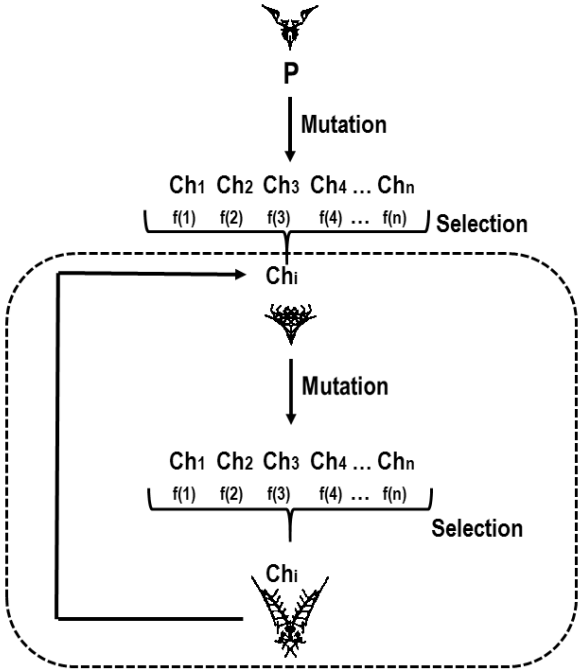


Figure 2. Dawkins' evolutionary algorithm. 'Human evaluation' is substituted by a fitness function. Note that no recombination or crossover mechanism is present. Therefore from a biological point of view we would be simulating a population with asexual reproduction.

First, we define the best individual, thus the optimal genotype or chromosome, referred as 'target biomorph'. The choice of a target individual was performed by applying one or other of the following criteria. A first protocol is the *Criterion of Equitable Distribution*. According to this criterion the Euclidean distance between the target individual and the parental individual is similar for the two parental individuals, being in the simulation experiments equal to 9.85 units. In addition, the selected genotype is obtained as follows: 50% is obtained by mutation and the remaining 50% results from the recombination or crossover of parental individuals. In the experiments conducted with crossover or sexual reproduction (Figure 3), in the initial generation (t = 0) the parental genotypes ($gene_1$, $gene_2$,…, $gene_8$) were (11, 0, 1, 2, 4, 0, 92, 10) and (16, 0, 3, 7, 6, 0, 95, 13). Likewise, the genotype of the target biomorph was (16, 5, 6, 2, 1, 2, 95, 10). The second protocol was termed *Restrictive Criterion*. In addition, fulfilled the above assumption with Euclidean distance (the distance between the target individual and the two parental individuals is equal to 9.85), in the conducted simulation experiments the maximum values of the first four genes in the genotype should be equal to a set of values: 16, 10, 8 and 8. The other values of genes are chosen within the interval [a+10, b-10], where a and b values are the higher and lower of each gene value in the parental biomorphs. According to this criterion we selected the following target biomorph (16, 5, 6, 2, 1, 2, 95, 10).

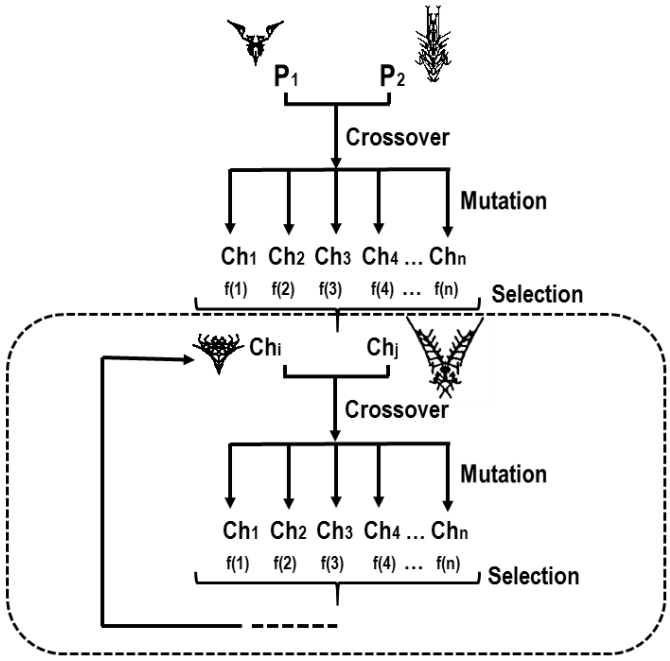


Figure 3. Dawkins' genetic algorithm. 'Human evaluation' is substituted by a fitness function. Since there is crossover, we would be simulating a population with sexual reproduction. Accordingly, Darwinian selection will select a pair of parental individuals: Chi and Chj.

Since in the experiments without crossover or asexual reproduction (Figure 2) there is only one parental individual at t = 0, all simulation experiments were performed with the initial genotype (16, 0, 3, 7, 6, 0, 95, 13).

Secondly, we calculate a 'genetic distance' (1) , i.e. the Euclidean distance d_i between the genotypes of biomorph i ($gene_i$) and target biomorph ($gene_i^{target}$):

$$d_i = \sqrt{\sum_i \left(gene_i - gene_i^{target} \right)^2} \qquad (1)$$

After calculating distance (1) the obtained value d_i will be the first argument of the fitness function. In this paper **F1-F4** (Table 2) are the proposed evaluation or fitness functions that we will use to transform Dawkins' algorithm into a true genetic algorithm. Given a fitness function and a set of distances d_i from individuals of the same generation, we obtain the minimum distance d_{min}, thus the second argument of the fitness function.

Simulation experiments were conducted based on the following fitness function parameters: $\alpha = 0.1$, $\beta = 0.9$ and $\gamma = 0.2$, where the *k* value was equal to zero (*k* = 0) for populations with a maximum of 500 individuals. Otherwise, *k* = 300 when the population size exceeded 500 individuals. Once we obtained the fitness value of each individual, the selection of parental individuals was conducted by a Bernoulli roulette [Lahoz-Beltra, 2004]. According to this procedure, the selection probability of an individual (2) represented by its chromosome *i* is calculated as the ratio between the individual fitness and total fitness:

$$p(i) = \frac{f(x_i)}{\sum_i f(x_i)} \tag{2}$$

Table 2.- Objective or fitness functions

F1	$f(\mathrm{d}_{\min}, \mathrm{d}_i) = \begin{cases} \dfrac{\alpha + d_{\min}}{\gamma - \beta(\alpha + d_{\min})} - \alpha(\alpha + d_{\min}) + k & , \quad d_i = 0 \\ \dfrac{\alpha + d_{\min}}{d_i - \beta(\alpha + d_{\min})} - \alpha(\alpha + d_{\min}) + k & , \quad d_i \neq 0 \end{cases}$
F2	$f(\mathrm{d}_{\min}, \mathrm{d}_i) = \begin{cases} \dfrac{d_{\min}}{\gamma - \beta d_{\min}} - \alpha d_{\min} & , \quad d_i = 0 \\ \dfrac{d_{\min}}{d_i - \beta d_{\min}} - \alpha d_{\min} & , \quad d_i \neq 0 \end{cases}$
F3	$f(\mathrm{d}_{\min}, \mathrm{d}_i) = \left\| \left(\dfrac{d_{\min}}{d_i - \beta d_{\min}} - \alpha d_{\min} \right) \right\|$
F4	$f(\mathrm{d}_{\min}, \mathrm{d}_i) = \begin{cases} \dfrac{d_{\min}}{\gamma - \beta d_{\min}} - \alpha d_{\min} + k & , \quad d_i = 0 \\ \dfrac{d_{\min}}{d_i - \beta d_{\min}} - \alpha d_{\min} + k & , \quad d_i \neq 0 \end{cases}$

Finally, given a random number U_i between 0 and 1, the individual or chromosome i is selected (R=1) for the next generation if it holds that:

$$\begin{cases} p(i) < U_i \,, R = 0 \\ p(i) \geq U_i \,, R = 1 \end{cases} \tag{3}$$

In the simulation experiments with populations displaying crossover, i.e. sexual reproduction (Figure 3), the *recombination operator* was simulated with one and two cutting points, as is usual in genetic algorithms. Regarding *mutation operator*, and since the chromosome is a vector of positive integers, it was not possible to use the flip-bit method [Lahoz-Beltra, 2004]. Mutation was simulated as follows. First, a gene is chosen randomly, increasing or decreasing its value by one. Obviously the sense of mutation, increase or decrease, is also conducted at random. Secondly, mutation is applied taking into account the allowable range of values of the genes. For example, in the simulation experiments genes 1, 2, 3 and 4 have maximum values equal to 16, 10, 8 and 8 respectively.

Simulation experiments

This study has been carried out for several years studying under different types of computer hardware (Tables 3-4) the evolution of biomorph populations. Populations were simulated based on two different versions of the Dawkins' algorithm (Figures 2 and 3). The first simulation experiments were conducted in the late 90s using an IBM PC-compatible computer with Pentium III processor 450 MHz and 218 MB of RAM. The algorithms depicted in Figures 2 and 3 were written at that time in TurboPascal 7.0. Preliminary experiments were performed with the program BIOMURFFS: a program showing the Dawkins' original algorithm (Figure 1) written in QBASIC for recreational purposes [Prata, 1993]. The simulation experiments (Table 3) were performed testing the fitness function **F1** (Table 2) with populations of 16 biomorphs, simulating the evolution during 500 generations. In each generation the offspring came from a single individual or a couple of individuals depending on whether the algorithm simulates asexual (Figure 2) or sexual (Figure 3) reproduction. In the latter case, and therefore when biomorphs display crossover, recombination was simulated with one and two cutting points, choosing different recombination probability values (0.25, 0.50 and 0.75).

Table 3.- Experimental conditions in the simulations conducted with IBM PC-compatible computer

	Standard population	
	Asexual reproduction	Sexual reproduction
Population size	16	16
Number parental individuals	1 individual	1 couple
Number of generations	500	500

Some years later, a second batch of simulation experiments was performed on a SGI-Cray ORIGIN 2000 supercomputer with 40 MIPS R10000 250 MHz microprocessors and 16 MIPS R12000 400 MHz microprocessors, with 12 GB of RAM and 190 GB hard drive. Of course, today many of these features have already been overcome but the results are still valid. Once again the two different versions of the Dawkins' algorithm (Figures 2 and 3) were implemented but this time in C language, and compiled with the MIPSproC compiler under IRIS 6.5 OS. The compilation was made with the option "-Ofast" in order to minimize runtime, using a C mathematical library implemented for the IRIS system. After several preliminary experiments we decided to evaluate the biomorphs fitness using **F4** function. Experiments with populations displaying sexual reproduction were performed with a two-point crossover operator and probability equal to 0.5. Simulation experiments were carried out increasing the population size, the number of parental biomorphs per generation and the number of simulated generations (Table 4).

Table 4.- Experimental conditions in the simulations conducted with SGI-Cray ORIGIN 2000 supercomputer

	Standard population				Increased population			
	Asexual reproduction		Sexual reproduction		Asexual reproduction		Sexual reproduction	
Population size	16		16		160		160	
Number parental individuals	1 individual		1 couple		10 individuals		10 couples	
Number of generations	1000	1500	1000	1500	1000	1500	1000	1500

Results

Despite the time that has elapsed since we conducted the experiments, in our opinion the results are still perfectly valid. In fact currently we are developing a quantum genetic algorithm version of the Dawkins' original algorithm. The results obtained under the original Dawkins' standard population conditions, i.e. a population size equal to 16 (Table 3 and 4), were similar in the two kinds of computers, i.e. in the experiments conducted with IBM PC-compatible computer and SGI-Cray ORIGIN 2000 computer. Therefore, we can conclude that for these experimental conditions has no influence the type of computer used to run the simulations and the number of studied generations (500, 1000 or 1500). However, the evolutionary convergence differs depending on the type of reproduction. Evolutionary convergence was analyzed for each biomorph plotting the genetic distances: on the y-axis from the parental biomorph and the x-axis from the target biomorph. In the experiments with asexual reproduction (Figure 4 a, c) populations exhibit higher evolutionary fluctuations, requiring a greater number of generations to achieve the target genotype. That is, sexually reproducing populations (Figure 4 b, d) reach the target genotype in a smaller number of generations. If we compare the evolutionary convergence of both types of reproduction with a card player, e.g. in the game of blackjack, the biomorphs with asexual reproduction would be "conservative players" avoiding a maximum adaption to their environment. Of course, in this metaphor the environment will be the casino where life is brought into play. By contrast, the biomorphs with sexual reproduction would be "risky players" showing a maximum adaptation to their environment. In both cases and for small values of genetic distances (near to the optimal genotype or target values), we observed a cluster of genetic distances which we have termed “arrowhead” (Figure 4 a-d).

However, when experiments were conducted under large population conditions (Table 4) some remarkable differences were observed. One of the most striking differences is the absence of an "arrowhead" cluster (Figure 4 e, f). Likely this result could be explained considering that in those populations with asexual reproduction the offspring is obtained by ‘bipartition’ of 10 parental individuals. Similarly, the explanation could be the same in those populations with sexual reproduction where the offspring is obtained by ‘sexual intercourse’ in 10 couples. Moreover, although we have increased the number of generations, populations do not reach the target genotype. Consequently, in large populations a lower evolutionary convergence might be due to a greater variability of individuals.

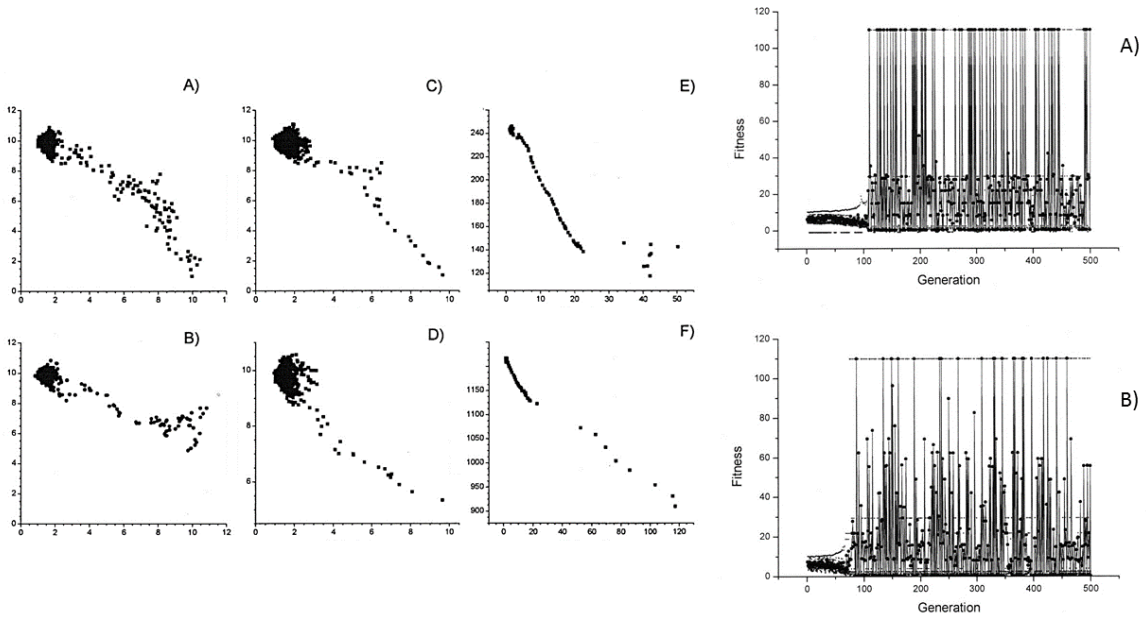


Figure 4.- Simulation experiments.

(Left) Evolutionary convergence plot (genetic distance from the parental biomorph=y-axis, genetic distance from the target biomorph=x-axis). For explanation see text.

(Right) Performance graph obtained in the simulation experiments (A) Dawkins' evolutionary algorithm (B) Dawkins' genetic algorithm

The performance graph [Lahoz-Beltra and Perales-Gravan, 2010] was similar in the two batches of experiments, the experiments conducted with IBM PC-compatible and SGI-Cray ORIGIN 2000 computers. However, the graphical representation of the average fitness and individual fitness per generation (Figure 4) depends on whether the reproduction is asexual (Figure 2) or sexual (Figure 3). For both kinds of reproduction we observed a first stage with low fitness value: from generation 1 to 108 in the populations with asexual reproduction and from 1 to 83 in populations with sexual reproduction. From 109 and 84 generations, depending on whether the reproduction is asexual or sexual, begins a second stage. In this stage individuals reach the target genotype (genetic distance near o equal to 0) or individuals are very close to the target genotype (the average fitness value is 109.89 units or equivalently a genetic distance equal to 1 unit). Nevertheless, variability is greater in the bimorphs with sexual reproduction compared to those with asexual reproduction. Moreover, if we consider the individual fitness value in both types of reproduction, we conclude the formation of genotypic classes or

clusters of individuals throughout generations. An analysis of the genotypic frequency of individuals per class, allows us to conclude that the observed number of clusters is greater in populations with sexual reproduction than asexual reproduction. In fact the number of categories or clusters increases with the variability and the number of simulated generations: 12, 23, 197, 223, 1796 and 2407 clusters for the case in which we studied asexual reproduction – 500 generations – 1 parental individual (Figure 5a), sexual reproduction – 500 generations – 1 couple parental individuals (Figure 5b), asexual reproduction – 1000 generations – 1 parental individual (Figure 5c), sexual reproduction – 1000 generations – 1 couple parental individuals (Figure 5d), asexual reproduction – 1000 generations – 10 parental individuals (Figure 5e) and sexual reproduction – 1000 generations – 10 couples parental individuals (Figure 5f), respectively. Assuming that the distribution of genotypic frequencies is multinomial, and confining the study to those experiments with 500 generations, we have e.g. that in the case of asexual reproduction with a single parent, the following frequency distribution:

$$f(x_1,x_2,x_3,x_4,x_5,x_6)=\frac{n}{x_1!\ x_2!\,x_3!\,x_4!\,x_5!\,x_6!}\left(\frac{1496}{5465}\right)^{x_1}\left(\frac{1389}{5465}\right)^{x_2}\left(\frac{327}{5465}\right)^{x_3}\left(\frac{0}{5465}\right)^{x_4}\left(\frac{919}{5465}\right)^{x_5}\left(\frac{1334}{5465}\right)^{x_6} \quad (4)$$

whereas for experiments with sexual reproduction and one couple of parents, we obtained the following frequency distribution:

$$f(x_1,x_2,x_3,x_4,x_5,x_6)=\frac{n}{x_1!\ x_2!\,x_3!\,x_4!\,x_5!\,x_6!}\left(\frac{1453}{5465}\right)^{x_1}\left(\frac{1043}{5465}\right)^{x_2}\left(\frac{189}{5465}\right)^{x_3}\left(\frac{720}{5465}\right)^{x_4}\left(\frac{440}{5465}\right)^{x_5}\left(\frac{1334}{5465}\right)^{x_6} \quad (5)$$

The study of above frequency distributions (4, 5) allows us to obtain the following conclusions. Firstly, it is noteworthy that there are certain classes that appear with high frequency regardless of type of reproduction. Secondly, when simulations are conducted with asexual reproduction there are more classes with zero frequency compared with those experiments with sexual reproduction. Finally, and for both types of reproduction, the classes with higher frequencies are those that contain a high number of individuals with high fitness values.

One of the achievements of this work was to introduce a fitness function (Figure 6) in the original Dawkins' evolutionary algorithm [Guil Lopez et al., 2000]. The aim was to replace the evaluation performed by a human (aesthetic selection) by a selection operator, transforming the Dawkins

interactive evolutionary algorithm into a true genetic algorithm. **F1** function was the first fitness function proposed in this study, evaluating biomorphs in the simulation experiments conducted with IBM PC-compatible. This function was a mathematical expression that was obtained from the original expression shown in Figure 6. In **F1** function and the remaining fitness functions we considered the case where the genetic Euclidean distance (1) is equal to or different from zero, avoiding the emergence of a 'dominant chromosome' with a disproportionately high fitness value. Parameters α and β were defined in the function with the following purpose. For large values of the genetic distance the α parameter included into the negative term of the fitness function decreases the fitness value. However the parameter plays the opposite role in the denominator of the fitness function. Another effect to correct occurs when small value of the Euclidean distance causes a large increase in the fitness value. Parameter β was introduced in order to moderate the increase in the fitness value. Finally, *k* term was introduced in order to ensure that the function is always positive, because when the population size increases also increases the minimum distance (d_{min}). **F2**, **F3** and **F4** fitness functions are very similar to **F1** function and were used to evaluate the biomorphs in the simulation experiments conducted with SGI-Cray ORIGIN 2000 supercomputer. **F2** displays a trouble taking negative values for large Euclidean distances. For this reason **F3** was introduced, returning the absolute value of **F2**. Finally, all simulation experiments with the supercomputer were performed with **F4**.

Conclusion

We show an example of how to transform an interactive evolutionary algorithm, i.e. the biomorphs model introduced by Dawkins, in a genetic algorithm. One of the critical steps was the search for a fitness function that measures the 'physical quality' of individuals. In addition we studied two experimental situations - biomorphs populations with only mutation (asexual reproduction) and populations including crossover (sexual reproduction). In both cases, significant evolutionary differences were observed, classifying individuals in different classes or clusters according to their genotypic frequencies. Finally, we found that the type of computer hardware has no significant effect on evolutionary computation experiments, as long as evolution is explained by the Darwinian principle of natural selection.

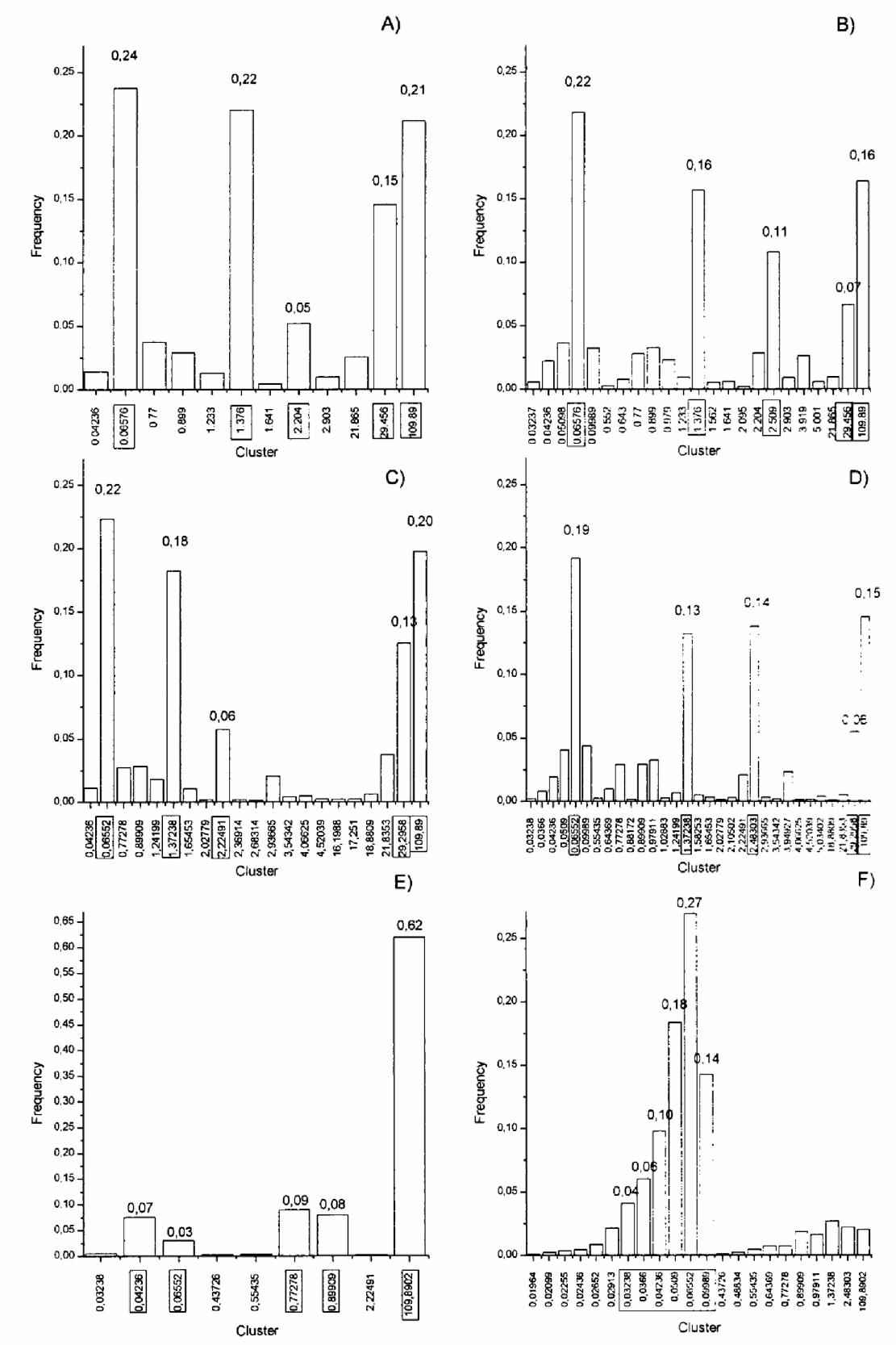
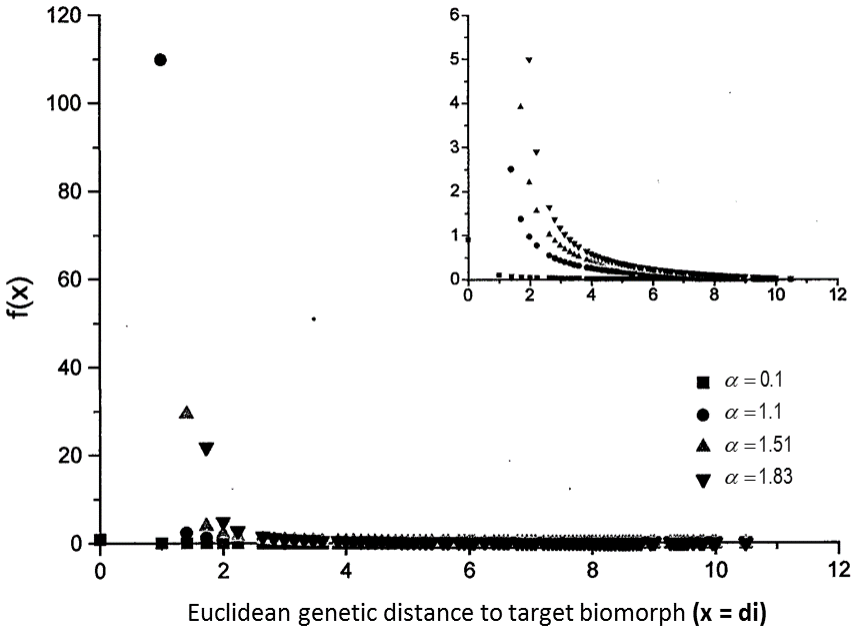


Figure 5.- Genotypic frequency of individuals per class or cluster (for explanation see text)



$$f(x)=\begin{cases}\dfrac{\alpha}{x-0.9\alpha}-0.1\alpha & , \quad x>0\\ \dfrac{\alpha}{0.2-0.9\alpha}-0.1\alpha & , \quad x=0\end{cases}$$

Figure 6.- 'Seminal fitness function' *f(x)* from which the functions **F1**-**F4** of the Table 2 were obtained

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