Genetic Algorithms: from Hegemony to Chaos

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Genetic algorithms are known to be convergent algorithms, with final population tending to become homogeneous. In this paper we show that it is possible to exhibit complex dynamics for a genetic algorithm by slightly modifying the canonical algorithm. Indeed, adding a meta level in the interpretation of the individuals, associated with a coupling between individuals gives rise to periodic or chaotic behavior.

The first part of the paper is dedicated to the presentation of the dual concept, together with an implementation of this concept : the dual genetic algorithm. Then a minimal model of the dynamical behavior of dual genetic algorithms is proposed and examined. This part emphasizes on the fact that dual genetic algorithms converge toward heterogeneous populations. This feature allows us to claim that dual genetic algorithms should be efficient in problems where the conservation of the polymorphism of the population is critical.

The second part of the paper presents how the introduction of a coupling between individuals in dual genetic algorithms leads to chaotic behaviors. Two routes towards chaos are observed, the period doubling one and the quasi-periodic one.

At last, we conclude by a discussion about the use of chaos in artificial evolving systems such as genetic algorithms.

Introduction

The goal of this paper is to show that it is possible to exhibit complex dynamics for a genetic algorithm (GA) by slightly modifying the basic algorithm. For standard GA, the dynamics of populations is rather simple since the population becomes homogeneous. Some authors enriched this dynamics by introducing couplings between the individuals, thus allowing to obtain polymorphic limit population (see [23] for a detailed state of art on diversity in genetic algorithms). But in the context of an

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haploid genetic algorithm working on a single population and without using technique such as sharing, it was not possible to exhibit complex dynamics as population oscillations or chaos.

The *duality* concept was primarily developed to improve the efficiency of the standard algorithm and to make it less representation dependent. The basic principle is to introduce a *meta level* in the individual representation. The effect of this *meta level* on deceptivity along with an implementation, called *dual genetic algorithm* (DGA), was first discussed by Collard and Aurand [5]. Collard and Escazut [7] introduced *relational schemata* and showed that a DGA handles standard schemata, as well as relational schemata. Several papers discuss the utility of duality for machine learning [7, 12], genetic programming [9], time dependent optimization [8] and multi objectives optimization [4]. In particular, it is shown, for explicit diversity preserving applications, such as *Pareto optimization*, the improvement due to the introduction of duality.

One of the main properties of DGA is that it has non trivial convergent behaviors : the final population is not necessarily a homogeneous population. This property ensures that there remains a diversity rate such that the search process never ends.

Indeed, the introduction of the duality concept deeply affects the way a GA works. In particular, their dynamical behaviors are deeply affected. The purpose of this paper is to propose a model of the dynamics of a dual genetic algorithm in order to better understand the mechanism involved. Since it is a rather difficult task to visualize such behaviors, we need to confine our analysis to simple cases featuring the main characteristics of the general dynamics. The minimal dual space (MDS) is designed to feature duality in a minimal way.

In addition, to emphasize the effect of dualism, we introduce the notion of *doupling*, which introduces an explicit coupling between dual pairs. This coupling induces non trivial dynamical behavior, leading to chaos in particular cases.

1. Dual Genetic Algorithms

Standard GA suffers from the problem of premature convergence ([25]), that is the optimum found may not be the global one, and the limit population is filled with copies of a local optimum. In this case, recombination operators have no effect and exploration is performed only by mutation operator, which is unable to perform efficient search. In order to solve this kind of problem, a lot of methods were developed, which aim at creating and preserving diversity within populations [23]. The naiver solution would simply be to increase the mutation rate in order to directly maintain diversity. However, this has the effect of disrupting the search process and this may be considered as equivalent to random search.

A more promising way to solve the exploration exploitation dilemma is to insert a meta level within chromosome interpretation while keeping the simplicity of genetic operators. This is the key principle of DGAs. Now, a lower mutation rate is required, since, as we will explain, diversity makes the recombination phase generate different solutions even while combining solutions with a same phenotype. Moreover, this meta-level allows to disconnect the phenotypical level from the genotypical one.

1.1 Basic principles

An intuitive characterization of the dual concept is "a same behavior for two distinct appearances". The implementation of the dual concept is quite simple : a head-bit is added to the genotype; this bit manages the interpretation of the rest of the string. When the head-bit is set to '0', the rest of the string remains unchanged. If the head-bit is set to '1', the chromosome is interpreted as the binary complement of the rest of the string. This way, the algorithm may manage individuals with the same phenotype, and so, the same fitness value, and different genotypes (i.e. chromosome strings are complementary strings).

Let us assume that a solution is coded by a binary string of length λ, then the search space is $\Omega = \{0,1\}^\lambda$, known as the *basic space*. The fitness of each solution is determined by a real function F defined on Ω. The objective is to optimize F. The product space $\langle\Omega\rangle = \{0,1\} \times \Omega$ is defined as the *dual space*. We can define a mapping E from $\langle\Omega\rangle$ to Ω by: $\forall 0\omega \in 0\Omega$, $\mathrm{E}(0\omega) = \omega$ and $\forall 1\omega \in 1\Omega$, $\mathrm{E}(1\omega) = \overline{\omega}$. For instance E(001)=E(110)=01. The composition <F> of the functions E and F is called the *dual function*. A GA is applied on the dual space in order to optimize the dual function <F> and so, in passing, the objective function F. We call *dual genetic algorithm* (DGA) this genetic algorithm operating on the dual space $\langle\Omega\rangle$ rather than on the basic one.

In the space $\langle\Omega\rangle$, the individuals 0ω, $1\overline{\omega}$, where $\overline{\omega}$ is the binary complement of ω, represent the same individual ω from Ω. So the DGA is an implementation of the dual concept, since two individuals from $\langle\Omega\rangle$ have the same phenotype (the same fitness value), though they have different genotypes (they are bitwise complement of each other).

In a way, duality may be viewed alike *diploidy*. With diploid genetic algorithms several genotypes can correspond to the same phenotype, and a more or less complex genotype phenotype mapping is introduced. However, there are two main differences between diploid GA and dual GA. The first one is that diversity preserving is not inherent to diploidy. This may be a side effect of environment changes or niching methods. The basic behavior of a diploid GA is to converge toward homogeneous populations. Whereas, as we will show in this paper, DGAs may never converge. The second difference is that DGAs are designed with a slight change from the canonical GA, while diploidy deeply alters its structure. For example, in the implementation found in [14], there is two genes at each locus with a triallelic alphabet and genetic operators are modified, and new ones are introduced in order to match this scheme. Whereas, the simplicity of the DGA allows to directly apply most of the improvement techniques, such as *sharing*.

The idea of maintaining complementary strings in the population is neither new nor original. For example, the *augmented genetic algorithm* proposed by Grefenstette [15] exploits such a technique. However, DGAs differ from this kind of method in the way they manage complementarity; the meta level introduced in the evaluation of individuals allows to maintain complementarity with a single population. The originality of DGA is to combine, in a simple way, idea from both diploidy and complementarity.

1.2 Crossover and mutation

Within standard GA the mutation rate is mostly handled as a global external parameter which is constant over time [27]. We showed elsewhere ([5]) that using a DGA, with the crossover operator only, mutations are implicit. Indeed, within DGAs, crossing over two dual strings (0ω and $1\overline{\omega}$) actually amounts to mutating ω.

For instance, let us consider the solution 101 in Ω, represented in $\langle\Omega\rangle$ either by 0101 or 1010. A 1-point crossover applied on locus 2 to the couple 0101 and 1010, followed by a 1-point crossover on locus 3, will give the two genotypes 0111 and 1000 representing 111 in Ω. These two consecutive crossovers have the same effect as an explicit mutation applied to the individual 101 on the second locus.

It is well known that standard crossover can be viewed as a biased mutation [11, 18, 26]. In the dual context, the implicit mutation rate due to crossover effects depends on the number of dual pairs; or, more generally, on the amount of duality in the population. The reason why the number of dual pairs decreases as the DGA converges has been examined in [6]. It follows that the rate of implicit mutation decreases to zero. This ensures that the DGA is able to achieve a tradeoff between exploration and exploitation.

1.3 Mirroring operator

The mirroring is an operator related to dualism. It aims at introducing diversity at the genotypical level while preserving phenotypical homogeneity of a given population. This operator transforms any genotype from $\langle\Omega\rangle$ into its bitwise complement. Mirroring is applied with a low probability (usually around 0.01). Combining it with standard genetic operators introduces a new component in the overall genetic algorithm dynamics which is opposed to the homogenizing ones, thus leading to a new dynamical equilibrium between bringing diversity and homogenizing.

It has been previously seen that crossover restores diversity, provided that there exists a certain amount of duality in the population. Mirroring is a way to increase duality, while not changing the overall quality of the population.

1.4 Conjugate Population and Mirror Population

Duality introduces a new type of equivalence relations between populations according to their phenotypes. Let P and Q be two populations such that:

$$\forall \omega \in \langle \Omega \rangle,\ p(\omega) = q(\overline{\omega}), \tag{1}$$

where $p(\omega)$ and $q(\omega)$ denotes the proportion of the chromosome ω, respectively in P and Q. P and Q are called *conjugate populations*. Two conjugates populations are phenotypicaly equivalent.

Mirror populations are the ones which are their own conjugate. So, a mirror population is a population in which the proportion of each chromosome is equal to the one of its complement, that is $p(\omega) = p(\overline{\omega})$.

The mirroring operator induces some interesting properties relating to mirror populations. Here are the most important ones:

1. A mirror population is a stationary distribution for the mirroring operator,
2. Repeated uses of the mirroring operator alone lead to a mirror population.

1.5 Beyond Duality

Extending the duality concept is out of the scope of this paper, since properties and dynamical behavior involved should be better understood before widening this work. However, one can think to two obvious way of generalization.

The first one is to introduce several meta bits. Each one manages a part of the chromosome with direct or complementary interpretation.

The second generalization concerns the application to non binary representations. Several schemes can be imagined. For alphabet on which a relation of complementarity is defined, a binary meta bit can still be used, and works as the meta bit for binary representation. The alternative would be to get the meta gene drawn from the basic alphabet, and to define how it transforms normal genes, according to its value. In the case of "special" representation, such as real coded chromosomes, or permutation chromosomes, there is no obvious integration of the duality concept. But, considering the wide range of application of such representations, *e.g.* operational research and parameter optimization, this point is, at the present time, one of our main preoccupations.

2. The Minimal Dual Space

In order to observe the dynamics induced by dualism, we propose a minimal model which captures duality in its simplest expression through a two genes long problem, where the first gene is the meta one. This allows a complete description of the dynamical behavior of a one locus problem with two alleles in the basic search space Ω. This restriction may appear severe but much of the work in mathematical genetics assumes single-locus models and large populations at equilibrium [3].

The distribution of genotypes, that is a population, is represented as usually by one point in the simplex $\{< \mathrm{p}_0, \mathrm{p}_1, \mathrm{p}_2, \mathrm{p}_3 > \in \mathbb{R}^4, \sum_i \mathrm{p}_i = 1\}$, where p_i represents the proportion of the individual i in the population. Duality imposes the equalities $\mathrm{f}_0 = \mathrm{f}_3$ and $\mathrm{f}_1 = \mathrm{f}_2$ (where f_i is the fitness of the individual i). We set $\mathrm{f}_1 = 1$ and $\mathrm{f}_0 = 1-\sigma$, where σ is a parameter which controls the *selective pressure*. The parameter σ takes its values from 0 (no selective pressure) to 1 (higher selective pressure). Since σ is always positive, f_0 is inferior or equal to f_1, so the two dual optima are 01 and 10, that is 1 in the basic space.

The iterated application of the genetic transformations can be represented by a trajectory in the simplex. In order to get a minimal (2D) and relevant graphical representation of this space, we need to restrict it to a particular view allowing to monitor all characteristic behaviors of the DGA. First, since $\sum_i \mathrm{p}_i = 1$, the space may be represented by 3D graphs. More, we consider only populations having p_0=p_3. This choice has been influenced by our wish to keep all mirror population represented in the minimal space. All previous restrictions have lead to consider the plane (p_0,p_1). Note that the constraint p_0=p_3 is only for visualization purposes. Most of the limit behaviors observed under this condition occur in the general case, but are less easily observable.

The symmetry between p_1 and p_2 induced by duality allows us to restrict the space to the triangle Δ, defined by the constraint $\mathrm{p}_0+\mathrm{p}_1 \leq 0.5$ (in the space Δ the chromosome 01 is dominant relatively to 10 as $\mathrm{p}_1 \leq \mathrm{p}_2$). The conjugate space Δ' is the set of populations which are conjugate of populations from the space Δ. The conjugate space Δ' is defined by the constraint $\mathrm{p}_0+\mathrm{p}_1 \geq 0.5$ (in this space the chromosome 10 is dominant relatively to 01 as $\mathrm{p}_1 \geq \mathrm{p}_2$). The vertices of Δ in the plane (p_0,p_1) are:

- $\alpha =< 0, 1/2 >$
  This population is a mirror one which contains at equal proportion individuals 01 and 10. These chromosomes both represent the expected

global optimum having fitness 1 (remember that we assume $f_1 > f_0$).

- $\beta =< 1/2, 0 >$
  This population is a mirror one which contains at equal proportion individuals 00 and 11. These chromosomes both represent misleading solutions having the lower fitness $(1 - \sigma)$.

- $\eta =< 0, 0 >$
  This population is an homogeneous one which contains the individuals 10 only. This chromosome represents the expected global optimum having fitness 1.

The side (α, β) of Δ is supported by the line of equation $p_0 + p_1 = \frac{1}{2}$; it represents the subspace of *mirror* populations. Finally, the point $\upsilon =< \frac{1}{4}, \frac{1}{4} >$ represents the *uniform* population which contains all the individuals in equal proportions. This point is the limit distribution for a population undergoing mutation only.

Figure 1 represents the MDS, in the plane (p_0, p_1). In order to get a convenient representation of both Δ and Δ', we operate a kind of folding, such that Δ' becomes the symmetric of Δ by the line (α, β) (the mirror population subspace). This way, two conjugate populations becomes symmetric by this line.

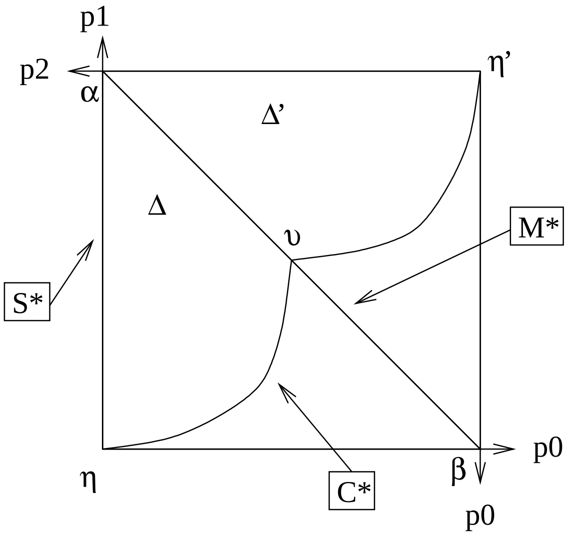

Figure 1. Symmetrical representation of the Minimal Dual Space.

2.1 Equations

We analyze the dynamics of the DGAs using the Whitley's executable model [29]. It uses an infinite population, no mutation and requires the enumeration of all points in the search space. Assuming proportionate reproduction, one-point crossover, and random mating of the reproduction products, an equational system can be used to modelize the evolution in time of the expected proportions of each of the competing chromosomes.

Let p_i^t be the proportion of the individual i in the current population P^t, where superscripts are generation indices, and subscripts denote each individual. The recurrence equations for the dual model are:

$$q_i^t = (1-\tau)\mathrm{p}_i^t + \tau.\mathrm{p}_{\bar{i}}^t \tag{2}$$
$$x_i^t = q_i^t.\frac{\mathrm{f}_i}{\overline{\mathrm{F}}} \tag{3}$$
$$\mathrm{p}_0^{t+1} = x_0^t + \chi.(x_1^t.x_2^t - x_0^t.x_3^t) \tag{4}$$
$$\mathrm{p}_1^{t+1} = x_1^t + \chi.(x_0^t.x_3^t - x_1^t.x_2^t) \tag{5}$$
$$\mathrm{p}_2^{t+1} = x_2^t + \chi.(x_0^t.x_3^t - x_1^t.x_2^t) \tag{6}$$
$$\mathrm{p}_3^{t+1} = x_3^t + \chi.(x_1^t.x_2^t - x_0^t.x_3^t) \tag{7}$$

where $\overline{\mathrm{F}}$ is the average fitness of the population ($\overline{\mathrm{F}} = \sum_{i\in\langle\Omega\rangle} \mathrm{f}_i.\mathrm{p}_i$), χ denotes the probability of having a crossover, τ the probability of having a mirroring, the q_i terms represent the population after application of mirroring and the x_i terms denote the effect of selection.

In the MDS, under the previous restriction, a reduced set of equations allows to express p_0^{t+1} and p_1^{t+1} according to p_0^t and p_1^t. In order to use this set, we should first prove that the transformed population of a population belonging to Δ belongs to Δ[1]. Note that we assume that the space of population is closed under the application of any genetic operators. So, the closure of Δ is ensured by checking the two conditions :

$$\mathrm{p}_0^t = \mathrm{p}_3^t \Rightarrow \mathrm{p}_0^{t+1} = \mathrm{p}_3^{t+1} \tag{8}$$
$$\mathrm{p}_1^t \leq \mathrm{p}_2^t \Rightarrow \mathrm{p}_1^{t+1} \leq \mathrm{p}_2^{t+1} \tag{9}$$

It is easily shown that these conditions are respected by each operators considered separately.

In the following, we will first examine the trajectories in the MDS induced by each operator separately, along with their respective fixed point sets. These "piece-wise" component analyses, while not exhibiting global behavior, will provide useful insights into the complete dynamical analysis.

[1] In fact, the relevance of the representation only needs that p_3 remains equal to p_0.

2.2 Dynamics of populations under selective pressure

2.2.1 Equations

Since the MDS is closed under selection, we can use the reduced equation set in the plane (p_0,p_1) for this operator:

$$p_0^{t+1} = p_0^t \cdot \frac{f_0}{\overline{\overline{F}}} = {p_0}^t \cdot \left(\frac{1-\sigma}{1-2\sigma {p_0}^t}\right) \tag{10}$$

$$p_1^{t+1} = p_1^t \cdot \frac{f_1}{\overline{\overline{F}}} = {p_1}^t \cdot \left(\frac{1}{1-2\sigma {p_0}^t}\right) \tag{11}$$

2.2.2 Trajectories

The trajectories induced by the selective pressure in the population space are linear (see figure 2). They are supported by lines passing by the initial population (p_0^0, p_1^0) and the population β, provided that the initial population is not β, and that there is an effective selective pressure ($\sigma \neq 0$). The equation of this line is:

$$p_1 = \frac{p_1^0}{(1-2p_0^0)}(1-2p_0) \tag{12}$$

2.2.3 Fixed points

The fixed points verify the equations: $p_i^{t+1} = p_i^t$. This leads to two equations:

$$p_0 = p_0 \cdot \frac{f_0}{\overline{\overline{F}}} \tag{13}$$

$$p_1 = p_1 \cdot \frac{f_1}{\overline{\overline{F}}} \tag{14}$$

If we assume that σ is different from 0, the first equation implies that $p_0 = 0$ or $p_0 = \frac{1}{2}$. The second equation implies that $p_0 = 0$ or $p_1 = 0$. This allows us to say that the fixed points set for selective pressure only is : $S^\star \cup \{\beta\}$, where $S^\star = \Delta \cap \{p_0 = 0\}$. If the initial population is different from β, it is easy to see that populations will converge toward $S^\star$, since p_0^{t+1} is always smaller than p_0^t.

2.3 Dynamics of populations under crossover

Crossover is the most distinguishing feature of genetic algorithm; so the case of no selection is particularly important as a test of the power of genetic search. In this section, we use results from mathematical genetics: the theory of recombination that characterizes the effects of recombination on multiple loci without selection [3, 13]. The probability that an individual has a 1 in a given locus remains constant under crossover is a fundamental property. That is, for any pair of parents, a crossover preserves the number of 1s at each position. So crossover does not change the distribution of alleles at any locus.

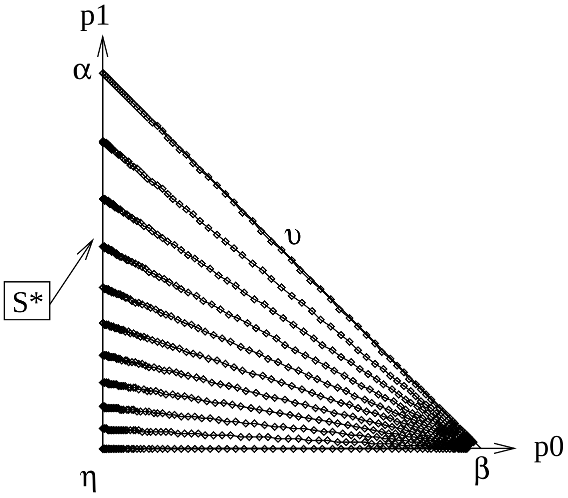

Figure 2. Trajectories for the selective pressure only ($\sigma = 0.1$), with different initial populations. They all converge toward $S^{\star}$.

Geiringer ([13]) analyzed the limiting distribution of genotypes: the main result is the crossover operator reduces the correlation between bits in different positions such that, in the limit, the probability becomes independent over bits. This equilibrium distribution is referred to as the "Robbin's equilibrium" ([3])

2.3.1 Equations

The reduced set of equations for crossover is:

$$\mathrm{p}_0^{t+1} = \mathrm{p}_0^t + \chi.(\mathrm{p}_1^t - (\mathrm{p}_0^t + \mathrm{p}_1^t)^2) \qquad (15)$$
$$\mathrm{p}_1^{t+1} = \mathrm{p}_1^t - \chi.(\mathrm{p}_1^t - (\mathrm{p}_0^t + \mathrm{p}_1^t)^2) \qquad (16)$$

2.3.2 Trajectories

As noted above, a fundamental property of crossover is the fact that this operator does not change the proportion of '1' over the population at a given locus. We call ω_i the proportion of '1' at the locus i. In the MDS, we have :

$$\omega_0 = \mathrm{p}_2 + \mathrm{p}_3 = 1 - (\mathrm{p}_0 + \mathrm{p}_1) \qquad (17)$$
$$\omega_1 = \mathrm{p}_1 + \mathrm{p}_3 = \mathrm{p}_0 + \mathrm{p}_1 \qquad (18)$$

The fact that ω_i remains constant over time implies that $\mathrm{p}_0 + \mathrm{p}_1$ remains also constant over time:

$$\omega_1^{t+1} = \omega_1^t \Rightarrow \mathrm{p}_0^{t+1} + \mathrm{p}_1^{t+1} = \mathrm{p}_0^t + \mathrm{p}_1^t \qquad (19)$$

So, trajectories induced by the crossover operator only are supported by the line for which $\mathrm{p}_0+\mathrm{p}_1$ is constant over time and passing by the initial population (p_0^0, p_1^0). The equation of this line is $p_1 = (p_0^0 + p_1^0) - p_0$. Figure 3 displays trajectories induced by the crossover for various initial populations.

2.3.3 Fixed points

The set of fixed points, $C^\star$, is supported by the parabola of equation :

$$(p_0 + p_1)^2 = p_1 \tag{20}$$

This is coherent with the Geiringer's theorem which claims that fixed points under crossover are those with zero correlation between the two genes. Indeed, it is easy to prove that the correlation between ω_0 and ω_1 is equal to zero for the points on the parabola $C^\star$ only. As noted by Spears ([28]), as the recurrent equations are non-linear, it is very difficult to determine the exact rate at which the crossover operator will drive a population to Robbin's equilibrium.

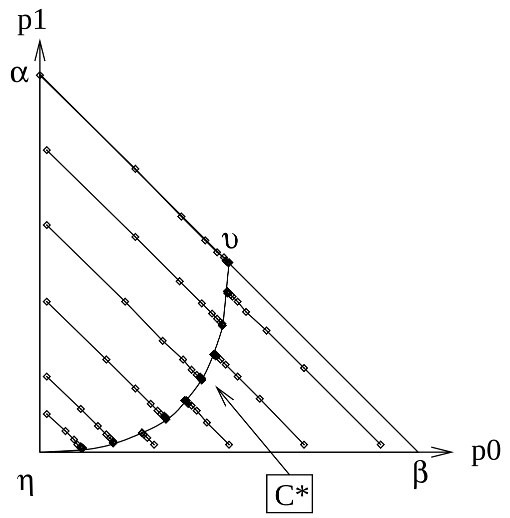

Figure 3. Trajectories for crossover only ($\chi = 0.5$), drawn from different initial populations. They all converge toward the parabola $C^\star$.

2.4 Dynamics of populations under mirroring

2.4.1 Equations

The equations for the mirroring dynamic are:

$$p_0^{t+1} = p_0^t \tag{21}$$
$$p_1^{t+1} = p_1^t - 2\tau p_1^t - 2\tau p_0^t + \tau \tag{22}$$

2.4.2 Trajectories

The trajectories induced by mirroring are lines for which p_0 remains constant over time, that is lines of equation : $p_0 = p_0^0$, where p_0^0 is the initial proportion of individual 00 (see figure 4).

2.4.3 Fixed points

As told above, the fixed points subset for mirroring is the set of mirror populations, $M^\star$.

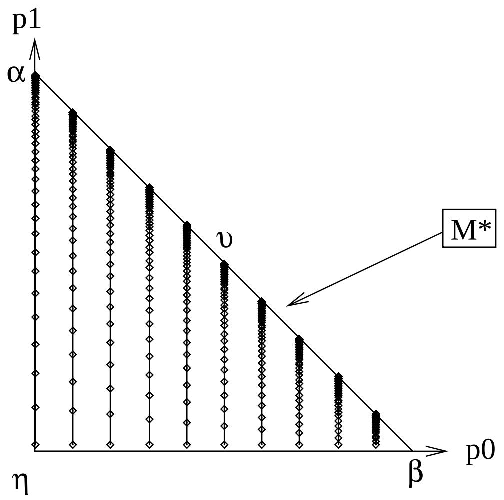

Figure 4. Trajectories for the mirroring only ($\tau = 0.01$), drawn from different initial populations. They all converge toward the line $M^\star$.

2.5 Genetic transformation as a composition of mirroring, selection and crossover

Previous sections have considered mirroring, selection and crossover apart from the other. Now we give the equations of the dynamics when the three operators act together. The genetic transformation, which produces the next population from the previous one, can be viewed as the composition of the three basic operators: mirroring, selection and crossover. Since the closure of Δ is established for each operator separately, we can say that Δ is closed under any composition of these operators. So, the dynamical equations for the MDS are:

$$\mathrm{q}_0^t = \mathrm{p}_0^t \quad (23)$$
$$\mathrm{q}_1^t = \mathrm{p}_1^t - 2\tau \mathrm{p}_1^t - 2\tau \mathrm{p}_0^t + \tau \quad (24)$$
$$\mathrm{x}_0^t = \mathrm{q}_0^t . \frac{1-\sigma}{1-2\sigma \mathrm{q}_0^t} \quad (25)$$
$$\mathrm{x}_1^t = \mathrm{q}_1^t . \frac{1}{1-2\sigma \mathrm{q}_0^t} \quad (26)$$
$$\mathrm{p}_0^{t+1} = \mathrm{x}_0^t + \chi.(\mathrm{x}_1^t - (\mathrm{x}_0^t + \mathrm{x}_1^t)^2) \quad (27)$$
$$\mathrm{p}_1^{t+1} = \mathrm{x}_1^t - \chi.(\mathrm{x}_1^t - (\mathrm{x}_0^t + \mathrm{x}_1^t)^2) \quad (28)$$

In the following, we use this set of equations to beget the dynamical behaviors of a DGA in the plane (p_0,p_1). We have seen that applying each operator separately implies linear trajectories in the space of populations. We now show that the composition of these operators gives non linear trajectories, and that the final population is the same whatever the initial population[2] is.

First, we consider the dynamics without mirroring. As expected, the final population is always η, for all couples ($\sigma \in]0,1]$,$\chi \in]0,1]$). Then, we introduce mirroring, and as it was expected, final populations are non homogeneous ones.

2.5.1 Dynamics of populations under selective pressure and crossover

With standard GA, we can conjecture that, under selective pressure and crossover and without mutation, the fixed points correspond to homogeneous populations, that is population which contains a single type of individual. As conventional GA, DGA converges toward homogeneous population if the initial population is not a mirror one. On the contrary, if the initial population is a mirror one, the fixed point is also a polymorphic mirror population (see figure 5).

2.5.2 Dynamics of populations under selective pressure, crossover and mirroring

With DGA, which is the composition of the three basic genetic transformations, mirroring, selection and crossover, it is possible to obtain stable polymorphic populations (see figure 6). If the system of non-linear equations is solved in order to found the fixed points, given σ, τ and χ, three solutions arise: two conjugate populations and a mirror one (equal proportions of 01 and 10). Each of these populations corresponds to one of the three basins of attraction: $\Delta \setminus M^\star$, $\Delta' \setminus M^\star$ and $M^\star$. The mirror population is by definition polymorphic. Given non null σ, τ and χ, the two others are polymorphic too.

So, duality allows to introduce and to maintain diversity in the population, without endogenous fitness evaluation, such as sharing.

[2] except for initial mirror populations

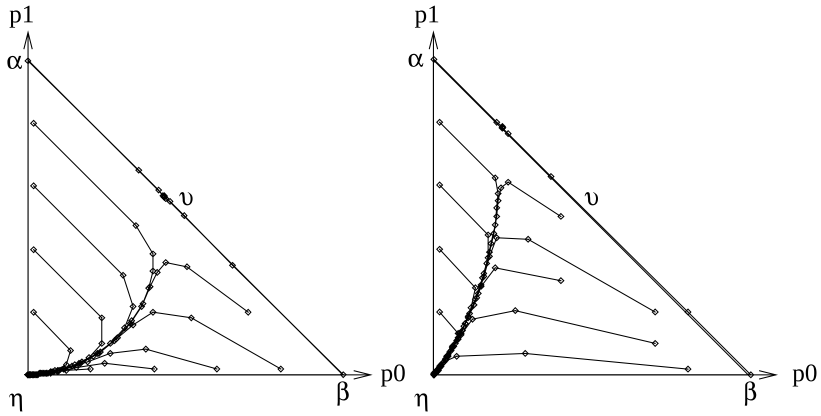

Figure 5. Trajectories induced by selection and crossover for different initial populations and for two sets of parameters. The left graph is for $\sigma = 0.5$ and $\chi = 0.7$. The right one is for $\sigma = 0.9$ and $\chi = 0.4$

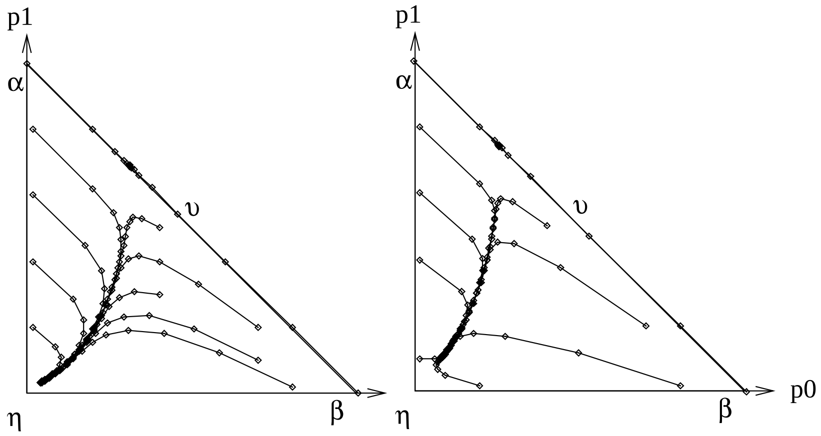

Figure 6. Trajectories induced by selection, crossover and mirroring for different initial population. The left graph is for $\sigma = 0.5$, $\chi = 0.4$ and $\tau = 0.01$. The right one is for $\sigma = 0.7$, $\chi = 0.4$ and $\tau = 0.03$.

3. Doupling : From Steady States to Cyclic Behaviors

The fact that biological systems do not always approach steady state, but may sometimes oscillate incites us to study the ways to introduce cyclic dynamics within GA. We propose to implement within GA one of the basic mechanisms of the chronobiology. Such an approach has not been yet explored in an artificial context, because, on one hand, only a few evolutionary theories are interested in the problem of the function of rhythm, and, on the other hand, the metaphor on which GA is based on, is extremely simplified compared with the natural model. The discover of the "per" gene among fruit flies and of the mutations altering it, has widely contributed to show that the rhythmic feature of hatching, the circadian cycle, and the periodicity of male songs are present in the animal's genotype. Instead to directly code an internal clock within the chromosome, we propose an implicit mechanism of rhythmogenese based on the duality of the genetic structures.

As M. Mitchell said [24], "explicit fitness evaluation is the most biologically unrealistic aspect of genetic algorithms". She suggests to move away from an external, static fitness measure toward more co-evolutionary and endogenous evaluations. Our motivation to use such techniques in the dual context is based on the fact that the dynamic of interactive complex systems is potentially a co-evolutive dynamic. Feedback mechanisms between the individuals undergoing selection provide a strong driving force toward complexity. Our technique has something in common with sharing which is classically used with GA ([23]). This kind of techniques lies in an alteration of the fitness value by endogenous factors; they take their spring from the ecological metaphor: the sharing of resources in the lap of a same niche. As chromosomes in a dual pair have the same phenotype, it seems natural that these two individuals act to increase their common gains. With the aim to induce a dual co-evolution, we propose to apply the sharing between two dual strings only. In this context, the relevant concept is not the sharing but rather the dual coupling. We refer to this kind of coupling as *doupling*.

3.1 A way to curve the space

In analogy with the concept of *adaptive topography* proposed by Wright ([30]), we consider a landscape where the distribution of genotypes in the population is represented by a point and the height represents the mean fitness in the population. The population would tend to move to peaks of this landscape. As said by R. Lande "the value of an adaptive topography is that it is easily visualized and so makes the evolutionary dynamics of the population intuitively clear" ([21]).

Doupling lies in the alteration of the exogenous fitness f_i of each string i. We propose to use the following transformation:

$$\tilde{\mathrm{f}}_i = \mathrm{f}_i . \left(\frac{2\mathrm{p}_{\bar{i}}}{\mathrm{p}_i + \mathrm{p}_{\bar{i}}} \right)^2 \tag{29}$$

where $\tilde{\mathrm{f}}_i$ is called *endogenous* fitness, and is used for selection.

We can observe on figure 7 the effect of doupling on the adaptive topography. Without doupling we have a flat landscape which declivity depends on the selective pressure σ. With doupling this surface

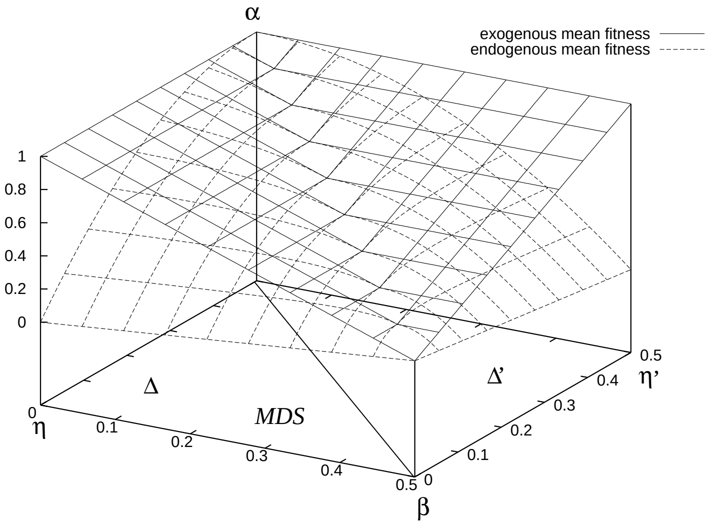

Figure 7. Effects of doupling on the adaptive topography

is curve around the mirror space with the space Δ on one side, and the conjugate space Δ' on the other side. We can note that doupling is neutral on mirror population, while the exogenous fitness of the homogeneous population η turns from 1 to an endogenous fitness of 0. Among all populations with close exogenous fitnesses, doupling promotes the more diverse ones. With doupling, the population α becomes the unique optimal population with the maximal mean fitness. According to this point of view, doupling can be thought as an implicit implementation of the mirroring operator. Indeed, one of the expected effects of doupling is to make selection act as an adaptive mirroring, since the doupling is not uniform over the population space. Considering doupling only from this point of view is limitative. We will see later that doupling induces more complex dynamics, since selection becomes a frequency-dependent process.

3.2 Two-points limit cycles in the MDS

We are going to show that doupling induces an internal clock of period two. We use a frequency-dependent selection process: the fitness of an individual changes according to the frequencies of its dual. Starting from a non mirror population, we observe a cyclic behavior with a convergence to two conjugate fixed points, one stands in the space Δ and the other in the conjugate space Δ'. Instead of a steady state we get an alternation between two conjugate populations.

We can observe on figure 8 (left graph) a typical trajectory, obtained for a particular low crossover rate (0.001). The population spirally converges toward a cycle of two conjugate populations belonging to $C^\star$. For higher crossover rate the spiral behavior tends to disappear, but the limit behavior is the same (i.e. cycle of period 2).

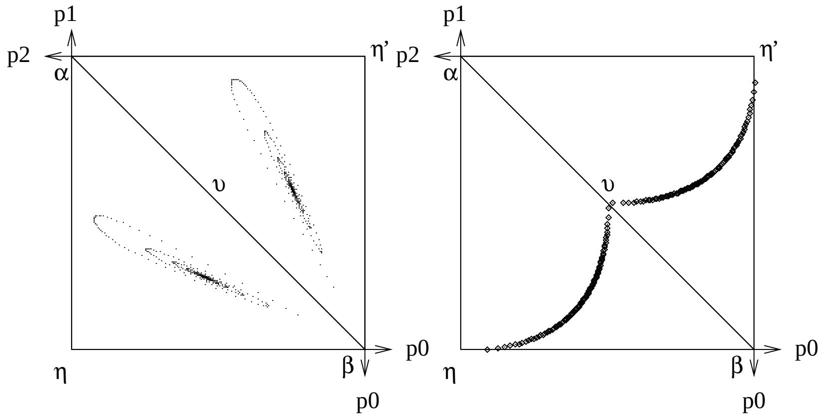

Figure 8. Left graph represents a trajectory in the MDS involving selection ($\sigma = 0.3$), crossover ($\chi = 0.01$) and doupling. Each generation, population jumps from one side of the MDS to the other one. Right graph shows the set of periodic attractors for σ values from 0 to 1. For each σ value there are two attractor, one in Δ and the symmetrical one in Δ'. They all belong to the parabola $C^\star$.

Populations converge to a two length periodic attractor in the phase space. When the selective pressure σ takes its values from 0 to 1, fixed points lie on the parabola $C^\star$ (right part of figure 8). However we must note that one point of $C^\star$ is not a fixed point for this dynamic: starting from one particular point on $C^\star$, the fixed point is another point of $C^\star$. Without selective pressure ($\sigma = 0$) the GA converges to the uniform population ν; if $\sigma = 1$, the final populations are the homogeneous ones η and η'; otherwise, we obtain polymorphic populations.

Remember that $C^\star$ is the set of fixed points for the crossover operator; that is the set of points for which the probability to have some bit value becomes independent over locus. So, populations on $C^\star$ have the best diversity among all populations which share the same probabilities of 1 on each locus.

These properties suggest to associate doupling with a simulated annealing technique in order to slide down the curve $C^\star$ toward the global optimum as the temperature decreases. This idea has been first proposed by Baluja and Caruana for *population-based incremental learning* ([2]). Their work is an extension of the Juels, Baluja and Sinclair's *equi-*

librium genetic algorithm ([19]). Their algorithm “simulates” crossover effects by maintaining populations on the vicinity of $C^\star$.

Doupling tends to put populations on $C^\star$, at a position which depends on the selective pressure. If the selective pressure is low, the population is near the uniform one, while higher pressure makes the population to get closer of the homogeneous one, filled with the optimal individual. In the first step of evolution, it is preferable to have more diversity to perform wide exploration, so selective pressure should be low. On the contrary, the final steps of evolution may be devoted to the exploitation by simply increasing the pressure. For example, selective pressure may be manage with technics such as fitness scaling.

3.3 Mirroring and Doupling

Combining mirroring and doupling, we obtain two kinds of attractor (see figures 9 and 10). When the selective pressure σ is under a point, populations converge to a mirror one ; beyond this threshold we observe a bifurcation and a two length periodic attractor. At this threshold point, we observe a break of symmetry : the pairs of dual chromosomes break down and the attractor gives way, as the selective pressure increases, to a periodic oscillation between two conjugate populations.

This last case reminds the no mirroring behavior. However, there are some differences. The first one is that limit populations do not belong to $C^\star$. The second one is that mirroring seems to delay the apparition of periodic behaviors according to the value of the selective pressure. Moreover, neither η nor η' are reached. So, in all cases, limit populations are polymorphic.

4. External Clock : a way to Chaos

We saw, in the previous section, how, under certain conditions, doupling may gives way to periodic behaviors. These behaviors, called endogenous behaviors, were of period 2. Now, we are going to dictate external rythmes to this bi-periodic system. The dynamical non-linear systems theory tells us that when periodic systems are subject to external oscillations incompatible with their free period, chaotic behaviors may arise. Effectively, we will observe, in the MDS, two kinds of transition toward chaos, the *period-doubling* one and the *quasi-periodic* one.

4.1 Clock driven fitness

Our aim is to introduce transitions from periodic to chaotic state by the way of variations of the selective pressure. Combining the dual coevolutionary framework with lifetime fitness evaluation, we propose to handle the system by an external clock which the rhythm controls the

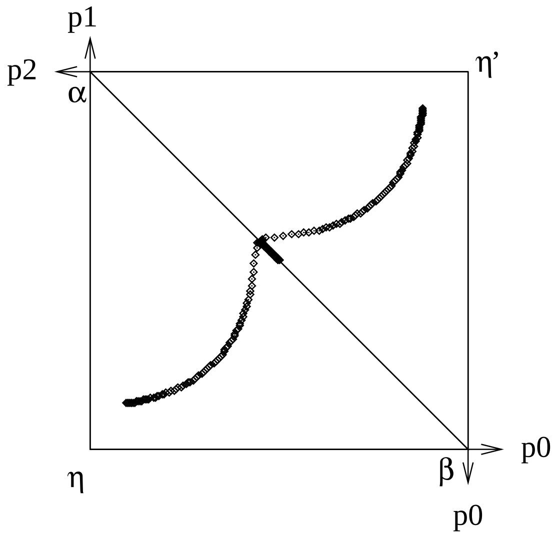

Figure 9. Periodic attractors in the phase space (p_0,p_1)

interactions between the system and its environment. More precisely, during some generations, the endogenous fitness relaxes back according to the doupling model:

$$\tilde{f}_i = \tilde{f}_i . \left(\frac{2p_{\bar{i}}}{p_i + p_{\bar{i}}} \right)^2 \tag{30}$$

Then, the endogenous fitness is reinitialized with the exogenous value, and it relaxes back again for some generations. So, there are two clocks: the endogenous one, induced by doupling and the external one, induced by the reset of the endogenous fitness.

Figure 11 shows the limit behavior of populations for an external clock of period 3. For σ values inferior to 0.6, the population "jumps" successively from three points. The period is 3, which is the period of the external clock. If the selective pressure increases, at a given σ value (around 0.65), the period of the system doubles. And so on, until the system becomes chaotic. This is the period-doubling route to chaos, which is also found with the logistic equation. When the behavior becomes chaotic the system is locally unstable: over short times nearby states move away from each other.

More generally, for odd period of the external clock, the behavior is qualitatively equivalent, that is a period-doubling route to chaos as σ increases.

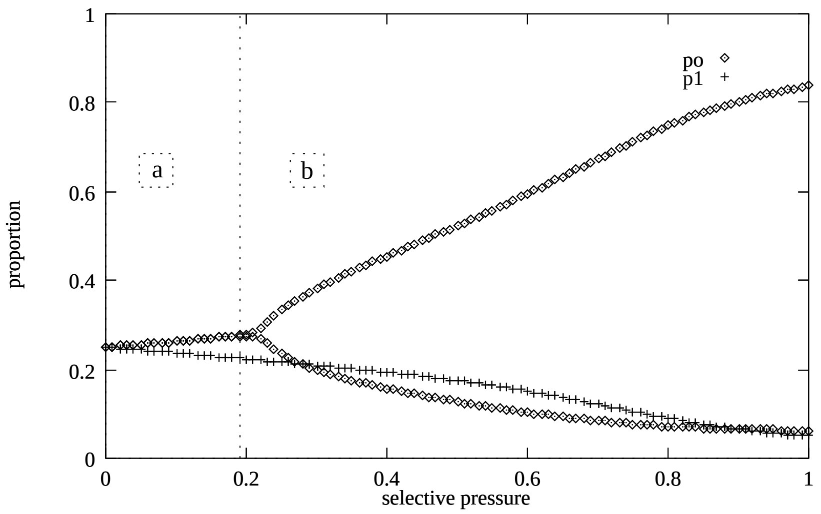

Figure 10. Distribution of the values of p_0 and p_1 for fixed points as a function of selective pressure σ from 0 to 1 with mirroring. (a) steady state: mirror population; (b) cycle of period 2: conjugate populations

4.2 Clock driven crossover

Now, we synchronize the crossover operator on the external clock. That is, crossover occurs only at each tip of the c_clock. So, crossover are concomitant with the re-initialization of the fitness value. Once more, and in the same way, we observe a number of attractors equal to the period of the external clock, for small value of σ (see figure 12).

When the selective pressure increases, a quasi-periodic state is observed. Figure 13, a zoom from figure 12, shows the first transition between a periodic state to a quasi-periodic one. When the pressure increases more, there are alternances of periodic, quasi-periodic and chaotic states (see Figures 14, 15 and 16). Figure 16 exhibits doubling period ways to chaos (eg. near $\sigma = 0.72$), and transitions to periodic states by period division (eg. near $\sigma = 0.74$).

The appearance of wavelet (see figures 13, 14 and 15) denotes quasi-periodic states. Indeed, these figures are, for each value of σ, the plot of p_1 for generations from 10000 to 10200. A quasi periodic system is a system which does not fall in the same state at each period, but in a close one. If the range of generation for plotting is increased, more and more space is covered, and in the limit, all the bounded space is filled.

The attractors of this system are composed of three continuous curves (see figure 17). Populations jump from one curve to another one at each generation. Obviously, the curve corresponding to the

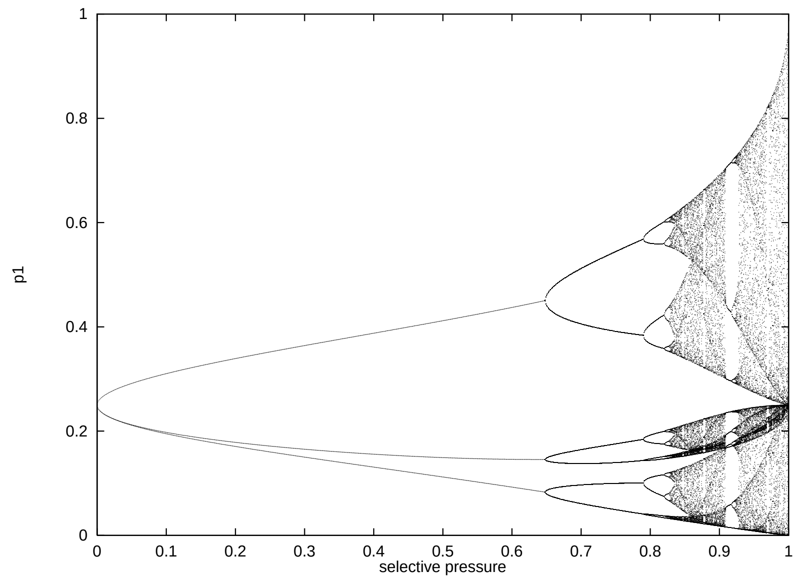

Figure 11. Bifurcation diagram showing the distribution of p_1 for fixed points as the selective pressure s is varied from 0 to 1. The period of the external clock is 3 and χ is 1.

generations where crossover occurs is the one supported by $C^{\star}$.

The previous remark concerning the space filling gets an easier explanation with figure 17 : after 5000 generations the attractor is nearly covered. With less generations, the attractor seems to be more dash plotted. The reason is that the value of σ used for this plot insures a quasi-periodic state. In the case of a chaotic behavior, the "sampling" of the attractors is more uniform. This is a feature which allows to distinguish between quasi-periodic and chaotic state.

4.3 Mirroring and External Clock

Adding mirroring, we observe four stages according to the value of the selective pressure (see figure 18). For small values of σ, the behavior is periodic, of period three, since the external clock is of period three. When the selective pressure is increased, the system becomes quasi-periodic, in the same way as the no mirroring case. Figure 19 is a closeup of figure 18. The quasi-periodicity is obvious on this plot. However, contrary to the no mirroring case, when σ increases again, instead of continuing on to chaos, the system goes through quasi-periodic states and finally ends up with a periodic behavior again. This kind of behavior has been exhibited in oscillating chemical reaction ([16], p. 635).

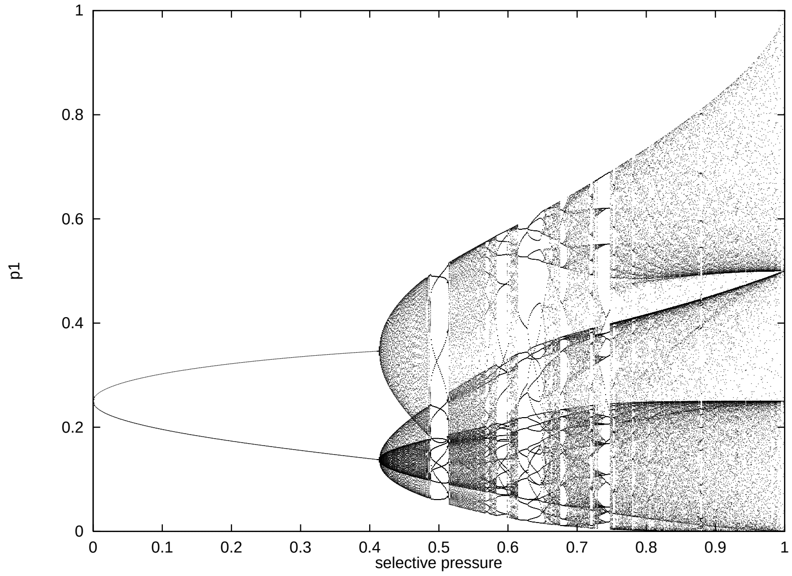

Figure 12. Bifurcation diagram showing the distribution of p_1 for fixed points as the selective pressure s is varied from 0 to 1. The period of the external clock is 3 and χ is 1.

It seems that the system always stays in periodic or quasi-periodic states. It can be thought that mirroring preserves from chaos, and allows the system to stay at the edge of chaos.

5. Discussion

The key idea with dualism is to add a level between genotype transcription and phenotype evaluation. This new level induces the existence of dual pairs, that is sets of two genotypes representing the same phenotype. The fact that the expression of genotype is controlled by the genotypes themselves, and that dual genotypes are bitwise complement, induces interesting properties for the resulting dynamics, such as convergence toward polymorphic populations.

Moreover, this meta level, together with the introduction of an explicit coupling between dual individuals, which induces a frequency-dependent selection scheme, allows complex behaviors, such as cycles and chaos, to emerge in population dynamics.

First, there is an obvious *per se* interest to exhibit chaotic behaviors in population dynamics. As far as we know, it is the first study where an haploid genetic algorithm with no mutation is bound to such behaviors, despite the fact that many works concern their conditions of emergence in models of natural evolution (see Altenberg [1] for a

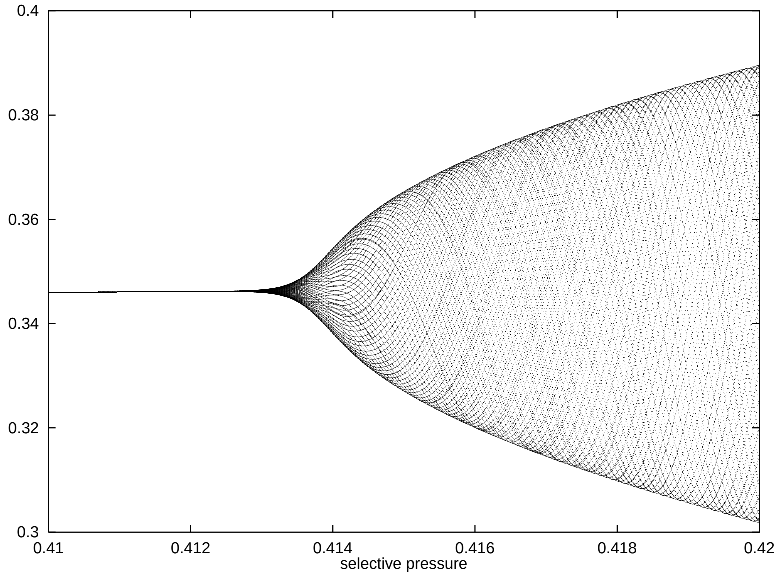

Figure 13. Closeup of figure 12. Periodic to quasi-periodic state transition.

wide discussion about this). The similitude between the bifurcation diagram obtained when the selective pressure is varying and the well known Feigenbaum's diagram is quite interesting. Moreover, it is a brand new two dimensional system featuring chaotic behavior. The study of the attractor structure and the population jumping behavior should give interesting insight on chaotic theory and non-linear dynamical systems studies.

However, one might enquire if there is a direct interest of such studies in the context of evolutionary computation. At this point we should ask for two questions: what is the relevance of the MDS as a model of DGA dynamics, and what is the interest to introduce complex behaviors in an evolutionary algorithm.

The MDS is a minimal model, based upon the hypothesis of a infinite population and derived from a probabilistic model of genetic algorithm dynamical behaviors. Nevertheless, this kind of model has already been widely used ([29]). And in population genetic, as noted in [29], it is often the case to study population of individuals with only one gene. The MDS may be seen as a way to study, in the general case of many genes, relations between a given gene and the meta one, without considering epistatic effects. Epistasis coupling between "normal" genes, far from simplifying behavior, should increase their complexity (for the relation between epistasis and complexity, one may have a look at Kauffman's work about NK-landscape in [20]). Thus it is consistent to make the hypothesis that observed complex dynamics on a simpli-

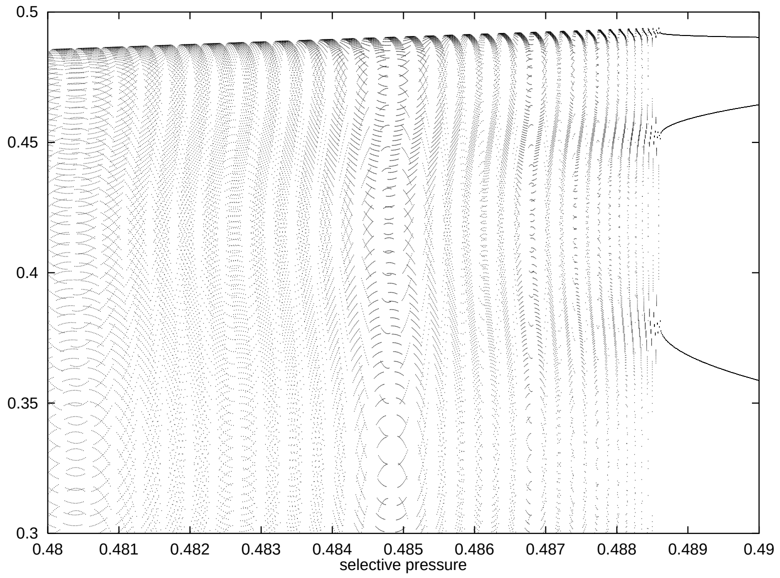

Figure 14. Closeup of figure 12. Quasi-periodic to periodic state transition.

fied model may exist in the actual system too. However, the study of the MDS is much simpler than the DGA one, since phenomena are more easily observable and analyzable.

The question "What is the use of chaos" has already been asked. In the natural adaptive systems context, Conrad ([10]) noted five chaotic mechanisms of adaptability

1. Search (diversity generation)
2. Defense (diversity preservation)
3. Maintenance (disentrainment processes)
4. Cross-level effects (interaction between population dynamics and gene structure)
5. Dissipation of disturbance (qualitative insensitivity to initial conditions)

In a more general way, most adaptive systems, including living systems, have to make a trade-off between the ability to continue to function in the face of uncertain or unknown environment and the ability to maintain their integrity in all case. Chaotic behaviors realize such a trade-off. "Life at the edge of chaos" (from the title of Langton's article [22]) is now a widely shared idea.

The enumeration of possible functional roles for chaos in adaptive systems may be transposed to genetic algorithms, since they are artificial adaptive systems. Obviously, the most expected role concerns

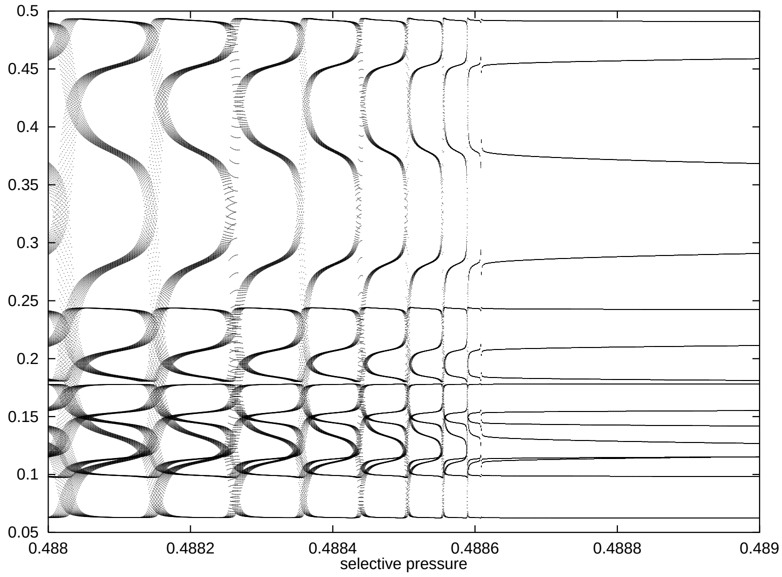

Figure 15. Closeup of figure 14. Quasi-periodic to periodic state transition.

the search (diversity preservation). While in chaotic state, the population follows a trajectory in the MDS passing through a great number of points, therefore "visiting" many different solutions. Moreover, insensitivity to perturbation and robustness are qualities of chaotic systems which may be useful to genetic algorithms, in particular for problems with incomplete or noisy information.

Finally, this work renews the Holland's exploration/exploitation dialectic [17], introduced while developing genetic algorithms. Considering genetic algorithms as adaptive systems, implies to study them as complex systems.

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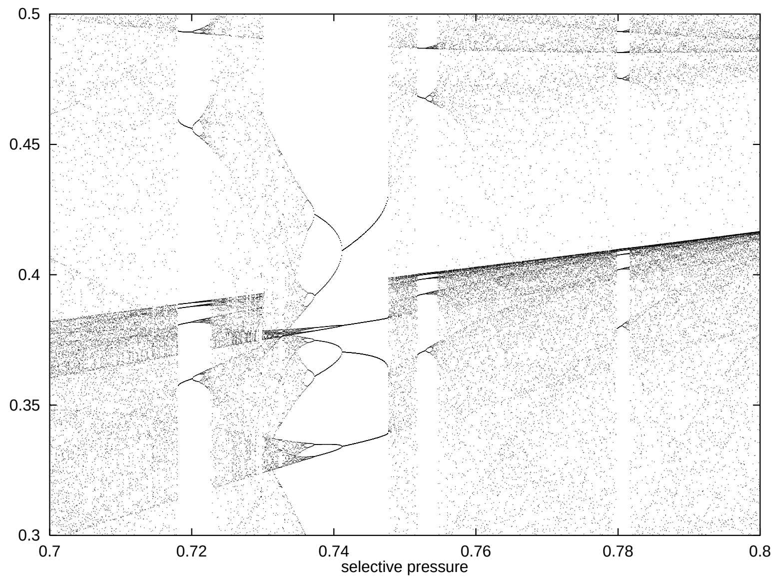

Figure 16. Closeup of figure 12. Chaos-periodic-chaos transitions

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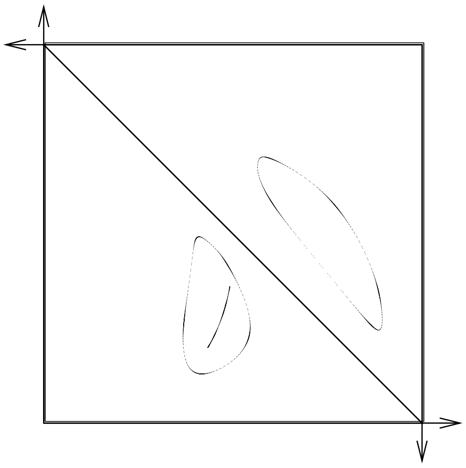

Figure 17. Attractor in the MDS for $\sigma = 0.4882$.

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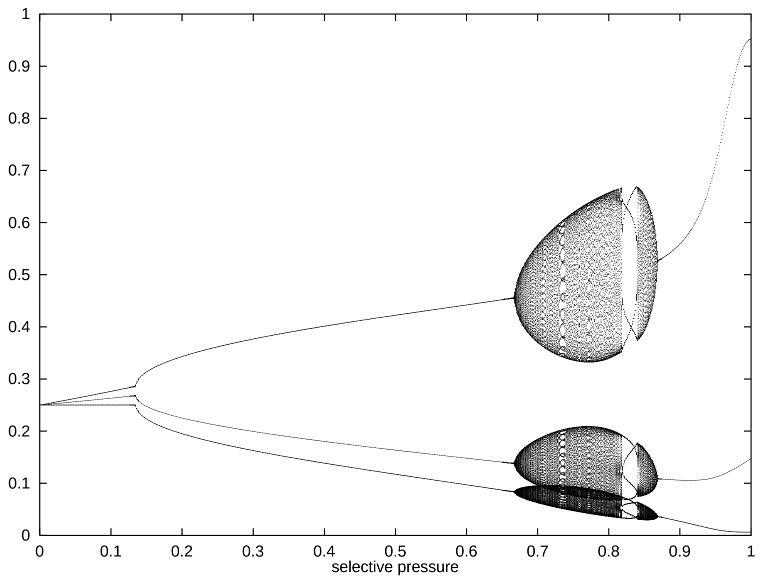

Figure 18. State diagram showing the values of p_1 reached by the system according to the selective pressure. The C_CLOCK period is three, the crossover probability is 1.0 and the mirror rate is 0.034.

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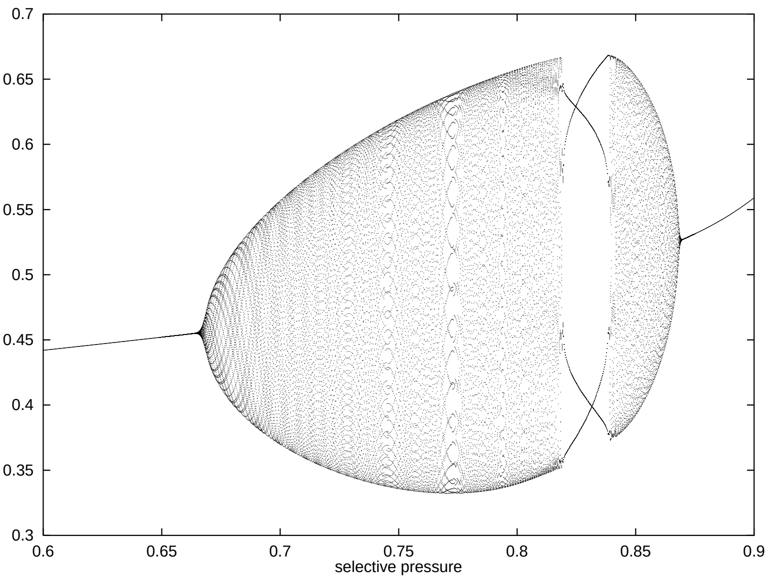

Figure 19. Closeup of figure 18. Quasi-periodic state.

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