Synthetic Neutrality for Artificial Evolution

Philippe Collard, Manuel Clergue and Michael Defoin-Platel

Laboratoire I3S, CNRS - UNSA
2000 route de lucioles, 06410 Biot, FRANCE
e-mail:{pc,clerguem,defoin}@i3s.unice.fr

Abstract. Recent works in both evolution theory and molecular biology have brought up the part played by selective neutrality in evolution dynamics. Contrary to the classical metaphor of fitness landscapes, the dynamics are not viewed as a climb towards optimal solutions but rather as explorations of networks of equivalent selective genotypes followed by jumps towards fitter networks. Although the benefit of neutrality is well known, it is hardly exploited in the genetic algorithm (GA) field. The only works about this subject deal with the influence of the inherent neutrality of a fitness landscape for evolution dynamics. In this paper, we propose a very different approach which consists to introduce "handmade" neutrality into the fitness landscape. Without any hypothesis about the inherent neutrality, we show that a GA is able to exploit new paths through the fitness landscape owing to the synthetic neutrality.

1 Introduction

A theory of the biological evolution at molecular level based on neutrality was first proposed by Kimura ([9]). According to this works, the most part of changes during evolution arises from a random drift at genotype level rather than from the effect of selective pressure. The neutral theory supposes firstly that there are sets of selectively equivalent genotypes and secondly that it is possible to move through those sets using selectively neutral mutations. Kimura is interested only in the influence of the neutrality for the dynamics in flat adaptive landscapes. Further, many simulations based on the RNA secondary structure ([6, 8]) shown that the neutrality plays an important role in the evolution dynamics at a molecular level.

Thus, the neutrality theory explains evolution by diffusion processes through neutral networks (i.e. sets of connected genotypes that are selectively equivalent). This diffusion increases the opportunity to find a part of the genotype space in which the selectively dominant network is closed to a more adapted network. More generally, there are a lot of interlaced networks; moving through a network, a population generates some mutants out of the network and then explores new phenotypes. A transition between two phenotypes appears in regions where networks become closer. This makes the classical vision of a rugged adaptive landscape, with peaks and valleys, no more relevant ([1]).

More recently, some adaptive landscapes owning a high neutrality level have been synthesized in the fields of cellular automata ([7]), sequential dynamic systems ([2]), and genetic algorithms ([1]).

Many fitness landscapes from genetic algorithms literature own an high level of neutrality, for example, the Royal Road functions or the unitation based functions (e.g. the "trap" function). Those landscapes have been generally designed to study one kind of difficulty : deceptivity, building blocks processing, etc. So, it is possible to build highly neutral fitness landscapes that are either GA-difficult or GA-easy. There is *a priori* no correlation between GA-difficulty and neutrality. But, can we say that a GA is not able to exploit the neutrality of a fitness landscape ? In this paper, we give a partial answer to this question. Rather than evaluating the neutrality level of a given landscape or designing fitness landscapes with controllable neutrality level, as for example, the NKp landscapes family ([1]), we propose to introduce, for any landscape, a structured neutrality. In this paper we show how the exploitation of such a neutrality can help a GA to find the way towards the global optimum. We propose a first step that consists in building some *ad hoc* fitness landscapes in which we think that the GA can exploit the synthetic neutrality. Then, we will study the populations dynamics in those landscapes. Our aim is twofold: firstly, we propose a new technique based on the synthetic neutrality concept; then, we build a family of adaptive landscapes owning a given neutrality level and we design some visualization and measure oriented tools to study the populations dynamics.

Finally, we want to say some words about the methodology. We think that we have to begin our studies with *ad hoc* landscapes because it is easier to define such landscapes than more realistic ones. We also notice that there are many things to understand about neutral dynamics in simple models and that we are not ready to study more complicated models in which the parts played by neutrality and selection could not be clearly discerned.

2 Synthetic neutrality

We've already reminded the role of neutrality in biological evolution. This led some authors to study the dynamics of GA from a neutral point of view (e.g. [1]). They analyzed the influence of the inherent neutrality of particular adaptive landscapes on the GA dynamics. Here, we propose a way to artificially introduce neutral networks into fitness landscapes.

2.1 Minimal synthetic neutrality

The basic idea of the synthetic neutrality is to create an extended genotype space, on which the GA works, and then, an application from this new space to the basic genotype space on which the evaluation function works.

Let $\Omega = \{0,1\}^\lambda$ be the basic genotype space. In a minimal way, the extended genotype space, $\langle\Omega\rangle$ is defined as $\{0,1\} \times \Omega$. It corresponds to the adjunction of an additional bit to the chromosomes from Ω. This new bit, called the *metabit*, controls the interpretation of the rest of the binary string.

We define the application T from $\langle\Omega\rangle$ to Ω as :

$$\forall\omega \in \Omega \; , T(0\omega) = T(1\overline{\omega}) = \omega$$

where $\overline{\omega}$ is the binary complement of ω. Let F be the evaluation function defined over Ω. From the point of view of $\langle\Omega\rangle$, the algorithm works on a new fitness landscape defined by the function $\langle F\rangle = F \circ T$ over $\langle\Omega\rangle$. The following relation can be established :

$$\forall\langle\omega\rangle \in \langle\Omega\rangle, \langle F\rangle(\langle\omega\rangle) = \langle F\rangle(\overline{\langle\omega\rangle}) = F(T(\langle\omega\rangle))$$

Thus we get, without any hypothesis about the inherent neutrality of Ω, two genotypes from $\langle\Omega\rangle$ with the same adaptive value, so selectively equivalent.

Now, we have to show how such genotypes could be connected in a same neutral network. Indeed, classical mutation is not adequate here since those genotypes are at maximal Hamming's distance $(\lambda + 1)$ of each other because of their complementarity. This leads us to introduce a neutral operator of mutation, also called mirror operator (according to its effects on the genotype or on the phenotype). This operator transforms a chromosome from $\langle\Omega\rangle$ to its binary complement. According to the above relation, this transformation doesn't induce any modifications on the phenotype. With this operator, two complementary chromosomes (that are selectively equivalent) are linked by a neutral network, since they are only one neutral mutation apart.

Such synthetic neutrality is said minimal, according to the size and the dimension of the induced networks. Indeed, in $\langle\Omega\rangle$, there are 2^λ networks which the size is 2. Their dimension (number of possible neutral mutation from a point) is equal to 1.

Despite its minimality, this synthetic neutrality (MSN) has interesting properties. The first one is that neutral mutations and classical mutations (that infer a change in the phenotype) are independent from each other. The neutral mutation rate is set on an high value (around 0.01), while the classical mutation is still fixed at its usual value (around $1/\lambda$). Thus, we can get an important ratio between neutral and classical mutation rates, as in neutral networks of high dimensions. The second property of the MSN affects the neighborhood of a neutral network. This neighborhood contains some chromosomes that could be very distant in $\langle\Omega\rangle$, as in Ω. Indeed, the introduction of synthetic neutrality alters the topology of Ω. This property of the MSN reminds the drifts in larger neutral networks that allow huge jumps through the search space.

2.2 Order n synthetic neutrality (SN_n)

Following the same idea, it is possible to synthesize a higher level of neutrality, according to the size and the dimension of neutral networks. Indeed, we can introduce several metabits, each influencing a part of the chromosome. Each part with its own metabit is called a block. The space of chromosomes becomes the space $\langle \Omega \rangle_n = \{0,1\}^n \times \Omega$ with n metabits. For $n = 0$, this is a standard GA, while the case $n = 1$ stands for the minimal synthetic neutrality. The maximal bound for n is λ, since this is uninteresting to have more blocks than bits in the chromosomes. Connections between equivalent genotypes are created by the partial mirror operator. This operator is selectively neutral and allows to complement just one block. The number of neutral networks stays equal to 2^λ, but their size and dimension become respectively 2^n and n. The two properties of the minimal synthetic neutrality are still true. The synthetic neutrality is structured and affects the search space topology by bringing closer initially distant chromosomes. For example, let us consider chromosomes 0010010011 and 1101110001. The Hamming's distance between them is high in Ω ($d_H = 6$). On the other hand, in $\langle \Omega \rangle_2$, they may be closer. Indeed, in this space, the distance may be as small as 2.

3 Populations dynamics and synthetic neutrality

Our goal, in this section, is to show how the synthetic neutrality can affect the dynamics of the populations.

3.1 Methodology

It's difficult to well understand how a population can exploit neutrality during the evolution. Indeed, classical and neutral evolution behaviors are often concomitant. That's why we propose to bring in light the exploitation of neutral networks in experimental situations specifically designed to promote it. For this purpose, we build particular GA-hard functions. Then we study the dynamics of the population.

3.2 Adaptive landscapes

A fitness function gives the distribution of adaptive values along the search space, also called the fitness landscape ([10]). The dimensions of such search space are often high, thus we propose to design fitness landscapes in the plan fitness / distance to the optimum. Let's notice that this projection implies that all genotypes at a given distance from the optimum own the same fitness. The global optimum is set, without loss of generality, to the genotype 0^λ (0.....0).

During our experimentations, we have considered first and second order synthetic neutrality oriented landscapes. When we design such landscapes, according to the theoretical model, we hope for being able to predict spatial and temporal circumstances of the appearance of particular events. There are at least two reasons that prevent us from *a priori* determining qualities of a given landscape in a neutral context. Firstly, as Barnett says ([1]), there is an independence between ruggedness measure of a landscape (given by the autocorrelation function) and the neutrality level. Secondly, it is hard to predict how transformations induced by synthetic neutrality will be exploited during evolution.

3.3 Visualization tools

Visualize the dynamics of the population in its globality is quite impossible because search space dimensions are generally too huge ([5]). So, we have to visualize these dynamics from a more restricted, then more ambiguous point of view. Nevertheless, varying points of view can remove many ambiguities.

Another problem is that these dynamics seem to be determined by many parameters such as : fitness landscapes characteristics, population polymorphism, "birth" of a dominant individual, *etc.* That is why we developed several tools, each one designed to observe particular features.

3.3.1 Macroscopic Visualization

Tools presented here allow to study the mean properties of a population.

Centroid trajectory :

Population centroid is the point representing the mean fitness and the mean distance to the global optimum plotted in the corresponding plan. By determining this point at each generation, we can get a trajectory which is a good reflect of the population dynamics through the associated landscape. We're able to study this trajectory in the basic search space, as well as in the extended search space.

Distance to the optimum per block :

When we have studied the order 2 neutrality, we were interested in blockwise evaluation of genotypes. This means that global fitness of a genotype is given by fitness function computed on each block. So the distances to the optimum of each block are relevant measures. Computing these two distances allows to draw both a three dimensional trajectory (mean distance from the block 1, mean distance from the block 2, mean fitness) or the time evolution of each block distance.

3.3.2 Microscopic vs. Macroscopic visualization

Tools presented here allow to study the relations between one individual and its population. The main objective is to show how some particulars events could influence the global populations dynamics.

Genotypes evolution :

The population evolution might be influenced by the coming out of a particular genotype. In order to verify this hypothesis, we propose to plot the added up proportions (computed at each generation) of all the genotypes of the population. Computational constraints force us to limit the genotype size to 64 bits. In order to observe possible moves of population through order 1 neutrality networks, we choose to draw those proportions according to two significant schemata : $0\#$ (positive ordinate) and $1\#$ (negative ordinate), with $\# \in \{0,1\}^{\lambda}$.

Mean and maximum fitness evolution :

This is a classical tool that bring in light the relations between the fittest genotype and the mean fitness of the population.

Relative trajectory of the centroid :

This relative trajectory is nearly similar the one previously described. The main difference is that the centroid is now the couple mean distance to the fittest genotype and mean fitness. So, each time a better individual emerges, the context changes.

3.4 Experimental studies

In this section, we present a set of results representing some typical examples of our experimentations. Each run, the GA works during 1000 generations, with 100 chromosomes each being 200 bits long. The classical mutation rate is fixed to 0.5 per chromosome (i.e. 0.0025 per bit) while the neutral mutation rate is set to 0.02. We choose to use the two points crossover at a rate of 0.7 and the 2-tournament selection scheme.

3.4.1 Order 1 neutrality

The landscape designed for this experimentation is defined with a piecewise affine function in the unitation fitness plan. Its global outline looks like the letter V from which some segments (8 in number) are set to zero.

Without synthetic neutrality, the population is trapped in a local optimum (cf. figure 1). A contrario, with order 1 synthetic neutrality (MSN), after some accumulations followed by jumps through the landscape, the population succeeds to converge towards the global optimum (cf. figure 2).

Observing the mean fitness evolution, we can distinguish three steps before important fitness gains (cf. figure 3). These steps, and associated accumulation, corresponds to the exploitation times of neutral networks, while gains and jumps are linked to inter networks moves. We also notice a degradation of the mean fitness value before the gains and during the jumps. Indeed, during accumulations, the population explores the two subspaces 0Ω et 1Ω. This phenomenon increases the genotype polymorphism and produces the coming out of more diversified individuals, who are potentially degraded.

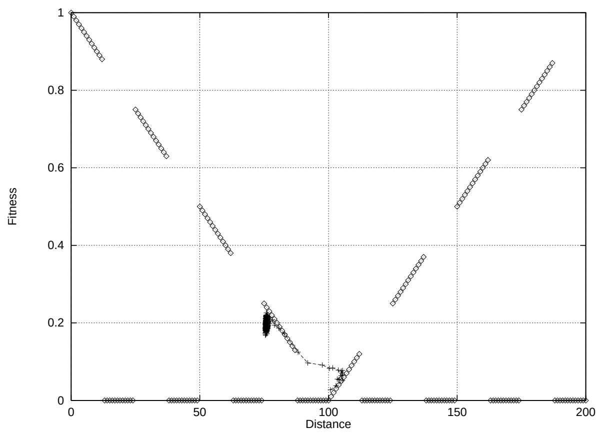

Fig. 1. Centroid trajectory without synthetic neutrality.

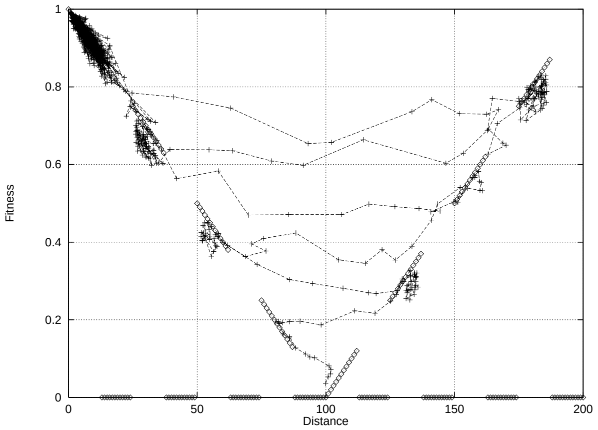

Fig. 2. Centroid trajectory with order 1 synthetic neutrality.

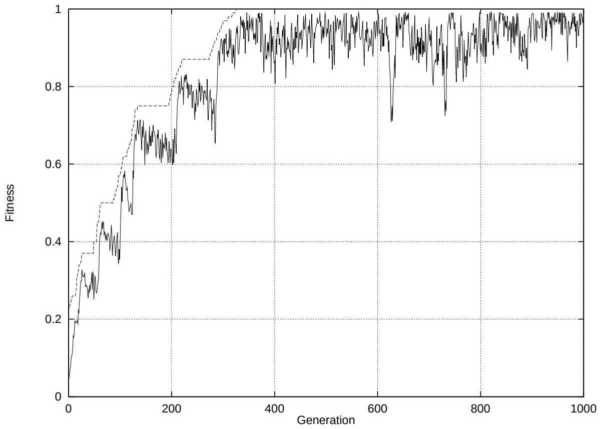

Fig. 3. Mean and max fitness evolution with order 1 synthetic neutrality.

Moves through neutral networks are equivalent to moves between the subspaces 0Ω and 1Ω. We can observe such moves on the figure 4. Note that this graph does not correspond to the same experiment than the previous one, since the length of the chromosome should be less than 64 bits. These migrations seem to be released by the exponential growth of particular genotypes.

The figure 5 shows the trajectory of the centroid obtained with the minimal synthetic neutrality when the crossover is turned off. The jumping behavior is still present and even more clearly observable. This indicates that the important feature in this experiments is the couple classical mutation and neutral mutation associated with the transformation of the structure of the search space. Nevertheless, experiments on other problems show the importance of crossover

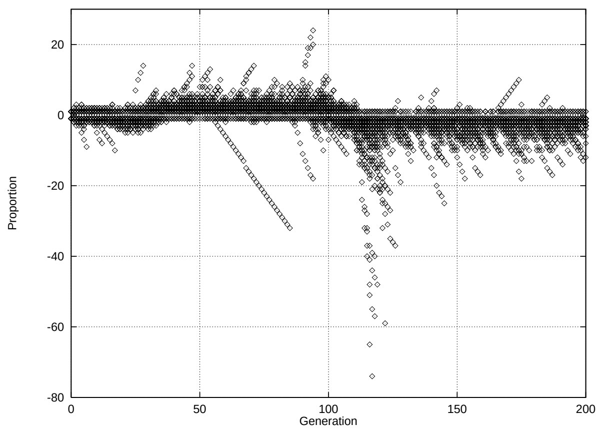

Fig. 4. Genotype cumulative proportions with order 1 synthetic neutrality.

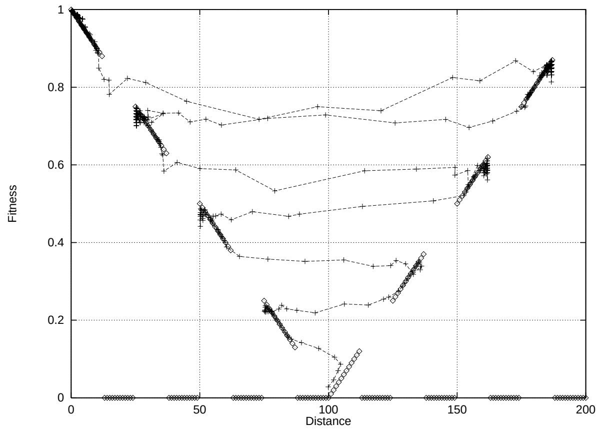

Fig. 5. Centroid trajectory with order 1 synthetic neutrality, no crossover.

to converge towards optimal solutions.

3.4.2 Order 2 neutrality

The landscape designed for this experimentation was obtained with a blockwise function. The first block is evaluated by the function used previously with only 4 zero fitness segments. The second block is evaluated according to the number of bits equal to zero (inverted unitation).

Even with order 1 neutrality synthesis, the problem is still difficult and the population doesn't attain the global optimum (cf. figure 6). Studying the relative trajectory (see figure 7), we observe two distinct jumps which correspond to the coming out of genotypes that are fitter and very distant from the mean population. These jumps are induce by jumps between neutral networks.

On the other hand, with order 2 synthetic neutrality, dynamics lead the

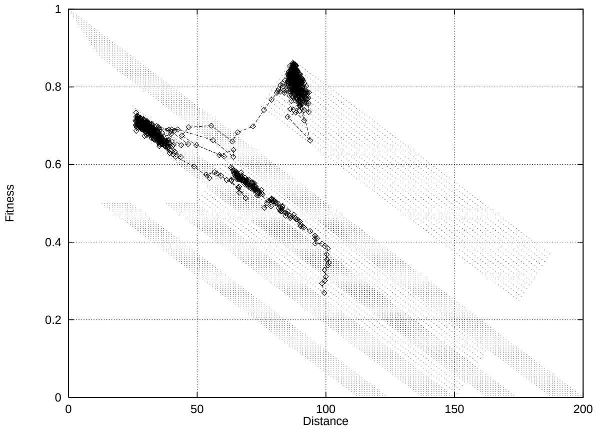

Fig. 6. Centroid trajectory with order 1 synthetic neutrality.

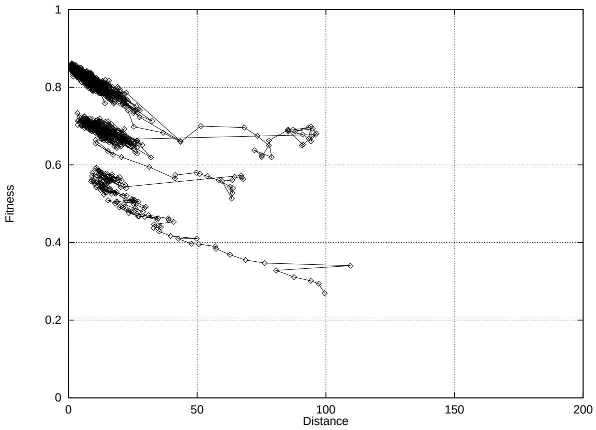

Fig. 7. Relative centroid trajectory with order 1 synthetic neutrality.

population to follow a path that allows it to converge to the global optimum after two jumps (cf. figures 8 and 9).

As we see in figure 10, the mean distance of the first block goes like in the order 1 neutrality experimentation. While the mean distance of the second block evolves according to its inverted unitation. The two jumps of the centroid trajectory may be linked to jumps of the first block. This allows us to bring in light the existence of parallel dynamics that are probably responsible of the right convergence of the population.

Again, the population, when the crossover is switched off, exhibits the jumping behavior, as showed on figure 11.

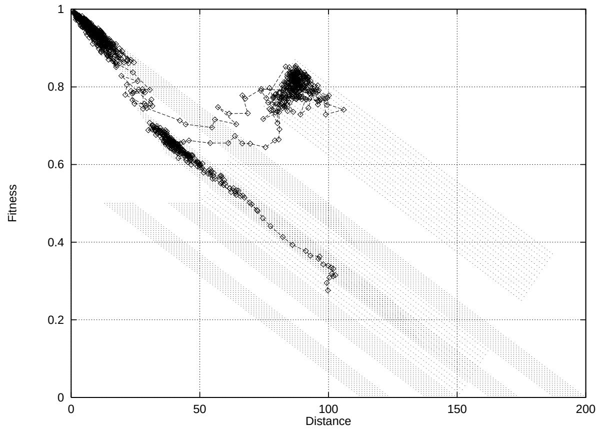

Fig. 8. Centroid trajectory with order 2 synthetic neutrality.

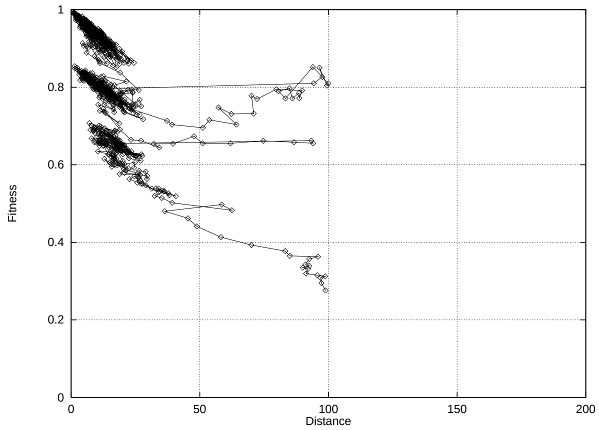

Fig. 9. Relative centroid trajectory with order 2 synthetic neutrality.

4 Conclusion

The main difference between neutral and selectionist theory of evolution relies on the explanation of the natural polymorphism. Indeed, genetic diversity is undoubtedly useful for the evolution, but this diversity is paradoxical since the selective pressure leads the populations to become homogeneous. Some people bring up selective arguments, others believe in neutral mutation hypothesis. The truth should lay between them.

This discussion can take place in GA field which is exposed to premature convergence, that is the loss of diversity. Until now, the classical techniques were selectionist, as sharing, which, modifying the selective value, allows to escape from local optima. We showed that synthetic neutrality with *ad hoc* evaluation functions also allows to escape from such optima. Neutral networks with a particular structure can be exploited by the algorithm.

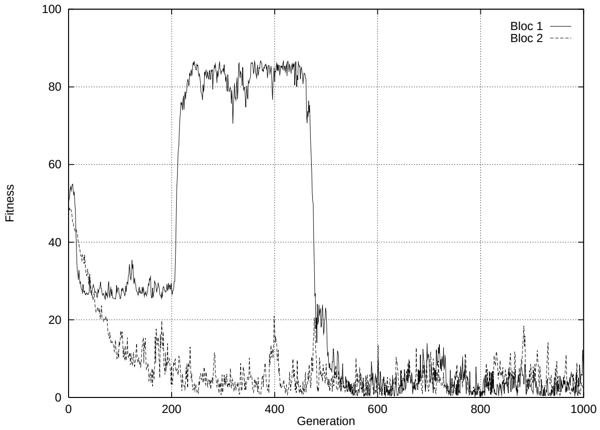

Fig. 10. Time evolution of the mean distance per block with order 2 synthetic neutrality.

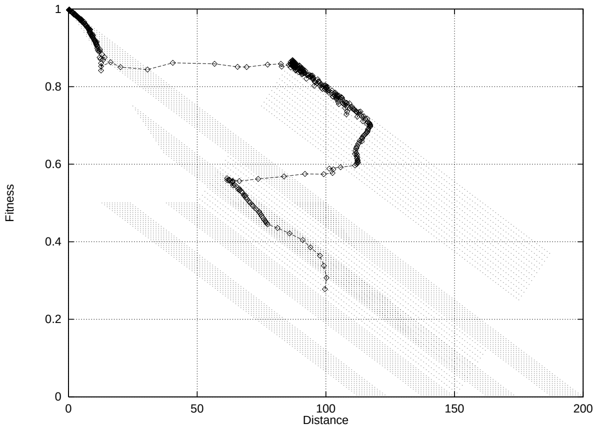

Fig. 11. Centroid trajectory with order 2 synthetic neutrality, no crossover.

Synthetic neutrality is for neutral theory of evolution as sharing for selectionist theory. In Nature, there is no clear evidence to use the neutral or the selectionist way of explanation for polymorphism. In the same way, in the artificial evolution field, the joint use of sharing and synthetic neutrality may and should be considered.

The neutrality concept has allowed us to review and to extend the concept of duality ([3, 4]). This has led us to build new analyze oriented tools for the dynamics; thus, we have shown the exploitation of neutral networks by a GA. Further works will deal with the importance of the synthetic neutrality compared to the inherent neutrality of an adaptive landscape. Indeed, we expect to be able to dissociate the different dynamics due to the inherent neutrality, the synthetic neutrality and the selective pressure. Of course, we also have to study the capacity of the synthetic model to solve more realistic problems. Finally, it would be very interesting to more deeply analyze the part played by crossover in the diffusion mechanisms.

References

1. L. Barnett. Evolutionary dynamics on fitness landscapes with neutrality. Master's thesis, University of East Sussex, Brighton, 1997.
2. C. L. Barrett, H. Mortveit, and C. M. Reidys. Elements of a theory of simulation ii : sequential dynamical systems. *Appl. Math. & Comp.*, 1998.
3. P. Collard and J.P. Aurand. DGA: An efficient genetic algorithm. In A.G. Cohn, editor, *ECAI'94: European Conference on Artificial Intelligence*, pages 487–491. John Wiley & Sons, 1994.
4. P. Collard and C. Escazut. Relational schemata: A way to improve the expressiveness of classifiers. In L. Eshelman, editor, *ICGA'95: Proceedings of the Sixth International Conference on Genetic Algorithms*, pages 397–404, San Francisco, CA, 1995. Morgan Kaufmann.
5. T.D. Collins. Using Software Visualization Technologies to Help Evolutionary Algorithm Users Validate their Solutions. In Thomas Bäck, editor, *Proceedings of the seventh International Conference on Genetic Algorithms*, pages 307–314. Morgan Kaufmann, 1998.
6. C. V. Forst, C. Reidys, and J. Weber. Evolutionary dynamics and optimization: Neutral networks as model-landscapes for rna secondary-structure folding-landscapes. In *Advances in Artificial Life*, volume 929 of *LNAI*. Springer Verlag, 1995.
7. W. Hordijk. Correlation analysis of the synchronizing-ca landscape. *Physica D*, 107:255–264, 1997.
8. M. A. Huynen, P. F. Stadler, and W. Fontana. Smoothness within ruggedness: the role of neutrality in adaptation. In *Proc. Natl. Acad. Sci. (USA)*, volume 93, pages 397–401, 1996.
9. M. Kimura. *The Neutral Theory of Molecular Evolution*. Cambridge University Press, Cambridge, UK, 1983.
10. S. Wright. The theory of gene frequency. In *Evolution and the genetics of Population*, volume 2, pages 120–143. University of Chicago Press, 1969.

This article was processed using the LaTeX macro package with LLNCS style