

(Co)evolution Leads towards ROMAs

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Abstract. This paper investigates the dynamics of a simple coevolutionary system. It consists of a predator-prey system in which one population maximizes its distance to the members of the other population, while the second population tries to minimize the distance to the first population. This results in a coevolutionary pursuer-evader (PE) system whose dynamics can easily be visualised and studied.

Next, a simple genotype-phenotype mapping is added to the system. This mapping - as well as other sources of increased selection - push the system towards regions of maximum adaptability (ROMAs). These ROMAs are a generalization of the concept "evolution to the edge of chaos".

1 Introduction

Three concepts are central in this paper: evolution to the edge of chaos, Genotype Phenotype Mappings (GPMs), and coevolution. Each of these concepts is briefly introduced in the long version of this paper [2].

In the past, the coevolutionary algorithm (CGA) has mainly been used as a tool for optimisation. Here, the dynamics of a CGA is studied. The coevolutionary interactions in nature are often complex. The goal of this paper consists of the design of a simple coevolutionary application and GPM which - despite their simplicity - still exhibits realistic, complex dynamics.

The structure of this article is as follows. First, the simple application which results in Pursuer Evader (PE) dynamics is described. Next, the genotype-phenotype mapping is introduced. The fourth section describes the empirical results associated with the GPM. Next, the relation between ROMAS and evolution to the edge of chaos is discussed. The sixth section discusses the model used and its relation to the real world. Finally, conclusions are given.

2 Pursuer-Evader Dynamics

Here, the CGA introduced in [1] is used. In the current paper, all parameter settings are identical to those described in [1] unless mentioned otherwise. For more detail, including pseudo-code of the basic cycle of the CGA, the reader is referred to [1] or [2].

In this particular application, each individual consists of two genes: real numbers in the interval [0,1]. The first population maximizes the cartesian distance to the individuals of the other population, the members of the second population minimize the distance to the individuals of the first population. This is achieved through inverse (predator-prey) fitness interaction between both populations. The fitness of an individual is calculated by sampling its (negative)

distance to members of the other population. Each individual represents one point in the plane $[0,1] \times [0,1]$. Furthermore, in order to allow for an unbounded evolution, this plane is considered to be a torus. Hence, the distance is the minimum of the two possible distances (one crossing (an) "edge(s)"). Furthermore, mutation can cross the "edges" as easy as it can move in the plane. Or, in other words, 0.95 is equally likely to be mutated into, for example, 0.085 or 0.05. Finally, a standard uniform crossover is used: new offspring receives each gene from one of its parents randomly and independently. It is worth noting that both populations reproduce at the same rate.

The dynamics of this application is fairly simple. The initial (random) populations are scattered randomly over the plane. Equal population sizes are assumed (50 individuals each). Fairly soon (typically in less than thousand cycles) during evolution two clusters appear (one for each population) where one cluster chases (pursuer) the other (evader). From time to time different behavior is observed. Sometimes the pursuers catch up on the evaders. At this moment the cluster of evaders breaks up. Most of the time the evader cluster breaks up in two or four sub clusters, which are located symmetrically with respect to the pursuers. These sub clusters virtually immobilize the pursuers while the evader sub clusters move radially and finally become one cluster again. Due to sampling errors and finite population sizes the evaders cluster (i.e. unite) again before the sub clusters have gone all the way. Once the evaders are clustered again, the "standard" pursuing of two clusters continues.

When the two populations have different population sizes then their respective speed changes. This is because both populations reproduce at the same rate. Hence, the smaller population evolves the fastest, i.e. moves faster on the plane. In case the pursuer population is smaller, the pursuers regularly catch up with the evaders. When this happens the evaders split up, again immobilizing the pursuers until the evaders form one cluster again. Then the chase resumes. In the other case, the evader population is the smallest population. Here, the evader population successfully keeps ahead of the pursuer population. Occasionally, the evaders even have to slow down in order not to get too close to the pursuers (remember the world consists of a torus).

3 Introducing a Genotype-Phenotype Mapping

In this section, the PE-model is extended with a simple GPM in order to study its contribution to the dynamics. This is achieved by adding two real numbers from the interval [0,1] to the gene string. This string then takes the following form: $(x \ y \ r_1 \ r_2)$. The two first parameters are as before. The last two define the GPM for each of the two parameters independently. Hence, the GPM is under evolutionary control.

Each time a new individual is born the GPM functions as follows. The two iterative mappings, equations (1), and (2), are applied on x

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and y , respectively, a fixed number of times. This number is called "preptime". Here, in all experiments, α is set to 0.001. After this, the individual's fitness (by sampling its distance to members of the other population) is calculated and if this individual is fit enough it is inserted in the population. Note that the GPM changes the original x and y genes. Or, more precisely, the genotype remains the same, the phenotype - which is originally a copy of the genotype - changes. Also the GPM considers the genes to live on a torus: if it becomes larger than 1, 1 is subtracted from it, if it becomes negative - which is not possible here - it is replaced by 1 plus that (negative) value.

$$x_{n+1} = x_n + \alpha r_1 x_n \quad (1)$$

$$y_{n+1} = y_n + \alpha r_2 y_n \quad (2)$$

After birth, these iterative functions are applied once during each cycle of the CGA and that during a fixed number of cycles. This constant is called "growtime". Both processes are simple models of a PGM operating in two phases. The first phase represents development during pregnancy, during which no interaction with the world occurs. The second one represents further development after birth, i.e. growth, during which the phenotype interacts with the world. Here, pregnancy as well as growth are represented by small positive increments of the phenotype.

4 Empirical Results

Given the PE behavior of the standard CGA described above, the question now is: How do the r 's evolve in various settings? In order to study this, 100 runs (of 20000 cycles) of the PE CGA with PGM were run. At the end of each run all r 's belonging to one population are printed on a $[0,1] \times [0,1]$ plane. Hence, at the end of the 100 runs, all final values of r per run are listed per population. Here, these results are described verbally. The actual figures can be found in [2]. Each experiment will be described by a quadruple: the first element is the size of the evader population, the second the size of the pursuer population, the third the preptime, and, finally, the growtime.

In the first experiment preptime and growtime are both zero. Hence, the r 's play no (evolutionary) role and they will be distributed (uniformly) random over the $[0,1] \times [0,1]$ plane. This experiment is represented by the quadruple 50-50-0-0: both population sizes are 50 and no GPM is used. Any pattern in the distribution of the r 's is due to random drift, small population size, and the relatively small number of runs (100).

In the next experiment, 50-50-80-20, preptime is set to 80 and growtime to 20. Now, structure appears in the distribution of the r 's: the r 's concentrate around the "edges". They even seem to concentrate most at the "corners". The explanation why this happens is deceptively simple: at these places mutation results in the largest variation of change (i.e. change of movement of the x,y genes on the $[0,1] \times [0,1]$ torus). At these edges, it switches from maximal movement to zero movement along any of the two axes. This allows the individuals of each population to out-maneuvre the individuals of the other population. The term regions of maximum adaptability (ROMAs) is coined here to define these regions where the r 's (and hence the GPM) evolve to. In terms of dynamic systems, these ROMAs are attractors and the density of the r 's give an indication of their strength. Again, due to symmetry (same population size, and same amount of GPM), the distribution of the r 's of the pursuers is similar to the distribution of the r 's of the evaders.

In the first two experiments the distribution of the r 's of evaders and pursuers was similar to each other. Now, the influence of differences in population size is investigated, again preptime is set to 80, and growtime is 20. In this experiment, 20-50-80-20, the population size of the evaders is set to 20, the pursuers are still with 50. In this experiment, there is no strong pressure on the r 's of the evaders towards the edges (or corners). This in contrast with the distribution of r 's of the pursuers: for the largest population (that is the pursuers) the pressure towards ROMAs is the strongest. The larger populations move slower. Hence, it is more important, for their survival, that they have access (genetically and / or through the GPM) to a wide variety of behavior. Such that they can out-maneuvre the smaller, faster population.

The same phenomenon is observed when the population of pursuers is smaller (20) than the evader population (50). Now, the r 's of the evaders are pushed more towards the ROMAs. Clearly, the effect of the GPM, pushing the r 's to the ROMAs, is enforced by the added pressure on the largest population.

5 ROMAs and "Evolution to the Edge of Chaos"

This paper provides a simple and general explanation for evolution to the edge of chaos: in a dynamic world, evolution leads towards ROMAs. In these regions, a maximum repertoire of behaviors is easily accessible through the application of genetic operators and / or the GPM. This is exactly what happens near the edge of chaos: it is there that the most diverse behaviors are situated. Hence, ROMAs generalize this concept of evolution to the edge of chaos.

6 Discussion

The fact that a very simple model is used here, can give raise to questions like: How realistic is this model? How do the results carry-over to the real world? Are the results not mere artefacts of the model chosen?

The experiments in the long version of this paper [2] clearly indicate the impact of non-toroidal mutation versus the toroidal mutation used earlier. Whereas increased selection pressure pushes the r 's to the edges and corners in case of toroidal mutation, non-toroidal mutation results in a pressure towards the centre. Summarizing, the toroidal nature of mutation, might seem artificial, but it compensates for the lack of epistasis in this simple PE model.

7 Conclusion

This paper studies the dynamics of a coevolutionary (predator-prey) algorithm by means of a simple pursuer evader application on a torus. This application allows for easy visual inspection of the dynamics. Next, a simple phenotype-genotype mapping (GPM) was introduced. This mapping is under evolutionary control as well. As selection pressure increases the GPM evolves towards regions of maximal adaptability (ROMAs). From these regions the GPM can easily change its behavior, and has access to a large repertoire of different behaviors. These ROMAs are a generalization of the concept "evolution to the edge of chaos". Or, in other words, the ROMAs are regions with high evolvability.

REFERENCES

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