Evolution of Heterogeneous Cellular Automata in Fluctuating Environments

First Author[1], Second Author[1,2], Third Author[1,2], Fourth Author[1,2] and Fifth Author[2]

[1]First affiliation
[2]Second affiliation
corresponding@author.email

Abstract

The importance of environmental fluctuations in the evolution by natural selection of living beings has been widely noted by biologists and linked to many important characteristics of life such as: modularity, plasticity, genotype size, mutation rate, and learning or epigenetic adaptations. However, in artificial life simulations, environmental fluctuations are usually seen as a problem to be solved rather than an essential characteristic of evolution. We propose in this paper to use HetCAis, a heterogeneous cellular automata characterized by its ability to generate open ended long-term evolution and evolutionary progress, to measure the impact of different forms of environmental fluctuations. Our results indicate that environmental fluctuations induce mechanisms analogous to epigenetic adaptations in HetCA.

Introduction

Environmental changes may include cyclic events such as seasonal changes or a daily cycle of light and darkness, occasional changes such as the introduction of new predator or the potential for a new source of food, or much more radical modifications such as environmental stresses induced by climate change.

Early population genetics theory assumed the environment to be constant. However, since then, work such as (Levins, 1968) or more recently (Jablonka et al., 2014), have put the emphasis on the importance of environmental fluctuations in the evolution by natural selection of living beings. Through these and other works many central questions about the mechanisms of evolution such as modularity, plasticity (West-Eberhard, 2005), size of the genotype, mutation rate and evolvability have been linked to environmental changes. Jablonka et al. (2014) stress that a changeable environment will unmask variations in the capacity of individuals to make adjustments to changed conditions and therefore promote plasticity. They advance that "For a lineage in a constantly changing environment, switching among several alternative heritable states was probably an advantage. While cells in one state survived in one set of conditions, those in other states did better in different circumstances."*(ibid. p. 318)*. For them, constantly changing environment or cycling variations might explain the origin of the Epigenetic Inheritance Systems considering that epigenetic mutations are more reversibles and occure more frequently than genetic mutations.

Lachmann and Jablonka (1996) have modelled the effects of cycling variations, such as seasonal or daily cycles, on phenotypical inheritances. Their model predicted that when the investigated cycles are longer than the reproductive cycle but relatively short otherwise, heritable variations produced by non-DNA inheritance systems are likely to be observed.

A proportion of existing works in artificial life, especially in evolutionary robotics (Floreano and Urzelai, 2000), considers the issue of environmental variations. Among this literature some have explicitly define the environment as a driving evolutionary power (Bredèche and Montanier, 2012). However and as far as we know, nobody has systematically studied the general properties induced by environmental fluctuation and a significant majority of the other works in that field still consider environmental changes only as a problem to be solved.

In this paper we propose a way to fill that gap with an experimental setup that allows to quantitatively measure the influence of cyclic environmental fluctuations on the course of the evolution of a Cellular Automata (CA). We show that such fluctuations lead to the emergence of processes similar to those exhibited by epigenetic inheritance systems.

The paper is organized as follows. Section , explain the general mechanisms of HetCA simulation. The implementation of environmental fluctuation in HetCA is then explained in Section . Section details the computer experimental setup while we reports experimental results in Section **??**. We discuss the implications of these results in Section **??**. Finally, Section concludes the paper.

Background

In (Lipson et al., 2002) Lipson demonstrated a correlation between the modularity and the rate of change of the environment resources. While in (Yu, 2007) Yu used observed that populations exploit neutrality to cope with environmental fluctuations and therefore evolve some sort of evolvabil-

ity under two alternating objective functions. Both of these simulations used Genetic Programming (GP) and employed explicit fitness functions.

HetCA

HetCA is based on classical two-dimensional Cellular Automata (CA), but has several added features: cells have *age*, *decay* and *quiescence* properties; cells utilize a heterogeneous transition function inspired by linear genetic programming (LGP); and there exists a notion of genetic transfer of transition functions between adjacent cells.

HetCA exhibits long term phenotypic dynamics, sustains a high level of variance over very long runs and displays greater behavioural diversity than classical cellular automata (Medernach et al., 2013). HetCA also exhibits Evolutionary Progress (EP) according to the three criteria : robustness, size and density of generated genotypes (Medernach et al., 2015), using Shanahan's definition of EP (Shanahan, 2012).

→ ALTERNATIVE SENTENCE : HetCA has been shown to exhibit long term phenotypic dynamics, high level of variance over very long run, a greater behavioral diversity than classical CA and evolves progress other three criteria (robustness size and density) given the Shanahan (2012)'s definition of Evolutionary Progress (Medernach et al., 2015).

Moreover, some emergent properties of HetCA are similar to two of the five major eukaryotic innovations which do not appear to have direct prokaryotic predecessors defined in (Smith and Szathmary, 1997) as : (1) the eukaryotic chromatin remodelling machinery; (2) the cell cycle regulation systems; (3) the nuclear envelope; (4) the cytoskeleton; and (5) the apoptosis apparatus (Koonin and Aravind, 2002). Indeed, in HetCA, the loss of the genotype of the cell as it turns to the quiescent state may seem similar to apoptosis while survival strategies such as the ones depicted in Figure 1 might akin cell cycle regulation systems.

Finally, controversy over the units of selection[1] in evolutionary biology (Okasha, 2006) are numerous and date back to the origins of this field and there is potentially several units of selection in HetCA: genotypic selection of the transition rules but also phenotypic selection of cell group replicating patterns that one can also find in cellular automata such as game of life. This issue is important when one is interested in environmental fluctuations because, as mentioned in introduction, it is anticipated that the existence of frequent environmental fluctuation could promote phenotypic selection compared to genotypic selection.

[1]Genotype selection, Phenotype selection, epigenetic selection, comportemental selection, multilevel selection...

Experimental Setup

Environmental Fluctuations

Originally, in HetCA, the new genotype of a cell was randomly chosen among candidate genotypes. In order to introduce environmental variations, we chose to vary the likelihood of spread of the genotype of a cell according to the state of this cell. The chances of the candidate genotype of the cell c to be selected are then: $c = K(S_c)/\sum_{i=1}^{n} K(S_{c_i})$ with S_c state of the cell c, $K(S)$ likelihood of spread of state S and n number of candidate genotypes. Therefore an environment is characterized by the odds of propagation of the five living states $\{K(S_1), K(S_2), K(S_3), K(S_4), K(S_5)\}$. To mimic environmental fluctuations we initialise the simulation with $K(S_i) = 1 \forall i \in [1, 5]$ and then we regularly change those values from iteration 3000 of the cellular automata.

We chose to introduce four forms of environmental fluctuations described in Table 3.

Short-cycle Fluctuation: consists of alternating between two environments every 100 iterations of the cellular automaton. We chose to vary the environment every 100 iterations to stay in the same range of frequency as described in Lispson (Lipson et al., 2002) examples 20 and 100 generations and (Yu, 2007) experiments 10, 20 and 50 generations. In fact we consider that a successful reproductive cycle involves passing a cell through the quiescent state. And this should take between two iterations (alternating between the quiescent state and a living state) and seven iterations (if a cell remains in a living state more than seven consecutive iterations it goes to the decay state and can not receive a genotype for an important period).

Light Fluctuation: consists of alternating between five environments every 5000 iterations of the cellular automaton. The first five each prohibit a different state from the five living state, the latter gives equal chance to each of the five states.

Strong Fluctuation: consists of alternating between twelve environments every 5000 iterations of the cellular automaton. The first eleven each prohibit a different combination of two states from the five living states, the latter gives equal chance to each of the five states.

Gradual Fluctuation: is similar to strong fluctuation except that it includes a transition phase of $T = 60$ iterations in between two environments where likelihood of spread of state values progressively switch from the value a previous environment to the ones of the new environment. Over this phase the state spreading is defined by the following formula : $K(S, t) = K_p(S) \times (T - t) + K_{p+1}(S) \times t$ where t is the number of iterations completed since the beginning of the transition phase; $K_p(S)$ and $K_{p+1}(S)$ are likelihood of state spread S for the current environment and the next environment respectively.

Short-cycle fluctuation may be analogous to the circadian rhythms for some bacteria: very regular cycles in

Parameter	Value
Number of living states	5
Successive living iterations before decay	7
Number of iterations for decay	375-1875
Direct transition to decay	enabled
Size of the grid	500x500
Grid boundaries	toric grid
Transition Rule (TR)	CA-LGP
Maximum (TR) size	50 program statements
Genotype copy neighbouring	Von Neumann
Transition rule neighbouring	Moore

Table 1: **HetCA parameters**.

op. name	**action** on inputs (x, y)
abs	$\|x\|$
plus	$x + y$
delta	1, if $\|x - y\| < 1/10000$; 0 o.w.
dist	$\|x - y\|$
inv	$1 - x$
inv2	safeDiv$(1, x)$
magPlus	$\|x + y\|$
max	$\max\{x, y\}$
min	$\min\{x, y\}$
safeDiv	x/y if $\|y\| > 1/10000$; 1 o.w.
safePow	x^y, if defined; 1 o.w.
thresh	1, if $x > y$; 0 o.w.
times	xy
zero	1, if $\|x\| < 1/10000$; 0 o.w.

Table 2: **Function set**.

which these organisms have enough time to reproduce several times. While *light fluctuation* may be similar to seasonal fluctuations and *strong and gradual fluctuations* would akin ecological crisis. Although, owing to the variety of both biological temporal rhythms and reproductive cycles, the relevance of these analogies may be limited.

Common Settings

For each form of environmental fluctuation and the stable non fluctuating environment, we performed 50 simulations, each on 500000 iterations with the parameters listed in Table 1. The genotypes of an individual are its transition rules encoded with CA-LGP using the function set depicted in Table 2. Mutation of genotypes is enabled and we use the Micro/Marco-mutation of CA-LGP as described in (Medernach et al., 2013).

Methodology

Genotype Size

We use the number of program statements (n_{prog}) as a measure of the genotype size and compute the average size of all the current genotypes of a run every 2500 iterations. We then report the average and standard error among all the fifty runs sharing the same settings.

Changes induced by environmental fluctuation

If, as postulated in (Jablonka et al., 2014), the introduction of environmental changes leads to the selection of plasticity of individuals mechanisms or, to the emergence of phenotypic selections[2] using easily reversible phenotypic mutations; then phenotypes from different individuals of the same lineage observed while environmental conditions are similar should be relatively close even though, between these measures, individuals from their lineage evolved in other environmental conditions; while one may think that if the adaptation to each environmental change is done exclusively through the selection of classical irreversible genotypic mutations, these phenotypes shall be quite different, despite the potential evolutionary convergence. That is why we want to develop a metric to measure phenotypic proximity between two iterations of the CA. To do this we simply compare the proportions of living cells in different states among the possible states. To do this we simply compare the proportions of living cells in each possible state. The phenotypic difference $\sigma(t_1, t_2)$ between two iterations t_1 and t_2 is then calculated as:

$$\sigma(t_1, t_2) = \sum_{s=1}^{5} \left| \frac{N(s, t_1)}{\sum_{s=1}^{5} N(s, t_1)} - \frac{N(s, t_2)}{\sum_{s=1}^{5} N(s, t_2)} \right|$$

where $N(s, t)$ is the number of cells at the state s for iteration t.

Density

We also collect the *most common genotype* (most frequently occurring) in iterations 2500[3], 102500, 202500, 302500, 402500 and 500000.

Regular phenotype characterization

In HetCA, to survive in the long term the genotypes must regularly release cells by transforming them into quiescent cells without genotypes. This generates patterns and cycles which are quite easy to observe in homogeneous simulations where a single genotype is tested as shown in Figure 1, but also observable, although with more difficulty, in normal, heterogeneous, HetCA simulations as seen in Figure 2. That is why, characterize phenotypes, we found it useful to measure these cycles as well as out-of regularities. At every iteration $t > 8$ of the homogenous genotype test, we compare the states S_t and S_{t-1} of each cell to their anterior state during the eight previous iterations of the CA. We then measure whether this sequence of two states is repeated during these eight previous iterations, and if so what is its periodicity p such as $p = \min p \in [2; 7], S_t = S_{t-p} \wedge S_{t-1} = S_{t-1-p}$. We use here a sequence of two states because, if the genotype of a cell adopts a stable strategy, i.e. repeats a sequence of states, this sequence must contain a minimum of two

[2] Similar to the epigenetic inheritance system

[3] (Medernach et al., 2015) has shown that the most common genotypes during the first iterations of HetCA were unlikely to have a viable survival strategy, therefore we chose to collect genotypes from iteration 2500.

states in order to ensure the survival of the genotype – the quiescent state and one of the living states. We have chosen to limit ourselves to a comparison of the eight previous iterations as the limit of the seven consecutive live iterations before decay involves a maximum periodicity of quiescent state of seven iterations. We have chosen to limit ourselves to a comparison of the eight previous iterations to reduce the computational cost and because the limit of the seven consecutive live iterations before decay involves, for a successful regular phenotype, a maximum periodicity of seven iterations for the quiescent state. We perform this measure only if there is at least a living state among the last two states and no state decay. We then report, for each iteration t of the CA, the sum $\Sigma(p,t)\forall p \in [2;7]$ of cells at every possible periodicity p.

Phenotype disturbance

To analyze the phenotypic plasticity and / or the existence of phenotypic selection it is necessary to have a measure of the stability of the phenotype. To achieve this, in each iteration t we compare the periodicity p_t of each cell to its previous periodicity p_{t-1}. We then report, for each iteration t of the CA, the number of cells that changed periodicity.

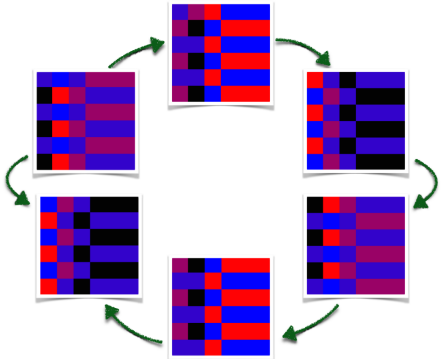

Figure 1: **Six steps survival strategy** from a genotype extracted from a HetCA simulation in a stable environment and tested here in a randomly initialized homogenous CA.

Qualitative Analysis

Analysis

Conclusions

Conlusion

Acknowledgement

The authors gratefully the support of Science Foundation Ireland, grant number:

References

Bredèche, N. and Montanier, J.-M. (2012). Environment-driven Open-ended Evolution with a Population of Autonomous Robots. In *Evolving Physical Systems Workshop*, East Lansing, États-Unis.

Floreano, D. and Urzelai, J. (2000). Evolutionary robots with on-line self-organization and behavioral fitness. *Neural Networks*, 13(4):431–443.

Heard, E. and Martienssen, R. A. (2014). Transgenerational Epigenetic Inheritance: Myths and Mechanisms. *Cell*, 157(1):95–109.

Jablonka, E., Lamb, M. J., and Zeligowski, A. (2014). *Evolution in Four Dimensions, revised edition: Genetic, Epigenetic, Behavioral, and Symbolic Variation in the History of Life*. MIT press.

Koonin, E. and Aravind, L. (2002). Origin and evolution of eukaryotic apoptosis: the bacterial connection. *Cell death and differentiation*, 9(4):394–404.

Lachmann, M. and Jablonka, E. (1996). The inheritance of phenotypes: an adaptation to fluctuating environments. *Journal of theoretical biology*, 181(1):1–9.

Laland, K., Matthews, B., and Feldman, M. W. (2016). An introduction to niche construction theory. *Evolutionary Ecology*, pages 1–12.

Levins, R. (1968). *Evolution in changing environments: some theoretical explorations*. Number 2. Princeton University Press.

Lipson, H., Pollack, J. B., and Suh, N. P. (2002). On the origin of modular variation. *Evolution*, 56(8):1549–1556.

Medernach, D., Fitzgerald, J., Carrignon, S., and Rya, C. (2015). Evolutionary progress in heterogenous cellular automata (hetca). In *Proceedings of the European*

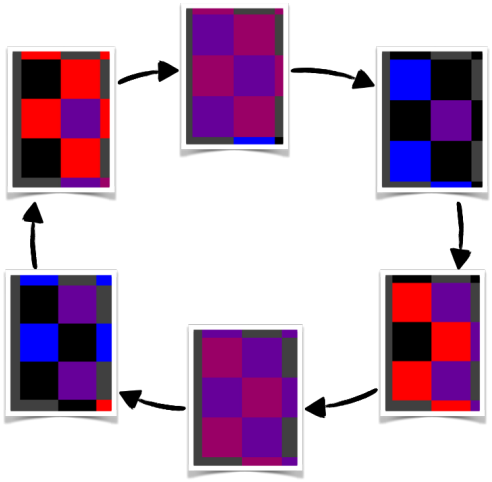

Figure 2: **Six steps survival strategy** from a HetCA simulation with *Short-cycle Fluctuation*.

Table 3: Environments.

Name	Short Name	Cycles	Transitions	Environment list
Stable Environment	[SE]	NA	NA	$\{1,1,1,1,1\}$
Short-cycle Fluctuations	[ScF]	100	1	$\{1,1,1,0,0\}, \{1,1,1,0,0\}$
Light Fluctuations	[LF]	5000	1	$\{1,1,1,1,0\}, \{1,1,1,0,1\}, \{1,1,0,1,1\}, \{1,0,1,1,1\}, \{0,1,1,1,1\}, \{1,1,1,1,1\}$
Strong Fluctuations	[SF]	5000	1	$\{0,0,1,1,1\}, \{1,1,1,0,0\}, \{0,1,0,1,1\}, \{1,0,1,1,0\}, \{0,1,1,0,1\}, \{1,1,0,1,0\}, \{1,0,1,0,1\}, \{0,1,1,1,0\}, \{1,0,0,1,1\}, \{1,1,0,0,1\}, \{1,1,1,1,1\}$
Gradual Fluctuations	[GF]	5000	60	$\{0,0,1,1,1\}, \{1,1,1,0,0\}, \{0,1,0,1,1\}, \{1,0,1,1,0\}, \{0,1,1,0,1\}, \{1,1,0,1,0\}, \{1,0,1,0,1\}, \{0,1,1,1,0\}, \{1,0,0,1,1\}, \{1,1,0,0,1\}, \{1,1,1,1,1\}$

Conference on Artificial Life 2015 (ECAL 2015), volume 13, pages 512–519.

Medernach, D., Kowaliw, T., Ryan, C., and Doursat, R. (2013). Long-term evolutionary dynamics in heterogeneous cellular automata. In *Proceedings of the 15th annual conference on Genetic and evolutionary computation*, pages 231–238. ACM.

Okasha, S. (2006). *Evolution and the levels of selection*, volume 16. Clarendon Press Oxford.

Shanahan, T. (2012). Evolutionary progress: conceptual issues. *eLS*.

Smith, J. M. and Szathmary, E. (1997). *The major transitions in evolution*. Oxford University Press.

West-Eberhard, M. J. (2005). Developmental plasticity and the origin of species differences. *Proceedings of the National Academy of Sciences*, 102(suppl 1):6543–6549.

Yu, T. (2007). Program evolvability under environmental variations and neutrality. In *Proceedings of the 9th annual conference companion on Genetic and evolutionary computation*, pages 2973–2978. ACM.