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1 Introduction

Artificial Life (AL; [1]) studies all kinds of biological phenomena as they occur in artificial organisms. Neural Networks (NNs; [2]) are commonly used in AL research as computational models of nervous systems that control organisms' behavior. However, organisms do not only possess nervous systems and other phenotypic traits but also genetic information stored in the nucleus of their cells (genotype). The nervous system is part of the phenotype which is derived from this genotype through a process called development. The information specified in the genotype determines aspects of the nervous system which are expressed as innate behavioral tendencies and predisposition to learn. As a consequence, in AL models NNs tend to be accompanied by genotypes (i.e., genetic algorithms; [3]) and to become members of evolving populations of networks in which genotypes are inherited from parents to offspring.

Cellular Automata (CAs; [4]) are dynamical systems in which elementary entities (cells) interacting at a low level according to local rules give rise to a high level 'behavior'. 'The Game of Life' [5] - one of the most well-known cellular automata - simulates the birth, death, etc., of organisms across generations and, from this point of view, could be considered the "ancestor" of simulations afterwards used in AL research [6].

An important difference that commonly distinguishes CAs from NNs is that the latter can be evolutionary or adaptive systems, that is, systems that change their local interaction 'rules' (i.e., connection weights) through evolution. As stressed by Mitchell and Forrest [7] "evolution of artificial systems is an important component of artificial life, providing an important modeling tool." On the contrary, in most CA models all cells obey the same local interaction rule that remains fixed over time. Therefore, in these models the genotype level is not considered in any way and only the phenotype level is observed and investigated. If we take an evolutionary perspective, however, the genotype level plays a very important role because it is at this level that novelties are produced through mutation, recombination, and selection.

In this paper we outline some interesting evolutionary biology issues that can be studied by using AL models in which the genotype and the phenotype are distinct entities.

2 Artificial Life Models as Multiple-Level Adaptative Systems

Wagner and Altenberg [8] stress that in both natural and artificial adaptative systems evolvability (i.e., the ability of random variations to sometimes produce improvement) critically depends on the way genetic variation maps onto phenotypic variation, an issue known as the representation problem. In nature both the information contained in the genotype and the mapping of the genetic information into the phenotype are usually complex. The mapping from genetic to phenotypical traits is not one to one, but one single genetic trait can enter into the determination of many different phenotypical traits (*pleiotropy*) and, vice versa, one phenotypical trait can be determined by the concurrent action of many different genetic traits (*poligeny*). Furthermore, the genotype contains not only information that directly maps into the phenotype but also information (e.g., modifier genes) that regulates the mapping. Finally, it should be considered that the external environment is an additional factor that, by interacting with the genetic information, determines the phenotype.

In most AL models there is no real distinction between genotype and phenotype. The inherited genetic information maps one to one into the phenotype and, therefore, the genotype and the phenotype are virtually identical. In research developed in our Research Group on Artificial Life (GRAL; http://kant.irmkant.rm.cnr.it/gral.html) we have examined some implications of a more biologically plausible genotype-to-phenotype mapping in genetic algorithms applied to populations of neural networks (e.g., [9], [10], [11], [12]).

In Calabretta et al. [9] the genotype and the phenotypical neural network are distinct entities and the genotype may exhibit diploidy, i.e., it may include two copies of each gene whose expression is governed by some dominance rules. We compared the performance of haploid and diploid populations of ecological neural networks living in both fixed and changing environments. Despite the enormous simplification of the model, our simulations confirmed some of the results obtained with real organisms, in particular concerning the role of diploidy in short-term adaptation to new environments in asexual organisms lacking the mechanism of recombination as a source of genetic variability. We observed that diploidy is useful in producing individuals that are able to adapt to non-stationary environments, especially in the case of fast changing environments. In these environments diploid individuals succeed in adapting to the quick environmental changes while haploid individuals tend to fail. The explanation for this could be that in changing environments diploid populations exhibit the capacity to keep a sort of genetic «memory» of the past recorded in their non-expressed genes (the shielding effect); in fact they recover faster and with a lesser decrease in fitness than haploids after environmental change.

In Calabretta et al. [10], [11], [12] we have investigated the role of genetic operator of gene duplication for the evolution of modularity. Various authors have stressed the role of genetic duplication for the emergence of evolutionary novelties, especially in complex organisms. For instance, Li [13] claims that "gene duplication is probably the most important mechanism for generating new genes and new biochemical processes that have facilitated the evolution of complex organisms from primitive ones." We have presented simulations of the evolution of populations of

artificial organisms focusing on the evolutionary emergence of functionally different modules at the neural-behavioral level from gene duplication. It is important to stress that neuro-physiologists in defining a module take into account only the nervous system and the higher level of organization (behavior) which is the result of the activity of the nervous system. However, they do not usually take into consideration lower levels such as the molecular and genetic level. They do not ascertain that what they have identified as a neural module is the result of a collection of genes that mainly codify for that phenotypic character [12]. On the contrary, in our model artificial organisms can be analyzed at the genetic level, at the neural and behavioral level, at the level of the effects of the network's output on the environment, at the level of the reproductive chances of each individual (fitness) and at the level of populations of individuals [10]. More specifically, we address the problem whether modules that start as repeated elements because of genetic duplication can develop to become specialized modules. Our simulation results, validated with a linear regression statistical analysis, confirm this hypothesis and suggest a new mode for the evolution of modularity ([11], [12]).

3 Conclusion

The cross-fertilization between Artificial Life and biology can take place since Artificial Life partially shares the theoretical apparatus and vocabulary of evolutionary biology and can offer additional methodological tools to biology. In AL models organisms can be analyzed at the genotypic level and at the phenotypic level. Then, the fact of having a more complex and biologically plausible genotype/phenotype mappings in the model of study allows us to observe and manipulate complex phenomena and nonlinear interactions among entities at each level and between levels.

Some researchers have made a significant attempt to shape their CA models according to AL's demands (e.g., [14], [15], [16]). In particular, Sipper [15] tries "to increase the 'capacity' for evolution while preserving the essential features of the CA model."

According to Mitchell [16] "CAs have the potential to model the behavior of complex systems in nature". In this paper we have outlined some important aspects of the genotype-to-phenotype mapping which could be considered in order to increase this potentiality.

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