Chapter 2

Artificial Cell Model Used for Information Processing

Enrique Fernández-Blanco
University of A Coruña, Spain

Jose A. Serantes
University of A Coruña, Spain

Nieves Pedreira
University of A Coruña, Spain

Julián Dorado
University of A Coruña, Spain

ABSTRACT

The main features of a new theoretical model inside the knowledge area called Artificial Embryogeny are described in this paper. Artificial Embryogeny is a term that identifies any model that uses embryological cells or embryological processes as inspiration. This chapter details the theoretical model and it also presents some its apllication to information processing problems. Specifically, this model was applied to solve classical problems such as pattern classification and pattern recognition problems. The Iris classification problem is the selected information processing problems presented in this paper. It must be remarked that a similar application was never been done with an artificial embryogeny model.

INTRODUCTION

Using biology as inspiration for the creation of computational models is not a new idea: Nature has already been the basis for artificial neuron models (McCulloch &Pitts, 1943), the genetic algorithms (Holland, 1975), etc. The cells of a biological organism are able to compose very complex structures from a unique cell, the zygote, with no need for centralized control (Watson & Crick, 1953). The cells can perform such process thanks to the existence of a general plan, encoded in the DNA for the development and functioning of the system. Another interesting characteristic of natural cells is that they form systems that are tolerant to partial failures: small errors do not induce a global collapse of the system. Finally, the tissues that are composed by biological cells present parallel information processing for the coordination of tissue functioning

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in each and every cell that composes this tissue. All these characteristics are very interesting from a computational viewpoint.

Another interesting point of view is to think that the biological structures process the input information of their environment and they use the DNA as a processor to operate with those inputs. to study the biological model as a design model. Actually, human designs use a top-down view, this methodology has served well. However the construction of software and hardware systems with a high number of elements, the design crisis is served. Verify formally the systems when interactions and possible states grows, becomes near impossible due the combinatorial explosion of configuration using a traditional way. Living systems suggest interesting solutions for these problems, such as that the information defining the organism is contained within each part. Consequently, if the designers want to increase the complexity of the systems, one way is to study the biological model trying to mimic its solutions.

This paper presents the development of a model that tries to emulate the biological cells and to take advantage of some of their characteristics by trying to adapt them to artificial cells. The model is based on a set of techniques known as *Artificial Embryogeny* (Stanley & Miikkulainen, 2003) or *Computational Embryology* (Kumar, 2004).

BACKGROUND

In 2003, Ken Stanley and Risto Miikulainen developed a methodology to classify the different models that appear in Evolutionary Computation (EC), which have defined the new Artificial Embryogeny (AE) area. This methodology is focused on the models which are inspired in abstractions of the embryological cells. This new research area has been called by different names, like Computational Embryology or AE, by different authors. The models try to keep features such as self-organizing, self-repairing, fault tolerance and parallel information processing, which are present in the biological model, in an abstraction to apply them to different problems.

Following this classification methodology, AE works can be classified in two main types which face the problem in two different ways. On one hand, works that are included under the grammatical approach can be found. These works are related with Lindermayer's studies and L-systems, which perform a top-down approach to the problem (1968). On the other hand, other works, with a chemical approach, are found. These last works are based in Turing's ideas and perform a bottom-up approach to the problem (1952).

Grammatical approach works have been mostly used to develop Artificial Neural Networks (ANNs). This process is called neuroevolution. The first neuroevolutive system was developed by Kitano (1990). This work shows how the connectivity matrix of an ANN can be evolved with a set of rewriting rules. Another remarkable work is the one developed by Hornby and Pollack (2002), where the authors develop both the structure of a body in a simulated 3D world and an ANN to control it. In this case, the authors use the L-systems to develop both parts. Finally, it is necessary to mention the work developed by Gruau (1994), where the authors use a grammatical tree to store the development of an ANN from a unique starting element.

On the chemical approach, the first work that has to be mentioned is the one done by Kauffmann (1969), where the theory about Gene Regulatory Networks is developed. From this one, different works that study how the expression of different genes causes the expression of other ones determining a complex behavior starts (Mjolness, Sharp, Reinitz, 1995).

One work that should be mentioned inside the chemical approach is the one developed by H. Kitano (1994). This work tries to develop a model close to the biological one, and its objective is to study the cell in deep. Other researchers have looked for this parallelism in the biological

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