Chapter IX
Artificial Cell Systems Based in Gene Expression Protein Effects

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ABSTRACT

The artificial embryogeny term overlaps all the models that try to adapt cellular properties into artificial models. This chapter presents a new model for artificial embryogeny that mimics the behaviour of biological cells, whose characteristics can be applied to solution of computational problems. The paper contains the theoretical development of the model and some test executed in an implementation of that model. The presented tests apply the model to simple structure generation and provide promising results with regard to its behaviour and applicability to more complex problems. The objective of the chapters is to be an introduction of the artificial embryogeny and shows an example of a model of these techniques.

INTRODUCTION

Use biology as inspiration for the creation of computational models is not a new idea: science has already been the basis for the famous artificial neuron models (Hassoun, 1995), 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 in each and every cell that composes this tissue. All these characteristics are very interesting from a computational viewpoint.

Another point of view is to study the biological model as a design model. At present human designs use a top-down view, this methodology has served well. However thinking on 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

The Evoluationary Computation (EC) field has given rise to a set of models that are grouped under the name of Artifial Embryogeny (AE), first introduced by Stanley and Mikkulainnen (Stanley & Miikkulainen, 2003). This group refers to all the models that try to apply certain characteristics of biological embryonic cells to computer problem solving, i.c. self-organisation, failure tolerance, and parallel information processing.

The work on AE has two points of view. On the one hand could be found the grammatical models based on L-systems (Lindenmayer, 1968) which do a top-down approach to the problem. On the other hand could be found the chemical models based on the Turing's ideas (Turing, 1952) which do a down-top approach.

On the last one, the starting point of this field could be found in the modelling of gene regulatory networks, performed by Kauffmann in 1969 (Kauffman, 1969). After that work, several develops were carried out on subjects such as the generation of complex behaviour by the differential expression of certain genes. This behaviour causes a cascade influence on the expressions of others genes (Mjolsness, Sharp & Reinitz, 1995).

The work performed by the scientific community can be divided into two main branches. The more theoretical branch uses the emulation of cell capabilities such as cellular differentiation and metabolism (Kaneko 2006; Kitano et al., 2005) to create a model that functions as a natural cell. The purpose of this work is to do an in-depth study of the biological model.

The more practical branch mainly focuses on the development of a cell inspired-model that might be applicable to other problems (Bentley, 2002; Kumar & Bentley (eds), 2003; Stanley & Miikkulainen, 2003). According to this model, every cell would not only have genetic information that encodes the general performance of the system, it would also act as a processor that communicates with the other cells. This model is mainly applied to the solution of simple 3D spatial problems, robot control, generative encoding for the construction of artificial organisms in simulated physical environments and real robots, or to the development of the evolutionary design of hardware and circuits (Endo, Maeno & Kitano, 2003; Tufte & Haddow, 2005).

The most relevant models are the following: the Kumar and Bentley model (Kumar & Bentley (eds), 2003), which uses the theory of fractal proteins (Bentley, 2002) for the calculation of protein concentration; the Eggenberger model (Eggenberger, 1996), which uses the concepts of cellular differentiation and cellular movement