Computer Morphogenesis in Self–Organizing Structures

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INTRODUCTION

Applying biological concepts to create new models in the computational field is not a revolutionary idea: science has already been the basis for the famous artificial neuron models, the genetic algorithms, 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 J.D. & Crick F. H. 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 the above characteristics are very interesting from a computational viewpoint. 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 Embryology* (Stanley K. & Miikkulainen R. 2003) or Embryology Computation (Kumar S. & Bentley P.J 2003).

BACKGROUND

The Evoluationary Computation (EC) field has given rise to a set of models that are grouped under the name of Artificial Embryology (AE), first introduced by Stanley and Miikkulainnen (Stanley K. & Miikkulainen R. 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 can be found the grammatical models based on L-systems (Lindenmayer A. 1968) which do a top-down approach to the problem. On the other hand can be found the chemical models based on the Turing's ideas (Turing A. 1952) which do a down-top approach.

On the last one, the starting point of this field can be found in the modelling of gene regulatory networks, performed by Kauffmann in 1969 (Kauffman S.A. 1969). After that, several works were carried out on subjects such as the complex behaviour generated by the fact that the differential expression of certain genes has a cascade influence on the expressions of others (Mjolsness E., Sharp D.H., & Reinitz J. 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 (Kitano H. 1994; Kaneko K. 2006) 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, P.J., Kumar, S. 1999; Kumar, S. 2004). 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 K., Maeno T. & Kitano H 2003; Tufte G. & Haddow P. C. 2005).

Considering the gene regulatory networks works, the most relevant models are the following: the Kumar and Bentley model (Kumar S. & Bentley P.J 2003), which uses the Bentley's theory of fractal proteins (Bentley, P.J. 1999); for the calculation of protein concentration; the Eggenberger model (Eggenberger P. 1996), which uses the concepts of cellular differentiation and cellular movement to determine cell connections; and the work of Dellaert and Beer (Dellaert F. & Beer R.D. 1996), who propose a model that incorporates the idea of biological operons to control the model expression, where the function assumes the mathematical meaning of a Boolean function.

All these models can be regarded as special cellular automata. In cellular automata, a starting cell set in a certain state will turn into a different set of cells in different states when the same transition function (Conway J.H. 1971) is applied to all the cells during a determined lapse of time in order to control the message concurrence among them. The best known example of cellular automats is Conway's "Game of Life", where this behaviour can be observed perfectly. Whereas the classical conception specifies the behaviour rules, the evolutionary models establish the rules by searching for a specific behaviour. This difference comes from the mathematical origin of the cellular automats, whereas the here presented models are based on biology and embryology.

These models should not be confused with other concepts that might seem similar, such as Gene Expression Programming (GEP) (Ferreira C. 2006). Although GEP codifies the solution in a string, similarly as how it is done in the present work, the solution program is developed in a tree shape, as in classical genetic programming (Koza, J. et. al.1999) which has little or nothing in common with the presented models.

ARTIFICIAL EMBRYOGENY MODEL

The cells of a biological system are mainly determined by the DNA strand, the genes, and the proteins contained by the cytoplasm. The DNA is the structure that holds the gene-encoded information that is needed for the development of the system. The genes are activated or transcribed thanks to the protein shaped-information that exists in the cytoplasm, and consist of two main parts: the sequence, which identifies the protein that will be generated if the gene is transcribed, and the promoter, which identifies the proteins that are needed for gene transcription.

Another remarkable aspect of biological genes is the difference between constitutive genes and regulating genes. The latter are transcribed only when the proteins identified in the promoter part are present. The constitutive genes are always transcribed, unless inhibited by the presence of the proteins identified in the promoter part, acting then as gene oppressors.

The present work has tried to partially model this structure with the aim of fitting some of its abilities into a computational model; in this way, the system would have a structure similar that is similar to the above and will be detailed in the next section.

Proposed Model

Various model variants were developed on the basis of biological concepts. The proposed artificial cellular system is based on the interaction of artificial cells by means of messages that are called proteins. These cells can divide themselves, die, or generate proteins that will act as messages for themselves as well as for neighbour cells.

The system is supposed to express a global behaviour towards the generation of structures in 2D. Such behaviour would emerge from the information encoded in a set of variables of the cell that, in analogy with the biological cells, will be named genes.

One promising application, in which we are working, could be the compact encoding of adaptive shapes, similar to the functioning of fractal growth or the fractal image compression.

Figure 1. Structure of a system gene