Gene Regulation Network Use for Information Processing

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INTRODUCTION

From the unicellular to the more complex pluricellular organism needs to process the signals from its environment to survive. The computation science has already observed, that fact could be demonstrated remembering the artificial neural networks (ANN). This computation tool is based on the nervous system of the animals, but not only the nervous cells process information in an organism. Every cell has to process the development and functioning plan encoded at its DNA and every one of these cells executes this program in parallel with the others. 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.

The present work proposes a model that is based on DNA information processing, but adapting it to general information processing. This model can be based on a set of techniques called Artificial Embryogeny (Stanley K. & Miikkulainen R. 2003) which adapts characteristics from the biological cells to solve different problems.

BACKGROUND

The Evolutionary 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 Miikkulainen (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.e. 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 chemical models based on the Turing’s ideas (Turing A. 1952) which do a down-top approach.

The grammatically approach, some times, has used the models for study the evolution of ANN, which is known as neuroevolution. The first neuroevolution system was development by Kitano (Kitano, H. 1990). In this work Kitano shows that it was possible to evolve the connectivity matrix of ANN through a set of rewrite rules. Another remarkable work is the application of L-systems do by Hornby and Pollack (Hornby, G. S. & Pollack J. B. 2002). At this work they simultaneously evolved the body morphologies and the neural network of artificial creatures in a simulated 3D physical environment. Finally, mention the works carry out by Gruau (Gruau F. 1994) where the author uses grammar trees to encode steps in the development of a neural network from a single antecesor cell.

On the chemical approach, the starting point of this field can be found in the modelling of gene regulatory networks, performed by Kauffman 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). 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 theory of fractal proteins Bentley, P.J., Kumar, S. 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.