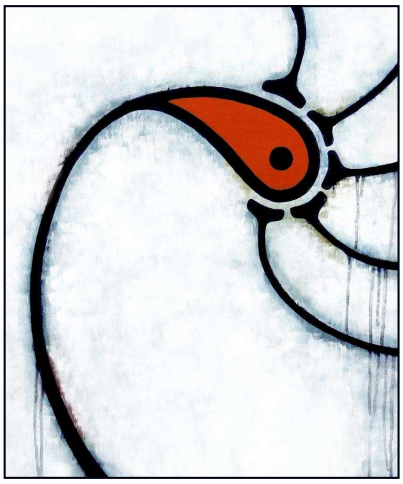

"Using GReaNs (Genetic Regulatory evolving artificial Networks) for 3-dimensional asymmetrical pattern formation and morphogenesis"

Borys Wróbel and Michel Joachimczak (Polish Academy of Sciences)

Abstract—Building a system that allows for pattern formation and morphogenesis is the first necessary step towards using a developmental-evolutionary approach to generate complex neural networks. In this extended abstract we present one such system, GReaNS (for Genetic Regulatory evolving artificial Networks). We review the results of previous experiments in which we investigated the evolvability of the encoding used in GReaNS to control 3-dimensional pattern formation and asymmetrical morphogenesis. We then present a road map towards using this system for evolution and development of neural networks.

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Using GReaNs (Genetic Regulatory evolving artificial Networks) for 3-dimensional Asymmetrical Pattern Formation and Morphogenesis

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***Abstract*— Building a system that allows for pattern formation and morphogenesis is a first step towards a biologically-inspired developmental-evolutionary approach to generate complex neural networks. In this extended abstract we present one such system, GReaNs (for Genetic Regulatory evolving artificial Networks). We review the results of previous experiments in which we investigated the evolvability of the encoding used in GReaNs to control 3-dimensional pattern formation and asymmetrical morphogenesis. We then present a road map towards using this system for evolution and development of neural networks.**

Keywords- gene regulatory networks; artificial evolution; artificial development; evo-devo; pattern formation; morphogenesis; genetic algorithm

I. INTRODUCTION

Biological development is a process in which large complex organized multicellular structures emerge from one cell, through stages in which initially the number of cells is small, and the structures simple. These complex structures emerge through several processes, which include pattern formation and morphogenesis. Pattern formation is the process in which cells differentiate in space. It allows laying out of a body plan (defining the main axes of the body). Morphogenesis is a process in which the developing embryo changes its shape, through mechanisms that include differential growth and cell migration. Both processes involve local interactions between cells, such as physical adhesion and signaling using diffusive substances (morphogens).

In biological multicellular organisms cells differ largely because they produce a different repertoire of proteins. These proteins are coded by genes. Which proteins are made in which cells is controlled by other proteins in the cell, often at the first step of gene expression (transcription). Such regulatory proteins are called transcriptional factors (TFs; sometimes: trans-regulators). TFs bind in the vicinity of regulated genes. Such regions in DNA close to regulated genes are sometimes called cis-regulators. These regions are often close to regions where transcription starts (promoters). A gene regulatory network (GRN) is a graph in which the links represent regulatory interactions between trans-regulators (through physical binding to cis-regulators). So also here the global behavior of the system emerges from local interactions. In the case of transcriptional gene regulation, the interactions are between TFs and DNA.

Biological multicellular development is remarkably robust to variability in environmental conditions and to damage at the genetic and cellular level. This robustness stems at least in part from the fact that biological systems emerge from local interactions, from the modularity and hierarchical organization of these systems.

We have built a biologically-inspired model that has some of these features [1-4], named GReaNs, for Genetic Regulatory evolving artificial Networks. The topology of the networks in the model is encoded in a linear genome in a way that is inspired by previous work by Eggenberger [5]. Similar model was recently used also by other authors (e.g., [6]), and several other models were formulated for evolving artificial gene regulatory networks regulating artificial embryology [7-13]. Important features of our model include: no limit on the number of links between nodes, no pre-set number of trans-regulators, and no grid in 3D space in which the cells divide (continuous space is used). We believe that removing such constraints allows using a model to test hypotheses about biological systems that are difficult to address otherwise.

In this extended abstract we present our research portfolio by reviewing some results previously obtained when using GReaNs to control development of 3-dimensional embryos [1], including the first successful attempt we are aware of at solving the so called “French flag problem” [14] in 3 dimensions [2]. The evolvability of this model was also investigated in computational and signal processing tasks at the level of single cells [3,4]. We then discuss the way the model could be

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extended to evolve-develop complex neural networks in a biologically-inspired manner.

II. Model of Artificial Gene Regulatory Networks Encoded in Linear Genomes

Artificial gene regulatory network in our model is specified by a linear genome. A *genome* (Fig. 1) is a list of *genetic elements* grouped in *regulatory units*. Genetic elements have several types. The most important division is between *trans-regulators* (*genes*: elements that encode products, transcriptional *factors*; *TFs*) and *cis-regulators* (*promoters*). In addition, an element can be *special* (special elements correspond to inputs to the GRN and specific cell actions, such as division, death or differentiation) or code a product that can diffuse between cells (such products are called *morphogens*).

Connectivity between the nodes in the GRN (nodes correspond to regulatory units) is determined by the affinity between the TFs and promoters. Special elements that are outputs can be seen as special promoters hardwired to one product with a specific function (for example, division). Inputs can be seen as special products whose concentration is determined externally to the cell.

Importantly, there is no pre-set limit on the number of products coded by the genome, and in particular, no limit on the number of morphogens. There is also no limit on the number of genetic elements in the genome, no limit on the number of nodes in the GRN, and no limit on the number of connections between nodes.

Each genetic element (Fig. 1) corresponds to a point in abstract *N*-dimensional space (*N* is a parameter in the model; typically, *N*=2). Euclidean distance between points corresponding to a promoter and a gene coding a product determines product-promoter affinity.

Concentration of each product is a real value in the interval [0,1]. Concentrations change in each simulation step, depending on the production rates calculated for each regulatory unit. All products degrade exponentially over time.

III. Model of 3-dimensional Development

Development takes place in a continuous 3D fluid-like environment with elastic cells. The embryo growth starts from a single cell and proceeds through cell divisions. Each cell is controlled by the same genome and GRN and has an associated division vector. Division is asymmetric and can be seen as a creation of a daughter cell by a mother in the direction of the mother's division vector. The daughter inherits product concentrations from the mother. At the time of division the direction of the daughter's division vector is set; it depends on the activation of special genetic elements in the mother. When two cells are close enough they adhere to each other, but when they are too close they push one another away. At division, the daughter cell is placed so close that the cells will push each other away. Fluid drag is simulated to prevent erratic movements. Division occurs when a cellular output (a special TF) responsible for division crosses the threshold.

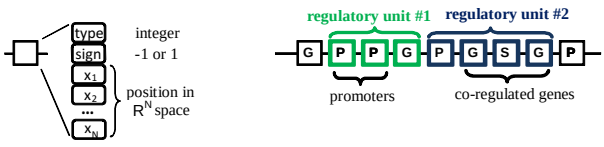

Figure 1. Schematic structure of the genome. Each genetic element (left) in the genome (right) is an ordered set of numbers: an integer specifying the type (*promoter*, P; gene, G; or *special*, S), sign (which determine if it is inhibitory/activatory), and real numbers that specify a point in space (which determines promoter-product affinity). A *regulatory unit*, a node in the *gene regulatory network* (GRN), is at least one promoter followed by at least one gene (G). Special elements correspond to GRN inputs and outputs.

The concentrations of morphogens perceived in a cell depend on the distance from the cells that produce them. Otherwise, in terms of their effects on promoters, they behave the same as internally produced TFs.

IV. Evolution of Assymmetrical Morphogenesis and Pattern Formation Using GReaNs

We have previously used a genetic algorithm to find out if our model allows evolving the development of non-trivial 3D morphologies [1,2]. An evolutionary run would typically take a few thousand generations with population size of 300. The genetic algorithm we used relies on operators that act either within a single genetic element or affect the number or order of elements in the genome. Operators acting on the level of individual elements cause changes in the numbers associated with the element: modification of element type, a number that determines whether the element will take an inhibitory or activatory role, changes to coordinates that affect the affect affinity of the element (product-promoter interactions). Operators acting on level of the genome include duplications and deletions of several continuous elements and exchange of elements between two genomes (recombination).

We have defined 3D targets for evolutionary experiments (see Fig. 2 for examples) and a fitness function that measures similarity of the developed shape or pattern of differentiation to the target. When evolving embryos with asymmetrical patterning, special products in the genome determined cell color.

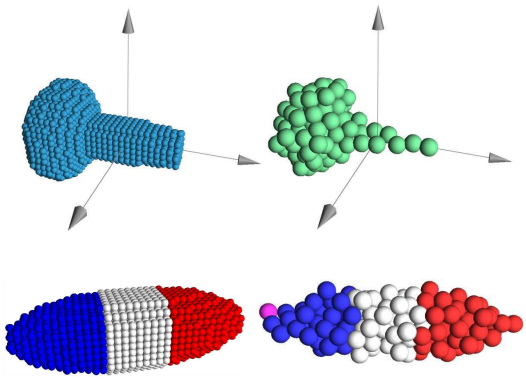

Figure 2. Evolved embryo with an asymmetrical shape (top) and pattern and patterning (bottom); right panels show evolved embryos; left panels show voxelized targets

V. Future Work: Towards Biologically-inspired Development of Artificial Neural Networks

A model of 3D patterning of complex shapes is a first step towards a biological-inspired approach to generation of artificial neural networks with no-trivial behavior in a way that could aid in the understating how the environment shapes biological cognitive systems through evolution and development. This issue has been thus far investigated to only a limited extent, using models with apparently poor evolvability (e.g., [7]), lacking biological realism (e.g., [9], in which genes are limited in number and body subunits do not correspond to cells), or in which only the brain was evolved (e.g., [8]).

In order to allow co-evolution/co-development of multicellular brains and bodies, the model will have to be extended to allow cell differentiation into neurons. This can be achieved in a manner similar to differentiation into colored cells. The parameters of the particular neuron model would be then specified by the concentrations of special proteins in the cell (using, for example, 4-parameter exponential [15] or quartic [16] adaptive neurons; concentration of additional proteins might influence synaptic properties, including learning).

A larger challenge is to find an appropriate way to specify the connections between neurons. Our initial proposal will be to use the chemical affinity of special products in each cell (this is inspired by the role of membrane proteins in determining the connectivity in the nervous system) rather than to model the growth of neurites (explicitly or by setting the direction/length of the neurites). In building such a system it will be necessary to consider the trade-offs between the biological realism and computational efficiency.

Perhaps the most important and difficult in this future work will be defining suitable targets for the evolutionary process. Evolution and development of brains for artificial bodies requires building a model of the interaction of the bodies with the physical world. Biologically-inspired approach to this, based on local interactions, modularity etc., is a challenge in itself. It may be advisable to avoid trying addressing several large challenges at once. We think that the question of building a model for specifying the biophysical parameters of the neurons and of specifying the connectivity in the network could be approached first using a simpler challenge, perhaps by evolving artificial neural networks able to perform signal processing tasks.

We have previously investigated both the issue of animat control and signal processing at the level of single cells. In these experiments, multicellular development was missing: a GRN was evolved to directly control the movement of a unicellular organism [3] or to process signals at the level of single cells [4]. What we propose to do now is to re-use parts of the existing software (the simulation platform that allows for development and interaction with artificial physics), and to evolve the formation of multicellular brains capable of computation or control of multicellular bodies through a developmental process.

VI. Summary

GReaNs provide a biologically-inspired approach towards the generation of multicellular systems that is based on the emergence of the properties of the system from local interactions. It has been created with the aim to capture such features of biological systems like efficient encoding and robustness to damage. We have previously used this approach to evolve embryos with asymmetrical shape and pattering. We believe this is the first step towards a biological-inspired, developmental-evolutionary approach for generation of artificial neural networks with no-trivial behavior.

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