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Bio-inspired computing tissues: towards machines that evolve, grow, and learn

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Abstract

Biological inspiration in the design of computing machines could allow the creation of new machines with promising characteristics such as fault-tolerance, self-replication or cloning, reproduction, evolution, adaptation and learning, and growth. The aim of this paper is to introduce bio-inspired computing tissues that might constitute a key concept for the implementation of 'living' machines. We first present a general overview of bio-inspired systems and the POE model that classifies bio-inspired machines along three axes. The Embryonics project—inspired by some of the basic processes of molecular biology—is described by means of the BioWatch application, a fault-tolerant and self-repairable watch. The main characteristics of the Embryonics project are the multicellular organization, the cellular differentiation, and the self-repair capabilities. The BioWall is intended as a reconfigurable computing tissue, capable of interacting with its environment by means of a large number of touch-sensitive elements coupled with a color display. For illustrative purposes, a large-scale implementation of the BioWatch on the BioWall's computational tissue is presented. We conclude the paper with a description of bio-inspired computing tissues and POEtic machines.

Keywords: Tissue; Growth; Evolution; Learning; BioWatch; BioWall; Embryonics

1. Introduction

Living organisms are complex systems exhibiting a range of desirable characteristics, such as evolution, adaptation, and fault tolerance, that have proved difficult to realize using traditional engineering methodologies. Many an engineer has been allured by certain features of natural processes, giving rise to such domains as artificial life, artificial neural networks, and evolutionary computation. Biological inspiration in the design of computing machines could allow the creation of new machines with promising characteristics such as fault-tolerance, self-replication or cloning, reproduction, evolution, adaptation and learning, growth, etc.

The skin is the largest organ of the human body. It is responsible for many vital functions and its large, extremely receptor-rich surface intensively interacts with the environment. The skin continuously adapts its form, porousness, blood circulation, etc. depending on the environmental

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conditions. The aim of this paper is to present bio-inspired computing tissues that might constitute a key concept for the implementation of 'living' machines, i.e. machines that evolve, grow, and learn. Bio-inspired computing tissues could help designing novel and intelligent man–machine interfaces, intelligent and adaptive prostheses, intelligent walls, floors, doors, blackboards, displays, etc. They might also help us understand natural phenomenon of human tissues and cells.

The paper is organized as follows: Section 2 presents bio-inspired computing machines and tissues as well as the POE model that partitions—in analogy to nature—the space of bio-inspired hardware along three different axes. The Embryonics project is presented in Section 3 by means of the BioWatch application. Its main features are the multi-cellular organization, the cellular differentiation, and the self-repair capabilities. The section terminates by a description of the Embryonics landscape. The BioWall, a large-scale reconfigurable computing tissue built in our lab is presented in Section 4. An implementation of the BioWatch using the BioWall's computational tissue is described in Section 5. Section 6 concludes the paper with an outlook on bio-inspired computing tissues and POEtic machines.

2. Bio-inspired computing machines

Biological systems grow, live, adapt, and reproduce, characteristics that are not truly encompassed by any existing computing system. The concept of 'living' has a number of consequences in terms of adaptation, interaction with the environment, and the ability to deal with limited resources. Methodologies and technologies that enable the construction of artificial systems that live, grow, adapt, and reproduce in hardware would allow a quantum leap in performance for many computing systems known so far.

If one considers life on Earth since its very beginning, three levels of organization can be distinguished (Sanchez et al., 1997; Sipper et al., 1997; Mange and Tomassini, 1998).

2.1. Phylogeny

The first level concerns the temporal evolution of the genetic program, the hallmark of which is the evolution of species, or phylogeny. The multiplication of living organisms is based upon the reproduction of the program, subject to an extremely low error rate at the individual level, so as to ensure that the identity of the offspring remains practically unchanged. Mutation (asexual reproduction) or mutation along with recombination (sexual reproduction) give rise to the emergence of new organisms. The phylogenetic mechanisms are fundamentally nondeterministic, with the mutation and recombination rate providing a major source of diversity. This diversity is indispensable for the survival of living species, for their continuous adaptation to a changing environment, and for the appearance of new species.

2.2. Ontogeny

Upon the appearance of multicellular organisms, a second level of biological organization manifests itself. The successive divisions of the mother cell, the zygote, with each newly formed cell possessing a copy of the original genome, is followed by a specialization of the daughter cells in accordance with their surroundings, i.e. their position within the ensemble. This latter phase is known as cellular differentiation. Ontogeny is thus the developmental process of a multicellular organism. This process is essentially deterministic: an error in a single base within the genome can provoke an ontogenetic sequence, which results in notable, possibly lethal, malformations.

2.3. Epigenesis

The ontogenetic program is limited in the amount of information that can be stored, thereby rendering the complete specification of the organism impossible. A well-known example is that of the human brain with some 10^{10} neurons and 10^{14} connections, far too large a number to be completely specified in the four-character genome of length approximately 3×10^9. Therefore, upon reaching a certain level of complexity, there must

emerge a different process that permits the individual to integrate the vast quantity of interactions with the outside world. This process is known as epigenesis and primarily includes the nervous system, the immune system, and the endocrine system. These systems are characterized by a basic structure that is entirely defined by the genome (the innate part), which is then subjected to modification through the lifelong interactions of the individual with the environment (the acquired part). The epigenetic processes can be loosely grouped under the heading of learning systems.

In analogy to nature, the space of bio-inspired systems can be partitioned along the same three axes: phylogeny, ontogeny, and epigenesis. We refer to this as the POE model (Fig. 1). While each of these models, taken separately, has to a greater or lesser extent been used as a source of inspiration for the development of computing machines, their amalgamation into hardware is a challenge yet to be met and will give birth to novel bio-inspired systems that go beyond traditional computing devices. The ultimate goal is to construct machines—called POEtic machines—that combine the three axes (P, O, E). As we will see later on, bio-inspired computing tissues might constitute an ideal substrate for the implementation of POEtic machines.

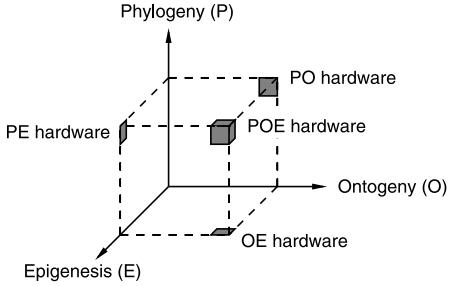

Fig. 1. The POE model. The combination of the three POE axes gives birth to novel bio-inspired computing systems, i.e. POEtic machines that combine evolution, growth (cellular development), and learning.

3. The Embryonics project

The Embryonics project (embryonic electronics; Mange et al., 1999, 2000; Mange and Tomassini, 1998; Tempesti, 1998; Ortega-Sánchez, 2000), an undergoing project in our lab, attempts to combine several of the above-mentioned characteristics. The main objective of the project—that essentially covers the ontogenetic axis of the POE model—is the design of highly-robust integrated circuits, endowed with the properties usually associated with the living world: self-repair (cicatrization) and self-replication. In the remainder of this section, the key-issues of the embryonics project are presented by means of an example.

3.1. Example: the BioWatch

In the framework of electronics, the environment in which our quasi-biological development occurs consists of a finite (but as large as desired) two-dimensional space of silicon. This space is divided into squares or cells. Since such cells (small digital processors) have an identical physical structure, i.e. an identical set of processing resources and of connections, the cellular array is homogeneous. Only the state of a cell, i.e. the contents of its registers, can differentiate it from its neighbors.

Our artificial organism, a bio-inspired watch called the BioWatch, is designed to count and display hours, minutes, and seconds, from 00 h 00 min 00 s to 23 h 59 min 59 s. The input signal is used for synchronizing the units of seconds is delivered by a wireless broadcast.

In the following, the main features of the BioWatch architecture and implementation are briefly discussed.

3.1.1. Multicellular organization

The multicellular organization divides an artificial organism (ORG) into a finite number of cells (see Fig. 2), where each cell (CELL) realizes a unique function, corresponding to a modulo counting called *gene* of the cell. The same organism can contain multiple cells of the same kind (in the same way as a living being can contain a large number of cells with the same function: nervous

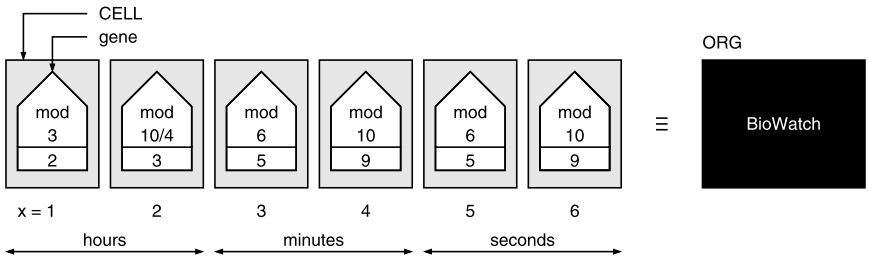

Fig. 2. Multicellular organization of theBioWatch organism. In this example, the BioWatch displays 23 h 59 min 59 s.

cells, skin cells, liver cells, etc.). Moreover, each cell is associated with some *output state*.

The artificial BioWatch is a one dimensional organism with six cells and featuring four distinct genes ('mod 10' for counting the units of seconds or minutes, 'mod 6' for counting the tens of seconds or minutes, 'mod 10/4' for counting the units of hours depending on the value of the tens of hours, and 'mod 3' for counting the tens of hours); the output state is the current value of the elapsed time and varies from 0 to 9 (for the units of seconds, minutes, and hours), from 0 to 5 (for the tens of seconds and minutes), and from 0 to 2 (for the tens of hours).

3.1.2. Cellular differentiation

Let us call *operative genome* (OG) the set of all the genes of an artificial organism, where each gene is a unique function characterized by its position (its coordinates X and Y). Fig. 3 shows the OG of the BioWatch, with the corresponding horizontal (X) coordinate; the vertical (Y) coordinate can be ignored in this particular case. Let then each cell contain the entire OG (Fig. 3): depending on its position in the array, i.e. its place in the organism, each cell can interpret the OG and extract and execute the gene which configures it.

In summary, storing the whole OG in each cell makes the cell universal: it can realize any gene of the OG, given the proper coordinates, and thus implement cellular differentiation.

In our artificial BioWatch, any cell CELL[X] computes its coordinate X by incrementing the coordinate WX of its neighbor immediately to the west (Fig. 3). Any cell CELL[OG,X] can thus be formally defined by a set of modulo-counting operations (its OG) and by its coordinate X.

3.1.3. Organism's self-repair

In order to implement self-repair, we need to add spare cells to the right of the original unidimensional organism (Fig. 4). These cells are defined by the coordinate $X = 7$.

The existence of a fault is detected by a KILL signal which is produced in each cell by a built-in self-test mechanism. The state KILL = 1 identifies the faulty cell which is deactivated (column $X = 4$ in Fig. 4). All the functions (X coordinate and gene) of the cells at the right of the column $X = 3$ are shifted by one column to the right. Obviously, this process requires as many spare cells, to the right of the array, as there were faulty cells to repair (two spare cells tolerating two successive faulty cells in the unidimensional example of Fig. 4). It also implies that the organism has the capability of bypassing the faulty cell and to divert to the right all the required signals (such as the OG and the X coordinate, as well as the data busses).

3.1.4. The cell's architecture

In each cell of every living being the genome is translated sequentially by a chemical processor, the ribosome, to create the proteins needed for the organism's survival. The ribosome itself consists of molecules, whose description is an important part of the genome.

As mentioned previously, each cell is a small processor that sequentially executes the instructions of the artificial genome, the OG. The need to realize organisms of varying degrees of complexity has led us to design an artificial cell characterized by a flexible architecture, that is, itself configurable. It will therefore be implemented using a new kind of fine-grained field-programmable gate array (FPGA). Each element of our FPGA (consist-

Fig. 3. Cellular differentiation of the BioWatch organism with OG and coordinates. (a) Global organization; OP, OG (genes and coordinates). (b) Central cell CELL[X] with its west neighbor CELL[X].

ing essentially of a multiplexer associated with a programmable connection network) is the equivalent to a molecule, and an appropriate number of these artificial molecules allow us to realize application specific processors (cells).

3.1.5. The embryonics landscape

The final architecture of the Embryonics project is based on four hierarchical levels of organization which, described from the bottom up, are the following (Fig. 5):

- The basic primitive of our system is the molecule, the element of our new FPGA consisting essentially of a multiplexer associated with a programmable connection network. The multiplexer is duplicated to allow the detection of faults. The logic function of each molecule is defined by its molecular code or MOLCODE.
- A finite set of molecules makes up a cell, essentially a processor with an associated memory. In a first programming step of the FPGA, the polymerase genome PG defines the topology of the cell, that is, its width, height, and the presence and positions of columns of spare molecules. In a second step, the ribosomic genome RG defines the logic function of each molecule by assigning its molecular code or MOLCODE.
- A finite set of cells makes up an organism, an application-specific multiprocessor system. In a third and last programming step, the OG is

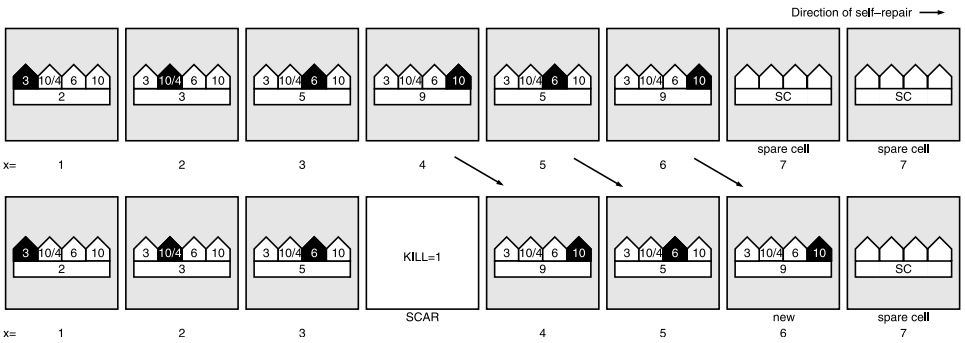

Fig. 4. Self-repair of a 6-cell BioWatch organism with two spare cells (SC, spare cell) and one faulty cell.

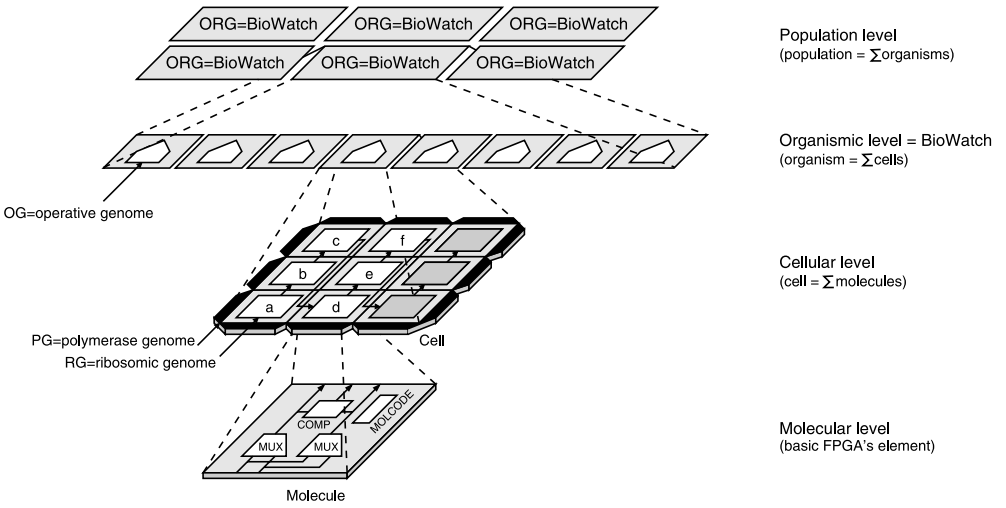

Fig. 5. The embryonics landscape of the BioWatch example: a four-level hierarchy.

copied into the memory of each cell to define the particular application, e.g. the BioWatch, executed by the organism.

- The organism can itself self-replicate, given rise to a population of identical organisms, the highest level of our hierarchy.

4. The BioWall: a large-scale reconfigurable computing tissue

The BioWall (Mange et al., 2001) is an undergoing project in our lab. The BioWall is intended as a reconfigurable computing tissue capable of interacting with its environment by means of a large number of touch-sensitive elements coupled with LED displays. The final implementation will have the respectable dimensions of approximatively 5.5×0.9 m. Fig. 6 shows the structure of the wall's fundamental element: the molecule. The entire tissue (see Fig. 7) contains 3200 molecules, each consisting of one two-color 8×8 dot LED display, one transparent touch-sensitive element, and one reconfigurable circuit (a Xilinx Spartan XCS10XL FPGA). The display and the transparent touch-sensitive element are physically joined by an adhesive film. Each molecule is interconnected with its four direct neighbors. The entire BioWall consists of about 32 mio. reconfigurable

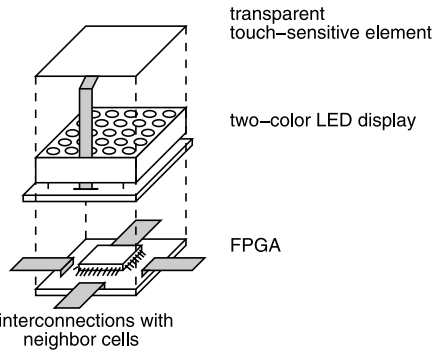

Fig. 6. A fundamental element—the molecule of the large-scale reconfigurable tissue. Each molecule consists of a transparent touch-sensitive element, a LED color display, and a reconfigurable chip (FPGA).

gates, 3200 binary inputs, and more than 50 000 two-color outputs.

Fig. 8 shows the current BioWall prototype, made up of about 2000 molecules.

5. The BioWatch on the BioWall's computing substrate

In this section, we will describe a large-scale implementation on the BioWall's computing substrate of the fault-tolerant and self-repairable BioWatch timer (first presented in Section 3.1).

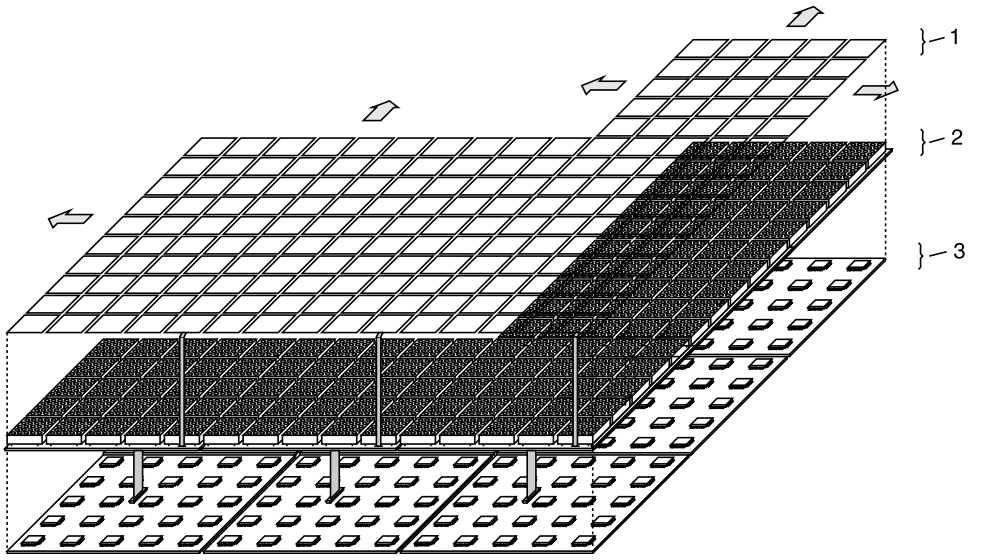

Fig. 7. The BioWall, a reconfigurable and completely scalable tissue capable of interacting with its environment by means of a large number of touch-sensitive element (1), coupled with two-color dot LED displays (2), and reconfigurable circuits (3).

A computer graphic of the BioWatch application is depicted in Fig. 9. Each of the six digits required to count the hours, minutes, and seconds represents an Embryonics cell built up of about 400 embryonics molecules, each molecule corresponding to the BioWall's fundamental element (Fig. 6). In addition to the six cells, two spare cells are added to the right of the wall (Fig. 9). Each cell also contains several spare columns of molecules.

Conception, birth, growth, maturity, illness, old age, death: this is the life cycle of living beings. The proposed demonstration will stage the life cycle of the BioWatch from conception to death. Visitors will face the BioWall, made up of a mosaic of

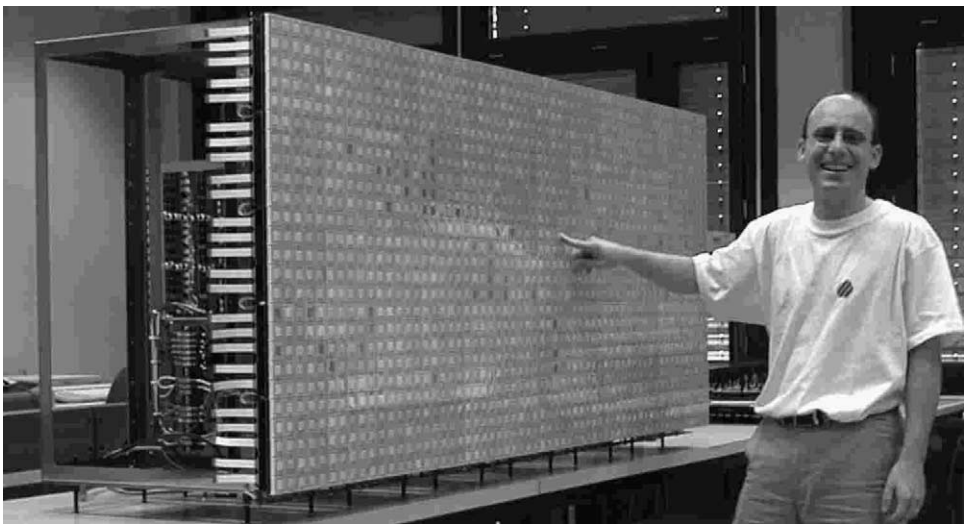

Fig. 8. Actual BioWall prototype consisting of about 2000 molecules.

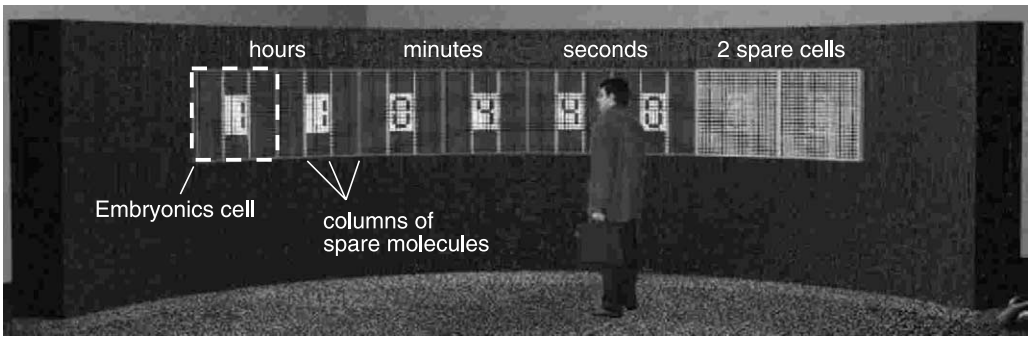

Fig. 9. A computer graphics of the BioWall, a fault-tolerant and self-repairable large-scale watch using the BioWall's computing and reconfigurable substance.

many thousand molecules each containing a display. At rest, all the molecules will be dark. A complex set of signals will the start to propagate through the space (conception) and program the molecules to realize the construction of a beating electronic watch (growth). Visitors will be invited to attempt to disable the watch: on each molecule a push-button will allow the insertion of a fault (wounding). As long as enough spare molecules are available, self-repair occurs on the molecular level and the operation of the cell is not affected. Once all spare molecules are used up, the entire cell dies and a spare cell will automatically be used to replace the dead cell. The programmable robustness of our system depends on a redundancy (spare molecules and spare cells), which is itself programmable. This feature is one of the main original contributions of the Embryonics project. It becomes thus possible to program (or reprogram) a greater number of spare molecules and spare cells for operation in a hostile environments (e.g. space exploration). A detailed mathematical analysis of the reliability of our system is currently under the way at the University of York (Ortega and Tyrrell, 1999a,b).

With respect to this design process, the programming of the molecular array, our reconfigurable tissue, takes place in the following order (Fig. 5):

- The polymerase genome is injected in order to set the boundaries between cells and in order to define the spare cells.
- The ribosomic genome is injected in order to configure the molecular FPGA and to fix the final architecture of the cell.
- The OG is stored within the read/write memory of each cell in order to execute the specification.

The existence of these different categories of genes is the consequence of purely logical needs deriving from the conception of our multicellular automaton.

On of the most promising domains of molecular biology, genomics, is the research of a syntax of the genome, that is, rules dictating the ordering of different parts of the genome, the genes (Duboule, 1997; Bentolila, 1996). One can imagine the artificial and the natural genomes sharing common, invariant properties. Should this indeed be the case, the embryonics project could contribute to biology itself (Barbieri, 1998; Gordon, 1999).

6. Conclusions

6.1. Towards bio-inspired computing tissues

A bio-inspired and reconfigurable computing tissue (Mange et al., 2001) is a completely homogeneous two-dimensional surface, built up of simple, locally-interconnected basic elements—also called molecules. Each molecule consists of at least one input, one output, and one reconfigurable computing unit (typically, an FPGA). Often, inputs, outputs, and computing units are organized in three hierarchical layers as depicted in Fig.

6. However, the layers might also be unified in a single physical substrate. The substrate might be rigid, flexible, organic, inorganic, etc. The molecule's physical size can range from a nano-electronic structure to a large-scale object. Molecule's inputs and outputs might include temperature sensors, force sensors, microphones, cameras, motors, speakers, displays, etc. The molecule's operation is determined by a configuration bitstream—or artificial genome. Both deterministic and non-deterministic genotype to phenotype mappings are imaginable. The system has a completely molecular structure that is scalable without any architectural limits. Molecules are simple and compute in parallel. Any computation is purely local since there are no global interconnection lines.

The concept of bio-inspired and reconfigurable computing tissues is new and promising. The idea clearly goes beyond a simple assembly of input, output, and reconfigurable computing elements. Recent research in display technology and organic electronics (e.g. Forrest et al., 2000) confirms a new tendency towards intelligent, interactive, and flexible systems. To the best of our knowledge, no current approach combines in one and the same substrate, a cellular, intelligent, and reconfigurable structure with embedded input and output channels.

6.2. Towards POEtic machines

The 21st century promises to be the century of bio- and nano-technology. Promising new technologies such as self-assembling systems, organic electronics, living intelligent machines (artefacts), hybrid electronical-biological machines, etc. and the ever-increasing complexity of systems will require new design and engineering methods. Machines will no longer be designed in every detail but evolutionary and adaptive methods will help in building more intelligent systems. The increasing overall complexity and the increasing number of elements (transistors, etc.) in a system will force designers—and mother nature does this job already very well—to build perfect systems out of imperfect components.

Evolving machines that grow, adapt, and are embedded into an ever-changing environment would allow a quantum leap in performance for many computing tasks. Computing tissues inspired by nature not only enable us to create better and more intelligent machines but could be useful by helping us understand natural phenomena. They might give us new insights into the functioning of human tissues and cells.

The BioWall is a first large-scale computing tissue that allows to implement machines according to the concepts of bio-inspired systems. Intelligent tissues are, above all, promising new systems because they could be applied to many different application domains like intelligent man-machine interfaces, intelligent and adaptive prostheses, intelligent walls, floors, doors, black boards, displays, etc.

Future work will focus on the miniaturization of the tissue, its integration into different physical substrates, and on the design of systems built up of a much larger number of molecules (more than 1 million). Our ultimate goal is to embed POEtic machines that evolve, grow, and learn.

Acknowledgements

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