

# METAMORPHIC MEMORY BASED BIO-INSPIRED RECONFIGURABLE CELLULAR SYSTEMS

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**Abstract** – *Living beings in nature are made up of structurally identical cells, where each cell contains a copy of its DNA, the unique characteristic of the individual. This DNA is like a memory. It remembers and defines the behaviour of the individual and remains constant throughout its life time. An artificial embryonic cell contains a similar memory map where the specific 'gene' it executes determines the functionality of the cell. An electronic system is then constructed by interconnecting a large number of identical cells. Each cell, similarly to nature, executes only a segment (gene) of the DNA and thus they all demonstrate different behaviour. However these cells will collectively determine the characteristic and configuration of the target system. This paper proposes a novel gene selection algorithm that doesn't use the common address decoding approach and provides easier reconfiguration of systems for a different behaviour.*

**Keywords:** Bio-Inspired Systems, Embryonics (embryonic electronics), Artificial Life, Artificial DNA, Self-Repair, Fault Tolerance.

## 1 Introduction

Embryonics (embryonic electronics) [1-5] was originally proposed in the mid-90's by the Swiss Federal Institute of Technology to design reliable electronic systems. It tries to adapt and transpose the development of living characteristics of organisms to the world of silicon integrated circuits. Systems are built by a homogenous array of identical cells similarly to that of commercial FPGAs. These cells however possess self-replication, self-repair and fault-tolerant properties [6]. Although system implementation approaches are structurally different, they all obey to and use the same bio-inspired fundamentals, namely:

1. **DNA (Genome):** Each embryonic cell includes a memory with at least one so called Configuration Register (CR) which holds the expected behaviour of the cell. This corresponds to a gene of the DNA. All the Configuration Registers together describe the functionality of the system and form the genome (DNA) of the application.
2. **Cellular Division:** It is the process whereby cells, starting from a mother cell, are successively divided and at the same time the genetic material (DNA) of the individual is passed on to their off-springs until the organism is formed.
3. **Cellular Differentiation:** The role of each cell in the organism is defined by the transcription of a segment (gene) of the DNA. Which gene a cell will decode, to determine its functionality, depends on its location and physical position in the organism. Gene selection is usually provided by an address generator.

Functional behaviour of an embryonic system is defined by its DNA stored in the memory of every one of its cells. The size of this memory and the required decoding circuit that selects the appropriate gene, that specialises the cell for a specific behaviour, can be large and consume a disproportionate area of the cell. Research to date [5, 9] tries to simplify and optimise this memory but little attention has been paid so far to more efficient memory address generation techniques.

This paper attempt to address the later problem by introducing a novel gene selection algorithm that eliminates the need for address generation during cellular division and cellular differentiation as well as during a fault initiated system repair process. The efficiency of our metamorphic cell-memory based cyclic gene selection algorithms is demonstrated by the implementation of a frequency divider using a Xilinx XC9500 CPLD device.

Section 2 introduces our proposed cyclic gene implemented memory and how it aids the processes of cellular division and cellular differentiation. Implementation and simulation results of a frequency divider example are detailed in section 3, followed by a brief conclusion in Section 4.

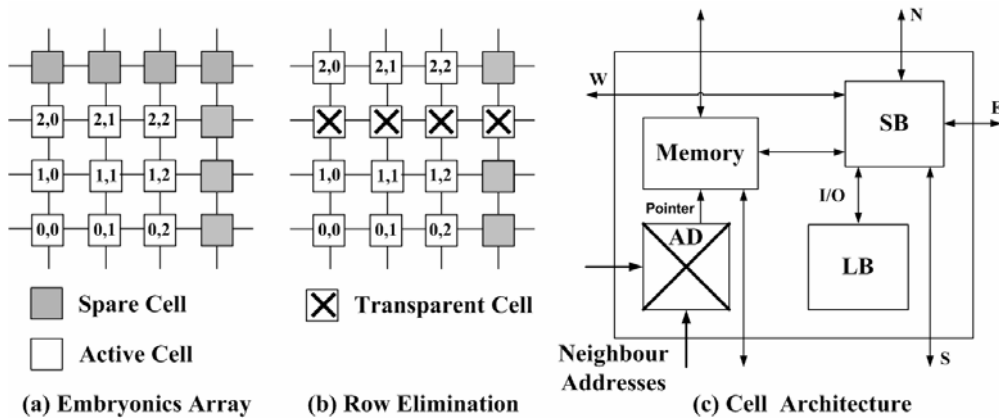


Fig. 1. Embryonic array based system, and cell architecture.

## 2 Embryonic Cell with Metamorphic Memory

Consider the case of an embryonic array where, for self-repair, row elimination strategy is used [11], Fig. 1-a & b. In such an array, the memory of every cell only contains a section of the DNA that is active in the column that the cell occupies. In Fig.1-a all cells in the same column will have the same memory content but only one of its genes, will be executed. The task of the address generator (AD), based on the cell's position with respect to its neighbours, is to calculate the memory address pointer during cellular division and then hold it during its lifetime, Fig. 1-c.

Although, following cellular division, all cells of the embryonic array will have the same genes; it is possible to alter the genetic behaviour of the system by changing the memory space environment in which the DNA is. In this case both processes of cellular division and cellular differentiation occur, in a single step, simultaneously. And the gene that is executed by the cell and provides its functional configuration is always placed in the 1<sup>st</sup> address location of its DNA segment memory (Configuration Register). Hence, it eliminates the need for a complex address generator, fig. 1-c.

The internal structure of an embryonic cell with particular emphasis given to the implementation of its DNA memory is described in Fig. 2. Each genetic code (a-b-c-d-e) has a bit sequence. During the operation of the system only a single gene of the genome will be active and be visible by the cell. Its task is to specialise the cell and determine its functionality. The memory is supported by a Logic Block (LB) or function unit, whose task is to interpret the gene and to execute the required combinational or sequential function that will specialise the cell. It is constructed from a multiplexer(s) or from a LUT (look-up-table) and a register. The functionality of the Switch Block (SB), the remaining element in the cell, is twofold. On one hand it provides the necessary interconnect between cells for the realisation of a particular target system, while on the other hand it is responsible for inter-cell communication and signal routing. Within each cell a special mechanism is provided that could change the size of the required memory space.

The configuration process takes place in three steps. First of all the Species Identity (similar to the different identity if the various species in nature) will be loaded into Species Identity Block. They will determine the number of genes of the cell. Every cell of a given column has same Species Identity, and thus the same data. The second step is to load the genes into the memory unit of the cells as the zygote and its daughter cells divide and differentiate. Finally, the growth process of the target system ends with all its cells configured.

Gene circulation is controlled by multiplexers  $SR_2$  and  $SR_3$ , while the size of the memory space, the metamorphic nature of the genome is supervised by some multiplexers. Each one of the last three multiplexers is associated with a control flag of Species Identity Block and together they provide access into or bypassing the Configuration Register they supervise. This type of variable size memory can support two different types of cellular division: Conventional Cellular Division, and Metamorphic Cellular Division, fig. 2-b. The conventional mode does have no effect on memory space and it remains at the size that it was originally set. This property is useful when upon the system detecting a fault, self-repair is requested. In the metamorphic mode of cellular division the daughter cell's memory space during cellular differentiation can, if so required, change. When the copy and cellular differentiation process are complete the genes in the mother cell's memory will assume their original position, while those in the daughter cell will suffer a one gene positional change. Both cells will display, in the 1<sup>st</sup> address location of their DNA memory map, the gene that they will execute.

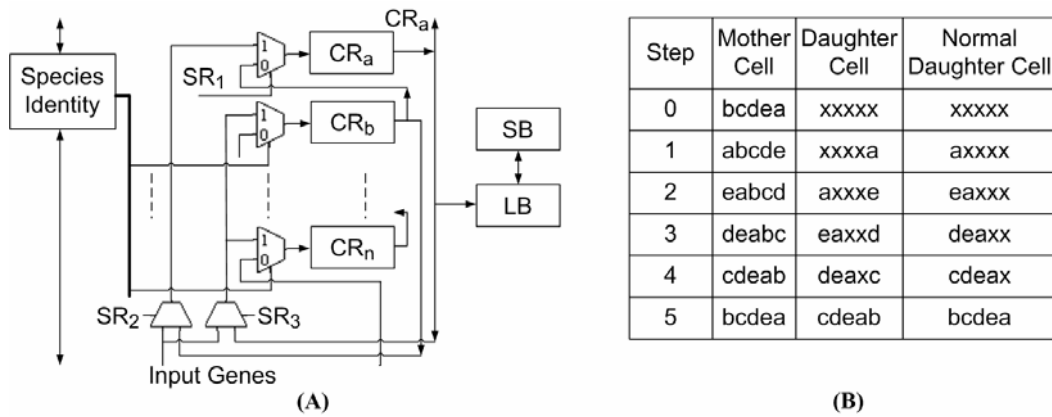


Fig. 2: An embryonic cell and its cyclic memory implemented artificial DNA.

One of the advantages of this memory mapping techniques is that the mother cell can be re-created form the last daughter cell in a single division. Since the genes demonstrate a cyclic metamorphic characteristic, the genetic material, the DNA of the system can be called having a cyclic metamorphic memory map.

A larger system can, in a hierarchical manner be built, from a number of smaller modules that have a variable size genetic material made up of a different number of genes. This property is similar to the different characteristics of species in nature. The variable length memory of each cell i.e. the possibility to alter both the size and make-up of the genome also facilitates evolutionary changes and genotype/phenotype translation of the organism.

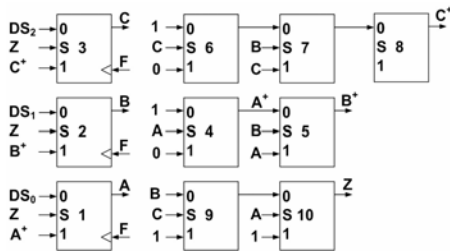


Fig. 3: Configuration Register Content.

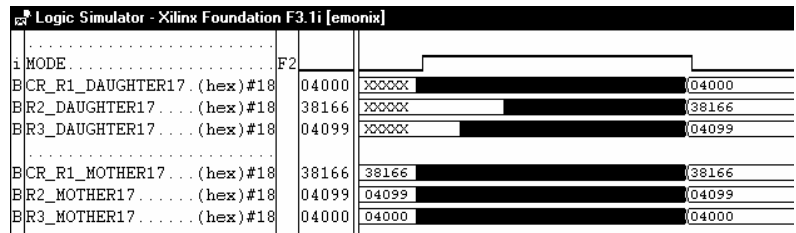


Fig. 4: Simulation of cellular division. CK= 100 ns.

### 3 Simulation Results

In order to demonstrate the efficiency of the metamorphic memory method, a programmable frequency divider that had already been designed by conventional methods [12] has been selected as a test vehicle. The implementation of this example using universal logic elements in form of 2:1 multiplexers with associated registers is shown in Fig. 3. For logic synthesis BDD (Binary Decision Diagrams) methodology was used. The circuit will divide the input frequency (F) by a pre-settable 3-bit number (DS).

For comparison purposes the same logic and switch block design was used as proposed by Prodan and Ortega [2, 12]. Self-check in each cell of the embryonic array is performed by BIST (Built-In Self-Test) logic proposed by Mange [13]. The DNA memory map was implemented using our proposed variable metamorphic memory space environment instead of the address generator technique used by other researchers.

For implementation platform of the frequency divider example a Xilinx XC9500 CPLD device was used. Simulation results of the cellular division and differentiation processes and how a daughter cell (CR\_R1\_DAUGHTER17) from a mother cell (CR\_R1\_MOTHER17) is generated, using our cyclic metamorphic memory, are demonstrated in Fig. 4. It shows how in column 1 the genes of the mother cell (in location 1,1 i.e. MOTHER) during the ‘birth’ of the first daughter cell (in location 1,2 i.e. DAUGHTER) are propagated. The genes are stored in 18-bit Configuration Registers of which in each cell only registers I, II and III (1<sup>st</sup>, 2<sup>th</sup> and 3<sup>th</sup> i.e. d, e and a) are selected. When genome propagation begins the three genes in the mother cell have the following content: 04000, 04099, 38166, while all the CRs in the daughter cell are still

00000. When DNA propagation is complete the mother cell's genome resumes its original state but the gene content of the daughter cell changes to 04099, 38166, 04000. Note how the 2<sup>nd</sup> gene in the mother cell becomes the active 1<sup>st</sup> gene, on the northern most position of the memory map, of the daughter cell that will configure it for its required functionality. Population of the rest of the array follows the same process.

## 4 Conclusion

This paper discusses how the cells' address generator can be replaced by a much simpler and more efficient cyclic memory approach. It also proposes a new artificial cellular division and system reconfiguration process in which the DNA and thus the behaviour of the system can be modified either by genetic operators or by facilitating an alterable genetic environment. A further advantage of our approach is that the gene that needs to configure and specialise the cell for a required functionality is always located at the northern most position of the memory map. The proposed method has the advantage of using variable length memory and therefore it is possible to use for each column of the array genes of different length. This in turn leads to a reduction on the overall size of the genome, resulting in turn shorter time for cellular division cellular differentiation and a larger number of available spare cells.

The paper proposes a variable length memory structure based on a fix number of registers that each cell contains. In certain applications however that require fewer genes some of these registers may not be needed and are thus surplus to requirement. We are currently investigating how such excess registers may form part of a memory map bank and shared by cells, and how registers may be optimised by using shared memory with duplexed DNA between two cells. This approach may also be exploited on a higher tissue level between groups of embryonic arrays.

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