

# BIO-INSPIRED CELLULAR SYSTEMS WITH CYCLIC METAMORPHIC MEMORY

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**Abstract** - *The unique characteristic of a biological system in nature is described by its DNA through the transcription of its genes. This is like a memory map that each cell of an organism contains. 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 a large number of identical cells where each possesses a different behaviour. The cells collectively however determine the characteristic of the target system. This paper proposes a new, variable size memory map based on a novel gene selection algorithm that no longer uses the hitherto common address decoding approach to access the cell's gene it will execute. Instead it applies the principle of cyclic metamorphic gene selection of the artificial DNA memory. A further benefit of the approach is that through genetic operators or variable memory space environment for enhanced behaviour the functionality of the system can also be easily altered.*

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

## 1 Introduction

The design of reliable electronic systems and ensuring their long-term fault free operation is one of the major challenges we are facing today. How can we design such complex but reliable systems? Nature offers some remarkable examples. One such important process is the development of the individual from a single fertilised egg (zygote) through its repeated division and differentiation. Embryonics (embryonic electronics) [1-5] tries to adapt and transpose the development of such processes and 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, but they possess self-replication, self-repair and fault-tolerant properties [6].

Unlike in nature however, if fault in a cell of a bio-inspired system develops or it dies, the silicon on which it is fabricated cannot grow new healthy cells to replace the damaged ones. In order to maintain fault free operation, in Embryonics spare standby cells are employed [7, 8]. These, as shown in Fig. 1, are usually distributed in rows and/or in columns around functional cells.

Functional behaviour of an embryonic system is defined, analogously to biological systems, 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 attempts to address the latter problem by introducing a novel gene selection technique 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.

Sections 2 of this paper will give a brief overview work done to date in Embryonics within the international research community. Section 3 introduces our proposed cyclic gene implemented memory and how it aids the processes of cellular division and cellular differentiation. In Section 4 a new metamorphic memory map based artificial DNA is presented. Finally, implementation and simulation results of a frequency divider example are detailed in section 5, followed by a brief conclusion in Section 6.

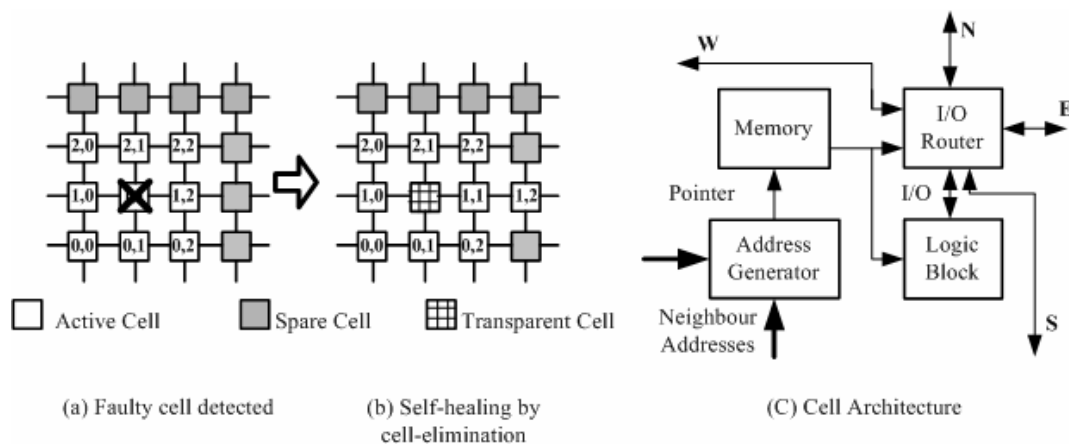


Fig. 1. Fault repairing algorithm array reconfiguration, and cell architecture.

## 2 Embryonics

Embryonics was originally proposed in the mid-90's by the Swiss Federal Institute of Technology. Currently there are three research groups actively working in the field [1, and 8-11]: Swiss Federal Institute of Technology (EPFL), University of York, and University of the West of England (UWE). Although they appear to be structurally different they obey to and use the same bio-inspired fundamentals, namely:

**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.

**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.

**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.

**Multi-Cellular Organism:** A set of cells that make up an organism.

Every cell of an embryonic array contains a DNA memory unit the task of which is to present a gene to the cell that it needs to execute. Depending on the size of the memory unit it is possible to differentiate between the various approaches such as: Full Genome (EPFL), and Partial Genome (University of York, UWE).

When the full genome memory approach is used then each embryonic cell will contain the entire genetic material of the system. This approach is analogous to the biological cell, where every cell of the individual contains its full DNA. In an artificial embryonic cell, during its normal mode of operation however, much of this genetic information is not required. Storing this unused part of the DNA in every cell's memory could result in a prohibitively large system.

In a partial genome memory approach only a portion of the DNA is stored by the cells. Researchers at York proposed that the genome should be divided amongst the cells either on the first row (or the first column). When it is, for example, loaded into the first row then each cell of a column would only contain those genes which are used in that particular column. In this case cellular division and differentiation can only take place in one direction. Distribution of the genome on the first column or row suits particularly well to a self-repairing process which is based on column or row elimination strategy.

A radically different approach to reduce the size of the genome that every cell of the system needs to store was proposed by researchers at UWE [9]. In this case the embryonic cell only stores its own gene and the genes of some of its neighbouring cells. The amount will depend on the cell-reconfigurable strategy and the number of spare columns used. In all cases however the size of the memory is very small.

### 3 Cyclic Gene Selection,

Consider the case of an embryonic array where, for self-repair, row elimination strategy is used [11]. 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-c all cells in the same column will have the same memory content but only one of its genes, as selected by the cell's address generator will be executed. The task of the address generator, 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.

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 either using genetic operators or by defining a different environmental setup for the DNA.

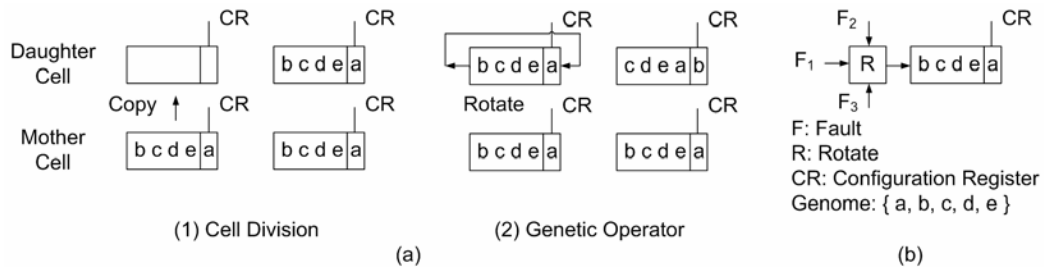
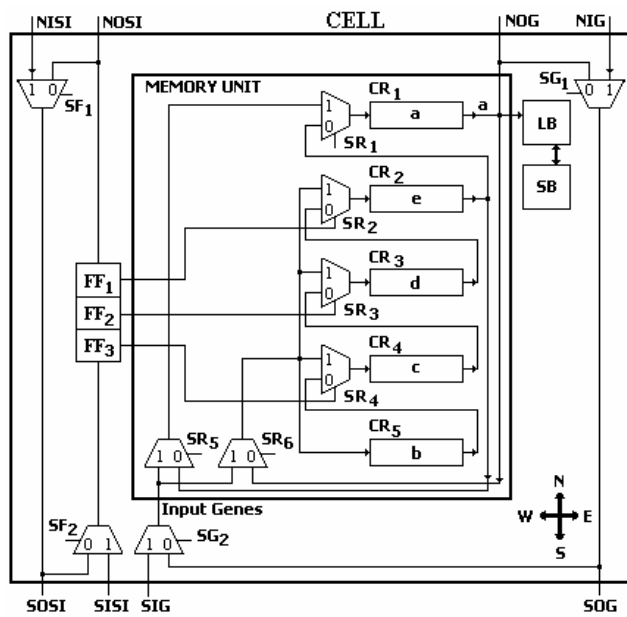


Fig. 2: DNA memory gene selection using genome rotation.

One way to achieve this, for example, is to cycle the embryonic cell's genome using genetic operators. In this case 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. This section of the memory is often called the Configuration Register. Fig.2 shows the way it is achieved. First during cellular division (Fig. 2a), the DNA's genes are copied from the mother cell to the daughter cell. The next step involves the rotation of genes in the daughter cell. The number of rotational steps required is calculated by the Rotation control unit (R). This will depend on the number rows found to be faulty and had to be eliminated in the array (Fig. 2b). The row that needs to be replaced is indicated by signal  $F_i$  ( $i = 0, 1, 2, \dots, n$ ), where  $i$  is the row number. Fig.2 shows how the daughter cell, in address location No.1, is assigned a new gene  $b$ , while the genes of the mother cell remain unchanged.

The advantages of the genome rotation algorithm as shown in Fig. 2 are threefold. First and foremost it eliminates the need for a complex address generator, secondly the genome could be easily altered if so required and finally by placing the active gene, whose task is to configure the cell, into address location No.1, its position is always known. Although the address generator, by using the genome rotation technique to calculate the cell's active gene, is eliminated the fundamental biological processes of cellular division and cellular differentiation are not effected. They remain as two distinctive steps in the growth of the organism.

The genetic behaviour of the cell and system can also be altered by changing the memory space environment in which the DNA is implemented, by using a metamorphic memory that is capable to expand or contract as required. In this case both processes of cellular division and cellular differentiation occur, in a single step, simultaneously (Fig. 3). The figure shows how, while the cell 'divides', the memory map changes and the gene is copied into the daughter cell. Again the gene that configures the cell and is interpreted to specialise it for a particular function, is placed in address location No.1 of the memory unit ( $CR_i$ ). For this no additional rotation is required. A further benefit of this technique, apart from eliminating the address generator, is the metamorphic ability of the memory. The following section will discuss this in detail.



NIRI: North Input Species Identity,  
 NORI: North Output Species Identity,  
 SIRI: South Input Species Identity,  
 SORI: South Output Species Identity,  
 NIG: North Input Genes,  
 NOG: North Output Genes,  
 SIG: South Input Genes,  
 SOG: South Output Genes,

Fig. 3: An embryonic cell and its cyclic memory implemented artificial DNA.

#### 4 Artificial DNA Using Metamorphic Memory Approach

The internal structure of an embryonic cell with particular emphasis given to the implementation of its DNA memory is described in Fig. 3. The memory is made up of a set of Configuration Registers (CR). They hold, in form of the genome, the expected behaviour of the target system and in particular that of the host cell. 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 multiplexer acts as a universal logic element and thus for example a 2:1 MUX can implement the combinational function of any type of a 2-input gate. The register provides sequential functionality if that is required from the cell. 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.

In the example of Fig. 3 the memory map is made up of five Configuration Registers and is thus able to store a five-gene DNA. Each genetic code (a-b-c-d-e) has a bit sequence. 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 FF<sub>1</sub>-FF<sub>2</sub>-FF<sub>3</sub>. 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. Data from the north or south can be externally loaded into the memory via multiplexers SG<sub>1</sub> or SG<sub>2</sub>. The programming of these multiplexers depends on operational conditions and on the position of the cell in the array.

Gene circulation is controlled by multiplexers SR<sub>5</sub> and SR<sub>6</sub>, while the size of the memory space, the metamorphic nature of the genome is supervised by SR<sub>2</sub>, SR<sub>3</sub>, and SR<sub>4</sub>. Each one of the last three multiplexers is associated with a control flag (FF<sub>1</sub>, FF<sub>2</sub> or FF<sub>3</sub>) 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.

In the conventional mode of operation SR<sub>6</sub> is set to “1”. This type of cellular division (Fig. 4a) does have no effect on memory space and it remains at the size that it was originally set. The DNA will, without any modification, be copied from mother to the daughter cell. This property is useful when upon the system detecting a fault, self-repair is requested.

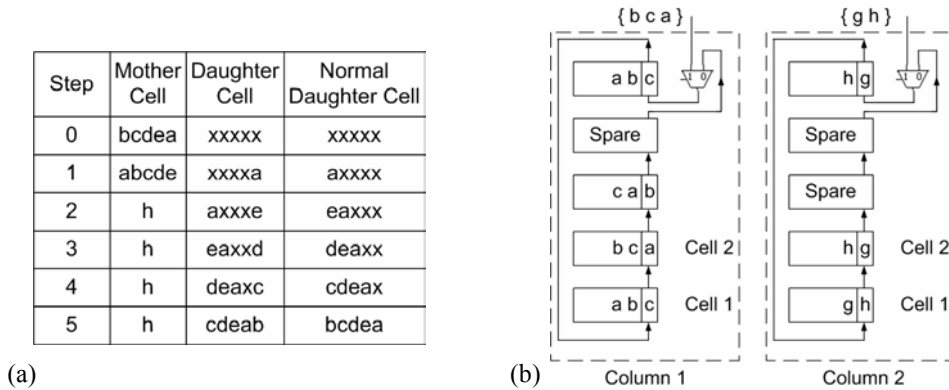


Fig. 4: a) Gene movement and transfer during cellular division, b) Gene loading examples.

In the metamorphic mode of cellular division the daughter cell’s memory space during cellular differentiation can, if so required, change. For this mode of operation SR<sub>1</sub>-SR<sub>5</sub>-SR<sub>6</sub> will be set to '1-1-0' in the daughter cell and to '0-0-0' in the mother cell. Additionally SG<sub>2</sub> in the daughter cell will also be set to '1'. The genes in the mother cell will rotate and will be bit-by-bit copied into the daughter cell. Gene movement in the memory unit of both cells is shown in Fig 4a. 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.

As discussed, the metamorphic approach of gene selection only requires a single memory access multiplexer (SR<sub>5</sub>). This is not only a far more efficient approach than using address generators for memory access but also enables to change the size of the memory. Thus genome, and therefore the number of genes, may vary in size when only a portion of the cell’s memory may need to be populated. The memory could then expand or contract, limited by the number of Configuration Registers (memory banks) used. By programming multiplexers SR<sub>2</sub>, SR<sub>3</sub> and SR<sub>4</sub>, this might be achieved. The minimal number of genes that a cell must have, in order that it can possess self-repair property, is limited to two.

Cellular division and system growth occurs in a bottom up vertical manner. The array is populated and the target system is built when its last cell (at step 5) has the same genetic material as the mother cell, and the required number of cellular division process steps has been completed. This also means that since the evolution of genes during cell division is cyclic, the growth process must be terminated as the mother cell (step 0 in Fig. 4a) is again re-created (step 5 in Fig. 4a).

One of the advantages of this memory mapping techniques is that the mother cell can be re-created from 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.

An example of an embryonic array configured system is shown in Fig. 4b. As it has already been mentioned, the configuration process comprises of three steps. It starts with loading the genome (genes of the Species and genes of the individual) of the artificial system into the northern most cells of the array. These cells also act as mother cells of the column. Cellular division will then populate each column and differentiate its cells in a bottom up vertical manner progressing from south to north.

The genetic material and thus the number of genes in each active cell of a column is the same. For example, each cell in column No.1 and column No.2 has 3 and 2 genes, respectively. The example also demonstrates how 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.

As discussed earlier, the cyclic metamorphic nature of gene selection can facilitate cell self-repair. If gene mutation is suffered by the first cell then this could be corrected by the northern most cell of the same column (the mother cell) transferring its entire genome.

Let's consider a worst case scenario where all the cells in a column suffer memory mutation in their active gene and therefore become functionality faulty. Since the southern most row (and cells) can no longer be used for gene recovery, the genome for the column is therefore lost. One way that this problem could be overcome is to use the northern most row instead of the southern most one for storing the original genes. This row could, at the same time, also act as a spare row and mutated genes of cells could be recovered using cyclic gene replacement. In this case cells in the northern most row would fulfil the role of both acting as mother cells for cellular division and cellular differentiations at the birth of the system and as spare cells during the lifetime of the system for self repair.

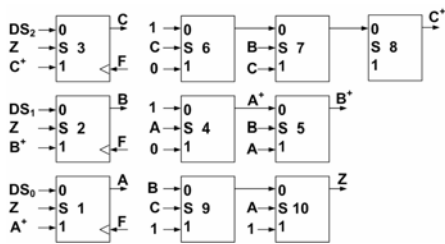


Fig. 5: Configuration Register Content.

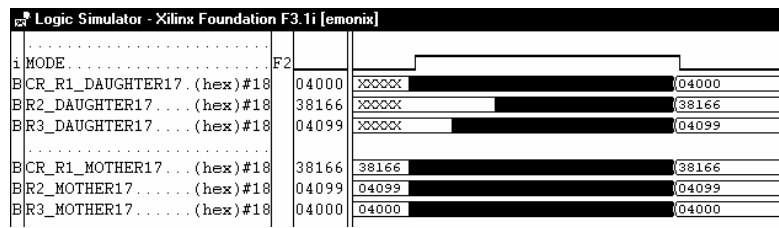


Fig. 6: Simulation of cellular division. CK= 100 ns.

## 5 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. 5. 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. 6. 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>nd</sup> and 3<sup>rd</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.

## 6 Conclusion

This paper discusses how the need for an address generator for each cell can be eliminated. It also proposes a new artificial cellular division 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. This can easily be implemented by the application of a novel algorithm to expand or to contract the size of the memory using cyclic metamorphosis to create the required artificial DNA. A further advantage of our approach is that the gene that should configure and specialise the cell for a required functionality is always located at the northern most position of the memory map. Further, if the genome is loaded to the northern most row of embryonic array then the row could also be used as a spare row for self-repair and system fault

recovery purposes. 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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