Embryonics: A New Methodology for Designing Field-Programmable Gate Arrays with Self-Repair and Self-Replicating Properties

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Abstract*— The growth and the operation of all living beings are directed through the interpretation, in each of their cells, of a chemical program, the DNA string or *genome*. This process is the source of inspiration for the Embryonics (embryonic electronics) project, whose final objective is the conception of very large scale integrated circuits endowed with properties usually associated with the living world: self-repair (cicatrization) and self-replication. We will begin by showing that any logic system can be represented by an ordered binary decision diagram (OBDD), and then embedded into a fine-grained field-programmable gate array (FPGA) whose basic cell is a multiplexer with programmable connections. The cellular array thus obtained is perfectly homogeneous: the function of each cell is defined by a configuration (or *gene*) and all the genes in the array, each associated with a pair of coordinates, make up the blueprint (or *genome*) of the artificial organism. In the second part of the project, we add to the basic cell a memory and an interpreter to, respectively, store and decode the complete genome. The interpreter extracts from the genome the gene of a particular cell as a function of its position in the array (its coordinates) and thus determines the exact configuration of the relative multiplexer. The considerable redundancy introduced by the presence of a genome in each cell has significant advantages: self-replication (the automatic production of one or more copies of the original organism) and self-repair (the automatic repair of one or more faulty cells) become relatively simple operations. The multiplexer-based FPGA cell and the interpreter are finally embedded into an electronic module; an array of such modules make it possible to demonstrate self-repair and self-replication.

***Index Terms*—Embryonic electronics, field-programmable gate arrays (FPGA's), multiplexer-based FPGA's, ordered binary decision diagrams, self-repairing FPGA's, self-replicating FPGA's.**

I. Introduction

A. Toward Embryonics

A HUMAN being consists of approximately 60 trillion (60×10^{12}) cells. At each instant, in each of these 60 trillion cells, the *genome*, a ribbon of 2 billion characters, is decoded to produce the proteins needed for the survival of the organism. This genome contains the ensemble of the genetic inheritance of the individual and, at the same time, the instructions for both the construction and the operation of the organism. The parallel execution of 60 trillion genomes in as many cells occurs ceaselessly from the conception to the death of the individual. Faults are rare and, in the majority of cases, successfully detected and repaired. This process is remarkable for its complexity and its precision. Moreover, it relies on completely discrete processes: the chemical structure of DNA (the chemical substrate of the genome) is a sequence of four bases, usually designated with the letters A (adenine), C (cytosine), G (guanine), and T (thymine).

Our research is inspired by the basic processes of molecular biology [16]. By adopting certain features of cellular organization, and by transposing them to the two-dimensional (2-D) world of integrated circuits on silicon, we will show that properties unique to the living world, such as self-replication and self-repair, can also be applied to artificial objects (integrated circuits).

B. Objectives and Strategy

Our final objective is the development of very large scale integrated (VLSI) circuits capable of self-repair and self-replication. These two properties seem particularly desirable for complex artificial systems meant for hostile (nuclear plants) or inaccessible (space) environments. Self-replication allows the complete reconstruction of the original device in case of a major fault, while self-repair allows a partial reconstruction in case of a minor fault.

Section II introduces the fundamental features of the Embryonics project (for embryonic electronics), which is based on a general hypothesis, defining the silicon environment in which the quasi-biological development occurs, and on three features, which roughly mimic the process of cellular development: multicellular organization, cellular differentiation, and cellular division.

To represent and implement a given digital system on a FPGA we select, in Section III, an efficient and universal representation: the ordered binary decision diagram (OBDD). We will show that the use of such a representation greatly simplifies the realization of a new family of FPGA's, based

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on a fine-grained cell. This cell, called MUXTREE, contains essentially a multiplexer with one control variable and a nontrivial programmable connection network. Section IV describes in detail the MUXTREE cell, which in fact constitutes the application layer of the FPGA, and its 20 configuration bits. According to our biological approach, these 20 bits are the gene of the cell and all the genes of a given digital system are its genome.

Section V introduces the two configuration layers which will perform the computation of the gene of each cell. The first layer computes the coordinates of a given cell from the coordinates of its neighbors. The second layer determines, from the complete genome and from the local coordinates of the cell, its gene. This is the equivalent of the process of cellular differentiation, and is implemented through the use a very simple binary decision machine, which we call NANOPASCALINE, charged with the execution of the GENOME program. Finally, Section VI briefly describes the realization of the cellular division process, that is, the duplication of the genome of a mother cell into one or two neighboring daughter cells.

The final cell, made up of an application layer (MUXTREE) and two configuration layers (NANOPASCALINE), is finally embedded into a demonstration module: the BIODULE. Section VII shows that any given digital system implemented by an array of BIODULES is endowed with the properties of self-repair and self-replication. Section VIII illustrates the limitations of the current project and outlines the ongoing research, aimed at the development of an integrated circuit endowed with quasi-biological properties.

II. The Foundations of Embryonics

A. The General Hypothesis about the Environment

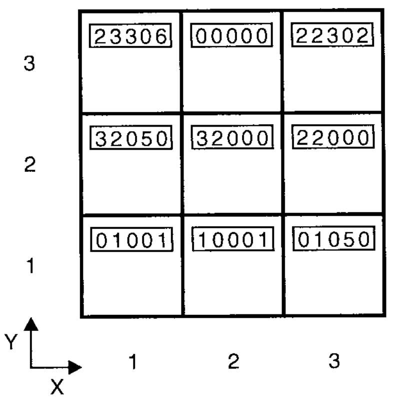
The general hypothesis describes the environment in which the quasi-biological development occurs. In the framework of electronics, it consists of a finite (but as large as desired) 2-D space of silicon, divided into rows and columns. The intersection of a row and a column defines a *cell*, and all cells have an identical structure, i.e., an identical network of connections and an identical set of logic operators. The physical space or *cellular array* is therefore *homogeneous*, that is, made up of absolutely identical cells: only the *state* of a cell can differentiate it from its neighbors.

B. First Feature: Multicellular Organization

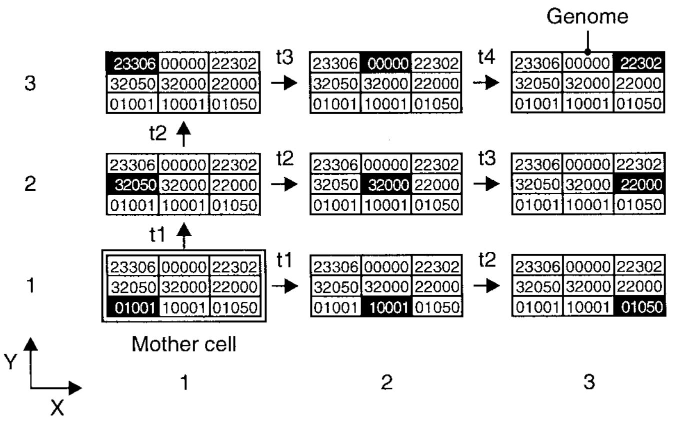
The first feature is that of *multicellular organization*: the artificial organism is divided into a finite number of cells [Fig. 1(a)], where each cell realizes a unique function, determined by a number called the *gene* of the cell. Fig. 1(a) illustrates the example of a simple artificial organism, an *up–down counter*, realized with nine cells, each cell being defined by a different gene (a five-digit hexadecimal number). The calculation of these genes will be analyzed in detail later.

C. Second Feature: Cellular Differentiation

Let us call *genome* the set of all the genes of an artificial organism, where each gene is characterized by its value and its position (its coordinates X, Y). Fig. 1(a) then shows the genome of the up–down counter, with the corresponding horizontal (X) and vertical (Y) coordinates. Let then each cell contain the entire genome [Fig. 1(b)]: depending on its position in the array, each cell interprets the genome and extracts the gene which configures it.



(a)



(b)

Fig. 1. The three features of embryonics applied to the example of an up–down counter. (a) Multicellular organization with a nine-gene genome. (b) Cellular differentiation with the complete genome in every cell and cellular division copying the genome of the mother cell into daughter cells ($t1 \cdots t4$: clock periods).

In summary, storing the whole genome in each cell makes this cell universal: it can realize any gene of the genome, given the proper coordinates.

D. Third Feature: Cellular Division

At startup, the mother cell [Fig. 1(b)], arbitrarily defined as having coordinates $X, Y = 1, 1$, holds the one and only copy of the genome. At time $t1$, the genome of the mother cell is copied into the two neighboring (daughter) cells to the north and to the east. The process then continues until the 2-D space is completely programmed. In our example, the furthest cell is programmed at time $t4$.

III. Synthesis of Ordered Binary Decision Diagrams (OBDD)

To fit our demands, we needed to find a method capable of generating, starting from a set of specifications, the configuration for a homogeneous network of cells, where each cell is defined by an identical architecture and a usually distinct function (gene).

To meet our requirements, we have selected a particular representation: the *ordered binary decision diagram* (OBDD). This representation, with its well-known intrinsic properties such as canonicity [2], [4], was chosen for two main reasons [see, for example, Fig. 2(c)]: on one hand, it is a graphical representation which exploits well the 2-D space and immediately suggests a physical realization on silicon; on the other hand, its structure leads us to a natural decomposition into cells realizing a logic test (a diamond), easily implemented by a multiplexer.

We will illustrate the handling of ordered binary decision diagrams through a simple example, an up–down counter. Our choice will lead us to define our new FPGA as a homogenous array where each cell contains a programmable multiplexer with one control variable, implementing precisely a logic test. Such an FPGA is said to be *fine-grained.*

A. Example of a Modulo-4 Up–Down Counter

As an example, let us consider the realization of the abovementioned modulo-4 up–down counter, defined by the following sequences:

$$\begin{aligned} &\text{for } M=0: Q1, Q0 = 00 \rightarrow 01 \rightarrow 10 \rightarrow 11 \rightarrow 00 \\ &\qquad\qquad\qquad\qquad\qquad\qquad \text{(counting up);} \\ &\text{for } M=1: Q1, Q0 = 00 \rightarrow 11 \rightarrow 10 \rightarrow 01 \rightarrow 00 \\ &\qquad\qquad\qquad\qquad\qquad\qquad \text{(counting down).} \quad (1) \end{aligned}$$

This definition is equivalent to the two state tables of Fig. 2(a), defining the future states $Q1+$ and $Q0+$.

B. Ordered Binary Decision Trees and Diagrams

We define a *complete (*or *canonical) binary decision tree* as a tree for n variables having 2^n branches corresponding to the 2^n possible input states; for the tree of Fig. 2(b), representing $Q1+$, we have $n=3$ and $2^3=8$. Each test element of the tree is represented by a diamond and defined by a test variable: it has a single input, a "true" output (test variable equal to "1") and a "complemented" output (test variable equal to "0"), identified by a small circle. The leaf elements, represented as squares, define the output value of the given function ($Q1+$ in our example).

In our case, the use of Karnaugh maps for simplifying trees [8], [9] shows that no simplification of $Q1+$ is possible (Fig. 2(a): there is no block, i.e., no pattern formed by 2^m adjacent "0"'s or "1"'s). On the other hand, the Karnaugh map for $Q0+$ [Fig. 2(a)] reveals one block of four "0"'s and one block of four "1"'s, which gives us to the *minimal simplified tree* of Fig. 2(b), representing $Q0+$ and containing only two branches.

A more detailed analysis of the Karnaugh maps of Fig. 2(a) reveals two types of *blocks of blocks* (ST0 and ST1), representing subtrees of the tree of $Q1+$ [Fig. 2(b)]. It can be observed, moreover, that the function $Q0+$ is equal to the subtree $\mathrm{ST0} = Q0'$.

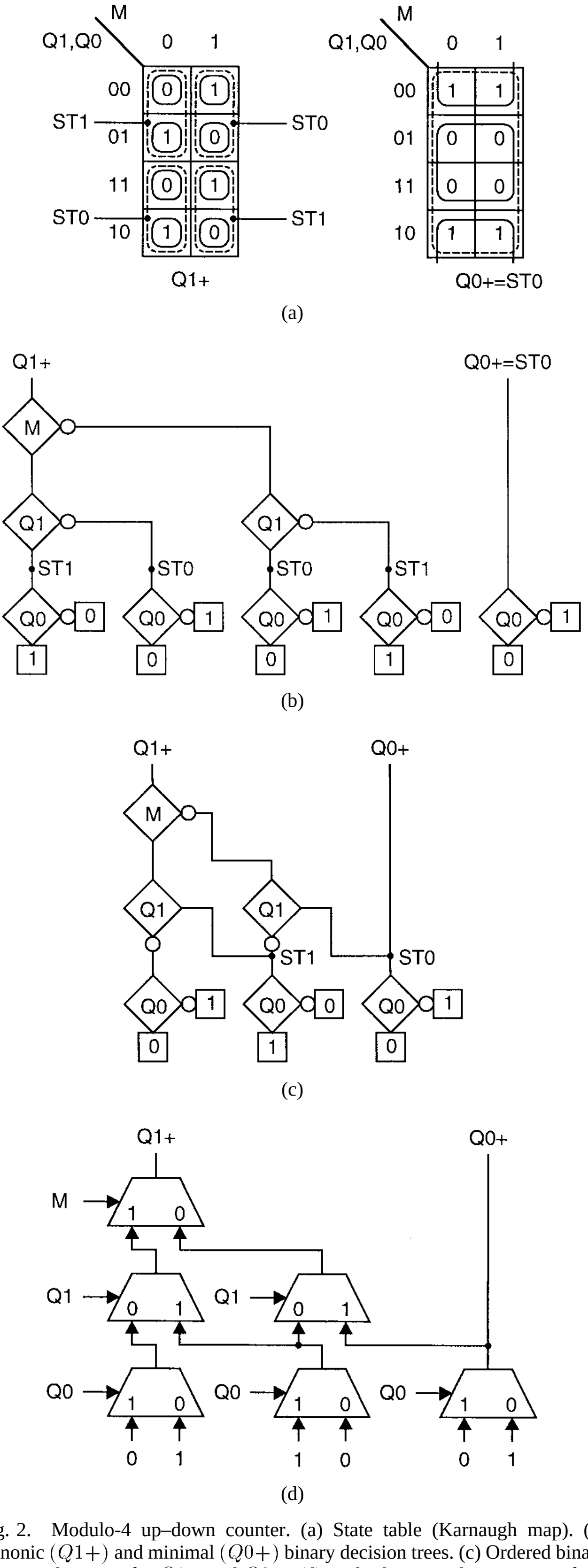


Fig. 2. Modulo-4 up–down counter. (a) State table (Karnaugh map). (b) Canonic $(Q1+)$ and minimal $(Q0+)$ binary decision trees. (c) Ordered binary decision diagrams for $Q1+$ and $Q0+$. (d) Multiplexer implementation of the OBDD's.

The sharing of identical subtrees implies the convergence of branches of the tree and its transformation into a new representation: the binary decision diagram (BDD). Finally, the sharing of a subtree (ST0) belonging to the two functions $Q1+$ and $Q0+$ and the permutation of the "0" and "1" outputs of certain diamonds lead us to the final diagram of Fig. 2(c), which represents a *forest of binary decision diagrams*.

In the above discussion, we have implied that the binary decision diagrams and trees were *ordered*, that is, characterized by a fixed position for the test variables: $Q0$ at the lower level, $Q1$ at the middle level, and M at the upper level. Using Bryant's notation [4], we will write

$$M < Q1 < Q0. \tag{2}$$

It can be observed that all logic systems, combinational or sequential, of n variables will require a cellular network of n rows. On the other hand, the minimal number of columns will depend on the simplification method adopted to obtain the ordered binary decision diagrams from the original specifications. For problems of up to six variables, the Karnaugh map allows a relatively simple manual computation [8], [9]. Beyond six variables, more complex analytical methods require the use of a computer [4], [5].

C. Hardware Implementation

Our design decision has been to implement directly the ordered binary decision diagrams on silicon, and to build our fine-grained basic cell around a test element (a diamond). Such an implementation is possible if one replaces each test element with a 2-to-1 multiplexer, keeps the same interconnection diagram, and assigns the values of the leaf elements to the corresponding multiplexer inputs [8]. Fig. 2(d) shows the direct multiplexer implementation of the up–down counter. The two state functions $Q1+$ and $Q0+$ are available at the outputs of the top multiplexers: the ordered diagrams of Fig. 2(c) are read bottom-up in Fig. 2(d).

IV. A New Field-Programmable Gate Array Based on a Multiplexer Cell

A. General Remarks

A simple examination of Fig. 2(d) allows us to identify the main features of the programmable cell, henceforth referred to as MUXTREE (for multiplexer tree).

- Each of the two inputs of the multiplexer (labeled "0" and "1") will be programmable. The input will be either a logic constant ("0" or "1") or the output of the multiplexer of one of the neighboring cells to the south, southeast, or southwest.
- The output of the multiplexer will be, therefore, connected to the inputs of the multiplexers in the neighboring cells to the north, northeast, and northwest.
- The realization of sequential systems requires the presence, in each cell, of a synchronous memory element, a D-type flip-flop, which will allow, in our example, to obtain directly the values $Q1$ and $Q0$ (instead of $Q1+$ and $Q0+$) needed for the display and for the retroaction of the secondary variables.
- Long-distance connections are necessary to connect a cell to any other cell in the array. In our example, the variable $Q1$ (itself obtained at the output of the mentioned flip-flop) must be brought back to the inputs of the multiplexers of the middle row of cells. This type of connection demands a system of universal buses, running through the entire array.

In brief, the heart of the cell remains the 2-to-1 multiplexer, optionally followed by a flip-flop. Inputs and outputs are programmable and can be connected either to immediate neighbors, according to a topology proper to binary decision diagrams (where information flows from the bottom to the top), or to faraway cells through a network of perfectly symmetric universal buses.

To facilitate the detailed description of the MUXTREE cell, we will separate it into two levels: the *logic level*, that is, the basic multiplexer and its immediate connections, and the *connection level*, that is, the bus network for faraway connections.

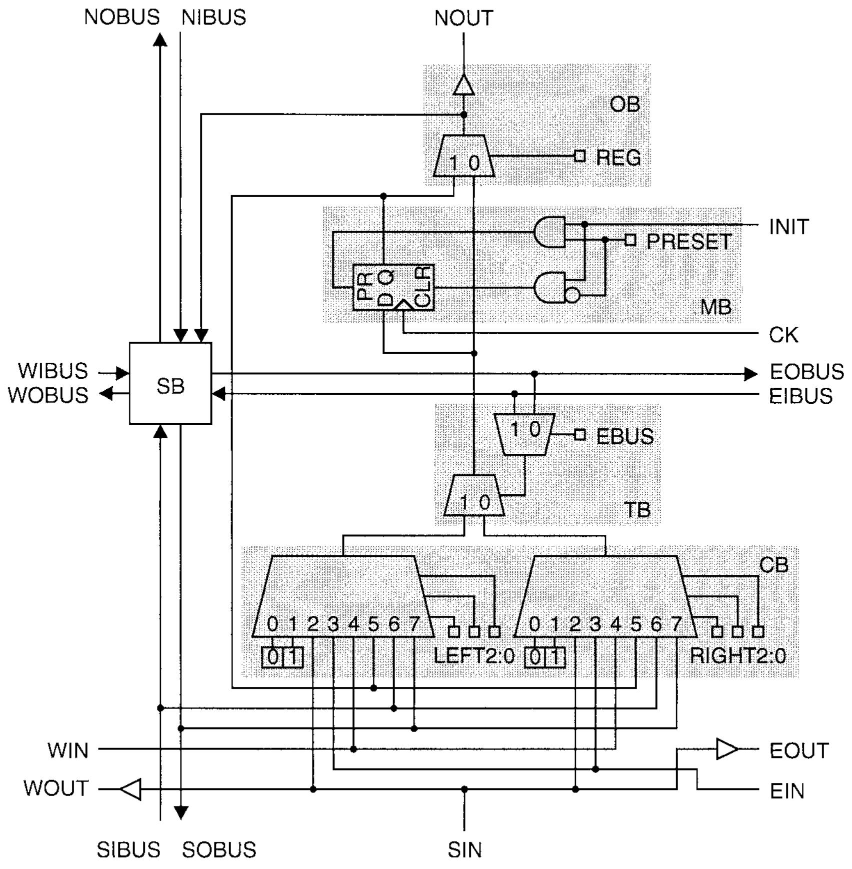
B. Description of the Logic Level

The MUXTREE cell (Fig. 3) is based on a 2-to-1 multiplexer (in the lower part of the test block TB) and a D-type flip-flop (in the memory block MB) for clocked sequential behavior. Connections to the inputs of the main multiplexer are defined using the 8-to-1 multiplexers of the connection block CB. The 6 bits LEFT2:0 and RIGHT2:0 select one out of eight inputs for the left and right branches of the main multiplexer. The second 2-to-1 multiplexer of TB selects one of the east buses (EOBUS, EIBUS) to control the main multiplexer. The 2-to-1 multiplexer of the output block OB allows the connection of the output of the main multiplexer or the output of the flip-flop to the north output (NOUT). A switch block SB, described in Section IV-C, provides interconnections between the input buses (NIBUS, EIBUS, SIBUS, WIBUS), as well as the output NOUT, and the output buses (NOBUS, EOBUS, SOBUS, WOBUS). Finally, the field-program bit REG (Fig. 3) controls the combinational or sequential behavior of the cell, while the field-program bit PRESET determines if an action on the INIT signal implies an asynchronous set or reset of the flip-flop.

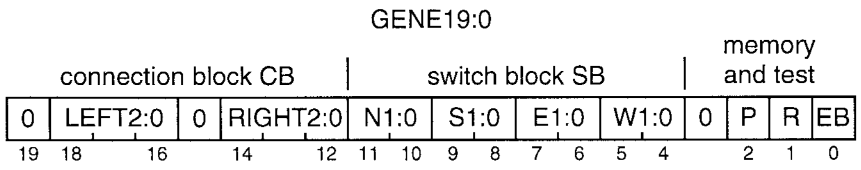
C. Description of the Bus Level and Global Representation

In order to implement long connections, the bus network includes one switch block SB per cell. Fig. 4(a) symbolizes the interconnection possibilities between the four input and four output oriented buses. All connections are possible, with the exception only of "U-turns." Fig. 4(b) shows the internal realization of the block. This realization, which also allows the north output (NOUT) to be connected to the four output buses, is realized using four 4-to-1 multiplexers. Each multiplexer is controlled by two field-program bits selecting one of the four possible inputs (the other directions input buses and the north output NOUT).

Fig. 11(b) summarizes the input and output signals of the MUXTREE cell. In order to facilitate the hexadecimal representation of its gene, the 17 field-program bits of the cell are organized as a 20-bit data GENE19:0 (Fig. 3).



(a)



(b)

Fig. 3. MUXTREE cell. (a) Detailed architecture (the switch block SB is described in Fig. 4). (b) The 20-bit data GENE19:0 with P = PRESET, R = REG, and EB = EBUS.

D. Application: Modulo-4 Up–Down Counter

It can be immediately seen that the counter described by the ordered decision diagrams of Fig. 2(c) can be realized using an array of three lines and three columns (that is, by a total of nine MUXTREE cells).

Fig. 2(c) is modified and leads to the final diagram [Fig. 5(a)] where we have the following:

- the use of two D-type flip-flops, symbolized with a square around the corresponding diamonds, generates the variables $Q1$ and $Q0$ in place of $Q1+$ and $Q0+$;
- a cell is completely unused, while another cell is used exclusively as a direct connection (transmission of $Q0+$).

Using the bus level notation defined in a detailed description of the MUXTREE cell [11], we can then draw the connection layout of the counter [Fig. 5(b)].

Combining the information of Fig. 5(a) and (b) allows us to compute manually the 17 control bits of each gene, according to the format defined in Fig. 3, and finally produces the *genome* of Fig. 1(a). For all indifferent conditions (Φ-conditions), the corresponding bits were set to "0."

E. Conclusion

Thanks to the conception of the new family of field-programmable gate arrays (FPGA's) MUXTREE, we are currently able to realize any given logic system using a completely homogeneous cellular network. This realization is simplified by the direct mapping of the ordered binary decision diagrams onto the array. Thus, we have satisfied the general hypothesis on the environment described in Section II-A, as well as the first feature of the Embryonics project, that is, multicellular organization [Section II-B and Fig. 1(a)].

The manual computation of the genes can be very awkward. Two software tools (running on an Apple Macintosh) have been devised to overcome this problem. The first is a graphical editor, capable of determining the individual 20-bit genes for the MUXTREE implementation of any given function

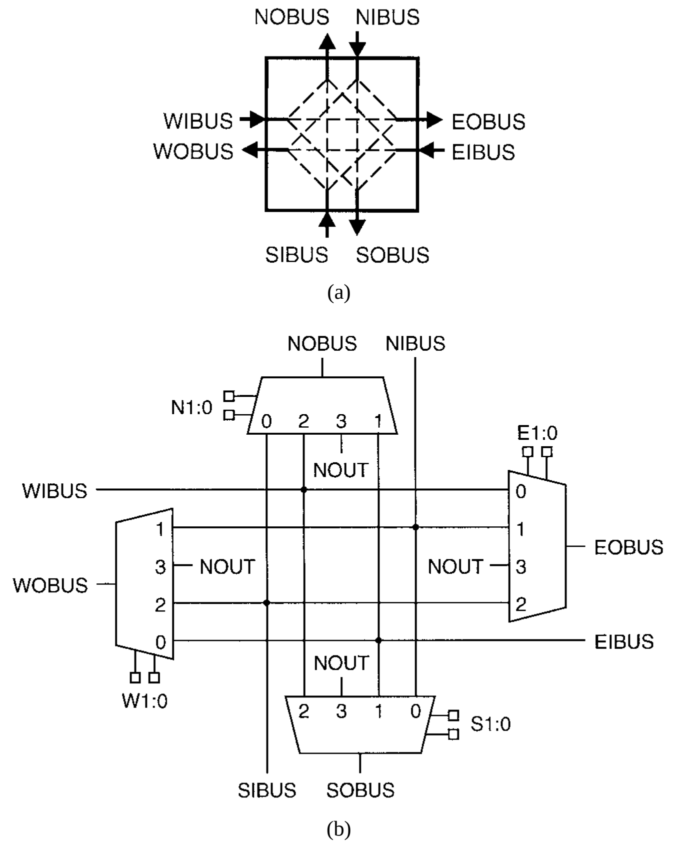


Fig. 4. The switch block SB. (a) Interconnection possibilities. (b) Detailed architecture.

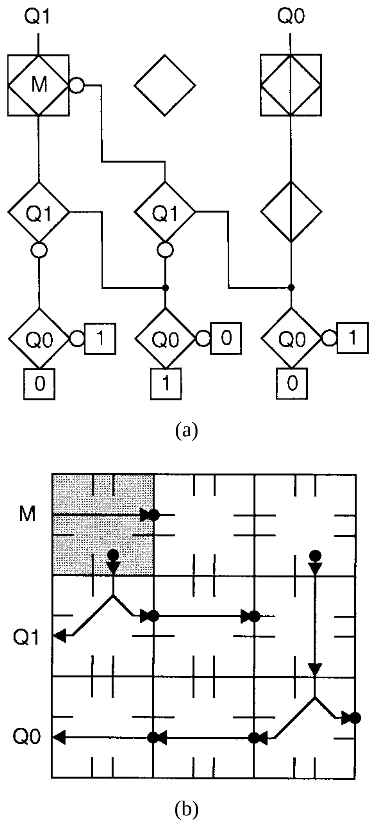


Fig. 5. Nine-cell implementation of the up–down counter. (a) Logic level and (b) bus level.

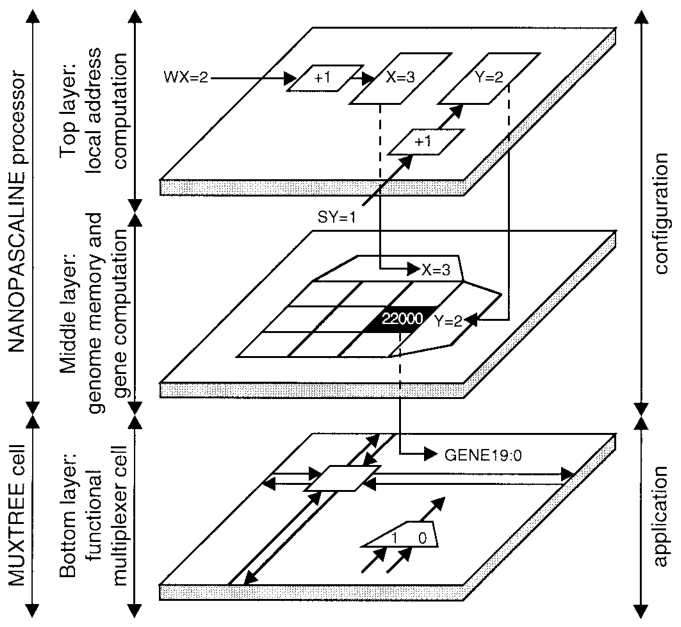

NANOPASCALINE processor
MUXTREE cell
Top layer: local address computation
Middle layer: genome memory and gene computation
Bottom layer: functional multiplexer cell
configuration
application
WX=2
+1
X=3
Y=2
+1
SY=1
X=3
22000
Y=2
GENE19:0
1 0

Fig. 6. Hierarchical overview of the three layers and the corresponding block schemes of the final embryonic cell.

represented by an OBDD. The second is a numerical simulator, allowing the functional verification of the implementation.

To this date, two physical realizations of arrays of MUXTREE cells have been implemented. The first consists of 20 programmable ACTEL 1020A circuits, realizing a homogeneous surface of $15 \times 16 = 240$ cells. The second, realized in collaboration with the CMP-Grenoble (Circuits multi projets, Prof. B. Courtois), is an integrated circuit MUXCHIP consisting of $8 \times 8 = 64$ cells. The chip was fabricated at an SGS-Thomson Microelectronics facility [6].

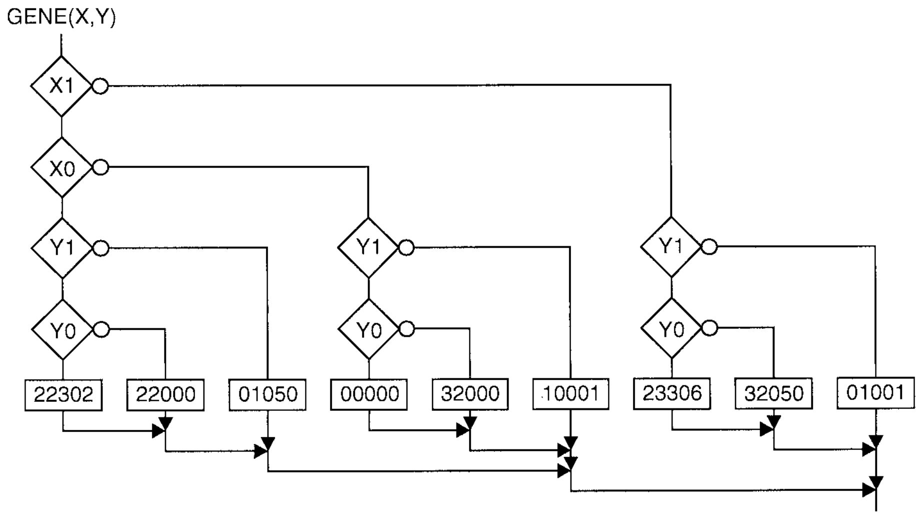
V. Cellular Differentiation: Genome Interpretation

A. A Hierarchical Overview

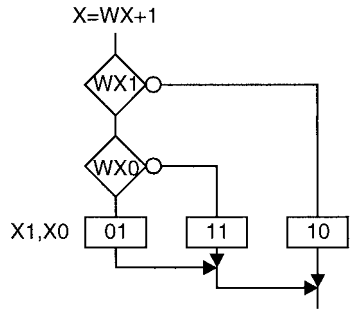
Rather than describing our final cell as a whole, we will, for the sake of simplicity, decompose it in three components or *layers* (Fig. 6) and describe each of these layers separately. The top layer is used to compute the local coordinates X, Y of the cell, usually by adding 1 to the coordinate WX of the western neighbor and to the coordinate SY of the southern neighbor. The middle layer contains a random access memory (RAM) and is used to store the entire genome: the memory stores a single gene per address, i.e., per pair of coordinates (X, Y). Finally, the selected gene controls the bottom layer, which contains the functional cell (i.e., the MUXTREE cell defined in the preceding section).

During normal operation, the top (address computation) and middle (genome) layers are fixed and the values they compute (X and Y coordinates, gene GENE19:0) are constant. We will say that these two layers, which are in fact *configuration layers*, are idle during operation. Modifications can only be effected at initialization (programming of the FPGA) or during the self-repair and self-replication processes.

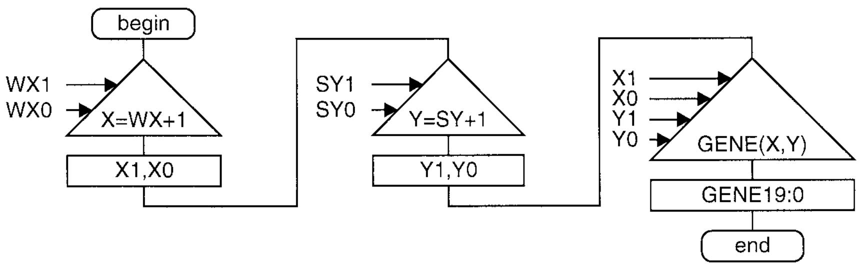
On the other hand, the bottom layer is the operational part or *application layer*. Its values usually change with time.



(a)



(b)



(c)

Fig. 7. Computation and genome representation. (a) Gene computation, (b) X coordinate computation, and (c) up–down counter genome.

B. Microprogrammed Realization

In all living beings, the genome is executed sequentially by a chemical processor, the *ribosome*. Drawing inspiration from this biological process, we will use a microprogram to compute the local coordinates X and Y and to extract from our artificial genome, as a function of the coordinates, the gene GENE19:0.

The artificial genome [for our example, that of the up–down counter of Fig. 1(a)] can be considered as a *truth table* (or *look-up table*) whose input states are the coordinates or addresses X and Y, and whose output states are the genes GENE19:0.

If we express the values of the coordinates X and Y in pure binary code, using the logic variables $X1$, $X0$, $Y1$ and $Y0$, we may apply the traditional simplification methods for binary decision trees [8], [9], and we finally obtain the structured subprogram GENE(X, Y) of Fig. 7(a), represented symbolically in the program of Fig. 7(c).

Assuming that the mother cell has coordinates $X, Y = 1, 1$, we observe the following (Fig. 6):

- each cell computes its horizontal coordinate X as a function of the horizontal coordinate WX of its western neighbor;
- each cell computes its vertical coordinate Y as a function of the vertical coordinate SY of its southern neighbor;
- the sequence of horizontal coordinates X is incremented and limited to a cycle $1 \rightarrow 2 \rightarrow 3 \rightarrow \cdots \rightarrow x$ by the width x of the cellular array;
- the sequence of vertical coordinates Y is incremented and limited to a cycle $1 \rightarrow 2 \rightarrow 3 \rightarrow \cdots \rightarrow y$ by the height y of the cellular array.

We can then write two subprograms realizing the expressions

$$X = (WX + 1) \bmod x \tag{3}$$
$$Y = (SY + 1) \bmod y \tag{4}$$

where $x = y = 3$ in the example of the up–down counter [Fig. 1(a)].

If we express the coordinates X and $WX \in \{1, 2, 3\}$ in pure binary code, using the logic variables $X1:0$ and $WX1:0$, the simplification of the binary decision tree generates the structured subprogram of Fig. 7(b). An identical computation can be performed on the $Y = Y1:0$ coordinate described by (4).

Merging the subprogram GENE(X, Y) [Fig. 7(a)] and the two subprograms which implement the increment of X as in (3) and of Y as in (4) generates the final structured microprogram or genome for the example of the up–down counter [Fig. 7(c)].

C. NANOPASCAL: A High-Level Language for Structured Microprogramming

We will now define a programming language particularly well suited for the description, the interpretation and the duplication of the genome. This language, called NANOPASCAL for historical reasons, consists in fact of an absolutely minimal subset of the MODULA-2 language [15].

The NANOPASCAL language is described by the *syntactic diagram* of Fig. 8(a), where we can count seven distinct terminal symbols (ovals), which make up the instructions of the language

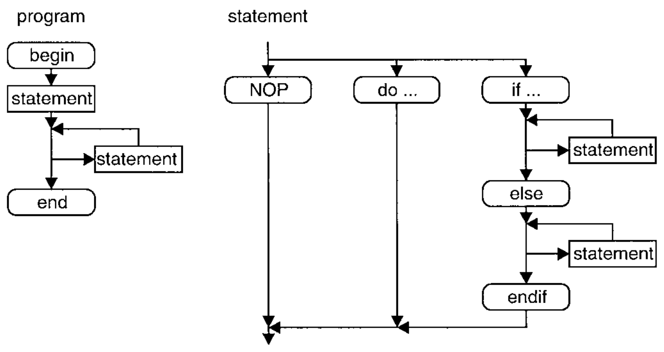
$$\{\mathbf{begin}, \mathbf{end}, \mathbf{NOP}, \mathbf{do}\ldots, \mathbf{if}\ldots, \mathbf{else}, \mathbf{endif}\}. \tag{5}$$

The pseudo-instruction **begin** is in fact never executed, and simply indicates the start of the program. The instruction **end** forces an unconditional jump to address "0" (this is in fact the only jump implemented by the language). The **NOP** (*No operation*) instruction represents the execution of a neutral operation. The assignment **do**... realizes the synchronous transfer REG$j \leftarrow$OUT of a constant OUT in a register REG of address j. Since no jumps are allowed by the language, all of the instructions making up the conditional construct **if** a **then** P **else** Q (where a is a test variable and P and Q are assignments) are read, and the execution of P or Q depends on the value of a signal EXEC (for EXECUTE) which, in turn, depends on the preceding values of the test variable a.

As an example, Fig. 8(b) shows the shape of the mnemonic program GENOME, realizing choosen parts of the final microprogram [Fig. 7(a) and (b)] in the syntax of the NANOPASCAL language.

Writing the microprogram for a relatively large genome can be a bothersome endeavor. Therefore, we have developed two software tools which successively allow the following:

- the compilation, starting from the truth table of the genome (Fig. 1(a), for example), of the complete NANOPASCAL mnemonic program, including the computation of the X and Y addresses [Fig. 8(b)];



(a)

```
begin
if WX1
    if WX0
        do X <- 1
    else
        do X <- 3
    endif
else
    do X <- 2
endif
if SY1
 ⋮
endif
if X1
    if X0
        if Y1
            if Y0
                do GENE <- 22302
            else
                do GENE <- 22000
            endif
        else
            do GENE <- 01050
        endif
    else
     ⋮
    endif
endif
end
```

(b)

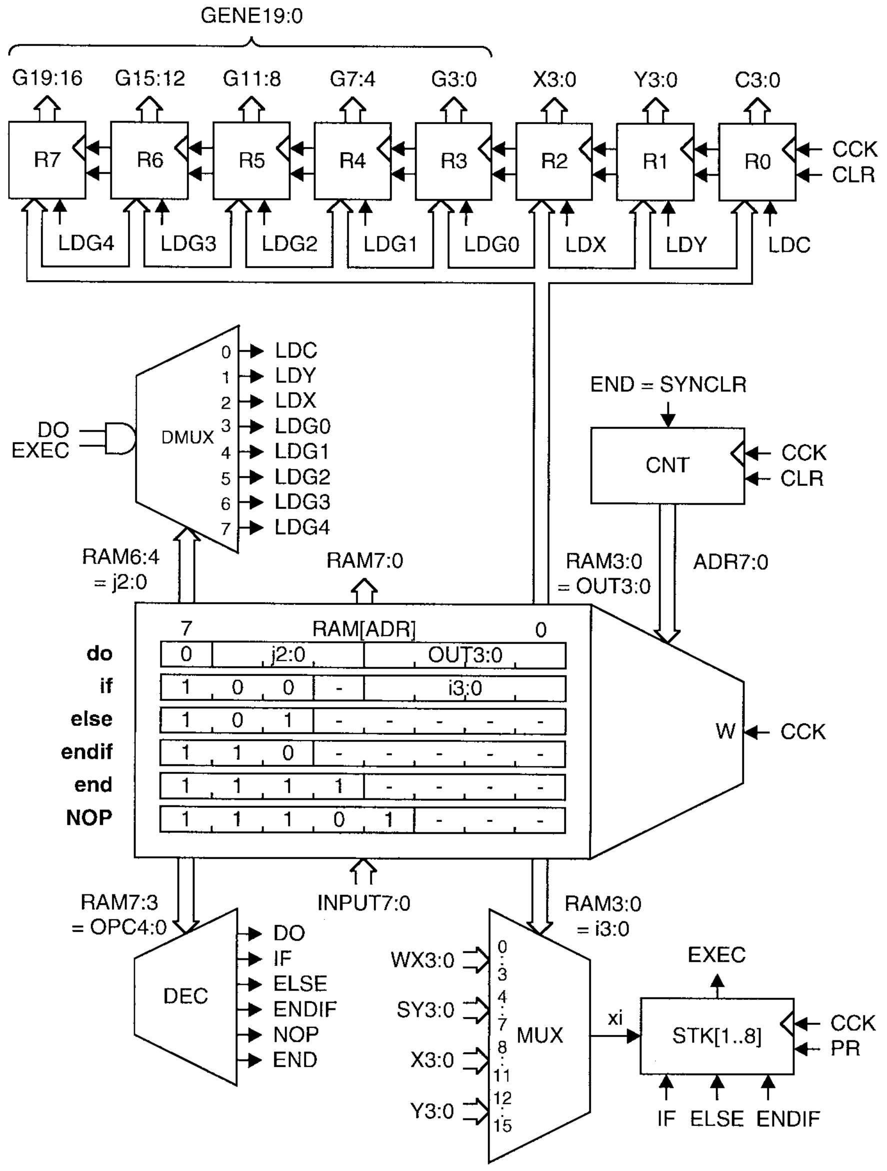
Fig. 8. NANOPASCAL language. (a) Syntactic diagram and (b) microprogram GENOME.

- the translation of the above-mentioned mnemonic program into a binary program directly executable by the interpreter (Section V-D).

D. NANOPASCALINE: An Interpreter for the NANOPASCAL Language

Fig. 9(a) suggests a possible format and operating code (OPC) for the six types of executable instructions of the NANOPASCAL language defined in (5). These six types of instruction are executed by a *binary decision machine* or *interpreter* of the NANOPASCAL language (NANOPASCALINE). It consists mainly of the following elements [Fig. 9(a)].

- A program memory RAM of 256 words of 8 bits.
- An address counter (CNT), whose output is the memory address ADR; ADR is incremented at each clock period (there are no jumps, with the exception of the instruction



(a)

instruction	operation	description
if xi	PUSH	STK[1] <- xi, STK[2..8] <- STK[1..7]
else	COMPLEMENT TOP	STK[1] <- STK[1]'
endif	POP	STK[1] <- STK[2], STK[2..7] <- STK[3..8], STK[8] <- 1
do ...	HOLD	NOP
NOP	HOLD	NOP
end	HOLD	NOP

(b)

Fig. 9. NANOPASCALINE: NANOPASCAL interpreter. (a) Detailed architecture with format and operation code (OPC) for the six instructions of the language. (b) Stack operation table.

end which assures the jump to the address ADR $= 0$ through the signal SYNCLR $= 1$).

- Eight assignment registers of 4 bits each ($R7 \cdots R3$: GENE19:0; $R2$, $R1$: coordinates X, Y; $R0$: display). The selection of one register out of eight is made by a demultiplexer DMUX and will only be effective if both the following two conditions are met: 1) an instruction **do**... (signal DO=1) is being decoded and 2) the order of execution EXEC=1 is set. This last signal is crucial, and its value depends on the sequence of values of the test variable xi: the computation of the value of EXEC is performed by the stack STK described below.
- A stack STK of eight levels of 1 bit for the computation of the signal EXEC. If we call STK[1] the variable of the

top level of the stack, and STK[2, $\cdots$,8] the values of the levels below, then the table of Fig. 9(b) describes the global operation of the stack. The logic product

$$\begin{aligned}\mathrm{EXEC} = \mathrm{STK}[1]\cdot\mathrm{STK}[2]\cdot\mathrm{STK}[3]\cdot\mathrm{STK}[4]\cdot\mathrm{STK}[5]\\ \cdot\mathrm{STK}[6]\cdot\mathrm{STK}[7]\cdot\mathrm{STK}[8] \qquad (6)\end{aligned}$$

which controls the execution of the assignment instructions do REGj ←OUT depends therefore on the succession of values of the test variable xi.

- A multiplexer MUX which selects one out of 16 test variable xi.
- A decoder DEC, controlled by the five bits of the operating code OPC4:0, which will generate the signals controlling the address counter CNT (signal END), the demultiplexer DMUX (signal DO) and the STK (signals IF, ELSE, and ENDIF).

In conclusion, our NANOPASCALINE is limited to the computation of artificial organisms composed of at most $16 \times 16 = 256$ MUXTREE cells.

E. Conclusion

Our choice for the execution of the NANOPASCAL language is thus the following: the interpreter executes linearly all the instructions of the microprogram by incrementing the address ADR of the memory. The synchronous assignments REGj ←OUT are executed only if the signal EXEC, generated by the stack, is one. This choice provides two main advantages:

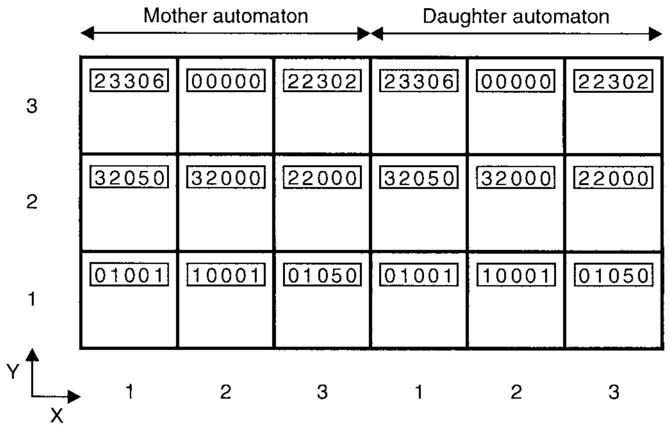
- the time of execution of the microprogram GENOME is constant and the same for all the cells;
- the duplication of the microprogram of a mother cell into an daughter cell can be executed in parallel with its interpretation (cellular division).

The time of execution of such a program is obviously greater than that of an equivalent program with jumps. This drawback is less important in our case, since the GENOME microprogram is active only during the configuration of the FPGA, and not during its operation.

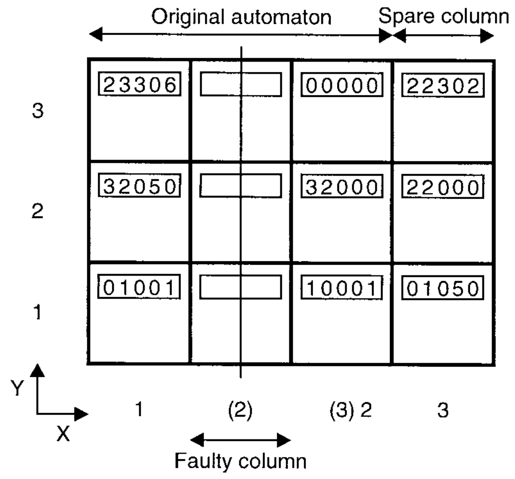
VI. Cellular Division: Duplication of the Genome

The duplication of the GENOME microprogram is accomplished automatically, in parallel with its interpretation. A register, controlled by the configuration clock CCK, is associated with the RAM in the NANOPASCALINE interpreter of each cell. At each rising edge of CCK, an instruction of the GENOME microprogram is copied into the cell through one of the SDATA or WDATA inputs selected by a physical jumper, manually set before start-up [Fig. 11(b)]. The copy of the instruction is then available on both of the NDATA and EDATA outputs.

The GENOME microprogram is thus duplicated in permanence, resulting in a great simplicity of wiring and an excellent reliability, since an eventual transient fault (copy error) during a cycle will be corrected in the next cycle.



(a)



(b)

Fig. 10. Properties of the up–down counter. (a) Self-replication and (b) self-repair.

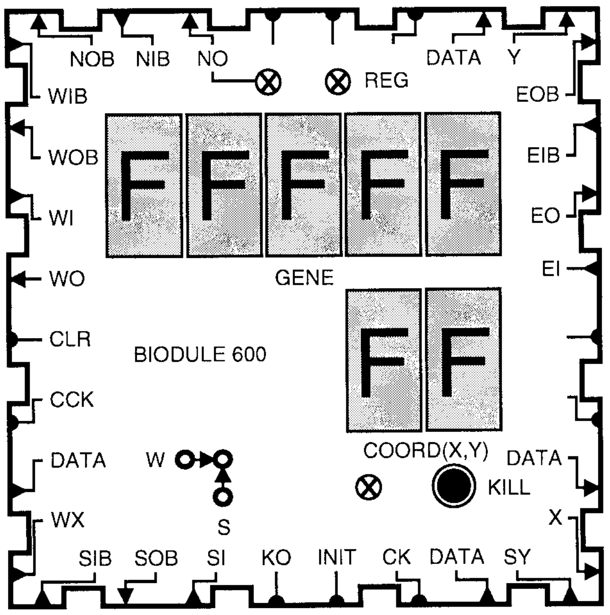
In the symbol of the NANOPASCALINE interpreter [Fig. 11(b)], KO = 1 characterizes a faulty cell.

VII. Self-Replication and Self-Repair Properties

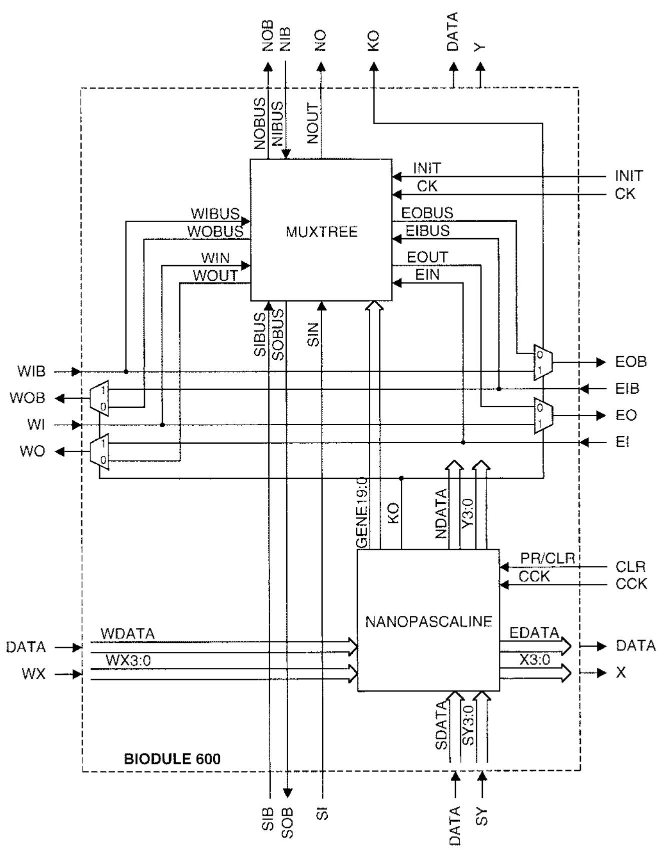
A. Self-Replication

The self-replication of an artificial organism, for example the up–down counter of Fig. 1(a), rests on two hypotheses: 1) there exists a sufficient number of spare cells (unused cells at the right hand side of the array, at least three columns of three cells for our example) and 2) the calculation of the coordinates produces a cycle [$X = 1 \rightarrow 2 \rightarrow 3 \rightarrow 1$ in Fig. 7(b)].

As the same pattern of coordinates produces the same pattern of genes, self-replication can be easily accomplished if the microprogram GENOME, associated to the homogeneous network of cells, produces several occurrences of the basic pattern of coordinates [$X = 1 \rightarrow 2 \rightarrow 3$ and/or $Y = 1 \rightarrow 2 \rightarrow 3$ in Fig. 1(a)]. In our example, the repetition of the horizontal coordinate pattern, i.e., the production of the pattern $X = 1 \rightarrow 2 \rightarrow 3 \rightarrow 1 \rightarrow 2 \rightarrow 3$ [Fig. 10(a)], produces one copy, the *daughter automaton*, of the original or *mother automaton*. Given a sufficiently large space, the self-replication process can be repeated for any number of specimens, both



(a)



(b)

Fig. 11. BIODULE: demonstration artificial digital cell. (a) The front panel and (b) detailed architecture.

in the X and the Y axes. For a given cell, the dimensions of the artificial organism are limited in the first place by the coordinate space ($X = 0 \cdots 15$ and $Y = 0 \cdots 15$, that is, at most 256 cells in our implementation), and then by the dimensions of the RAM which will contain the GENOME microprogram (256 words of 8 bits in our case).

B. Self-Repair

Even if our long-term objective is the development of very large scale integrated circuits, we have started by realizing a demonstration system, based on *artificial digital cells* called BIODULES [Fig. 11(a)]. In this context, the existence of a fault is decided by the human user by pressing the KILL button of a cell. Therefore, fault detection and fault location, two features which will be indispensable in the final system, where they will be implemented using BIST (built-in self-test) techniques [1], [11]–[13], are not present in the BIODULES.

To implement self-repair, we have chosen, favoring simplicity, the following process [Figs. 10(b) and 11(a)]:

- pressing the KILL button identifies the faulty cell;
- the entire column to which the faulty cell belongs is considered faulty, and is deactivated (column $X = 2$ in Fig. 10(b) in the example of the up–down counter);
- all the functions of the application layer (MUXTREE) and of the configuration layers (NANOPASCALINE) of the column are shifted by one column to the right.

Obviously, this process requires as many spare columns, to the right of the array, as there are columns to repair [one spare column in the example of Fig. 10(b)]. It also implies some modifications to the application and configuration layers, so as to add the capability of jumping the faulty column and shifting to the right all or part of the original cellular array [Fig. 11(b)].

Finally, it should be mentioned that the final BIODULE [Fig. 11(a)] also realizes the series-parallel conversion of the data (DATA) and of the coordinates (X, Y) at the input, and the opposite conversion at the output. This conversion minimizes the number of connections between each BIODULE.

VIII. Conclusion

A. Results

The first result of our research is the development of a new family of FPGA's called MUXTREE and based on a fine-grained cell containing a multiplexer with one control variable. The original features of this FPGA are essentially the following:

- a completely homogenous organization of the cellular array;
- an integration of the routing into each cell, both for the short- and long-distance (bus) connections;
- a cell architecture allowing the direct mapping of binary decision diagrams onto the array.

The FPGA satisfies both the general hypothesis (Section II-A) and the first feature of the Embryonics project, that of multicellular organization (Section II-B). Two physical implementations have been realized: a prototype array of 240 cells, itself implemented using FPGA's of the ACTEL family, and a complementary metal–oxide–semiconductor (CMOS) integrated circuit containing 64 cells.

The second result is the realization of a quasi-biological cell based on an application layer (the MUXTREE cell) and two configuration layers computing, as a function of the local coordinates and of the genome, the specific gene controlling the application layer MUXTREE. The configuration layers are realized using a binary decision machine called NANOPASCALINE, which interprets the GENOME microprogram. The three layers of application and of configuration are finally embedded into a complete cell, implemented using an FPGA and a RAM, and then built as a demonstration module called BIODULE. We then show that an array of BIODULES satisfies the second and third features of the Embryonics project (Sections II-C and -D: cellular differentiation and division) and that it is endowed with the properties of self-replication and self-repair.

The interest of self-repair is immediately obvious, as this property allows the repair of isolated faults, for example, the fault of a single cell. The importance of self-replication is less evident, and can be justified by the following:

- the complete reconstruction of a device, in case of massive faults;
- the automatic realization of homogeneous 2-D cellular automata, by repetition of the same basic cell;
- the simplicity of moving a device in the cellular array by the simple alteration of the coordinates of the mother cell.

B. Future Perspectives

The main drawback of the BIODULE cell is the lack of balance between the application layer (MUXTREE), which realizes the universal function with a single variable, and the configuration layers (NANOPASCALINE), which store and interpret a rather complex microprogram. The development of a new coarse-grained FPGA cell will aim at correcting this imbalance [11]. The second drawback of the BIODULE, which is primarily a demonstration system, is the absence of a system for the detection and location of faults. While such a system could be implemented using relatively well-known techniques, we are trying to exploit the peculiar features of FPGA's (homogeneous cellular organization, possibility of reconfiguration) to obtain a BIST realization capable of being embodied into the integrated circuit which will finally have to possess all the computational power of an array of BIODULES [1], [11]–[13].

C. Historical and Theoretical Perspectives

The early history of the theory of self-replicating machines is basically the history of John von Neumann's thinking on the matter [7], [14]. Von Neumann's automaton is in accord with the general hypothesis outlined in Section II-A, as each of its elements is a finite state machine with 29 states. In his historic work [14], von Neumann successively showed that a possible configuration (a set of elements in a given state) of his automaton can implement a *universal constructor* endowed with the three following properties: constructional universality, self-replication of the universal constructor and self-replication of a universal calculator. In biology, the *cell* is the smallest part of a living being containing the complete blueprint of the being, the *genome*. On the basis of this definition, it can be shown that von Neumann's automaton is a *unicellular organism*, since it contains a single copy of the genome, i.e., the description of the universal constructor and computer [11]. Each element of the automaton is thus a part of the cell, or, in biological terms, a *molecule*. Von Neumann's automaton, therefore, is a *molecular automaton*, and universal construction and self-replication are complex processes, as they are caused by the interaction of thousands of elements, the molecules, each one realized by a finite state machine with 29 states.

Arbib [3] was the first to suggest a truly "cellular" automaton, in which every cell contains a complete copy of the genome, and a hierarchical organization, where each cell is itself decomposed into smaller and regular parts, the "molecules." Following this concept, the automaton we propose is a multicellular organism, as each of its elements contains a copy of the genome [nine copies in the case of the up–down counter of Fig. 1(a)]. Each element of our automaton is thus a *cell* in the biological sense, and our automaton is truly a *multicellular automaton*. Self-replication and self-repair are straightforward processes, as the BIODULE cell has been conceived especially to carry out globally the operations of cellular differentiation and division.

The property of *universal computation*, that is, the possibility of realizing, repairing, and replicating a universal Turing machine, can theoretically be verified with the BIODULE cell. But the implementation of such a machine will be strongly simplified by the creation of a second generation of cells, coarse-grained [10].

The property of *universal construction* poses problems of a different nature, since it requires (always according to von Neumann) that BIODULE cells be able to implement artificial organisms of any dimension. The finite dimensions of our cells (memories, registers, etc.) are, for the moment, preventing us from meeting this requirement, a challenge which remains one of our main concerns and which could be solved, according to Arbib's suggestion, by decomposing a cell into molecules.

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