L-Systems and Artificial Chemistry to Develop Digital Organisms

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Abstract—**With the purpose of populating virtual worlds with various adapted artificial organisms, we propose an ontogenetic and phylogenetic hybrid model to generate complete organisms possessing metabolism, morphology, and behavior from a single initial cell. The initial purpose of our work is to generate organisms that are thereafter used to define complete organisms. In this paper, we introduce a bio-inspired cellular developmental model that links different approaches of ontogenesis systems: grammatical and cell chemistry approaches. Thus, we propose an alternative to parametric L-systems (*APL-systems*) in order to simulate morphogenesis of organisms according to their internal states. The developed organisms have a metabolism using environmental substrates to grow and to act. Moreover, they are able to exhibit almost perfect self-healing characteristics afterwards or even during their development.**

Keywords- ontogeny; phylogeny; metabolism; evolutionary parametric L-systems; cell lineage

I. INTRODUCTION AND MOTIVATIONS

A number of different models exist for the creation of artificial creatures. These models use different levels of abstraction to produce organisms of various shapes and sizes. Whereas, phylogenetic approaches [1], [2], [3] attempt to evolve sophisticated behaviors through the simultaneous evolution of the brains and bodies of organisms in a 3-D simulated world, ontogenetic approaches [4], [5], [6], [7] aim to simulate the cellular development of organisms from a single element: a cell. The purpose of this subfield of artificial life, called artificial embryogeny, is to build on the mechanisms deployed during the growth of living organisms to produce more complex artificial organisms and to propose to the evolutionary robotics field new prototypes capable of self-modeling, self-repairing and self-assembly.

Furthermore, the previous work in artificial ontogeny falls into two broad categories [8], [9]: the grammatical approach [10], [11], [12], originated by Lindenmayer [13] and the cell chemistry approach [14], [15], [16], [17], [18], that draws inspiration from the early work of Turing [19]. Grammar based techniques are convenient for describing cell lineage[1] and genetic control of cell division [20]. These systems use production rules to sequentially modify symbols which represent organisms, and are able to create realistic-looking models of biological structures.

Cell chemistry approaches generally utilize lower level representations and are more strictly motivated by the biological mechanisms of development such as: diffusion, reaction-diffusion, expression and regulation of genes, metabolism, genetic regulatory networks, differentiation, cell division, etc. We argue that development models based on these mechanisms, in particular genetic regulatory networks, take into account more elementary phenomena than those proposed by the grammatical approach, and that generally they provide more expressive encodings (the size of the genotype is smaller than that of the phenotype). However, as Dellaert and Beer [21] note, the genetic operators are more difficult to define and the loss of convergence performance is not compensated by the potential gain of expression. In addition, within the framework of the development of neural networks for example, grammatical approaches are powerful.

Thus, we propose in this paper a unified model based on these two approaches to take advantage of both. As a grammatical approach, L-systems are considered to be an appropriate formalism for describing many growth processes in organisms [22]. They constitute an adequate genetic representation for studies which simulate natural morphological evolution. They allow a necessary and very suitable distinction between genotype and phenotype, and provide a well-defined process (morphogenesis) for generating the latter from the former. Repetition and regularity, intrinsic concepts of L-systems, are also necessary ingredients for natural morphogenesis. In addition, many studies have successfully explored the evolution of these systems notably for the construction of models which best describe natural target structures. We cite: the development of plants and flowers [12], [23], modeling the blood vessels of the eye [24] or proteins [25], evolutionary neurogenesis [10], [26] and also the generation of artificial organisms [27] and real robots [28]. All these reasons motivate us to take advantage of the flexibility of evolutionary L-system in a unified cellular developmental model.

So, in order to generate whole organisms from a single cell and possessing a morphology, a metabolism and a behavior, we propose an ontogenetic and phylogenetic hybrid approach. To develop initially multicellular organisms

[1] Lineage mechanisms are employed where an individual module determines its own fate using information passed from parent to child module.

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(the ontogeny part) which could be used thereafter to synthesize complete organisms (the phylogeny part), we propose, in this paper, a cellular development model unifying grammatical and cell chemistry approaches. To develop multicellular organisms, we simulate their metabolism, their cellular and environmental interactions, their morphogenesis and their evolution.

II. The Cellular Developmental Model

A. Environment

Our artificial multicellular organisms evolve in an embryonic environment represented by a 2-D toric grid similar to the one presented in [29]. A toric grid is obtained by connecting the opposite edges of a simple grid. In our model, a grid is a n*m matrix of sites or patches. Each patch can contain one or more substrates and zero or one cell. The environment contains different molecules that diffuse into the grid and cells that can perform different tasks.

1) Diffusion: The goal of the diffusion is to balance the quantities of substrates in the environment by minimizing the variations of the quantities of molecules between two neighbooring sites in the grid. The initial distribution of these substrates is achieved in a non-uniform way. Then, each substrate can diffuse towards the eight neighboring sites in the grid. Diffusion acts in two stages as illustrated in figure1:

- First, the substrate diffuses towards the four cardinal sites.
- Then, if the quantity of molecules is sufficient, the molecule diffuses on the diagonals.

If the quantity of substrates is not sufficient to spread evenly, the last diffusions of the stage of diffusion are chosen randomly. Moreover, if a site close to the currently computed diffusion site contains more substrates, the diffusion will not occur in this direction. Finally, no diffusion can occur between a cell and its environment in either direction. Only an action triggered by the cell may allow an exchange of substrates with the environment.

2) Cells: The cells evolve in the embryonic environment and more precisely in its diffusion grid. Each cell has:

- an internal state which represents the cell constitution of intracellular molecule and energy level,
- a set of sensors positioned on its membrane (described in section C),
- a list of capacities, in other words, a list of actions (described in section C),
- an action selection system allowing the cell to choose the best action to perform at every moment of the simulation (described in section C).

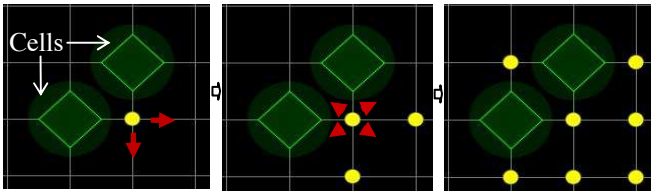


Figure 1. The diffusion of molecules in the environment.

B. Metabolism

With the purpose of simulating the metabolism of our artificial multicellular organisms, our model integrates a simplified artificial chemistry. Formally, an artificial chemistry is defined by a triple (*S; R; A*) [30], where:

- S is the set of all possible molecules,
- R is a set of collision or reaction rules representing the interaction among the molecules,
- and A is an algorithm describing the reaction vessel or domain and how the rules are applied to the molecules inside the vessel.

In our model, we define a simple chemical system consisting of a finite number of molecules that we call substrates. These substrates diffuse in the grid and have a unique name (A, B, C...) and several properties such as diffusion rate, color and type (intracellular or environmental). Substrates can interact via a finite set of reaction rules. To reduce complexity, the list of valid reaction rules is given explicitly when specifying the environment.

To simulate the dynamics of a population of molecules, we propose a stochastic molecular collision approach. A typical algorithm takes a sample of molecules randomly from the set S and checks whether a rule $r \in R$ can be applied. If so, the substrates are replaced by the right hand side substrates given by *r*. Otherwise, no rule can be applied and the process is repeated.

Note that these reaction rules can be triggered only inside the cells. Thus, when a cell carries out the substrate transformation action (described in next section), using some substrates, a reaction rule creates new substrates by consuming or producing energy. For example, the transformation $A + 2B \rightarrow C$ (-62), produces one unit of C substrate, with a unit of A substrate and two units of B substrate. This transformation consumes 62 units of vital energy. From a biological site of view, C can viewed as a waste from a cell which has the ability to convert A and B in energy.

The algorithm:

intracellular substrates: S= {s_1, s_2, …};

reactions: R= {r_1, r_2 , …};

begin

S' = all_possible_combinations_of (S);while (S'!=Ø)

n := random_number ([S]);

s_1 := random_substrate (S);

s_2 := random_substrate (S);

s_n := random_substrate (S);

if (∃ r = (a_1s_1, a_2s_2,…,a_ns_n⟶ a'$_1s_1$', a'$_2s_2$',…, a'$_ms_m$') ∈ R

and can_be_triggered (r))

then execute r;

update (S');

end while

end

The produced substrates can be rejected in the environment and thus another cell can absorb and transform them into other substrates. However, there are substrates which are only intracellular, i.e. they cannot be present in the environment. Therefore, the cell can neither absorb nor reject them into the environment but must produce them. Intracellular substrates can be used by the cell to perform specific actions like mitosis. Environmental substrates are used to produce intracellular ones, and to serve in the indirect intercellular interaction.

C. *Environmental and Cellular Interactions*

The cells can interact with the environment and also with other cells via an action selection system. To simulate this interaction, cells are provided with membranous sensors and can carry out various cellular actions.

Sensors are positioned on the membrane of each cell. They measure the amount of substrate available in its Von Neumann neighborhood. Thus, for each possible environmental substrate, the cell has an associated sensor. Only the sensor corresponding to a given substrate can measure its density. For example, in Figure 2, the cell has sensors for A and D substrates in the bottom corner. The results of the measure of the corresponding substrate densities are:

- 1 unit of A substrate,
- 2 units of D substrates because of the presence of two units of D substrate in the bottom corner of the cell.

Cellular actions, which we simulate in our model, are as follows:

1) Absorption or release of a substrate: These actions can trigger (or respectively, be triggered by) a transformation of substrates. They consume vital energy.

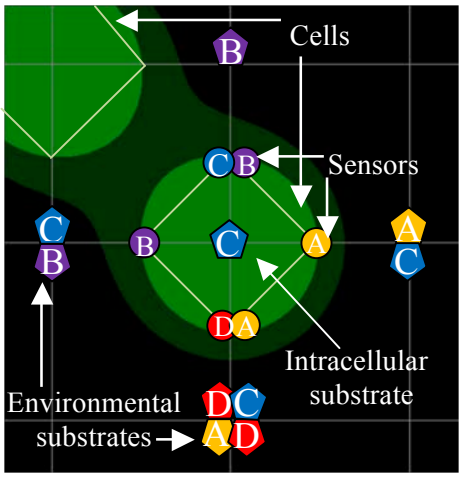


Figure 2. The artificial cell in its environment. It contains sensors (circles) to measure the density of valid substrates (pentagons) in its neighborhhod.

2) Substrate transformation: This action can trigger a stochastic collision of substrates within the cell. The collision of substrates will catalyze the formation of new substrates via a reaction rule. Thus, substrates are destroyed to create the right hand side substrates given by a rule. The substrate transformation consumes or produce energy.

3) Survival: This action allows the cell to await a signal from the environment or its internal state. It consumes vital energy.

4) Apoptosis: This action allows the cell to commit suicide if it does not have enough vital energy to survive. When a cell dies, all its constitution in substrates returns to the environment.

5) Mitosis: When a cell divides, it creates a new daughter cell towards the direction specified by the L-systems controlling the morphogenesis of the organism. Mitosis can be carried out by the cell, only if the following conditions are respected:

- The cell must have enough vital energy to divide.
- The quantities of certain substrates, necessary for the creation of a new cell, must exceed a certain threshold.
- The orientation of mitosis corresponds to a position non-occupied by another cell.
- During mitosis, intracellular substrates as well as vital energy are shared equitably between the mother and the daughter cell.

The action selection system allows the cell to select the best action to perform at every moment of the simulation. The action selection system of each organism is inspired by Pittsburgh [31], [32] classifier system. It uses a genetic algorithm for its evolution and its evaluation which is applied to a population of classifier systems. The individuals are thus a set of classifiers that are trying to solve the problem.

In our action selection system, each classifier has three parts: condition, action and priority:

- *The condition* serves to capture the signal coming from the environment or the internal state of the cell. It constitutes the cell sensors.
- *The action* part determines the action to be carried out by the cell if the corresponding condition is fulfilled.
- *The priority* allows to choose only one action if several classifiers are active at the same time. The higher the coefficient is, the more probable is the selection of the rule.

Each organism's action selection system works by using data from the cell sensors and matching them with the condition part of each classifier to produce a matching set. Once completed, it selects the best action to perform from this set, using the highest priority.

D. Morphogenesis

Genetic factors such as cell lineage are also important in the generation of developmental patterns. Some simple grammar-based systems, which only model cell lineage, are able to synthesize biologically relevant patterns [22]. The abilities of these models lie behind our inclusion of genetic mechanisms. L-systems are based on formal grammars with recursive applications of production rules. Starting from a canonical embryological start symbol, embryos are grown by simultaneously and repeatedly applying rules to the symbols in the developing embryo [8]. The possibility of simultaneous productions reflects the biological motivation of L-systems, intended to capture mitosis in multicellular organisms. Although our representation is somewhat different from the classical representation. Indeed, instead of using a symbol to represent a cell, we use a symbol to represent a cell division action, mitosis. Moreover, the L-systems that we use are an alternative to parametric L-systems.

1) L-systems alphabet: The alphabet we use is described in the table below. Uppercase characters are non-terminal symbols and denote the predecessors of rules, while lowercase letters represent terminal symbols where: "d" is a symbol denoting a mitosis action, the symbols "+" and "-" represent 2-D rotations determining the direction where the mother cell will put its daughters. Finally, the symbols "[", "]" are used to push and pop the current state.

TABLE I. THE L-SYSTEMS ALPHABET

Symbol	Function
A …Z	Non-terminals representing predecessors of rules.
d	Terminal denoting a cell mitosis action.
+,-	Terminals representing a two-dimensional rotation.
[,]	Terminals indicating branching.

2) APL-systems: To simulate the growth of our artificial multicellular organisms, we propose a variant of parametric L-systems, which we call APL-systems (Alternative Parametric L-systems). This extension to basic L-systems allows the simulation of the development of multicellular organisms according to the internal state of each cell. However, unlike traditional parametric L-systems, all production rules can be triggered. The predecessors of rules do not have pre-conditions unlike terminal symbols which do have pre-conditions. Figure 3 illustrates the difference between a traditional parametric rule and the new parametric rule defined in our APL-systems.

Formally, an APL-systems can be defined as an ordered quadruplet (V,Σ,ω,P), where:

- $V=V1\cup V2$ is the alphabet of L-systems, with V1 is the set of non-terminals and V2 is the set of terminals,
- Σ is an axiom,
- $\omega\in V$ is the axiom,
- $P\subset V\times(V1\times(V2\times C(\Sigma)))^*$ is a finite set of production rules. V is the set of the production predecessors, and $V1\times(V2\times C(\Sigma))$ is the set of the production successors where $C(\Sigma)$ is the set of preconditions.

Thus, the alphabet V and the set of the formal parameters are defined as in traditional parametric L-system. Nevertheless, the axiom ω and the set of productions P are redefined. The axiom is a non-parametric word and production rules do not have pre-conditions, but in fact the terminal symbols have pre-conditions.

A precondition $C(\Sigma)$ attached to a terminal means that it cannot be interpreted unless its precondition is fulfilled. For example, the terminal "d" cannot be interpreted in a cell mitosis action unless the mitosis conditions are respected by the cell concerned.

In this manner, this alternative will allow the interpretation of all the substrings, produced by the application of a production rule in a given generation, to the first terminal that does not fulfill its precondition. Whereas, in traditional parametric L-systems, all substrings generated by this rule would not be generated since the rule would not be triggered. In this way, all cells that wish to divide, during this generation, can do so if they fulfill their preconditions.

E. Evolution

To find the organism the most adapted to a specific problem, we use a genetic algorithm. Each organism is coded with a genome composed of two different chromosomes: the *APL-systems*, specifying the rules of growth, and the action selection system, that contains a rule list to apply available actions. The developed organism is evaluated at the end of the simulation.

III. EXPERIMENTS AND RESULTS

We have implemented our model in Java using a multi-threaded architecture. All cells are coded as independent threads running in parallel and sharing common resources: environmental substrates.

A. Development of Simple Organisms

We wish to synthesize multicellular organisms with the proposed development model. Self-similarity is used as a selection criterion for the morphological development of our multicellular organisms. We made this choice, to produce organisms similar to those of Karl Sims [1]. From the long view perspective, they could be immersed in a physical simulator and have a high level behavioral module enabling them to move in their environment.

In order to reduce the convergence time of the genetic algorithm and have a better comprehension of the results, the evolutionary experiments are conducted in two stages. Initially, we use a fitness favoring bilateral self-similarity. Then, once the best chromosomes describing cell lineage are found, the second stage consists in learning the organisms how to survive in the environment by developing their metabolisms.

1) Experiment 1: In this experiment, we studied the evolution of L-systems. The fitness of each individual consists in estimating the balance of the " weight" of its morphology. Thus, the sum of the absolute values of X-coordinates X, on the left (and on the right) of the vertical axis of the organism is calculated: X_g (X_d). The best fitness is allotted to the best balanced structures. In this way the goal of the genetic algorithm is to minimize the difference between X_g and X_d. The final formula of fitness is given by the following:

$$\text{fitness}=| X_g - X_d |.$$

In all experiments, we simulate 50 chromosomes per population, for 500 generations. Each experiment produced a different morphology. Figure 4 shows a range of morphologies that have emerged.

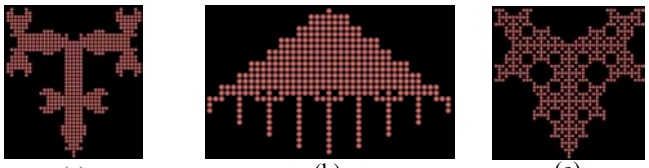
2) Experiment 2: The purpose of this experiment is to teach organisms how to survive in the environment by developing their metabolism, and to study their ability to use this metabolism for growth thanks to our *APL-systems*.

To develop our multicellular organisms, we define an artificial chemistry model with a set of molecules composed of 3 substrates:

- A and B: blue (yellow respectively) environmental substrate used by the organism as nutriment. These substrates have the property of spreading in the environment.
- C: red intracellular substrate produced by cells using environmental substrates and used as material of mitosis.

The grid size is 100*100. The diffusion property of the substrate will spread rapidly environmental substrates in the grid. The set of reactions of the artificial chemistry consists of two reactions, R={r1: A+2B→C (-10), r2: A→{} (+60)}.

The mother cell is initialized with some units of vital energy and C substrate (so it can survive in the early



(a) (b) (c)

Figure 3. morphologies emerged from the evolution of L-system chromosome.

moments of the simulations). The genetic algorithm uses tournament selection. Fitness function of the organism is divided into two sub-functions:

- The longevity of the organism, *length* (duration of the simulation in milliseconds)
- The size of the organism measured by the number of cells composing it, *nbCells*.

The final evaluation function is given by the formula:

fitness=a*length+b*nbCells/(a+b), with a= 10, b=100.

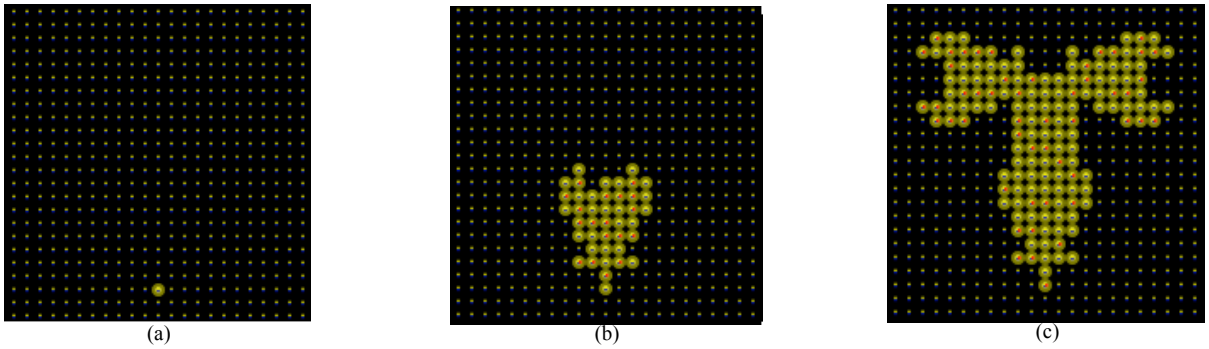
The coefficients of this formula are given to more take into account the final goal of the organism which is its capacity to develop than its metabolism. The goal of the genetic algorithm is to maximize this Fitness. The parameters of this algorithm are as follows:

- selection algorithm: 6 tournament selections with elitism,
- mutation rate: 5%; crossover rate: 65%,
- substitution algorithm: worst individuals,
- population size: 100 individuals.

Figure 4 shows the results of the best organism produced by evolution (a kind of "an artificial crayfish"). The development starts from a single mother cell and proceeds over discrete time steps. It stops either when a maximum time step is reached or when an individual embryo exhausts its initial energy. When the mother cell divides, it creates a new cell which is placed in the position specified by the APL-systems, controlling the growth of the multicellular organism. At the initial state, the expression of the APL-system starts with the axiom. The cell, at this state, uses its initial intracellular substrates to create its first daughter cells. Subsequently growth requires the acquisition of the environment resources.

In the first generations, simulations take only a few seconds. Not having developed their metabolism, the newly created cells die quickly after consumption of their initial vital energy. Over generations, the cells gradually learn how to use the environmental substrates in order to survive in the environment.

Observing the action selection system produced by the genetic algorithm, we notice that it could be possible to



(a) (b) (c)

Figure 4. Growth of an organism composed of 146 cells reprensenting a kind of crayfish. (a) Beginning of the simulation. (b) The organism develops by using environmental resources. (c) End of the development.

produce other organisms with the same chromosome. To verify the hypothesis, we decide to develop another organism: a kind of an "artificial bat". To do that, we keep the same substrates and the same possible actions. Using the L-systems chromosome of Figure 4 (c), we launch the simulation and we obtain the organism shown by Figure 5.

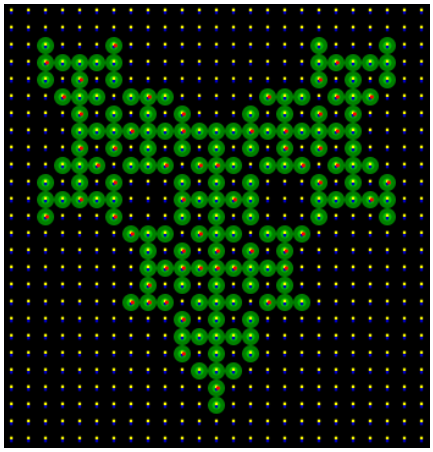


Figure 5. Development of an organism (an artificial "bat") composed of 164 cells.

B. Self-Healing Abilities

Our resulting organisms show a remarkable ability to repair themselves when subjected to damage.

To demonstrate this ability, we remove a small part of the "artificial bat's" cell structure during and after its development. In the first experiment, we inflict a wound in the center of the organism. Figure 6 shows the number of cells of the organism during the simulation. The mark on the curve points out the time of the wound inflicted to the organism, (38 cells are killed by the user in Figure 8 (a)).

At this moment, the organism is composed of 164 cells. Thus, 23% of the cells have been deleted. The curve shows that the organism reacts positively by quickly regenerating the dead cells. This regeneration is illustrated by the sequence composed of Figure 8 (b)-(e).

In the second experiment, the wound is also performed during the development phase of the organism, and particularly on the newly created cells (the first thunder on Figure 7). In this case, the regeneration of the dead cells takes more time since the mitosis requires energy, and the newly created cells have not yet reach this energy level. Before the end of development, we proceed again with two simultaneous injuries on different parts of the organism: the first is below the center of the organism and the second is on the upper left. The second thunder on Figure 7 represents this new wound. In the same manner, the organism is able to regenerate (illustrated by Figure 9 (h)-(j)). The left side branch of the organism takes more time to develop, because the hole affects a greater number of cells (29 cells) than the one in the center (17 cells).

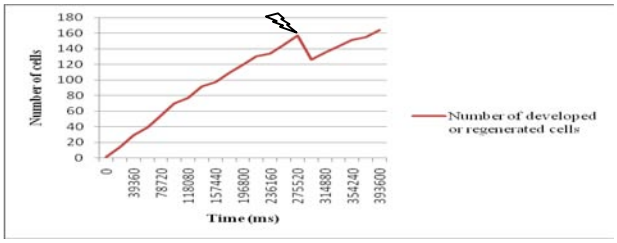


Figure 6. Number of cells of the organism. Wounds inflicted after development.

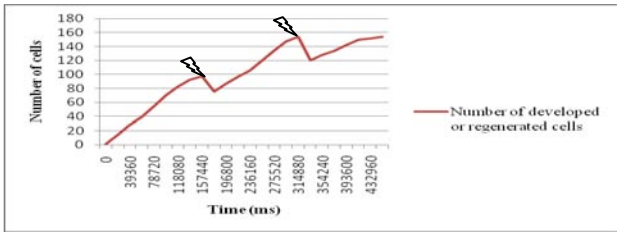
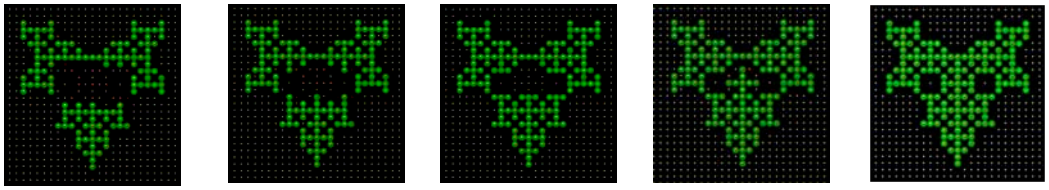


Figure 7. The number of cells of the organism. Wounds inflicted during development.

I. DISCUSSION

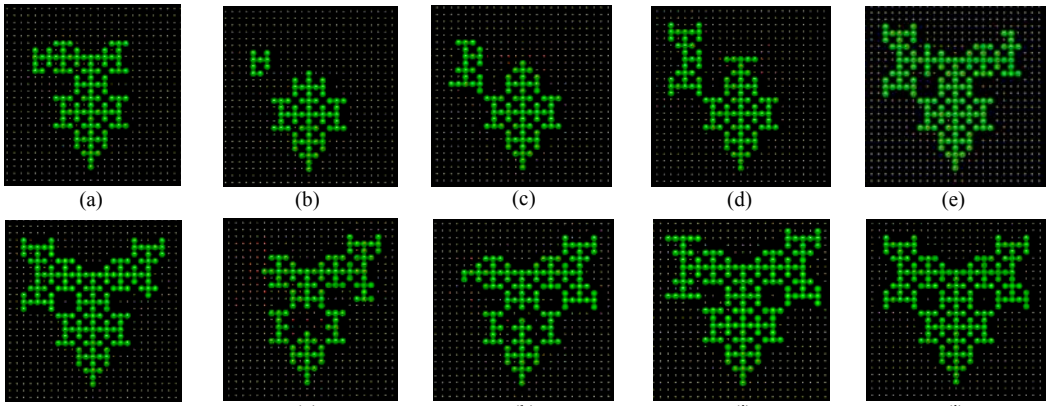
In Nature, the transformation of a stem cell into an embryo is the result of a complex sequence of interactions between genes, their phenotypic effects and the environment in which the embryo develops (an ontogeny) [33].

By analogy to biological development, the proposed model is able to simulate environmental and indirect cellular interactions. In terms of genetic interactions, in L-systems,



(a) (b) (c) (d) (e)

Figure 8. Wounds after the development. (a) The organism after having inflicted a wound in the center (38 killled cells at 296692 ms). (b-e) The organism regenerates itself (at 393618 ms).



(a) (b) (c) (d) (e)

(f) (g) (h) (i) (j)

Figure 9. Wounds inflicted during the development. (a) The organism develops (107 cells developed). (b) Realization of a central hole in the newly created cells (33 killed cells at 168995 ms). (c, d, e, f) The organism develops and regenerates itself. (g) Simultaneous realization of two wounds (at 321051 ms): the first on the left lateral branch of the organism (29 killed cells), the second in the lower center of the organism (17 killed cells). (h, i, g) The organism is regenerated (at 428713 ms).

gene activation can correspond to the appearance of a non-terminal symbol which creates a reference to an inactive rule. Thus, as a rule activation or deactivation of L-systems can have a drastic effect on the resulting phenotype. Each production rule can thus be related to the role of regulatory genes in natural organisms.

This does not mean that the growth of natural multicellular organisms is guided by a mechanism similar to L-systems. This is just a metaphor, because the goal of the model is in no case to conceive a biologically plausible model but to create a system which allows the development of more complex developmental patterns.

I. Conclusion and Future Works

We proposed in this paper, a cellular developmental model based on the combination of two approaches recognized in the field: the grammatical and the cellular chemistry approaches. On the one hand, this model simulates the major elements of a cellular chemistry model, such as chemical reactions in a simplified manner, the diffusion of substrates in the environment, cellular and environmental interactions, and some cellular actions such as mitosis or apoptosis. On the other hand, morphogenesis is based on a grammatical approach using growth rules coded in *APL-systems*, an alternative parametric L-system, which we proposed to simulate the adaptive growth of multicellular organisms according to the internal state of cells composing them.

Largely more bio-inspired than biologically plausible, this model is able to produce various artificial organisms, starting from a single cell. The developed organisms, have a morphology generated by a lineage mechanism, based on L-systems, and a metabolism allowing them to grow and act. In the lineage of our previous works [5], [27], the proposed model is among the rare cellular development models taking metabolism into account, often omitted in the classical models. However, metabolism is primarily essential for the integrity of each multicellular organism, because it allows each cell composing the organism to be surveyed. Moreover, our model is able to exhibit almost perfect self-healing proprieties, if the organism is wounded afterwards or even during its development.

This model proposes the use of L-systems, for directing the morphogenesis of an artificial multicellular organism. We made this choice, in order to explore the potential of these systems widely used with success in many fields, and particularly in the artificial life research field.

Furthermore, our *APL-system* is a unique alternative to parametric L-systems. It has the particularity of being independent of the proposed model and can thus be used in a broad range of applications which use parametric L-systems.

The model has employed the simplest type of L-systems (basic L-systems). Further studies may be done using complex ones, considering: stochastic L-systems [31] to simulate cellular development according to the neighboring cells, and context sensitive L-systems [31] to increase the variety of generated morphologies using the same set of

rules. Another improvement that could be made to achieve greater complexity is the inclusion of 3-D morphologies.

Our long-term goal is to conduct our work in order to generate complete artificial organisms which have a metabolism, a morphology, and which can evolve in the environment. This evolution could occur according to some adaptation functions, such as the capacity of locomotion. To do this, a multicellular organism created with the proposed model can be translated into an abstraction then immersed in a physical simulator. The movements of the organisms could then occur thanks to a neural network controller as in [1].

The objective of the synthesis of these organisms is that they can serve, in the future, as design models of autonomous organisms. Compared to Karl Sims's organisms, metabolism introduced into our cellular developmental model can provide more autonomy to these models of organisms, because metabolism is a means of obtaining energy. Thus, substrates, for example, can be considered as metaphor for batteries that artificial organisms can retrieve from the environment and use to perform specific tasks.

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