P Systems with Active Cells

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Summary. P systems with active membranes is a widely studied framework within the field of Membrane Computing since the creation of the discipline. The abstraction of the structure and behavior of living cells is reflected in the tree-like hierarchy and the kinds of rules that can be used in these kinds of systems.

Resembling the organization and communication between cells within tissues that form organs, tissue-like P systems were defined as their abstractions, using symport/antiport rules, that is, moving and exchanging elements from one cell to another one. All the cells are located in an environment where there exist an arbitrary number of some elements.

Lately, symport/antiport rules have been used in the framework of cell-like membrane systems in order to study their computational power. Interesting results have been reached, since they act similarly to their counterparts in the framework of tissue P systems.

Here, the use of the former defined rules (that is, evolution, communication, dissolution and division/separation rules) is considered, but not working with a tree-like structure. Some remarks about choosing good semantics are given.

Key words: Membrane Computing, Active cells, Computational Complexity, **P** versus **NP** problem.

1 Introduction

Membrane Computing is a distributed parallel computing paradigm inspired by the way the living cells process chemical substances, energy and information. The processor units in the basic model are abstractions of biological membranes, selectively permeable barriers which give cells their outer boundaries (plasma membranes) and their inner compartments (organelles). They control the flow of information between cells and the movement of substances into and out of cells and they are also involved in the capture and release of energy. Biological membranes play an active part in the life of the cell. In fact, the passing of a chemical substance

through a biological membrane is often implemented by an interaction between the membrane itself and the protein channels present in it. During this interaction, the chemical substance and the membrane itself can be modified at least locally.

P systems with active membranes [7] include rules inspired on the behavior of the proteins inside the cells. Recalling, evolution rules are the abstraction of the mutation of the chemical compounds within singular organelles, communication rules give us the idea of the transport of the proteins through the membranes of the cells, dissolution rules remember the process of *apoptosis*, which makes the cell to "kill itself" (in this case, we take the inspiration and apply it to membranes). At last, division and separation rules are the rules that can create an exponential workspace in polynomial time. These are inspired by the asexual and sexual cell processes, that give birth to new cells.

All of those rules can be successfully applied in the framework of tissue-like P systems. Moreover, it would be a more natural way to describe the functioning of these rules at the cells that in the membranes. As an analogy to *P systems with active membranes*, we are going to call them *P systems with active cells*

The paper is organized as follows. Next section briefly introduces some preliminaries needed to make the work self-contained. Section 3 will be devoted to present both syntax and semantics of tissue-like P systems with active cells, letting Section 4 dedicated to present some results concerning the computational complexity classes reached by this kind of membrane systems. The paper ends with some open problems and concluding remarks.

2 Preliminaries

An *alphabet* Γ is a non-empty set and their elements are called *symbols*. A *string* u over Γ is an ordered finite sequence of symbols, that is, a mapping from a natural number of $n \in \mathbb{N}$ onto Γ. The number n is called the *length* of the string u and it is denoted by $|u|$. The empty string (with length 0) is denoted by λ. The set of all strings over an alphabet Γ is denoted by Γ^*. A *language* over Γ is a subset of Γ^*.

A multiset over an alphabet Γ is an ordered pair (Γ, f) where f is a mapping from Γ onto the set of natural numbers $\mathbb{N}$. The *support* of a multiset $m = (\Gamma, f)$ is defined as $supp(m) = \{x \in \Gamma | f(x) > 0\}$. A multiset is finite (respectively, empty) if its support is a finite (respectively, empty) set. We denote by $\emptyset$ the empty multiset. We denote by $M_f(\Gamma)$ the set of all finite multisets over Γ. The *cardinal* of a finite multiset m is defined as $\sum_{x \in \Gamma} m(x)$.

Let $m_1 = (\Gamma, f_1)$, $m_2 = (\Gamma, f_2)$ be multisets over Γ, then the union of m_1 and m_2, denoted by $m_1 + m_2$, is the multiset (Γ, g), where $g(x) = f_1(x) + f_2(x)$ for each $x \in \Gamma$. We say that m_1 is contained in m_2 and we denote it by $m_1 \subseteq m_2$, if $f_1(x) \leq f_2(x)$ for each $x \in \Gamma$. The relative complement of m_2 in m_1, denoted by $m_1 \setminus m_2$, is the multiset (Γ, g), where $g(x) = f_1(x) - f_2(x)$ if $f_1(x) \geq f_2(x)$, and $g(x) = 0$ otherwise.

A *rooted tree* is a connected, acyclic, undirected graph in which one of the vertices (called the *root of the tree*) is distinguished from the others. Given a node x (different from the root) in a rooted tree, if the last edge on the (unique) path from the root to the node x is $\{x, y\}$ (so $x \neq y$), then y is **the** *parent* of node x and x is **a** *child* of node y. We denote it by $y = p(x)$ and $x \in ch(y)$. The root is the only node in the tree with no parent. A node with no children is called a *leaf* (see [2] for details).

Let us recall that the *pair function* $\langle n, m\rangle = ((n + m)(n + m + 1)/2) + n$ is a polynomial-time computable function which is also a primitive recursive and bijective function from $\mathbb{N} \times \mathbb{N}$ to $\mathbb{N}$.

A *decision problem* X is one whose solution is either "`yes`" or "`no`". This can be formally defined by an ordered pair (I_X, θ_X), where I_X is a language over a finite alphabet and θ_X is a total boolean function over I_X. The elements of I_X are called *instances* of the problem X.

2.1 Recognizer membrane systems

In this section, a membrane system designates any variant of P system. Recognizer membrane systems were introduced in [4] and they provide a natural framework to solve decision problems by means of devices in Membrane Computing.

Definition 1. *A membrane system Π is a recognizer membrane system if the following holds:*

1. *The working alphabet Γ of Π has two distinguished objects* `yes` *and* `no`.
2. *There exists an (input) alphabet Σ strictly contained in Γ.*
3. *The initial multisets $\mathcal{M}_1, \ldots, \mathcal{M}_q$ of Π are multisets over $\Gamma \setminus \Sigma$.*
4. *There exists a distinguished membrane called the input membrane.*
5. *The output region i_{out} is the environment.*
6. *All computations halt.*
7. *If $\mathcal{C}$ is a computation of Π, then either object* `yes` *or object* `no` *(but not both) must have been released into the environment, and only at the last step of the computation.*

In recognizer membrane systems any computation is either an *accepting computation* (when object `yes` is released into the environment at the last step).

For each finite multiset m over the input alphabet Σ, the *computation of the system Π with input m* starts from the configuration obtained by adding the input multiset m to the contents of the input membrane, in the initial configuration of Π. Therefore, in this kind of systems we have an initial configuration associated with each input miltiset m (over the input alphabet Σ). We denote $\Pi + m$ the membrane system Π with input multiset m.

2.2 Polynomial complexity classes of recognizer membrane systems

Next, let us recall the concept of efficient solvability by means of a family of recognizer membrane systems (see [4] for more details).

Definition 2. *A decision problem $X = (I_X, \theta_X)$ is solvable in polynomial time by a family $\mathbf{\Pi} = \{\Pi(n) | n \in \mathbb{N}\}$ of recognizer membrane systems from a class $\mathcal{R}$, in a uniform way, denoted by $X \in \mathbf{PMC}_{\mathcal{R}}$, if the following statements hold:*

- *the family $\mathbf{\Pi}$ is polynomially uniform by Turing machines, that is, there exists a deterministic Turing machine working in polynomial time which constructs the system $\Pi(n)$ from $n \in \mathbb{N}$;*
- *there exists a pair (cod, s) of polynomial-time computable functions over the set I_X such that:*
  - *for each instance $u \in I_X$, $s(u)$ is a natural number and $cod(u)$ is the input multiset of the system $\Pi(s(u))$;*
  - *for each $n \in \mathbb{N}$, $s^{-1}(n)$ is a finite set;*
  - *the family $\mathbf{\Pi}$ is polynomially bounded with regard to (X, cod, s), that is, there exists a polynomial function p, such that for each $u \in I_X$ every computation of $\Pi(s(u)) + cod(u)$ is halting and it performs at most $p(|u|)$;*
  - *the family $\mathbf{\Pi}$ is sound with regard to (X, cod, s), that is, for each $u \in I_X$, if there exists an accepting computation of $\Pi(s(u)) + cod(u)$, then $\theta_X(u) = 1$;*
  - *the family $\mathbf{\Pi}$ is complete with regard to (X, cod, s), that is, for each $u \in I_X$, if $\theta_X(u) = 1$, then every computation of $\Pi(s(u)) + cod(u)$ is an accepting one.*

The polynomial complexity class $\mathbf{PMC}_{\mathcal{R}}$ is closed under polynomial-time reduction and under complement [5].

3 Tissue-like P Systems with Active Cells

This new kind of P systems keeps the inspiration keeps the foundations of classical tissue P systems, that is, the exchange of elements between the cells. Here, instead of the use of symport/antiport rules, we are going to introduce the application of the rules typically used in cell-like P systems with active membranes.

3.1 Syntax

Definition 3. *A tissue-like P system with active membranes and separation rules of degree $q \geq 1$ is a tuple $(\Gamma, \Gamma_0, \Gamma_1, H, H_0, H_1, \mu, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$, where:*

- *Γ is a finite alphabet and $H = \{1, \ldots, q\}$;*
- *$\{\Gamma_0, \Gamma_1\}$ is a partition of Γ and $\{H_0, H_1\}$ is a partition of H;*
- *$\mathcal{M}_1, \ldots, \mathcal{M}_q$ are finite multisets over Γ;*
- *$\mathcal{R}$ is a finite set of rules over Γ of the following forms:*

- *(a)* $[a \to u]_h^\alpha$ *for* $h \in H, \alpha \in \{+,-,0\}, a \in \Gamma, u \in M_f(\Gamma)$ *(object evolution rules).*
- *(b)* $a\ [\ \ ]_h^{\alpha_1} \to [\,b\,]_h^{\alpha_2}$ *for* $h \in H, \alpha_1, \alpha_2 \in \{+,-,0\}, a, b \in \Gamma$ *(send-in communication rules).*
- *(c)* $[\ a\ ]_h^{\alpha_1} \to b\ [\ \ ]_h^{\alpha_2}$ *for* $h \in H, \alpha_1, \alpha_2 \in \{+,-,0\}, a, b \in \Gamma$ *(send-out communication rules).*
- *(d)* $[\ a\ ]_h^\alpha \to b$ *for* $h \in H, \alpha \in \{+,-,0\}, a, b \in \Gamma$ *(dissolution rules).*
- *(e)* $[\ a\ ]_h^{\alpha_1} \to [\ b\ ]_h^{\alpha_2}[\ c\ ]_h^{\alpha_3}$ *for* $h \in H, \alpha_1, \alpha_2, \alpha_3 \in \{+,-,0\}, a, b, c \in \Gamma$ *(division rules for elementary membranes).*
- *(e)* $[\ a\ ]_h^{\alpha_1} \to [\ \Gamma_0\ ]_h^{\alpha_2}[\ \Gamma_1\ ]_h^{\alpha_3}$ *for* $h \in H, \alpha_1, \alpha_2, \alpha_3 \in \{+,-,0\}, a \in \Gamma$ *(separation rules for elementary membranes).*
- *(f)* $[[\ \ ]_{h_0}^{\alpha_1}[\ \ ]_{h_1}^{\alpha_2}]_h^\alpha \to [[\ \ ]_{h_0}^{\alpha_3}]_h^{\alpha_5}[[\ \ ]_{h_1}^{\alpha_4}]_h^{\alpha_6}$ *for* $h, h_0, h_1 \in H$, $\alpha, \alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5, \alpha_6 \in \{+,-,0\}$ *(division rules for non-elementary membranes).*
- *(f)* $[[\ \ ]_{h_0}^{\alpha_1}[\ \ ]_{h_1}^{\alpha_2}]_h^\alpha \to [\Gamma_0[\ \ ]_{h_0}^{\alpha_3}]_h^{\alpha_5}[\Gamma_1[\ \ ]_{h_1}^{\alpha_4}]_h^{\alpha_6}$ *for* $h \in H, h_0 \in H_0, h_1 \in H_1$, $\alpha, \alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5, \alpha_6 \in \{+,-,0\}$ *(separation rules for non-elementary membranes).*

• $i_{out} \in H \cup \{env\}$*, where* $env \notin \Gamma \cup H$*.*

A tissue-like P system with active cells of degre $q \geq 1$ can be viewed as a set of q *cells*, labelled by elements of H, arranged in a directed structure μ given by a directed graph (the *cell* structure) whose nodes h that have $outdegree(h) = 0$ are called *elementary cells*, such that: (a) $\mathcal{M}_1, \ldots, \mathcal{M}_q$ represent the finite multisets of *objects* (symbols of the working alphabet Γ) initially placed in the q cells of the system; (b) $\mathcal{R}$ is a finite set of rules over Γ associated with the system; and (c) $i_{out} \in H \cup \{env\}$ indicates the output region. We use the term *region* i to refer to cell i in the case $i \in H$ and to refer to the "environment" of the system in the case $i = env$. If the membrane system makes no use of separation rules for non-elementary cells, then sets H_0 and H_1 will be omited. If separation rules either for elementary and non-elementary cells are not used, then we can omit either the sets H_0 and H_1 and Γ_0 and Γ_1. The *length* of a rule is the number of objects involved in it (for instance, the length of the object evolution rule $[\ a \to u\ ]_h^\alpha$ is $1 + |u|$. Let us notice that in this framework we can change (classical) object evolution rules by cooperative evolution rules (see [11] for more details).

For each cell h different for cells h with $indegree(h) \neq 0$, we denote $p(h)$ the label of the parent of h in μ. By convention, the "parent" of cells h with $indegree(h) = 0$ is the environment of the system

3.2 Semantics

An *instantaneous description* or a *configuration* $\mathcal{C}_t$ at an instant t of a P system with active cells is described by the cell structure at instant t and all multisets of objects over Γ associated with all the membranes present in the system at the moment.

An object evolution rule $[a \to u]_h^\alpha$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α in $\mathcal{C}_t$ which contains object a. When applying such a rule, object a is consumed and all objects from multiset u are produced in that membrane.

A send-in communication rule $a\,[\quad]_h^{\alpha_1} \to [\,b\,]_h^{\alpha_2}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α_1 in $\mathcal{C}_t$ such that $indegree(h) > 0$ and its parent one of its parent cells contain object a. When applying such a rule, object a is consumed from the selected parent cell and object b is produced in the corresponding cell h, and the polarization of cell h changes to α_2.

A send-out communication rule $[\ a\ ]_h^{\alpha_1} \to b\,[\quad]_h^{\alpha_2}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α_1 in $\mathcal{C}_t$ such that it contains object a. When applying such a rule, object a is consumed from such cell and object b is produced in the one of its parent cells chosen in a non-deterministic way, and the polarization of cell h changes to α_2.

A dissolution rule $[\ a\ ]_h^{\alpha} \to b$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α in $\mathcal{C}_t$, different from the output region, such that it contains object a. When applying such a rule, object a is consumed, cell h is dissolved and its objects are sent to one of the parents cells, chosen non-deterministically (or ancestors that have not been dissolved). For all h' such that $f(h') = h$ and h'' such that $f(h) = h''$, when h is dissolved, then new edges from all h'' to all h' are created, and edges from h'' to h and from h to h' are removed.

A division rule $[\ a\ ]_h^{\alpha_1} \to [\ b\ ]_h^{\alpha_2}[\ c\ ]_h^{\alpha_3}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α_1 in $\mathcal{C}_t$, different from the output region, such that it is an elementary cell and contains object a. When applying such a rule, the cell is divided into two cells with the same label, one with polarization α_1 and the other one with polarization α_2; at the same time, object a is consumed and object b appears in the first cell, and c in the second one, and the remaining objects get duplicated in the two created cells. For all h' such that $f(h') = h$ and h'' such that $f(h) = h''$, when h is dissolved, then edges from all h'' to h and from h to h' are duplicated.

A separation rule $[\ a\ ]_h^{\alpha_1} \to [\ \Gamma_0\ ]_h^{\alpha_2}[\ \Gamma_1\ ]_h^{\alpha_3}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α_1 in $\mathcal{C}_t$, different from the output region, such that it is an elementary cell and contains object a. When applying such a rule, the cell is separated into two cells with the same label, one with polarization α_1 and the other one with polarization α_2; at the same time, object a is consumed and the multiset of objects contained in membrane h get distributed: the objects from Γ_0 are placed in one cell, those from Γ_1 are placed in the second one. For all h' such that $f(h') = h$ and h'' such that $f(h) = h''$, when h is dissolved, then edges from all h'' to h and from h to h' are duplicated.

A division rule $[[\quad]_{h_0}^{\alpha_1}[\quad]_{h_1}^{\alpha_2}]_h^{\alpha} \to [[\quad]_{h_0}^{\alpha_3}]_h^{\alpha_5}[[\quad]_{h_1}^{\alpha_4}]_h^{\alpha_6}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α in $\mathcal{C}_t$, different from the output region, such that it is the parent of a cell labelled by

h_0 with polarization α_1 and of another cell labelled by h_1 with polarization α_2. When applying such a division rule to a cell labelled by h in a configuration $\mathcal{C}_t$, that cell is divided into two cells with the same label with polarizations α_5 and α_6, in such a way that the contents (multiset of objects) and relations (children and parent cells) are duplicated into the two new cells, except from cells labelled by h_0, that becomes a child cell of the first one, with polarization α_3, and h_1, that becomes a child cell of the second one, with polarization α_4. For all h' such that $f(h') = h$ and h'' such that $f(h) = h''$, when h is dissolved, then edges from all h'' to h and from h to h' are duplicated (except for edges from h to h_0 and h_1, which ones remains one for each new created cell).

A separation rule $[[\ \ ]_{h_0}^{\alpha_1}[\ \ ]_{h_1}^{\alpha_2}]_h^{\alpha} \rightarrow [\Gamma_0[\ \ ]_{h_0}^{\alpha_3}]_h^{\alpha_5}[\Gamma_1[\ \ ]_{h_1}^{\alpha_4}]_h^{\alpha_6}$ is *applicable* to a configuration $\mathcal{C}_t$ at an instant t, if there exists a cell labelled by h with polarization α in $\mathcal{C}_t$, different from the output region, such that it is the parent of a cell labelled by h_0 with polarization α_1 and of another cell labelled by h_1 with polarization α_2. When applying such a separation rule to a cell labelled by h in a configuration $\mathcal{C}_t$, that cell is separated into two cells with the same label with polarizations α_5 and α_6, in such a way that the contents (multisets of objects) and relations (children cells) are distributed as follows: The first cell receives the multiset of objects from Γ_0, and all child cells whose label belongs to H_0; and the second cell receives the multiset of objects from Γ_1, and all child cells whose label belongs to H_1. For all h' such that $f(h') = h$ and h'' such that $f(h) = h''$, when h is dissolved, then edges from all h'' to h are duplicated, and edges from h to h' are distributed depending on whether they belong to H_0 or H_1.

In tissue-like P systems with active cells, the rules are applied according to the following principles:

- The rules associated with membranes labelled with h are used for all copies of this membrane.
- At one transition step, one object can be used by only one rule (chosen in a non-deterministic way).
- At one transition step, a *cell* can be subject of *only one* rule of types (b)–(f), and then it is applied at most once.
- Object evolution rules can be simultaneously applied to a cell with one rule of types (b)–(f). Object evolution rules are applied in a maximally parallel manner.
- If at the same time a membrane labelled with h is divided/separated by a rule of type (e) or (f) and there are objects in this cells which evolve by means of rules of type (a), then we suppose that first the evolution rules of type (a) are used, changing the objects, and then the separation is produced. Of course, this process takes only one transition step.
- Output cell can never get divided, separated, nor dissolved.

Let us consider a tissue-like P systems with active cells Π We say that configuration $\mathcal{C}_t$ yields configuration $\mathcal{C}_{t+1}$ in one *transition step*, denoted by $\mathcal{C}_t \Rightarrow_\Pi \mathcal{C}_{t+1}$, if we can pass from $\mathcal{C}_t$ to $\mathcal{C}_{t+1}$ by applying the rules from the system following the

previous remarks. A *computation* of Π is a (finite or infinite) sequence of configurations such that: (a) the first term is the initial configuration of the system; (b) for each $n \geq 1$, the n-th configuration of the sequence is obtained from the previous configuration in one transition step; and (c) if the sequence is finite (called *halting computation*) then the last term is a *halting configuration* (a configuration where no rule of the system is applicable to it).

All computations start from an initial configuration and proceed as stated above; only halting computations give a result, which is encoded by the objects present in the output region i_{out} associated with the halting configuration. If $\mathcal{C} = \{\mathcal{C}_t\}_{t<r+1}$ of Π ($r \in \mathbb{N}$) is a halting computation, then the *length* of $\mathcal{C}$, denoted by $|\mathcal{C}|$, is r, that is, $|\mathcal{C}|$ is the number of non-initial configurations which appear in the finite sequence $\mathcal{C}$. For each i ($1 \leq i \leq q$) we denote by $\mathcal{C}_t(i)$ the finite multiset of objects over Γ contained in all cells labelled by i (by applying division or separation rules different cells with the same label can be created) at configuration $\mathcal{C}_t$.

3.3 Families of tissue-like P systems with active cells

We use the following notations:

- $\mathcal{NAC}(\alpha, \beta, \delta)$, where $\alpha \in \{+e, -e\}$, $\beta \in \{+c, -c\}$ and $\delta \in \{+d, -d\}$, is the class of all recognizer P systems with active cells without using division nor separation rules.
- $\mathcal{DAC}(\alpha, \beta, \delta, \gamma)$, where $\alpha \in \{+e, -e\}$, $\beta \in \{+c, -c\}$, $\delta \in \{+d, -d\}$ and $\alpha \in \{+n, -n\}$,is the class of all recognizer P systems with active cells and division rules.
- $\mathcal{SAC}(\alpha, \beta, \delta, \gamma)$, where $\alpha \in \{+e, -e\}$, $\beta \in \{+c, -c\}$, $\delta \in \{+d, -d\}$ and $\alpha \in \{+n, -n\}$,is the class of all recognizer P systems with active cells and separation rules.

The meaning of parameters is the following:

- if $\alpha = +e$ (resp., $-e$) then evolution rules are permitted (resp., forbidden).
- if $\alpha = +c$ (resp., $-c$) then communication rules are permitted (resp., forbidden).
- if $\alpha = +d$ (resp., $-d$) then dissolution rules are permitted (resp., forbidden).
- if $\alpha = +n$ (resp., $-n$) then division/separation rules for elementary and non-elementary cells are permitted (resp., only division/separation rules for elementary cells are permitted).

3.4 Another (not so relevant) approach

One question discussed when this framework was being created was:

In tissue-like membrane systems, the natural definition would be the one where when we do a communication rule, the cell interacts the environment (objects go

to the environment in send-out communication rules and comes from it in send-in communication rules. The same goes to dissolution rules, that is, when a cell dissolves, its contents go to the environment.

This definition seems the best in order to capture the behavior of tissue P systems. But because of the simple structure created, it has little interest regarding the computational complexity of these systems.

If this kind of systems is defined, we can suppose that there are q cells disposed in the environment, and they can interact with it through communication and dissolution rules. But we can simulate this behavior with P systems with active membranes with $q+1$ membranes, where q membranes are situated within one that acts as the environment in the previous system. So complexity classes where these families of P systems were involved in would be weaker than classical P systems with active membranes, therefore it will not be considered.

4 Some Results About Computational Complexity

First of all, it is easy to see that every P system with active cells is at least as powerful as its active membranes counterpart. It can be proved because every P system with active membranes structure is defined by a rooted tree μ. A tree is a particular case of a graph, where cycles are not allowed. For every P system with active membranes, we can define a P system with active cells that simulates its behavior. Let $\Pi = (\Gamma, \Gamma_0, \Gamma_1, H, H_0, H_1, \mu, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$ a P system with active membranes. We can create (in polynomial time) a P system with active membrane that simulates its behavior. Let $\Pi' = (\Gamma, \Gamma_0, \Gamma_1, H, H_0, H_1, \mu', \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$ be the P system with active cells that simulates its behavior. μ' is constructed as follows:

- Let μ' be a single node h, where h is the label of the skin membrane of Π.
- For every membrane h' situated within another membrane h in Π, we create a node h' in μ' and add an edge from h to h'.

The directed graph obtained has the shape of a directed rooted tree, and as it has the same set of rules, semantics of the system makes Π' simulate the behavior of Π'. We can conclude with:

Theorem 1. $\mathbf{PMC}_{\mathcal{AM}(\alpha,\beta,\delta,\gamma)} \subseteq \mathbf{PMC}_{\mathcal{AC}(\alpha,\beta,\delta,\gamma)}$,

no matter which kinds of rules we are using.

4.1 Some complexity classes

As it happened with P systems with active membranes, we can use the Milano Theorem [14] to state that no computationally hard problems can be solved in polynomial time without using rules allowing the generation of an exponential number of membranes/cells in polynomial time. Then:

Theorem 2. $\mathbf{P} = \mathbf{PMC}_{\mathcal{NAC}}$

In [8, 9], an upper bound of the complexity of P systems with active membranes was given. In fact, algorithms used there did not complain about the "direction of the edges" in the graph defining the systems, so the same technique can be used here.

Theorem 3. $\mathbf{PSPACE} = \mathbf{PMC}_{\mathcal{DAC}(+e,+c,+d,+n)}$

In fact, we can use this technique to define an upper bound for systems that use separation rules instead of division rules.

Theorem 4. $\mathbf{PMC}_{\mathcal{SAM}(+e,+c,+d,+n)} \cup \mathbf{PMC}_{\mathcal{SAC}(+e,+c,+d,+n)} \subseteq \mathbf{PSPACE}$

4.2 Polarizationless P systems with active cells

In previous works, P systems with active membranes were demonstrated to be too powerful in order to obtain new frontiers to tackle the problem **P** vs. **NP**. In order to obtain less powerful systems, polarizationes were avoided, giving place to polarizationless P systems with active membranes. Some frontiers of efficiency were obtained in this new framework. We can do the same in P systems with active cells, so we would obtain *polarizationless* P systems with active cells. These systems are defined as polarizationless P systems with active membranes are defined to P systems with active membranes.

We use the following notations:

- $\mathcal{DAC}^0(\alpha, \beta, \delta, \gamma)$, where $\alpha \in \{+e, -e\}$, $\beta \in \{+c, -c\}$, $\delta \in \{+d, -d\}$ and $\alpha \in \{+n, -n\}$,is the class of all recognizer polarizationless P systems with active cells and division rules.
- $\mathcal{SAC}^0(\alpha, \beta, \delta, \gamma)$, where $\alpha \in \{+e, -e\}$, $\beta \in \{+c, -c\}$, $\delta \in \{+d, -d\}$ and $\alpha \in \{+n, -n\}$,is the class of all recognizer polarizationless P systems with active cells and separation rules.

The meaning of parameters is the same than before.

In [3, 12] that families of P systems which make no use of dissolution rules can only solve tractable problems in an efficient way. The technique used is the dependency graph technique, and we can adapt it to P systems with active cells, so:

Theorem 5. $\mathbf{P} = \mathbf{PMC}_{\mathcal{DAC}^0(+e,+c,-d,+n)} = \mathbf{PMC}_{\mathcal{SAC}^0(+e,+c,-d,+n)}$

Proof. Here, the creation of the graph differs from the original one since a cell can have two parent cells, unlike in active membranes, where each membrane could have at most one parent membrane. So, we have to contemplate this in the next algorithm:

`Input:` Π (with $\mathcal{R}$ as its set of rules and H as its label set)

$V_\Pi \leftarrow \emptyset$; $E_\Pi \leftarrow \emptyset$
`for each` rule $r \in \mathcal{R}$ of Π `do`
  `if` $r = [\ a \rightarrow u\ ]_h \wedge alph(u) = \{a_1, \ldots, a_s\}$ `then`
    $V_\Pi \leftarrow V_\Pi \cup \sum_{j=1}^{s} \{(a,h),(a_j,h)\}$
    $E_\Pi \leftarrow E_\Pi \cup \sum_{j=1}^{s} \{((a,h),(a_j,h))\}$
  `else if` $r = [\ a\ ]_h \rightarrow b\ [\ \ ]_h$ `then`
    $V_\Pi \leftarrow V_\Pi \cup \sum_{h'=f(h)} \{(a,h),(b,h')\}$
    $E_\Pi \leftarrow E_\Pi \cup \sum_{h'=f(h)} \{((a,h),(b,h'))\}$
  `else if` $r = a\ [\ \ ]_h \rightarrow [\ b\ ]_h$ `then`
    $V_\Pi \leftarrow V_\Pi \cup \sum_{h=f(h')} \{(a,h),(b,h')\}$
    $E_\Pi \leftarrow E_\Pi \cup \sum_{h=f(h')} \{((a,h),(b,h'))\}$
  `else if` $r = [\ a\ ]_h \rightarrow [\ b\ ]_h[\ c\ ]_h$ `then`
    $V_\Pi \leftarrow V_\Pi \cup \{(a,h),(b,h),(c,h)\}$
    $E_\Pi \leftarrow E_\Pi \cup \{((a,h),(b,h)),(a,h),(c,h)\}$
  `else if` $r = [\ a\ ]_h \rightarrow [\ \Gamma_0\ ]_h[\ \Gamma_1\ ]_h$ `then`
    $V_\Pi \leftarrow V_\Pi \cup \{(a,h)\}$

The running time of this algorithm is bounded by $O(|\mathcal{R}| \cdot q)$, where q is the value $max(max\{length(r) : r \in \mathcal{R}\}, |H|)$. The rest of the demonstration is similiar to the given in [3, 12].

□

In [1], a uniform solution to `QSAT` problem was given with polarizationless P systems with active membranes that make use of dissolution and division rules for elementary and non-elementary membranes. This solution, of course, can be adapted to polarizationless P systems with active cells. Thus:

Theorem 6. PSPACE = $\mathbf{PMC}_{\mathcal{DAC}^0(+e,+c,+d,+n)}$

Here, a new version of the Păun's conjecture can be outlined:

$$\mathbf{P} \stackrel{?}{=} \mathbf{PMC}_{\mathcal{DAC}^0(+e,+c,+d,-n)}$$

4.3 Minimal cooperation in polarizationless P systems with active membranes

Some interesting results have been reached in the framework of P systems with active membranes when *minimal cooperation* has been introduced. That is, with this kind of rules, we can make the objects in the regions collaborate with each other. The term *minimal* tell us that the left part of a rule can have at most two

objects, but even with this restriction, these systems are powerful enough to solve computationally hard problems.

In the context of polarizationless P systems with active cells, the following kinds of minimal cooperation in object evolution rules are considered.

- Primary minimal cooperation (**pmc**): object evolution rules are of the form $[\ u \rightarrow v\ ]_h$, where $h \in H$, u, v are multisets over Γ, and $1 \leq |u|, |v| \leq 2$, but at least one object evolution rule verifies $|u| = 2$.
- Bounded minimal cooperation (**bmc**): object evolution rules are of the form $[\ u \rightarrow v\ ]_h$, where $h \in H$, u, v are multisets over Γ, and $1 \leq |u| \leq |v| \leq 2$, but at least one object evolution rule verifies $|u| = 2$.
- Minimal cooperation and minimal production (**mcmp**): object evolution rules are of the form $[\ a \rightarrow b\ ]_h$, $[\ a \rightarrow b\ ]_h$, where $h \in H$, $a, b, c \in \Gamma$, but at least one object evolution rule is of the second type.

We use the same notations that in polarizationless P systems with active cells (that make use of classical object evolution rules), but now $\alpha \in \{pmc, bmc, mcmp\}$.

In [10], the use of *bounded minimal cooperation* were demonstrated to be strong enough to solve **NP**-complete problems.

Theorem 7. $\mathbf{NP} \cup \mathbf{co} - \mathbf{NP} \subseteq \mathbf{PMC}_{\mathcal{DAC}^0(bmc,+c,-d,-n)}$

In [13], this result was improved by using *mcmp* rules, that is:

Theorem 8. $\mathbf{NP} \cup \mathbf{co} - \mathbf{NP} \subseteq \mathbf{PMC}_{\mathcal{DAC}^0(mcmp,+c,-d,-n)}$

Nevertheless, it is different when we use separation rules instead of division rules. In this framework, it was demonstrated in [11] that the use of *bounded minimal cooperation* is not powerful enough to solve **NP**-complete problems. It was demonstrated with the algorithmic technique, and in this case we can adapt the algorithm to deal with polarizationless P systems with active cells.

Theorem 9. $\mathbf{P} = \mathbf{PMC}_{\mathcal{SAC}^0(bmc,+c,+d,+n)}$

Bearing in mind that minimal cooperation with minimal production in object evolution rules is a particular case of bounded minimal cooperation, we deduce the following result:

Theorem 10. $\mathbf{P} = \mathbf{PMC}_{\mathcal{SAC}^0(mcmp,+c,+d,+n)}$

In order to obtain efficient solutions to presumably intractable problems in the framework of polarizationless P systems with active cells, we have to make use of *primary minimal cooperation*. We can use the same solution to `SAT` problem that in [12], therefore:

Theorem 11. $\mathbf{NP} \cup \mathbf{co} - \mathbf{NP} \subseteq \mathbf{PMC}_{\mathcal{SAC}^0(pmc,+c,-d,-n)}$

5 Conclusions

In this work, we present a new kind of families of P systems, the so-called P systems with active cells. The union of the syntax and semantics of P systems with active membranes and the structure of tissue-like P systems give this kind of membrane systems some interesting properties. It is useful in order to obtain new frontiers of efficiency regarding the *direction* of the edges. We can see P systems with active membranes as directed graphs that have edges in only one direction. If we remove the restriction of the direction of the edges, we obtain P systems with active membranes. It is no surprising that these membrane systems are at least as powerful as the former ones.

Some classical results in P systems with active membranes are reviewed to obtain their equivalent when we are treating with P systems with active cells. Both systems with polarizations and polarizationless ones are studied, giving an upper bound of them and, like in the framework of active membranes, is **PSPACE**.

Minimal cooperation have been recently investigated to study its relevance in the power of polarizationless P systems with active membranes, and here we give their counterpart active cells definitions. All the results given here are quite similar to their active membranes counterparts, therefore a first question appear:

- Does the direction matter? That is, does:

$$\mathbf{PMC}_{\mathcal{AM}(\alpha,\beta,\delta,\gamma)} = \mathbf{PMC}_{\mathcal{AC}(\alpha,\beta,\delta,\gamma)}$$

  remains?

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