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The Efficiency of Tissue P Systems with Cell Separation Relies on the Environment

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Abstract. The classical definition of tissue P systems includes a distinguished alphabet with the special assumption that its elements are available in an arbitrarily large amount of copies. These objects are shared in a distinguished place of the system, called the *environment*. This ability of having infinitely many copies of some objects has been widely exploited in the design of efficient solutions to computationally hard problems by means of tissue P systems.
This paper deals with computational aspects of tissue P systems with cell separation where there is no such environment as described above. The main result is that only tractable problems can be efficiently solved by using this kind of P systems. Bearing in mind that **NP**–complete problems can be efficiently solved by using tissue P systems without environment and with cell division, we deduce that in the framework of tissue P systems without environment, the kind of rules (separation versus division) provides a new frontier of the tractability of decision problems.

Keywords: Membrane Computing, Tissue P System, Cell Separation, Environment of a Tissue, Computational Complexity, Borderline of Tractability

1 Introduction

Membrane Computing is a young branch of *Natural Computing* initiated by Gh. Păun in the end of 1998 [15]. The computational devices of this paradigm, called *P systems*, operate in a distributed, parallel and non-deterministic manner, getting inspiration from living cells (their structure and functioning), as well as from the way cells are organized in tissues, organs, etc.

Several different models of cell-like P systems have been successfully used to solve computationally hard problems efficiently, by trading space for time, usually following a brute force approach: an exponential workspace is created

in polynomial time by using some kind of rules, and then massive parallelism is used to simultaneously check all the candidate solutions. Inspired by living cells, several ways for obtaining exponential workspace in polynomial time were proposed: membrane division (*mitosis*) [16], membrane creation (*autopoiesis*) [7], and membrane separation (*membrane fission*) [12]. These three ways have given rise to the following models: *P systems with active membranes*, *P systems with membrane creation*, and *P systems with membrane separation*.

A new type of P systems, the so-called *tissue P systems*, was considered in [10]. Instead of considering a hierarchical arrangement, membranes/cells are placed in the nodes of a virtual graph. This variant has two biological justifications (see [11]): intercellular communication and cooperation between neurons. The common mathematical model of these two mechanisms is a net of processors dealing with symbols and communicating these symbols along channels specified in advance. The communication among cells is based on symport/antiport rules, which were introduced to P systems in [18]. These models have a special alphabet associated with the environment of the system and it is assumed that the symbols of that alphabet appear in an arbitrary large amount of copies at the initial configuration of the system.

From the seminal definitions of tissue P systems [10, 11], several research lines have been developed and other variants have arisen (see, for example, [1, 2, 4, 8, 9, 14]). One of the most interesting variants of tissue P systems was presented in [19], where the definition of tissue P systems is combined with the one of P systems with active membranes, yielding *tissue P systems with cell division*.

In the biological phenomenon of fission, the contents of the two new cells evolved from a cell can be significantly different, and membrane separation inspired by this biological phenomenon in the framework of cell-like P systems was proved to be an efficient way to obtain exponential workspace in polynomial time [12]. In [13], a new class of tissue P systems based on cell fission, called *tissue P systems with cell separation*, was presented. Its computational efficiency was investigated, and two important results were obtained: (a) only tractable problems can be efficiently solved by using cell separation and communication rules with length at most 1, and (b) an efficient (uniform) solution to the `SAT` problem by using cell separation and communication rules with length at most 8 was presented.

In this paper we study the efficiency of tissue P systems with communication rules and cell separation where the alphabet associated with the environment is empty. These systems are called tissue P systems *without environment* and, specifically, we prove that only tractable problems can be solved in polynomial time by families of tissue P systems with communication rules, with cell separation and without environment.

The paper is organized as follows: first, we recall some preliminaries, and then, the definition of tissue P systems with cell separation, recognizer tissue P systems and computational complexity classes in this framework, are briefly described. Section 4 is devoted to the main result of the paper: the polynomial

complexity class associated with $\widehat{\mathbf{TSC}}$ is the class $\mathbf{P}$. Finally, conclusions and further works are presented.

2 Preliminaries

An *alphabet*, Σ, is a non–empty set whose elements are called *symbols*. A finite sequence of symbols is a *string* over Σ. If u and v are strings over Σ, then so is their *concatenation* uv, obtained by juxtaposition, that is, writing u and v one after the other. The number of symbols in a string u is the *length* of the string, and it is denoted by $|u|$. As usual, the empty string (with length 0) will be denoted by λ. The set of all strings over an alphabet Σ is denoted by Σ^*. In algebraic terms, Σ^* is the free monoid generated by Σ under the operation of concatenation. Subsets of Σ^*, finite or infinite, are referred to as *languages* over Σ.

The *Parikh vector* associated with a string $u \in \Sigma^*$ with respect to the alphabet $\Sigma = \{a_1, \ldots, a_r\}$ is $\Psi_\Sigma(u) = (|u|_{a_1}, \ldots, |u|_{a_r})$, where $|u|_{a_i}$ denotes the number of ocurrences of the symbol a_i in the string u. This is called the *Parikh mapping* associated with Σ. Notice that in this definition the ordering of the symbols from Σ is relevant. If $\Sigma_1 = \{a_{i_1}, \ldots, a_{i_s}\} \subseteq \Sigma$ then we define $\Psi_{\Sigma_1}(u) = (|u|_{a_{i_1}}, \ldots, |u|_{a_{i_s}})$, for each $u \in \Sigma^*$.

A *multiset* m over a set A is a pair (A, f) where $f : A \to \mathbb{N}$ is a mapping. If $m = (A, f)$ is a multiset then its *support* is defined as $supp(m) = \{x \in A \,|\, f(x) > 0\}$. A multiset is empty (resp. finite) if its support is the empty set (resp. a finite set). If $m = (A, f)$ is a finite multiset over A, and $supp(m) = \{a_1, \ldots, a_k\}$ then it will be denoted as $m = \{a_1^{f(a_1)}, \ldots, a_k^{f(a_k)}\}$. That is, superscripts indicate the multiplicity of each element, and if $f(x) = 0$ for $x \in A$, then the element x is omitted. A finite multiset $m = \{a_1^{f(a_1)}, \ldots, a_k^{f(a_k)}\}$ can also be represented by the string $a_1^{f(a_1)} \ldots a_k^{f(a_k)}$ over the alphabet $\{a_1, \ldots, a_k\}$. Nevertheless, all permutations of this string identify the same multiset m precisely. Throughout this paper, whenever we refer to "the finite multiset m" where m is a string, this should be understood as "the finite multiset represented by the string m".

If $m_1 = (A, f_1), m_2 = (A, f_2)$ are multisets over A, then we define the union of m_1 and m_2 as $m_1 + m_2 = (A, g)$, where $g = f_1 + f_2$, that is, $g(a) = f_1(a) + f_2(a)$, for each $a \in A$. We also define the difference $m_1 \setminus m_2$ as the multiset (A, h), where $h(a) = f_1(a) - f_2(a)$, in the case $f_1(a) \geq f_2(a)$, and $h(a) = 0$, otherwise. In particular, given two sets A and B, $A \setminus B$ is the set $\{x \in A \,|\, x \notin B\}$.

In what follows, we assume the reader is already familiar with the basic notions and the terminology of P systems. For details, see [17].

2.1 Tissue P Systems with Communication Rules and with Cell Separation

A *tissue P system with communication rules and with cell separation* of degree q ($q \geq 1$) is a tuple $\Pi = (\Gamma, \mathcal{E}, \Gamma_0, \Gamma_1, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$, where:

1. Γ is a finite *alphabet*.
2. $\mathcal{E} \subseteq \Gamma$.
3. $\{\Gamma_0, \Gamma_1\}$ is a partition of Γ, that is, $\Gamma = \Gamma_0 \cup \Gamma_1$, $\Gamma_0, \Gamma_1 \neq \emptyset$, $\Gamma_0 \cap \Gamma_1 = \emptyset$;
4. $\mathcal{M}_1, \ldots, \mathcal{M}_q$ are strings over Γ.
5. $\mathcal{R}$ is a finite set of rules of the following forms:
   Communication rules: $(i, u/v, j)$, for $i, j \in \{0, \ldots, q\}, i \neq j$, $u, v \in \Gamma^*$, $|u| + |v| > 0$;
   Separation rules: $[a]_i \to [\Gamma_0]_i[\Gamma_1]_i$, where $i \in \{1, \ldots, q\}$, $a \in \Gamma$ and $i \neq i_{out}$.
6. $i_{out} \in \{0, \ldots, q\}$.

A *tissue P system with communication rules and with cell separation* $\Pi = (\Gamma, \mathcal{E}, \Gamma_0, \Gamma_1, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$, of degree q can be viewed as a set of q cells, labelled by $1, \ldots, q$ such that: (a) $\mathcal{M}_1, \ldots, \mathcal{M}_q$ represent the finite multisets of objects initially placed in the q cells of the system; (b) $\mathcal{E}$ is the set of objects initially located in the environment of the system, all of them available in an arbitrary number of copies; and (c) i_{out} represents a distinguished *region* which will encode the output of the system. We use the term *region* i $(0 \leq i \leq q)$ to refer to cell i in the case $1 \leq i \leq q$ and to refer to the environment in the case $i = 0$.

A communication rule $(i, u/v, j)$ is called a *symport rule* if $u = \lambda$ or $v = \lambda$. A symport rule $(i, u/\lambda, j)$, with $i \neq 0, j \neq 0$, provides a virtual arc from cell i to cell j. A communication rule $(i, u/v, j)$ is called an *antiport rule* if $u \neq \lambda$ and $v \neq \lambda$. An antiport rule $(i, u/v, j)$, with $i \neq 0, j \neq 0$, provides two arcs: one from cell i to cell j and the other from cell j to cell i. Thus, every tissue P system has an underlying directed graph whose nodes are the cells of the system and the arcs are obtained from communication rules. In this context, the environment can be considered as a virtual node of the graph such that its connections are defined by communication rules of the form $(i, u/v, j)$, with $i = 0$ or $j = 0$.

When applying a rule $(i, u/v, j)$, the objects of the multiset represented by u are sent from region i to region j and, simultaneously, the objects of multiset v are sent from region j to region i. The length of communication rule $(i, u/v, j)$ is defined as $|u| + |v|$.

When applying a separation rule $[a]_i \to [\Gamma_0]_i[\Gamma_1]_i$, in reaction with an object a, the cell i is separated into two cells with the same label; at the same time, object a is consumed; the objects from Γ_0 are placed in the first cell, those from Γ_1 are placed in the second cell; the output cell i_{out} cannot be separated.

The rules of a system like the above one are used in a non-deterministic maximally parallel manner as customary in membrane computing. At each step, all cells which can evolve must evolve in a maximally parallel way (at each step we apply a multiset of rules which is maximal, no further applicable rule can be added). This way of applying rules has only one restriction: when a cell is separated, the separation rule is the only one which is applied for that cell at that step; thus, the objects inside that cell do not evolve by means of communication rules. The new cells resulting from separation could participate in the interaction with other cells or the environment by means of communication rules at the next step – providing that they are not separated once again. The label of a cell precisely identifies the rules which can be applied to it.

An *instantaneous description* or a *configuration* at any instant of a tissue P system with cell separation is described by all multisets of objects over Γ associated with all the cells present in the system, and the multiset of objects over $\Gamma - \mathcal{E}$ associated with the environment at that moment. Recall that there are infinitely many copies of objects from $\mathcal{E}$ in the environment, and hence this set is not properly changed along the computation. The *initial configuration* is $(\mathcal{M}_1, \cdots, \mathcal{M}_q; \emptyset)$. A configuration is a *halting configuration* if no rule of the system is applicable to it.

Let us fix a tissue P system with cell separation Π. We say that configuration $\mathcal{C}_1$ yields configuration $\mathcal{C}_2$ in one *transition step*, denoted by $\mathcal{C}_1 \Rightarrow_\Pi \mathcal{C}_2$, if we can pass from $\mathcal{C}_1$ to $\mathcal{C}_2$ by applying the rules from $\mathcal{R}$ following the previous remarks. A *computation* of Π is a (finite or infinite) sequence of configurations such that:

1. the first term of the sequence is the initial configuration of the system;
2. each non-initial configuration of the sequence is obtained from the previous configuration by applying rules of the system in a maximally parallel manner with the restrictions previously mentioned; and
3. if the sequence is finite (called *halting computation*) then the last term of the sequence is a halting configuration.

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 cell i_{out} in 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* $\mathcal{C}$ is r, that is, the number of non-initial configurations which appear in the finite sequence $\mathcal{C}$. We denote it by $|\mathcal{C}|$. We also denote by $\mathcal{C}_t(i)$ the contents of region i ($0 \leq i \leq q$) at the configuration $\mathcal{C}_t$.

2.2 Recognizer Tissue P Systems

In order to study the computing efficiency, the notions from classical *computational complexity theory* are adapted for membrane computing, and a special class of cell-like P systems is introduced in [22]: *recognizer P systems* (called *accepting P systems* in a previous paper [21]). For tissue P systems, with the same idea as recognizer cell-like P systems, *recognizer tissue P systems* is introduced in [19].

A *recognizer tissue P system* with communication rules and with cell separation of degree q ($q \geq 1$) is a tuple $\Pi = (\Gamma, \mathcal{E}, \Sigma, \Gamma_0, \Gamma_1, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$, where:

- $(\Gamma, \mathcal{E}, \Gamma_0, \Gamma_1, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$ is a tissue P system with communication rules and with cell separation of degree q, as defined in the previous subsection.
- The working alphabet Γ has two distinguished objects `yes` and `no`, at least one copy of them present in some initial multisets $\mathcal{M}_1$, ..., $\mathcal{M}_q$.
- Σ is an (input) alphabet strictly contained in Γ such that $\Sigma \cap \mathcal{E} = \emptyset$.
- $\mathcal{M}_1, \ldots, \mathcal{M}_q$ are strings over $\Gamma \setminus \Sigma$.

- $i_{in} \in \{1, \ldots, q\}$ is the input cell.
- $i_{out} = 0$ is the output region, that is, the output of the system is encoded in the environment.
- All computations halt.
- If $\mathcal{C}$ is a computation of Π, then either object `yes` or object `no` (but not both) must have been released into the output region, and only at the last step of the computation.

For each $w \in \Sigma^*$, the *computation of the system Π with input $w \in \Sigma^*$* starts from the configuration of the form $(\mathcal{M}_1, \ldots, \mathcal{M}_{i_{in}} + w, \ldots, \mathcal{M}_q; \emptyset)$, that is, the input multiset w has been added to the contents of the input cell i_{in}, and we denote it by $\Pi + w$. Therefore, we have an initial configuration associated with each input multiset w (over the input alphabet Σ) in this kind of systems.

Given such a recognizer tissue P system and a halting computation $\mathcal{C} = \{\mathcal{C}_t\}_{t<r+1}$ of Π ($r \in \mathbb{N}$), we define the result of $\mathcal{C}$ as follows:

$$Output(\mathcal{C}) = \begin{cases} \texttt{yes}, & \text{if } \Psi_{\{\texttt{yes},\texttt{no}\}}(M_{r,0}) = (1,0) \wedge \\ & \quad \Psi_{\{\texttt{yes},\texttt{no}\}}(M_{t,0}) = (0,0) \text{ for } t = 0, \ldots, r-1 \\ \texttt{no}, & \text{if } \Psi_{\{\texttt{yes},\texttt{no}\}}(M_{r,0}) = (0,1) \wedge \\ & \quad \Psi_{\{\texttt{yes},\texttt{no}\}}(M_{t,0}) = (0,0) \text{ for } t = 0, \ldots, r-1 \end{cases}$$

where Ψ is the Parikh mapping, and $M_{t,0}$ is the multiset over $\Gamma \setminus \mathcal{E}$ associated with region 0 at the configuration $\mathcal{C}_t$, in particular, $M_{r,0}$ is the multiset over $\Gamma \setminus \mathcal{E}$ associated with region 0 at the halting configuration $\mathcal{C}_r$.

We say that a computation $\mathcal{C}$ is an *accepting computation* (respectively, *rejecting computation*) if $Output(\mathcal{C}) = \texttt{yes}$ (respectively, $Output(\mathcal{C}) = \texttt{no}$), that is, if object `yes` (respectively, object `no`) appears in the output region of the corresponding halting configuration of $\mathcal{C}$, and neither object `yes` nor `no` appears in the output region of any non–halting configuration of $\mathcal{C}$.

We denote by **TSC** the class of recognizer tissue P systems with cell communication and with cell separation. For each natural number $k \geq 1$, we denote by **TSC**(k) the class of recognizer tissue P systems with cell separation and with communication rules of length at most k.

3 Tissue P Systems with Communication Rules, with Cell Separation and without Environment

Definition 1. *A tissue P system with communication rules, with cell separation and without environment of degree $q + 1$ is a tuple*

$$\Pi = (\Gamma, \Gamma_0, \Gamma_1, \mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out}),$$

where:

1. *Γ is a finite* alphabet.
2. *$\{\Gamma_0, \Gamma_1\}$ is a partition of Γ, that is, $\Gamma = \Gamma_0 \cup \Gamma_1$, $\Gamma_0, \Gamma_1 \neq \emptyset$, $\Gamma_0 \cap \Gamma_1 = \emptyset$;*

3. $\mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q$ *are strings over* Γ.
4. $\mathcal{R}$ *is a finite set of rules of the following forms:*

   Communication rules*:* $(i, u/v, j)$*, for* $i, j \in \{0, \ldots, q\}, i \neq j$*,* $u, v \in \Gamma^*$*,* $|u| + |v| > 0$*;*

   Separation rules*:* $[a]_i \to [\Gamma_0]_i[\Gamma_1]_i$*, where* $i \in \{0, \ldots, q\}$*,* $a \in \Gamma$ *and* $i \neq i_{out}$.
5. $i_{out} \in \{0, \ldots, q\}$.

A *tissue P system with communication rules, with cell separation and without environment* is a tissue P system with communication rules and with cell separation such that the alphabet $\mathcal{E}$ of the environment is empty.

Definition 2. *A* recognizer tissue P system *with communication rules, with cell separation and without environment of degree* $q + 1$ *is a tuple*

$$\Pi = (\Gamma, \Sigma, \Gamma_0, \Gamma_1, \mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$$

where:

- $(\Gamma, \Gamma_0, \Gamma_1, \mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$ *is a tissue P system with communication rules, with cell separation and without environment of degree* $q + 1$*, as defined previously.*
- *The working alphabet* Γ *has two distinguished objects* `yes` *and* `no`*, at least one copy of them present in some initial multisets* $\mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q$.
- Σ *is an (input) alphabet strictly contained in* Γ.
- $\mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q$ *are strings over* $\Gamma \setminus \Sigma$.
- $i_{in} \in \{1, \ldots, q\}$ *is the input cell.*
- $i_{out} = 0$ *is the output cell.*
- *All computations halt.*
- *If* $\mathcal{C}$ *is a computation of* Π*, then either object* `yes` *or object* `no` *(but not both) must have been released into cell 0, and only at the last step of the computation.*

For each $w \in \Sigma^*$, the *computation of the system* Π *with input* $w \in \Sigma^*$ starts from the configuration of the form $(\mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_{i_{in}} + w, \ldots, \mathcal{M}_q; \emptyset)$, that is, the input multiset w has been added to the contents of the input cell i_{in}, and we denote it by $\Pi + w$. Therefore, we have an initial configuration associated with each input multiset w (over the input alphabet Σ) in this kind of systems.

Given a recognizer tissue P system with cell separation, and a halting computation $\mathcal{C}$ of Π, the result of $\mathcal{C}$ is defined as in the previous section.

We denote by $\widehat{\mathbf{TSC}}$ the class of recognizer tissue P systems with cell communication, cell separation and without environment. For each natural number $k \geq 1$, we denote by $\widehat{\mathbf{TSC}}(k)$ the class of recognizer tissue P systems with cell separation, without environment, and with communication rules of length at most k.

3.1 Polynomial Complexity Classes

Next, we define what solving a decision problem in a uniform and efficient way means in the framework of tissue P systems. Since we define each tissue P system to work on a finite number of inputs, to solve a decision problem we define a numerable family of tissue P systems.

Definition 3. *We say that a decision problem $X = (I_X, \theta_X)$ is solvable in a uniform way and polynomial time by a family $\mathbf{\Pi} = \{\Pi(n) \mid n \in \mathbb{N}\}$ of recognizer tissue P systems with communication rules, with cell separation and without environment if the following holds:*

- *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 I_X such that:*
  - *for each instance $u \in I_X$, $s(u)$ is a natural number, and $cod(u)$ is an 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 $\Pi(s(u))$ with input $cod(u)$ is halting and it performs at most $p(|u|)$ steps;*
  - *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 $\Pi(s(u))$ with input $cod(u)$, 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 $\Pi(s(u))$ with input $cod(u)$ is an accepting one.*

>From the soundness and completeness conditions above, we deduce that every P system $\Pi(n)$ is *confluent*, in the following sense: every computation of a system with the *same* input multiset must always give the *same* answer.

Let $\mathbf{R}$ be a class of recognizer tissue P systems. We denote by $\mathbf{PMC_R}$ the set of all decision problems which can be solved in a uniform way and polynomial time by means of families of systems from $\mathbf{R}$. The class $\mathbf{PMC_R}$ is closed under complement and polynomial–time reductions [21].

4 Efficiency of Tissue P Systems with Cell Communication, with Cell Separation and without Environment

4.1 Representation of Tissue P Systems from $\widehat{\mathbf{TSC}}$

Let $\Pi = (\Gamma, \Sigma, \Gamma_0, \Gamma_1, \mathcal{M}_0, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$ be a recognizer tissue P system of degree $q+1$ with communication rules, with cell separation and without environment.

1. We denote by R_C (R_S respectively) the set of communication rules (separation rules respectively) of Π. We will fix total orders in R_C and R_S.
2. Let $\mathcal{C}$ be a computation of Π, and $\mathcal{C}_t$ a configuration of $\mathcal{C}$. The application of a communication rule keeps the multiset of objects of the whole system unchanged because only movement of objects between the cells of the system is produced. On the other hand, the application of a separation rule causes that an object is removed from the system, and since there is no objects replication, the rest remain unchanged. Thus, the multiset of objects of the system in any configuration $\mathcal{C}_t$ is contained in $\mathcal{M}_0 + \cdots + \mathcal{M}_q$. Moreover, if $M = |\mathcal{M}_0 + \cdots + \mathcal{M}_q|$ then the total number of copies of cell $i \in \{0, \ldots, q\}$ at configuration $\mathcal{C}$ is, at most, M because the copies can only be produced by the application of a separation rule, and each application of this kind of rule consumes one object. Consequently, $(q+1) \cdot M$ is an upper bound of the number of cells at any configuration of the system.
3. In order to identify the cells created by the application of a separation rule, we modify the labels of the new membranes in the following manner:
   - The label of a cell will be a pair (i, σ) where $0 \leq i \leq q$ and $\sigma \in \{0,1\}^*$. At the initial configuration, the labels of the cells are $(0, \lambda), \ldots, (q, \lambda)$.
   - If a separation rule is applied to a cell labelled by (i, σ), then the new created cells will be labelled by $(i, \sigma 0)$ and $(i, \sigma 1)$, respectively. Cell $(i, \sigma 0)$ will contain the objects of cell (i, σ) which belong to Γ_0, and cell $(i, \sigma 1)$ will contain the objects of cell (i, σ) which belong to Γ_1.
   - Note that we can consider a lexicographical order over the set of labels (i, σ) in a natural way.
4. If cells labelled by (i, σ_i) and (j, σ_j) are engaged by a communication rule, then, after the application of the rule, both cells keep their labels.
5. A configuration of Π can be described by a multiset of labelled objects from $\{(a, i, \sigma) |\ a \in \Gamma \cup \{\lambda\}, 0 \leq i \leq q, \sigma \in \{0,1\}^*\}$.
6. Let $r \equiv (i, a_1 \cdots a_s / b_1 \cdots b_{s'}, j)$ be a communication rule of Π. If n is a natural number, then denote by $n \cdot LHS(r, (i, \sigma_i), (j, \sigma_j))$ the multiset of labelled objects "consumed" by applying n times rule r over cells (i, σ_i) and (j, σ_j). That is, $n \cdot LHS(r, (i, \sigma_i), (j, \sigma_j))$ is the following multiset

   $$(a_1, i, \sigma_i)^n \cdots (a_s, i, \sigma_i)^n (b_1, j, \sigma_j)^n \cdots (b_{s'}, j, \sigma_j)^n$$

   Similarly, $n \cdot RHS(r, (i, \sigma_i), (j, \sigma_j))$ denotes the multiset of labelled objects produced by applying n times rule r over cells (i, σ_i) and (j, σ_j). That is, $n \cdot RHS(r, (i, \sigma_i), (j, \sigma_j))$ is the following multiset

   $$(a_1, j, \sigma_j)^n \cdots (a_s, j, \sigma_j)^n (b_1, i, \sigma_i)^n \cdots (b_{s'}, i, \sigma_i)^n$$

7. If $\mathcal{C}_t$ is a configuration of Π we denote by $\mathcal{C}_t + \{(x, i, \sigma)/\sigma'\}$ the multiset obtained by replacing in $\mathcal{C}_t$ every occurrence of (x, i, σ) by (x, i, σ'). Besides, $\mathcal{C}_t + m$ ($\mathcal{C}_t \setminus m$, respectively) is used to denote that a multiset m of labelled objects is added (removed, respectively) to the configuration.

4.2 Efficiency of Tissue P Systems from $\widehat{\mathbf{TSC}}$

The goal of this section is to show that only tractable problems can be solved efficiently by using tissue P systems with communication rules, separation rules and without environment. That is, we will prove that $\mathbf{P} = \mathbf{PMC}_{\widehat{\mathbf{TSC}}}$.

For this purpose, given a family of recognizer tissue P system, we provide a deterministic algorithm $\mathcal{A}$ working in polynomial time that receives as input a recognizer tissue P system from $\widehat{\mathbf{TSC}}$ together with an input multiset, and reproduces the behaviour of a computation of such system. In particular, if the given tissue P system is confluent, then algorithm will provide the same answer of the system, that is, the answer of the algorithm is affirmative if and only if the input tissue P system has an accepting computation.

The pseudocode of the algorithm $\mathcal{A}$ is described as follows:

Input: A recognizer tissue P system Π from $\widehat{\mathbf{TSC}}$ and an input multiset m
  Initialization stage: the initial configuration $\mathcal{C}_0$ of $\Pi + m$
  $t \leftarrow 0$
  while $\mathcal{C}_t$ is a non halting configuration **do**
    Selection stage: Input $\mathcal{C}_t$, Output $(\mathcal{C}'_t, A)$
    Execution stage: Input $(\mathcal{C}'_t, A)$, Output $\mathcal{C}_{t+1}$
    $t \leftarrow t + 1$
  end while
Output: *Yes* if $\mathcal{C}_t$ is an accepting configuration, *No* otherwise

The selection stage and the execution stage implement a transition step of a recognizer tissue P system Π. Specifically, the selection stage receives as input a configuration $\mathcal{C}_t$ of Π at an instant t. The output of this stage is a pair $(\mathcal{C}'_t, A)$, where A encodes a multiset of rules selected to be applied to $\mathcal{C}_t$, and $\mathcal{C}'_t$ is the configuration obtained from $\mathcal{C}_t$ once the labelled objects corresponding to the application of rules from A have been consumed. The execution stage receives as input the output $(\mathcal{C}'_t, A)$ of the selection stage. The output of this stage is the next configuration $\mathcal{C}_{t+1}$ of $\mathcal{C}_t$. Specifically, at this stage, the configuration $\mathcal{C}_{t+1}$ is obtained from $\mathcal{C}'_t$ by adding the labelled objects produced by the application of rules from A.

Next, selection stage and execution stage are described in detail.

Selection stage.

Input: A configuration $\mathcal{C}_t$ of Π at instant t
  $\mathcal{C}'_t \leftarrow \mathcal{C}_t$; $A \leftarrow \emptyset$; $B \leftarrow \emptyset$
  for $r \equiv (i, u/v, j) \in R_C$ according to the order chosen **do**
    for each pair of cells $(i, \sigma_i), (j, \sigma_j)$ of $\mathcal{C}'_t$ according to the lexicographical order **do**
      $n_r \leftarrow$ maximum number of times that r is applicable to $(i, \sigma_i), (j, \sigma_j)$
      if $n_r > 0$ **then**
        $\mathcal{C}'_t \leftarrow \mathcal{C}'_t \setminus n_r \cdot LHS(r, (i, \sigma_i), (j, \sigma_j))$
        $A \leftarrow A \cup \{(r, n_r, (i, \sigma_i), (j, \sigma_j))\}$
        $B \leftarrow B \cup \{(i, \sigma_i), (j, \sigma_j)\}$

```
        end if
    end for
end for
for r ≡ [a]_i → [Γ_0]_i[Γ_1]_i ∈ R_S according to the order chosen do
    for each (a, i, σ_i) ∈ C'_t, according to the lexicographical order, and
         such that (i, σ_i) ∉ B do
        C'_t ← C'_t \ {(a, i, σ_i)}
        A ← A ∪ {(r, 1, (i, σ_i))}
        B ← B ∪ {(i, σ_i)}
    end for
end for
```

This algorithm is deterministic and works in polynomial time. Indeed, the cost in time of the previous algorithm is polynomial in the size of Π because the number of cycles of the first main loop **for** is of order $O(|R| \cdot \frac{(2M+q)(2M+q-1)}{2})$, and the number of cycles of the second main loop **for** is of order $O(|R| \cdot |\Gamma| \cdot (2M+q))$. Besides, the last loop includes a membership test of order $O(2M+q)$.

In order to complete the simulation of a computation step of the system Π, the execution stage takes care of the effects of applying the rules selected in the previous stage: updating the objects according to the RHS of the rules.

Execution stage.

```
Input: The output C'_t and A of the selection stage
    for each (r, n_r, (i, σ_i), (j, σ_j)) ∈ A do
        C'_t ← C'_t + n_r · RHS(r, (i, σ_i), (j, σ_j))
    end for
    for each (r, 1, (i, σ_i)) ∈ A do
        C'_t ← C'_t + {(λ, i, σ_i)/σ_i0}
        C'_t ← C'_t + {(λ, i, σ_i1)}
        for each (x, i, σ_i) ∈ C'_t according to the lexicographical order do
            if x ∈ Γ_0 then
                C'_t ← C'_t + {(x, i, σ_i)/σ_i0}
            else
                C'_t ← C'_t + {(x, i, σ_i)/σ_i1}
            end if
        end for
    end for
    C_{t+1} ← C'_t
```

This algorithm is deterministic and works in polynomial time. Indeed, the cost in time of the previous algorithm is polynomial in the size of Π because the number of cycles of the first main loop **for** is of order $O(|R|)$, and the number of cycles of the second main loop **for** is of order $O(|R| \cdot |\Gamma| \cdot (2M+q))$. Besides, inside the body of the last loop there is a membership test of order $O(|\Gamma|)$.

Throughout this algorithm we have deterministically simulated a computation of Π in such manner that the answer of the algorithm is affirmative if and only if the simulated computation is accepting.

Theorem 1. $\mathbf{P} = \mathbf{PMC}_{\widehat{\mathbf{TSC}}}$.

Proof. It suffices to prove that $\mathbf{PMC}_{\widehat{\mathbf{TSC}}} \subseteq \mathbf{P}$. Let $k \in \mathbb{N}$ such that $X \in \mathbf{PMC}_{\widehat{\mathbf{TSC}}(k)}$ and let $\{\Pi(n) : n \in \mathbb{N}\}$ be a family of tissue P systems from $\widehat{\mathbf{TSC}}(k)$ solving X according to Definition 3. Let (cod, s) be a polinomial encoding associated with that solution. If $u \in I_X$ is an instance of the problem X, then u will be processed by the system $\Pi(s(u)) + cod(u)$.

Let us consider the following algorithm $\mathcal{A}'$:

Input: `an instance` u `of the problem` X`.`
`Construct the system` $\Pi(s(u)) + cod(u)$`.`
`Run algorithm` $\mathcal{A}$ `with input` $\Pi(s(u)) + cod(u)$`.`
Output: *`Yes`* `if` $\Pi(s(u))+cod(u)$ `has an accepting computation,` *`No`* `otherwise`

The algorithm $\mathcal{A}'$ receives as input an instance u of the decision problem $X = (I_X, \theta_X)$ and works in polynomial time. The following assertions are equivalent:

1. $\theta_X(u) = 1$, that is, the answer of problem X to instance u is affirmative.
2. Every computation of $\Pi(s(u)) + cod(u)$ is an accepting computation.
3. The output of the algorithm with input u is *Yes*.

Hence, $X \in \mathbf{P}$.

□

Remark 1. From the previous theorem we deduce that $\mathbf{P} = \mathbf{PMC}_{\widehat{\mathbf{TSC}}(3)}$. In [23], a polynomial time solution of the `SAT` problem was given by a family of tissue P systems from $\mathbf{TSC}(3)$ according to Definition 3. Thus, $\mathbf{NP} \cup \mathbf{co\text{-}NP} \subseteq \mathbf{PMC}_{\mathbf{TSC}(3)}$. Hence, in the framework of tissue P systems with cell separation and communication rules of length at most 3, the environment provides a new borderline between efficiency and non-efficiency, assuming $\mathbf{P} \neq \mathbf{NP}$.

Remark 2. From the previous theorem we deduce that $\mathbf{P} = \mathbf{PMC}_{\widehat{\mathbf{TSC}}(2)}$. In [24], it was shown that $\mathbf{PMC}_{\mathbf{TDC}(k+1)} = \mathbf{PMC}_{\widehat{\mathbf{TDC}}(k+1)}$, for each $k \in \mathbb{N}$. In [25], a polynomial time solution of the `HAM-CYCLE` problem was given by a family of tissue P systems from $\mathbf{TDC}(2)$ according to Definition 3. Thus, $\mathbf{NP} \cup \mathbf{co\text{-}NP} \subseteq \mathbf{PMC}_{\mathbf{TDC}(2)} = \mathbf{PMC}_{\widehat{\mathbf{TDC}}(2)}$. Hence, in the framework of tissue P systems with communicaction rules of length at most 2 and without environment, the kind of rules (separation versus division) provides a new borderline between the efficiency and non-efficiency, assuming $\mathbf{P} \neq \mathbf{NP}$.

5 Conclusions and Further Works

The efficiency of cell-like P systems for solving **NP**-complete problems has been widely studied. The usual approach is to perform a space-time tradeoff that allows "efficient" (in terms of the number of steps of the computations) solutions to **NP**-complete problems in the framework of *Membrane Computing*. For instance, membrane division, membrane creation, and membrane separation are three efficient ways of obtaining exponential workspace in polynomial time that have been used in the literature. Such tools have been adapted to tissue–like P systems, and linear-time solutions to the `SAT` problem have been designed both in the model with cell division rules [19], as well as in the case of cell separation [13].

In this paper, the computational efficiency of tissue P systems with cell separation and *without environment* has been studied. We highlight the relevant role played by the environment in this framework from the point of view of efficiency.

Finally, two new borderlines between efficiency and non-efficiency are presented, assuming $\mathbf{P} \neq \mathbf{NP}$. The first of them is related with the environment and the second one is related to the kind of rules (separation versus division).

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