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THE ROLE OF THE DIRECTION IN TISSUE P SYSTEMS WITH CELL SEPARATION

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ABSTRACT

Tissue P systems with cell separation where the communication among cells is performed by means of symport and antiport rules are able to efficiently solve computationally hard problems in a feasible time by a space-time trade off. Symport and antiport rules formally capture the cases where a number of chemical substances pass through a membrane at the same time, with the help of each other, either in the same direction (*symport*) or in opposite directions (*antiport*).

The present paper investigates the role of the direction in communication rules from a computational complexity point of view. More precisely, the efficiency of tissue P systems with cell separation is analyzed in the case when their communication rules are all of the same type: either symport rules or antiport rules.

The main result is that in the framework of tissue P systems with cell separation, passing from using only symport rules to using only antiport rules amounts to passing from non-efficiency to efficiency, assuming that $\mathbf{P} \neq \mathbf{NP}$.

Keywords: Membrane Computing, Tissue P Systems, Cell Separation, Symport/antiport rules. Computational complexity

1. Introduction

Membrane Computing is an emergent branch of *Natural Computing* introduced by Gh. Păun at the end of 1998. It is inspired by the structure and functioning of living cells, and provide unconventional distributed, parallel, synchronous and non-deterministic computing devices, called P systems. The basic model consists of a hierarchical structure (a rooted labeled tree) composed by several membranes (the nodes of the tree), embedded into a main membrane called the skin (the root of the tree), and delimiting *compartments/regions* (space between a membrane and the immediately inner membranes, if any) in which one places *multisets* of *objects*. The objects evolve and pass through membranes in a synchronous parallel manner according to given *evolution rules*, also associated with the membranes.

Tissue P systems considered in this paper have two biological justifications: intercellular communication and cooperation between neurons. The common mathematical model of these two mechanisms is a net of processors (cells) dealing with symbols (chemical substances) and communicating these symbols by means of symport and antiport rules which were introduced to P systems in [7]. Moreover, two additional cell-inspired mechanisms have been considered in the framework of tissue P systems: *cell division* [8] and *cell separation* [4]. In the first case, the two new cells created during the cell division process contain exactly the same objects except for at most a pair of different objects, thus cell division produces *replication* of objects between two new cells. Cell separation is biologically justified by the phenomenon of cell fission: a cell is divided into two new cells such that the contents of the initial cell is *distributed* between two new cells. A class of *tissue P systems with cell separation* was presented in [5] and its computational efficiency was investigated in [5] and [10].

In this paper we study the efficiency of tissue P systems with cell separation such that either only the use of symport rules or only the use of antiport rules is allowed. That is, we analyze the relevance of the direction in the application of communication rules allowed in tissue P systems with cell separation, from a computational complexity point of view.

The paper is organized as follows: first, we recall some preliminaries, and then, the definition of tissue P systems with cell separation is given. Next, recognizer tissue P systems are briefly described and polynomial complexity classes associated with this kind of systems are introduced. Sections 3 and 4 are devoted to study properties of tissue P systems with cell separation and symport rules, and to analyze their efficiency, yielding the main result of the paper. Finally, conclusions and open problems are presented in the last section.

2. Preliminaries

An *alphabet* Γ is a non–empty set whose elements are called *symbols*. An ordered finite sequence of symbols of Γ is a *string* or *word* over Γ. As usual, the empty string (with length 0) will be 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* m over an alphabet Γ is a pair $m = (\Gamma, f)$ where $f : \Gamma \to \mathbb{N}$ is a mapping. For each $x \in \Gamma$ we say that $f(x)$ is the *multiplicity* of the symbol x in m. If $m = (\Gamma, f)$ is a multiset then its *support* is defined as $supp(m) = \{x \in \Gamma \mid f(x) > 0\}$. A multiset is finite if its support is a finite set. A *set* is a multiset such that the multiplicity of each element of its support, is equal to 1.

If $m = (\Gamma, f)$ is a finite multiset over Γ, and $supp(m) = \{a_1, \ldots, a_k\}$ then it will be denoted as $m = a_1^{f(a_1)} \ldots a_k^{f(a_k)}$ (here the order is irrelevant), and we say that $f(a_1) + \cdots + f(a_k)$ is the cardinal of m, denoted by $|m|$. The empty multiset is denoted by $\emptyset$. We also denote by $M_f(\Gamma)$ the set of all finite multisets over Γ.

Let $m_1 = (\Gamma, f_1)$ and $m_2 = (\Gamma, f_2)$ multisets over Γ. Then,

- The *union* of m_1 and m_2, denoted by $m_1 + m_2$, is the multiset (Γ, g), where $g = f_1 + f_2$, that is, $g(x) = f_1(x) + f_2(x)$ 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 $g = f_1(x) - f_2(x)$ if $f_1(x) \geq f_2(x)$ and $g(x) = 0$ otherwise.
- m_1 is a submultiset of m_2, denoted by $m_1 \subseteq m_2$, if $f_1(x) \leq f_2(x)$ for each $x \in \Gamma$.

Let $m = (\Gamma, f)$ be a multiset over Γ and let A be a set. We define the intersection $m \cap A$ as the multiset (Γ, g), where $g(x) = f(x)$ for each $x \in \Gamma \cap A$, and $g(x) = 0$ otherwise.

2.1. Tissue P Systems with Cell Separation

In formal models of membrane systems with cell separation, the cells are not polarized; the two cells obtained by separation have the same labels as the original cell, and if a cell is separated, its interaction with other cells or with the environment is blocked during the separation process. These assumptions, together with the original abstract concept of a P system [6], and previous models studied in [1, 2] and [4], motivated the following definition:

Definition 1 A *tissue P system with cell separation and communication rules* of degree $q \geq 1$ is a tuple $\Pi = (\Gamma, \Gamma_0, \Gamma_1, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$, 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. $\mathcal{E} \subseteq \Gamma$ is a finite alphabet.
4. $\mathcal{M}_1, \ldots, \mathcal{M}_q$ are multisets over Γ.
5. $\mathcal{R}$ is a finite set of rules of the following forms:

   Communication rules: $(i, u/v, j)$, for $i, j \in \{0, 1, \ldots, q\}, i \neq j$, $u, v \in M_f(\Gamma)$, $|u| + |v| > 0$;

   Separation rules: $[a]_i \rightarrow [\Gamma_0]_i[\Gamma_1]_i$, where $i \in \{1, \ldots, q\}$, $a \in \Gamma$ and $i \neq i_{out}$.
6. $i_{out} \in \{0, 1, \ldots, q\}$.

A tissue P system with cell separation and communication rules can be viewed as a set of q cells, labeled by $1, \ldots, q$ 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) $\mathcal{E}$ 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 an *antiport rule* if $u \neq \lambda$ and $v \neq \lambda$, otherwise it is a *symport rule*. This rule formally captures the cases where a number of chemical substances (represented by multisets u and v) pass through a cell at the same time, with the help of each other, either in the same direction (*symport*) or in opposite directions (*antiport*). A symport rule $(i, u/\lambda, j)$ provides a virtual arc from region i to region j. An antiport rule $(i, u/v, j)$ provides two arcs: one from region i

to region j and the other from region j to region i. Thus, every tissue P system has an underlying directed graph whose nodes are the regions of the system and the arcs are obtained from communication rules.

A communication rule $(i, u/v, j)$ is applicable to regions i, j if the multiset u is contained in region i and multiset v is contained in region j. When applying a communication 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 $|u|+|v|$.

A separation rule $[a]_i \to [\Gamma_0]_i[\Gamma_1]_i$ is applicable to cell i if object a is contained in that cell. 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, the 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. Note that if there are several copies of a, only one of them is consumed, the rest goes into one of the new cells. The output cell i_{out} cannot be separated.

The rules are used in a non-deterministic maximally parallel manner. At each step, all cells which can evolve must evolve in a maximally parallel way: we apply a multiset of rules which is maximal, no further applicable rule can be added. Separation rules impose a restriction: when a cell is separated, the separation rule is the only one which is applied for that cell at that step.

A *configuration* at any instant of a tissue P system is described by all multisets of objects over Γ associated with all the cells present in the system, and the multiset of objects over $\Gamma \setminus \mathcal{E}$ associated with the environment at that moment. The *initial configuration* is $\mathcal{C}_0 = (\mathcal{M}_1, \cdots, \mathcal{M}_q; \emptyset)$. 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 and communication rules 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: (a) the first term of the sequence is the initial configuration $\mathcal{C}_0$ of the system; (b) each non-initial configuration of the sequence is obtained from the previous configuration by applying rules of the system in the manner described above; and (c) if the sequence is finite (called *halting computation*) then the last term of the sequence is called *halting configuration.* Only halting computations give a result, which is encoded by the objects present in the output region i_{out} in the halting configuration.

If $\mathcal{C} = \{\mathcal{C}_t\}_{0 \le t \le r}$ 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 $\mathcal{C}$. We denote by $\mathcal{C}_t(i)$ the multiset of objects over Γ contained in <u>all cells</u> labeled by i (by applying separation rules different cells with the same label can be created) at configuration $\mathcal{C}_t$, and $\mathcal{C}_t(0)$ denotes the multiset of objects over $\Gamma \setminus \mathcal{E}$ contained in the environment at configuration $\mathcal{C}_t$. Finally, we denote by $\mathcal{C}_t^*$ the multiset $\mathcal{C}_t(0) + \mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$.

2.2. Recognizer Tissue P Systems with Cell Separation and Communication Rules

In order to study the computational efficiency of membrane systems, the notion of *recognizer tissue P systems* is introduced in [8].

Definition 2 A recognizer tissue P system with cell separation and communication rules of degree $q \geq 1$ is a tuple $\Pi = (\Gamma, \Gamma_0, \Gamma_1, \Sigma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$, where:

1. $(\Gamma, \Gamma_0, \Gamma_1, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{out})$ is a tissue P system with cell separation and communication rules of degree $q \geq 1$ (as defined in the previous section).
2. The working alphabet Γ has two distinguished objects `yes` and `no` being, at least, one copy of them present in some initial multisets $\mathcal{M}_1, \ldots, \mathcal{M}_q$, but none of them are present in $\mathcal{E}$.
3. Σ is an (input) alphabet strictly contained in Γ such that $\mathcal{E} \subseteq \Gamma \setminus \Sigma$.
4. $\mathcal{M}_1, \ldots, \mathcal{M}_q$ are multisets over $\Gamma \setminus \Sigma$.
5. $i_{in} \in \{1, \ldots, q\}$ is the input cell, and 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.

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

We say that a computation $\mathcal{C}$ is an *accepting computation* (respectively, *rejecting computation*) if object `yes` (respectively, object `no`) appears in the environment associated with the corresponding halting configuration of $\mathcal{C}$.

Note that, because of the condition that all computations halt, rules of the type $(i, \lambda/v, 0)$ with $v \subset \mathcal{E}$ are not allowed for recognizer systems.

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

Previous results in the literature concern the classes **TSC** and **TSC**(k), of recognizer tissue P systems with cell separation and no restriction on the direction of its communication rules.

For the case of recognizer tissue P systems using division rules instead of cell separation rules, the corresponding classes are denoted by **TDS**, **TDA** and **TDC**, respectively.

2.3. Polynomial Complexity Classes of Recognizer Tissue P systems

Let us recall that a *decision problem* is a pair (I_X, θ_X) where I_X is a language over a finite alphabet (whose elements are called *instances*) and θ_X is a total Boolean function over I_X. Next, we define the meaning of "efficient solution" to a decision problem in the framework of tissue P systems. Bearing in mind that tissue P systems are devices with a finite description, a countable family of tissue P systems will be necessary in order to solve (any instance of) a decision problem.

Definition 3 We say that a decision problem $X = (I_X, \theta_X)$ is solvable in polynomial time by a family $\mathbf{\Pi} = \{\Pi(n) \mid n \in \mathbb{N}\}$ of recognizer tissue P systems with cell separation and communication rules if the following holds:

1. The family $\mathbf{\Pi}$ is *polynomially uniform* by Turing machines, that is, there exists a deterministic Turing machine working in polynomial time such that on input 1^n, constructs the system $\Pi(n)$.
2. There exists a pair (cod, s) of polynomial-time computable functions over I_X such that:
   (a) for each instance $u \in I_X$, $s(u)$ is a natural number and $cod(u)$ is an input multiset of the system $\Pi(s(u))$;
   (b) for each $n \in \mathbb{N}$, $s^{-1}(n)$ is a finite set;
   (c) 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;
   (d) 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 $\theta_X(u) = 1$;
   (e) 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 polynomial time by means of families of systems from $\mathbf{R}$, as defined above. The class $\mathbf{PMC_R}$ is closed under complement and polynomial–time reductions [9].

2.4. On Efficiency of Tissue P Systems with Cell Separation

It is worth pointing out two important results related to the computational efficiency of tissue P systems with cell separation and communication rules: (a) only tractable problems can be efficiently solved by using families of such tissue P systems with

communication rules of length at most 2 ([3]), that is, $\mathbf{P} = \mathbf{PMC}_{\mathbf{TSC(2)}}$; and (b) an efficient solution to the SAT problem has been given by means of a family of such tissue P systems with communication rules of length at most 3 ([10]), hence $\mathbf{NP} \cup \mathbf{co} - \mathbf{NP} \subseteq \mathbf{PMC}_{\mathbf{TSC(3)}}$. Therefore, 3 is an optimal bound on the length of communication rules, with respect to the efficiency of tissue P systems with cell separation and communication rules (assuming that $\mathbf{P} \neq \mathbf{NP}$).

3. Representation of Tissue P Systems from TSS

First, we prove a technical result concerning recognizer tissue P systems with cell separation and symport rules.

Lemma 1 *Let $\Pi = (\Gamma, \Gamma_0, \Gamma_1, \Sigma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$ be a recognizer tissue P system of degree $q \geq 1$ from $\mathbf{TSS}(k)$, $k \geq 1$. Let $M = |\mathcal{M}_1 + \cdots + \mathcal{M}_q|$. Let $\mathcal{C} = \{\mathcal{C}_0, \ldots, \mathcal{C}_r\}$ be a computation of Π. For each t, $0 \leq t \leq r$, the following holds:*

1. *If $t < r$ then $\mathcal{C}^*_{t+1} \cap (\Gamma \setminus \mathcal{E}) \subseteq \mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E})$.*
2. *$\mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E}) \subseteq (\mathcal{M}_1 + \cdots + \mathcal{M}_q) \cap (\Gamma \setminus \mathcal{E})$, and $|\mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E})| \leq M$.*
3. *$|\mathcal{C}^*_0| = M$ and $|\mathcal{C}^*_{t+1}| \leq |\mathcal{C}^*_t| + M \cdot k$, for each $t < r$.*
4. *$|\mathcal{C}^*_t| \leq M \cdot (1 + k \cdot t)$.*
5. *The total number of objects handled by the system along the computation $\mathcal{C}$ (including objects from $\Gamma \setminus \mathcal{E}$ in the environment) is*

$$\mathcal{C}^*_0 + \mathcal{C}^*_1 + \cdots + \mathcal{C}^*_r \leq M \cdot (1 + r) \cdot (1 + \frac{k \cdot r}{2})$$

6. *The number of created cells along the computation $\mathcal{C}$ by the application of separation rules, is bounded by $M \cdot (1 + r) \cdot (2 + k \cdot r)$.*

Proof. 1. Let x be an object of the multiset $\mathcal{C}^*_{t+1} \cap (\Gamma \setminus \mathcal{E}) = (\mathcal{C}_{t+1}(0) + \mathcal{C}_{t+1}(1) + \cdots + \mathcal{C}_{t+1}(q)) \cap (\Gamma \setminus \mathcal{E})$. Let us start recalling that separation rules do not replicate objects and do not produce new objects. Then, at the $(t+1)$th transition step there are two possible scenarios:

- x has not been involved on the application of any communication rule, and then $x \in \mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E})$.
- x has been involved on a communication rule. In this case, either x came from the environment, and then $x \in \mathcal{C}_t(0) \cap (\Gamma \setminus \mathcal{E})$, or x came from another cell, and then $x \in (\mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)) \cap (\Gamma \setminus \mathcal{E})$. In both cases $x \in \mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E})$.

The multisets inclusion that we just proved can be strict for some values of t, in case separation rules were applied in that step, thus consuming some objects.

2. By induction on t. For $t = 0$ the result is trivial because of

$$\mathcal{C}^*_0 \cap (\Gamma \setminus \mathcal{E}) = (\mathcal{C}_0(0) + \mathcal{C}_0(1) + \cdots + \mathcal{C}_0(q)) \cap (\Gamma \setminus \mathcal{E}) = (\mathcal{M}_1 + \cdots + \mathcal{M}_q) \cap (\Gamma \setminus \mathcal{E})$$

Let t be such that $t < r$ and let us assume the result holds for t (*inductive hypothesis*). Then

$$\mathcal{C}^*_{t+1} \cap (\Gamma \setminus \mathcal{E}) \overset{(1)}{\subseteq} \mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E}) \overset{(i.h.)}{\subseteq} (\mathcal{M}_1 + \cdots + \mathcal{M}_q) \cap (\Gamma \setminus \mathcal{E})$$

Thus, $|\mathcal{C}^*_t \cap (\Gamma \setminus \mathcal{E})| \leq |(\mathcal{M}_1 + \cdots + \mathcal{M}_q) \cap (\Gamma \setminus \mathcal{E})| \leq M$.

3. Obviously, $|\mathcal{C}^*_0| = |\mathcal{C}_0(0) + \mathcal{C}_0(1) + \cdots + \mathcal{C}_0(q)| = |\mathcal{M}_1 + \cdots + \mathcal{M}_q| = M$. Now, let us compute $\mathcal{C}^*_{t+1} = \mathcal{C}_{t+1}(0) + \mathcal{C}_{t+1}(1) + \cdots + \mathcal{C}_{t+1}(q)$.
First, let us see what is the contribution to $\mathcal{C}^*_{t+1}$ of multiset $\mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$.

- Some objects from $\mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$ either do not evolve, or evolve by the application of symport rules between different cells of the system of the type $(i, u/\lambda, j)$ with $u \in \mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$. These objects will pass to $\mathcal{C}_{t+1}(1) + \cdots + \mathcal{C}_{t+1}(q)$.
- Some objects from $\mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$ evolve by the application of symport rules of the type $(i, u/\lambda, 0)$ with $u \in \mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)$. Only objects from $u \cap (\Gamma \setminus \mathcal{E})$ will be produced in $\mathcal{C}_{t+1}(0)$.

Now, let us see what is the contribution of multiset $\mathcal{C}_t(0)$ to $\mathcal{C}^*_{t+1}$.

- Some objects from $\mathcal{C}_t(0)$ do not evolve and they directly pass to $\mathcal{C}_{t+1}(0)$.
- The remaining objects from $\mathcal{C}_t(0)$ will evolve by means of rules of the type $(i, \lambda/v, 0)$. In this case, string v must contain some objects from $\mathcal{C}_t(0) \subseteq \Gamma \setminus \mathcal{E}$. Then, the number of new objects that can arrive to cells by the application of these rules is, at most, $|\mathcal{C}_t(0)| \cdot (k-1)$.

Hence, $|\mathcal{C}^*_{t+1}| \leq |\mathcal{C}_t(1) + \cdots + \mathcal{C}_t(q)| + |\mathcal{C}_t(0)| \cdot k \leq |\mathcal{C}^*_t| + M \cdot k$.

4. By induction on t. For $t = 0$ the result is trivial because of $|\mathcal{C}^*_0| = M$.
Let t be such that $t < r$ and the result holds for t. Hence,

$$|\mathcal{C}^*_{t+1}| \overset{(3)}{\leq} |\mathcal{C}^*_t| + M \cdot k \overset{(i.h.)}{\leq} M \cdot (1 + k \cdot t) + M \cdot k = M \cdot (1 + k \cdot (t+1))$$

5. It suffices to note that

$$\mathcal{C}^*_0 + \mathcal{C}^*_1 + \cdots + \mathcal{C}^*_r \leq M + (M(1+k)) + \cdots + (M(1+k \cdot r)) =$$
$$M \cdot (1+r) + M \cdot k \cdot \tfrac{r(r+1)}{2} = M \cdot (1+r) \cdot (1 + \tfrac{k \cdot r}{2})$$

6. Follows from (5) noting that the each application of a separation rule consumes one object and produces two new cells. □

Let $\Pi = (\Gamma, \Gamma_0, \Gamma_1, \Sigma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out})$ be a recognizer tissue P system from $\mathbf{TSS}(k)$, $k \geq 1$

1. We denote by $\mathcal{R}_{SY}$ (respectively, $\mathcal{R}_{SP}$) the set of symport rules (respectively, separation rules) of Π. We will fix total orders in $\mathcal{R}_{SY}$ and $\mathcal{R}_{SP}$.
2. In order to uniquely identify the cells created by the application of a separation rule, we modify the labels of the new cells in the following recursive manner:

- The label of a cell will be represented by a pair (i, σ) where $1 \leq i \leq q$ and $\sigma \in \{0,1\}^*$. At the initial configuration, the labels of the cells are $(1, \lambda), \ldots, (q, \lambda)$.
- If a separation rule is applied to a cell labeled by (i, σ), then we create two new labels by appending to the string σ a symbol 0 or a symbol 1. That is, the new created cells will be labeled by $(i, \sigma 0)$ and $(i, \sigma 1)$, respectively. Cell $(i, \sigma 0)$ will only contain the objects of cell (i, σ) which belong to Γ_0, if any, and cell $(i, \sigma 1)$ will only contain the objects of cell (i, σ) which belong to Γ_1, if any.
- Note that we can consider a lexicographical order over the set of labels of cells in the system along any computation.

3. If cells labeled 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.
4. A configuration $\mathcal{C}_t$ of Π is characterized by the multisets of objects over Γ contained in each individual cell and the multiset of objects over $\Gamma \setminus \mathcal{E}$ inside the environment. Then, $\mathcal{C}_t$ can be described by a multiset of labeled objects from $\{(a, i, \sigma) |\ a \in \Gamma \cup \{\lambda\}, 1 \leq i \leq q, \sigma \in \{0,1\}^*\} \cup \{(a, 0) |\ a \in \Gamma \setminus \mathcal{E}\}$. If $(a, i, \sigma) \in \mathcal{C}_t$ then we say that object a and cell labeled by (i, σ) are in configuration $\mathcal{C}_t$.

   Let us notice that the number of labels σ we need to identify all cells appearing along a computation of a tissue P system from **TSS** is cubic in the size of the initial configuration of the system and the length of the computation.
5. Let $r \equiv (i, a_1 \cdots a_s / \lambda, j)$ be a symport rule of Π, where $1 \leq i, j \leq q$ and $1 \leq s \leq k$. If n is a natural number, then we denote by $n \cdot LHS(r, (i, \sigma_i), (j, \sigma_j))$ the multiset of objects over Γ in cell (i, σ_i) consumed by applying n times the rule r to cells (i, σ_i) and (j, σ_j). That is, $n \cdot LHS(r, (i, \sigma_i), (j, \sigma_j))$ is the following multiset of objects $(a_1, i, \sigma_i)^n \cdots (a_s, i, \sigma_i)^n$. We also denote by $n \cdot RHS(r, (i, \sigma_i), (j, \sigma_j))$ the multiset of objects produced in cell (j, σ_j) by applying n times the rule r to cells (i, σ_i) and (j, σ_j). That is, $n \cdot RHS(r, (i, \sigma_i), (j, \sigma_j))$ is the following multiset of objects $(a_1, j, \sigma_j)^n \cdots (a_s, j, \sigma_j)^n$.
6. Let $r \equiv (i, \lambda / a_1 \cdots a_s, 0)$ be a symport rule of Π, where $1 \leq i \leq q$ and $1 \leq s \leq k$. If n is a natural number, then we denote by $n \cdot LHS(r, (i, \sigma_i), 0)$ the multiset of objects over $\Gamma \setminus \mathcal{E}$ in the environment consumed by applying n times the rule r involving the environment and cell (i, σ_i). That is, $n \cdot LHS(r, (i, \sigma_i), 0)$ is the following multiset of objects $((a_1, 0)^n \cdots (a_s, 0)^n) \cap ((\Gamma \setminus \mathcal{E}) \times \{0\})$. We also denote by $n \cdot RHS(r, (i, \sigma_i), 0)$ the multiset of objects produced in cell (i, σ_i) by applying n times the rule r involving the environment and cell (i, σ_i). That is, $n \cdot RHS(r, (i, \sigma_i), 0)$ is the following multiset of objects $(a_1, i, \sigma_i)^n \cdots (a_s, i, \sigma_i)^n$.
7. Let $r \equiv (i, a_1 \cdots a_s / \lambda, 0)$ be a symport rule of Π, where $1 \leq i \leq q$ and $1 \leq s \leq k$. If n is a natural number, then we denote by $n \cdot LHS(r, (i, \sigma_i), 0)$ the multiset of objects consumed in cell (i, σ_i) by applying n times the rule r involving the environment and cell (i, σ_i). That is, $n \cdot LHS(r, (i, \sigma_i), 0)$ is the following multiset of objects $(a_1, i, \sigma_i)^n \cdots (a_s, i, \sigma_i)^n$. We also denote by $n \cdot RHS(r, (i, \sigma_i), 0)$ the multiset of objects over $\Gamma \setminus \mathcal{E}$ in the environment produced by applying n times

the rule r involving the environment and cell (i, σ_i). That is, $n \cdot RHS(r, (i, \sigma_i), 0)$ is the following multiset of objects $((a_1, 0)^n \cdots (a_s, 0)^n) \cap ((\Gamma \setminus \mathcal{E}) \times \{0\})$.

8. If $\mathcal{C}_t$ is a configuration of Π, described as has been expressed in (4), then 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'), for $1 \leq i \leq q$. Besides, $\mathcal{C}_t + m$ ($\mathcal{C}_t \setminus m$, respectively) is used to denote that a multiset m of labeled objects is added (removed, respectively) to the configuration.

4. Efficiency of Tissue P Systems from TSS

The goal of this section is to show that only tractable problems can be solved efficiently by using tissue P systems with cell separation and symport rules. Specifically, we will show that $\mathbf{P} = \mathbf{PMC}_{\mathbf{TSS}(k)}$, for each $k \geq 1$.

For this purpose, we provide a deterministic algorithm $\mathcal{A}$ working in polynomial time that receives as input a pair (Π, m), where Π is a confluent tissue P system from $\mathbf{TSS}(k)$ that has a finite number of computations, all of them being halting computations, and m is an input multiset of Π.

Then, algorithm $\mathcal{A}$ reproduces the behaviour of one computation of $\Pi + m$, that is, the answer of $\mathcal{A}$ is affirmative if and only if the system $\Pi + m$ has an accepting computation (and then, any computation is an accepting one).

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

```
Input: a confluent system Π from TSS(k) and an input multiset m
  Initialization stage: the initial configuration C_0 of Π + m
  t ← 0
  while C_t is a non halting configuration do
     Selection stage: Input C_t, Output (C'_t, A)
     Execution stage: Input (C'_t, A), Output C_{t+1}
     t ← t + 1
  end while
Output: Yes if Π + m has an accepting computation, No otherwise
```

Figure 1: Pseudocode of Algorithm $\mathcal{A}$

Let (Π, m) be an input of $\mathcal{A}$. Let

$$\Pi = (\Gamma, \Gamma_0, \Gamma_1, \Sigma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, \mathcal{R}, i_{in}, i_{out}) \in \mathbf{TSS}(k).$$

Let $M = |\mathcal{M}_1 + \cdots + \mathcal{M}_q|$. Let p be a natural number such that any computation of $\Pi + m$ performs, at most, p transition steps. Then, from Lemma 1 the number of created cells along any computation by the application of separation rules, is bounded by $M \cdot (1 + p) \cdot (2 + k \cdot p)$.

The selection stage and the execution stage implement a transition step of a recognizer tissue P system $\Pi + m$. Specifically, the selection stage receives as input a configuration $\mathcal{C}_t$ of $\Pi + m$ at an instant t. The output of this stage is a pair $(\mathcal{C}'_t, A)$, where A encodes a maximal 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 labeled objects corresponding to the application of rules from A have been consumed. The selection is done taking into account that, for each step, a separation rule cannot be applied together with any other rule on the same cell (a special variable B is used for this). The execution stage receives as input the pair $(\mathcal{C}'_t, A)$ obtained from the selection stage. The output of this stage is the configuration in the next step, $\mathcal{C}_{t+1}$. Specifically, at this stage, the configuration $\mathcal{C}_{t+1}$ is obtained from $\mathcal{C}'_t$ by adding the labeled objects produced by the application of rules from A.

Selection stage and execution stage are described in detail in Figures 3 and 2, respectively.

Execution stage.
Input: The output C'_t and A of the selection stage
  for each $(r, n_r, (i, \sigma_i), (j, \sigma_j)) \in A$ **do**
    $C'_t \leftarrow C'_t + n_r \cdot RHS(r, (i, \sigma_i), (j, \sigma_j))$
  end for
  for each $(r, n_r, (i, \sigma_i), 0) \in A$ **do**
    $C'_t \leftarrow C'_t + n_r \cdot RHS(r, (i, \sigma_i), 0)$
  end for
  for each $(r, 1, (i, \sigma_i)) \in A$ **do**
    $\mathcal{C}'_t \leftarrow \mathcal{C}'_t + \{(\lambda, i, \sigma_i)/\sigma_i 0\}$
    $\mathcal{C}'_t \leftarrow \mathcal{C}'_t + \{(\lambda, i, \sigma_i 1)\}$
    for each $(x, i, \sigma_i) \in \mathcal{C}'_t$ according to the lexicographical order **do**
      if $x \in \Gamma_0$ **then**
        $\mathcal{C}'_t \leftarrow \mathcal{C}'_t + \{(x, i, \sigma_i)/\sigma_i 0\}$
      else
        $\mathcal{C}'_t \leftarrow \mathcal{C}'_t + \{(x, i, \sigma_i)/\sigma_i 1\}$
      end if
    end for
  end for
  $\mathcal{C}_{t+1} \leftarrow \mathcal{C}'_t$

Figure 2: Execution stage

The algorithm for Selection stage is deterministic and works in polynomial time. Indeed, the cost in time of such algorithm is polynomial on the size of Π because the number of cycles of the first main loop `for` is of the order

$$O(|\mathcal{R}| \cdot \frac{M(1+p)(2+kp) \cdot (M(1+p)(2+kp)-1)}{2}) \subseteq O(|\mathcal{R}| \cdot M^2 \cdot k^2 \cdot p^4)$$

and the number of cycles of the remaining loops `for` are of the order $O(|\mathcal{R}| \cdot M \cdot (1+kp))$. The algorithm for Execution stage is also deterministic and works in polynomial time. Indeed, the cost in time of such algorithm is polynomial on the size of Π because the number of cycles of the first main loop `for` is of the order $O(|\mathcal{R}| \cdot M^2 \cdot k^2 \cdot p^4)$, and the number of cycles of the second and the third main loop `for` are of the order

Selection stage.
Input: A configuration $\mathcal{C}_t$ of $\Pi + m$ at the instant t
$\mathcal{C}'_t \leftarrow \mathcal{C}_t$; $A \leftarrow \emptyset$; $B \leftarrow \emptyset$
for each $r \equiv (i, \lambda/v, j) \in \mathcal{R}_{SY}, 1 \leq i, j \leq q, i \neq j$ 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 each $r \equiv (i, \lambda/v, 0) \in \mathcal{R}_{SY}$ according to the order chosen **do**
  for each cell (i, σ_i) of $\mathcal{C}'_t$ according to the lexicographical order **do**
    $n_r \leftarrow$ maximum number of times that r is applicable to (i, σ_i)
    if $n_r > 0$ **then**
      $\mathcal{C}'_t \leftarrow \mathcal{C}'_t \setminus n_r \cdot LHS(r, (i, \sigma_i), 0)$
      $A \leftarrow A \cup \{(r, n_r, (i, \sigma_i), 0)\}$
      $B \leftarrow B \cup \{(i, \sigma_i)\}$
    end if
  end for
end for
for each $r \equiv (i, v/\lambda, 0) \in \mathcal{R}_{SY}$ according to the order chosen **do**
  for each cell (i, σ_i) of $\mathcal{C}'_t$ according to the lexicographical order **do**
    $n_r \leftarrow$ maximum number of times that r is applicable to (i, σ_i)
    if $n_r > 0$ **then**
      $\mathcal{C}'_t \leftarrow \mathcal{C}'_t \setminus n_r \cdot LHS(r, (i, \sigma_i), 0)$
      $A \leftarrow A \cup \{(r, n_r, (i, \sigma_i), 0)\}$
      $B \leftarrow B \cup \{(i, \sigma_i)\}$
    end if
  end for
end for
for each $r \equiv [a]_i \rightarrow [\Gamma_0]_i[\Gamma_1]_i \in \mathcal{R}_{SP}$ according to the order chosen **do**
  for each $(a, i, \sigma_i) \in \mathcal{C}'_t$ according to the lexicographical order **do**
    if $(i, \sigma_i) \notin B$ **then**
      $\mathcal{C}'_t \leftarrow \mathcal{C}'_t \setminus \{(a, i, \sigma_i)\}$
      $A \leftarrow A \cup \{(r, 1, (i, \sigma_i))\}$
      $B \leftarrow B \cup \{(i, \sigma_i)\}$
    end if
  end for
end for

Figure 3: Selection stage

$O(|\mathcal{R}| \cdot M \cdot k \cdot p^2)$. Besides, inside the body of the last loop there are two loops `for` giving a number of cycles of the order $O(|\Gamma|)$.

Throughout Algorithm $\mathcal{A}$ we have simulated a computation of Π in such manner that the answer of the algorithm is affirmative if and only if the computation simulated is an accepting computation.

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

Proof. We prove that $\mathbf{P} = \mathbf{PMC}_{\mathbf{TSS}(k)}$, for each $k \geq 1$. It suffices to prove that $\mathbf{PMC}_{\mathbf{TSS}(k)} \subseteq \mathbf{P}$, for each $k \geq 1$. For that, let $X \in \mathbf{PMC}_{\mathbf{TSS}(k)}$ and let $\{\Pi(n) : n \in \mathbb{N}\}$ be a family of tissue P systems from $\mathbf{TSS}(k)$ solving X according to Definition 3. Let (cod, s) be a polynomial 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 the pair $(\Pi(s(u)), cod(u))$.
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 a 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 $\mathcal{A}'$ with input u is *Yes*.

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

□

Consequences:

1. From the previous theorem we deduce that $\mathbf{P} = \mathbf{PMC}_{\mathbf{TSS}(3)}$.

2. In [10] a polynomial time solution of the `SAT` problem by a family of tissue P systems from $\mathbf{TSC}(3)$ according to Definition 3 was given. In that solution, the symport rules that appear are of the type $(i, u/\lambda, 0)$, with $|u| \leq 2$. Then we can rearrange the rules adding a new object # to the alphabet $\mathcal{E}$ of the environment, in such a way that symport rules $(i, u/\lambda, 0)$ can be replaced by equivalent antiport rules $(i, u/\#, 0)$. This proves that $\texttt{SAT} \in \mathbf{PMC}_{\mathbf{TSA}(3)}$. Thus, $\mathbf{NP} \cup \mathbf{co\text{-}NP} \subseteq \mathbf{PMC}_{\mathbf{TSA}(3)}$.

3. In the framework of tissue P systems with cell separation and communication rules with length at most 3, the kind of communication rules (only symport rules versus only antiport rules) provides a new borderline between the efficiency and non-efficiency.

5. Conclusions and Further Works

Cell separation provides a mechanism to generate an exponential workspace in linear time expressed in the number of cells of the system.

There are many cases where two chemical substances pass through a membrane at the same time, with the help of each other, either in the same direction, or in opposite directions.

In this paper we have shown that applying communication rules always in the same direction (symport rules), tissue P systems with cell separation are not computationally efficient, in the sense that they cannot solve **NP**–complete problems in polynomial time (according to Definition 3).

We have also obtained a surprising result, proving that in the framework of tissue P systems with cell separation and communication rules of length bounded by 3, the direction of the communication plays a crucial role. More precisely, we have shown that passing from using only symport rules to using only antiport rules amounts to passing from non-efficiency to efficiency, assuming that $\mathbf{P} \neq \mathbf{NP}$.

$$\begin{aligned} \mathbf{P} &= \mathbf{PMC}_{\mathbf{TSS}}(3) \\ \mathbf{NP} \cup \mathbf{co\text{-}NP} &\subseteq \mathbf{PMC}_{\mathbf{TSA}}(3) \end{aligned}$$

If we restrict ourselves to the case of antiport rules only, then we have a borderline of the efficiency related to the length of antiport rules: the cooperation of pairs of objects is not enough, we need three objects interacting together to reach efficiency

$$\begin{aligned} \mathbf{P} &= \mathbf{PMC}_{\mathbf{TSA}}(2) \\ \mathbf{NP} \cup \mathbf{co\text{-}NP} &\subseteq \mathbf{PMC}_{\mathbf{TSA}}(3) \end{aligned}$$

Nevertheless, when cell division is used in the framework of tissue P systems to generate exponential workspace in polynomial time, there is an advantage which needs to be taken into account: all the other objects in the cell are duplicated except the object that activates the cell division operation. Note that Lemma 1 will not be valid for this case.

We summarize here previous results obtained in the framework of tissue P systems with cell division. If no cooperation is allowed (that is, if we use only communication[1] rules of length 1), then only problems from class **P** can be efficiently solved. On the other hand, a solution to `HAM-CYCLE` has been given using a family in $\mathbf{TDC}(2)$, which can be adapted and transformed into a solution within either $\mathbf{TDS}(3)$ or $\mathbf{TDA}(3)$. Studying the computational power of classes $\mathbf{TDS}(2)$ and $\mathbf{TDA}(2)$ remains an open problem to be addressed in the future.

$$\begin{aligned} \mathbf{P} &= \mathbf{PMC}_{\mathbf{TDC}}(1) \\ \mathbf{NP} \cup \mathbf{co\text{-}NP} &\subseteq \mathbf{PMC}_{\mathbf{TDS}}(3) \\ \mathbf{NP} \cup \mathbf{co\text{-}NP} &\subseteq \mathbf{PMC}_{\mathbf{TDA}}(3) \end{aligned}$$

[1]Note that, by definition, antiport rules require objects on two regions, so communication rules of length 1 are actually symport rules.

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