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A Quick Survey of Tissue-Like P Systems

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Abstract. Membrane computing is a branch of natural computing, which abstracts from the architecture and the functioning of living cells. The models investigated in membrane computing are distributed and parallel computing devices, which are generically called P systems. Three main families have been considered until now: cell-like P systems, tissue-like P systems and neural-like P systems. In this work, we first present the definitions of tissue-like P systems and several variants of these systems, then some results about Turing universality and computational efficiency are recalled. Finally, a computational complexity theory within the framework of tissue-like P systems is introduced, polynomial complexity classes associated with several variants of tissue-like P systems are defined and some relevant results are presented. Different borderlines between efficiency and non-efficiency on the basis of the length of communication rules are presented.

Key-words: Bio-inspired computing, Membrane computing, Tissue P system, Universality, Computational complexity

1. Introduction

The research area of membrane computing was motivated by the structure and functioning of living cells, more specifically, by the role of membranes in compartmentalization of living cells into "protected reactors". This direction of research was initiated by Gh. Păun [40], and initial models were based on a cell-like arrangement of membranes, delimiting compartments where multisets of objects evolve according to (reaction) rules. The next important step in the development of membrane computing was to consider other membrane structure; thus, in [29], tissue-like

membrane systems were considered, where the membrane structure corresponds to an arbitrary graph. The latest development of this research area is neural-like membrane systems [23], which are motivated by spiking neural networks. For general information about membrane computing, one may consult [42, 44]; for up-to-date source of information and several software products for simulating P systems, one can go to the P systems web page `http://ppage.psystems.eu`.

After twenty years of development, a large number of bibliographic references has been achieved, including theory, applications and implementation software. From a theoretical point of view, most variants of P systems are Turing complete even when using a small number of membranes, rules of simple forms, and several ways of controlling the use of rules. Moreover, most of P systems are efficient, that is, with enhanced parallelism, P systems can solve **NP**-complete problems, even **PSPACE**-complete problems in a feasible time by trading space for time, that is, P systems can generate an exponential workspace in a linear time. The way to obtain such an exponential workspace is membrane division [41], string replication [27], membrane separation [32], membrane creation [30] and other operations.

As a modeling framework, P systems have several attractive features for handling discrete biological processes: scalability and programmability, ability to handle discrete data, easy understandability, inherent compartmentalization, etc. Until now applications of P systems have been investigated in several areas, e.g., optimization problem [60], ecology [6, 10], systems biology [28], computer graphics [31], fault diagnosis [45], fuzzy reasoning [47], and so on. One can refer to [9, 19, 59] for more details.

In this work, we focus on the theory of tissue P systems. We first present the definitions of tissue P systems and several variants of these systems, then some results about Turing universality and computational efficiency of the variants of tissue P systems are recalled. Finally, a computational complexity theory within the framework of tissue P systems is introduced, polynomial complexity classes associated with different variants of tissue P systems are defined and some relevant results are presented. Several frontiers between efficiency and non-efficiency on the basis of the length of communication rules are presented.

2. Tissue-like P systems

2.1. Basic tissue-like P systems

Tissue P systems are inspired by the structure of tissues and the way of communicating substances between two cells or between a cell and the environment. The membrane structure of a tissue P system is described by a graph whose nodes are the cells (the environment is viewed as a distinguished node) of the system and the arcs are obtained from communication rules. If an arc between two nodes exists, then they can communicate by means of communication (symport/antiport) rules [38]. Symport rules move objects from one region to other region together in one direction, while antiport rules move objects between two regions in opposite directions. We remark that in [29], rules are rewriting rules, and target indications are associated with each object obtained. The present work focuses on tissue P systems with communication rules evolving through applications of symport/antiport rules.

Formally, we recall the definition of tissue P systems (resp., tissue P systems with cell division and tissue P systems with cell separation [34]) [43].

1. *A tissue P system of degree $q \geq 1$ is a construct*

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

where:

(1) Γ *is a finite set of objects;*

(2) $\mathcal{E} \subseteq \Gamma$ *is the set of objects initially placed in the environment of the system, all of them available in an arbitrary number of copies;*

(3) $\mathcal{M}_i, 1 \leq i \leq q$, *are finite multisets of objects initially placed in the* q *cells of the system;*

(4) R *is a finite set of rules of the following forms:*

- *Symport rules:* $(i, u/\lambda, j)$, *where* $0 \leq i \neq j \leq q$, $u \in \Gamma^+$;
- *Antiport rules:* $(i, u/v, j)$, *where* $0 \leq i \neq j \leq q$, $u, v \in \Gamma^+$;

(5) $i_{out} \in \{0, 1, 2, \ldots, q\}$ *is the output region.*

When applying a symport rule $(i, u/\lambda, j)$, the multiset u of objects is sent from region i to region j; while when applying an antiport rule $(i, u/v, j)$, the multiset u of objects is sent from region i to region j, and simultaneously the multiset v of objects is sent from region j to region i.

2. *A tissue P system with cell division of degree $q \geq 1$ is a construct*

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

where:

(1) $\Pi = (\Gamma, \mathcal{E}, \Sigma, \mathcal{M}_1, \ldots, \mathcal{M}_q, R, i_{out})$ *is a tissue P system;*

(2) R *also contains cell division rules of the form:* $[\, a \,]_i \rightarrow [\, b \,]_i [\, c \,]_i$, *for* $i \in \{1, \ldots, q\}$, $i \neq i_{out}$, $a, b, c \in \Gamma$.

When applying a division rule $[\, a \,]_i \rightarrow [\, b \,]_i [\, c \,]_i$ to such cell i, under the influence of object a, such cell is divided into two new cells with the same label; in the first copy, object a is replaced by object b and in the second one, object a is replaced by object c; all the other objects residing in such cell i are replicated and copies of them are placed in the two new cells.

3. *A tissue P system with cell separation of degree $q \geq 1$ is a construct*

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

where:

(1) $\Pi = (\Gamma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, R, i_{out})$ *is a tissue P system;*

(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) R *also contains cell separation rules of the form:* $[\, a \,]_i \rightarrow [\, \Gamma_0 \,]_i [\, \Gamma_1 \,]_i$, *for* $i \in \{1, \ldots, q\}$, $i \neq i_{out}$, $a \in \Gamma$.

When applying a separation rule $[\, a \,]_i \rightarrow [\, \Gamma_0 \,]_i [\, \Gamma_1 \,]_i$ to such cell i, under the influence of object a, the cell with label i is separated into two new cells with the same label; at the same time, object a is consumed; the objects from Γ_0 are placed in the first cell and those from Γ_1 are placed in the second cell.

2.2. Some variants of tissue-like P systems

Tissue P systems with symport/antiport rules have been first investigated in [39], and then the model has been extended in [17] by adding a notion of state to communication channels, which can be modified when a communication rule is applied. Instead of using maximal parallelism, in [17], rules are used in a sequential manner for each channel and in a parallel manner for the system, that is, for each channel, at most one rule is used, but all communication channels evolve in parallel at the same time.

Besides the maximal parallelism, other strategies of using rules were also considered in membrane computing. In [33], the notion of the flat maximal parallelism was first proposed, where in each membrane, a maximal set of applicable rules is chosen and each rule in the set is applied exactly once in each step. In [55], the flat maximal parallelism strategy was investigated for tissue P systems with channel states, where on each channel, a maximal set of applicable rules is chosen and each rule in the set is applied once in each step. The flat maximal parallelism was also considered in tissue P systems with promoters [37].

Inspired from the living cell, several ways of generating new cells have been considered: membrane division [41], membrane separation [32], membrane creation [27], which make it possible to generate an exponential workspace, and can solve computationally hard problems in a feasible time. In [43], cell division is introduced into tissue P systems, and the SAT problem is solved by tissue P systems with cell division (see [13, 14, 16] for more details and solutions to different NP-complete problems using these systems). Tissue P systems with cell separation were proposed in [34], and a computational complexity theory in the framework of such P systems was investigated.

In biological systems the parallelism occurs at various levels and involves different components and chemical elements. If rules used involve objects from one or two regions, there have been proposed tissue P systems with conditional uniport [57] or evolution-communication [4, 5, 7]. If rules used involve objects from four regions, two acting as inputs and two as outputs, generalized communication P systems were proposed [11, 12, 24, 58].

Recently, tissue P systems with evolutional symport/antiport rules were proposed in [56], where objects were moved between cells or between a cell and the environment, and may be evolved during this process. Moreover, cell division is introduced into tissue P systems with evolutional symport/antiport rules, and a variant of P systems, called tissue P systems with evolutional symport/antiport rules and cell division was proposed [56]. In [36], cell separation is introduced into tissue P systems with evolutional symport/antiport rules, and a computational complexity theory in the framework of such P systems was investigated. There are several other classes of tissue P systems, for instance, introducing promoters or inhibitors [52], energy [1], proteins [8, 54], etc.

2.3. Computation power of tissue-like P systems

Many variants of tissue P systems have been proposed, and most of the models are Turing universal [2,3,18,25,53]. Here we briefly present the computation power of tissue P systems with channel states and tissue P systems with evolutional symport/antiport rules. For the computation power of other classes of tissue P systems, one can refer to [44] for more details.

Tissue P systems with channel states were proposed in [17], where the systems with one cell, rules of any weight and any number of states can only compute Parikh sets of matrix languages, while the systems with two cells are Turing universal when using minimal antiport rules and

arbitrarily many states or antiport rules of weight two and one state. Also the systems with arbitrarily many cells, minimal antiport rules and three states are Turing universal. In [55], the computation power of tissue P systems with channel states working in a flat maximally parallel way were investigated, where the systems with arbitrarily many cells, arbitrarily many states and antiport rules of length two are able to compute Parikh sets of finite languages; the systems with one cell, arbitrarily many states and noncooperative symport rules can compute at least all Parikh sets of matrix languages; moreover, the systems are Turing universal with one cell, one state and symport rules of length three or with two cells, arbitrarily many states and symport rules of length one or with arbitrarily many cells, four states and symport rules of length one.

In tissue P systems, objects evolve by means of symport/antiport rules, and objects just change their place within the system. In [56], tissue P systems with evolutional symport/antiport rules were considered, where objects may be evolved when they are moved between cells or between a cell and the environment. It is proved that tissue P systems with evolutional symport/antiport rules are Turing universal by using one cell and evolutional symport rules of length at most three or evolutional antiport rules of length at most four [56].

In the next section, we will recall the computational complexity results for tissue P systems with symport/antiport rules (resp., tissue P systems with evolutional symport/antiport rules) and cell division or cell separation.

3. Computational complexity of tissue P systems

3.1. Recognizer tissue P systems with cell division or cell separation

In order to solve decision problems, the notions from classical Computational Complexity Theory are considered in membrane computing. Here we define recognizer tissue P systems with cell division [43] or cell separation [34].

4. *A recognizer tissue P system with cell division of degree $q \geq 1$ is a tuple*

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

where

- $(\Gamma, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, R, i_{out})$ *is a tissue P system with cell division of degree $q \geq 1$;*
- Γ *contains two distinguished objects* `yes` *and* `no`*;*
- Σ *is an (input) alphabet contained in Γ;*
- $\mathcal{M}_1, \ldots, \mathcal{M}_q$*, are finite multisets over $\Gamma \setminus \Sigma$;*
- $i_{in} \in \{1, \ldots, q\}$ *is the input cell, and $i_{out} = 0$;*
- *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 environment at the last step of the computation.*

5. *A recognizer tissue P system with cell separation of degree $q \geq 1$ is a tuple*

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

where

- *the tuple $(\Gamma, \Gamma_0, \Gamma_1, \mathcal{E}, \mathcal{M}_1, \ldots, \mathcal{M}_q, R, i_{out})$ is a tissue P system with cell separation of degree $q \geq 1$, where Γ strictly contains an (input) alphabet Σ and two distinguished objects* `yes`, `no`, *and $\mathcal{M}_i$ $(1 \leq i \leq q)$ are multisets over $\Gamma \setminus \Sigma$;*
- *$i_{in} \in \{1, \ldots, q\}$ is the input cell and i_{out} is the label of the environment;*
- *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 at the last step of the computation.*

A computation $\mathcal{C}$ is said to be an accepting computation (resp., rejecting computation) of a recognizer tissue P system with cell division or with cell separation if object `yes` (resp., object `no`) appears in the environment when the computation reaches the halting configuration, while neither object `yes` nor `no` appears in the environment when the computation cannot stop.

We denote by TC (resp., TDC, TSC) the class of recognizer tissue P systems (resp., with cell division or cell separation). For each natural number $k \geq 1$, we denote by $TC(k)$ (resp., $TDC(k)$, $TSC(k)$) the class of recognizer tissue P systems (resp., with cell division or cell separation) and communication rule of length at most k (the length of a symport/antiport rule is the total number of objects involved in the rule). If the alphabet of the environment is empty, then we denote by $\widehat{TC}$, $\widehat{TDC}$, $\widehat{TSC}$, $\widehat{TC}(k)$, $\widehat{TDC}(k)$, $\widehat{TSC}(k)$, respectively, the corresponding classes.

We denote by TEC (resp., $TDEC$, $TSEC$) the class of recognizer tissue P systems with evolutional symport/antiport rules (resp., and cell division or cell separation). If the length of an evolutional communication rule is the total number of objects involved in the rule, for each natural number $k \geq 1$, we denote by $TEC(k)$ (resp., $TDEC(k)$, $TSEC(k)$) the class of recognizer tissue P systems (resp., with cell division or cell separation) and evolutional symport/antiport rule of length at most k. If the alphabet of the environment is empty, then we denote by $\widehat{TEC}$, $\widehat{TDEC}$, $\widehat{TSEC}$, $\widehat{TEC}(k)$, $\widehat{TDEC}(k)$, $\widehat{TSEC}(k)$, respectively. If the length of an evolutional symport/antiport rule is defined as an ordered pair whose first component is the total number of objects involved in the left hand side of the rule and the second component is the total number of objects involved in the right hand side of the rule, then we denote by $TEC(k_1, k_2)$, $TDEC(k_1, k_2)$, $TSEC(k_1, k_2)$, $\widehat{TEC}(k_1, k_2)$, $\widehat{TDEC}(k_1, k_2)$, $\widehat{TSEC}(k_1, k_2)$, respectively.

Next, we present the definition of solving a problem in a uniform way by means of families of recognizer tissue P systems with cell division or cell separation [46].

6. *Let $\mathcal{R}$ be a class of recognizer tissue P systems with input cell. 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 tissue P systems from $\mathcal{R}$ in a uniform way, and we denote this by $X \in \mathbf{PMC}_{\mathcal{R}}$ if the following conditions hold:*

- *The family $\mathbf{\Pi}$ is polynomially uniform by Turing machines.*
- *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; and (c) the family $\mathbf{\Pi}$ is polynomially bounded, sound and complete with regard to (X, cod, s).*

Let $\mathcal{R}$ be a class of recognizer tissue P systems (resp., with cell division or with cell separation). We denote by $\mathbf{PMC}_{\mathcal{R}}$ the set of all decision problems that can be solved in polynomial time by means of families of systems from $\mathcal{R}$. The class $\mathbf{PMC}_{\mathcal{R}}$ is closed under complement and polynomial-time reductions [49].

3.2. Efficiency of tissue P systems with cell division or cell separation

In this subsection, we give some known results about the computational efficiency of several models of tissue P systems, that is, their capability to solve computationally hard problems in an efficient way.

(1) *Basic tissue P systems*

A basic tissue P system is defined as in Definition 1. In [15], it was shown that families of recognizer tissue P systems which solves a decision problem can be efficiently simulated by a family of recognizer transition P systems solving the same problem. Moreover, it is well known that families of recognizer transition P systems can only solve problems in class **P** in polynomial-time [22]. Hence we have the following result.

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

(2) *Tissue P systems with cell division or cell separation*

By using the technique of dependency graph, it is shown that tissue P systems with cell division and communication rules of length at most 1 can only efficiently solve problems in class **P** [21].

Theorem 2. $\mathbf{P} = \mathbf{PMC}_{TDC(1)}$.

If we consider tissue P systems with cell division and communication rules of length at most 2, it is shown that the HAM−CYCLE problem (a well known **NP**-complete problem [20]) can be efficiently solved in polynomial-time by such systems [51]. Hence we have:

Theorem 3. $\mathtt{HAM-CYCLE} \in \mathbf{PMC}_{TDC(2)}$.

Theorem 4. $\mathbf{NP} \cup \mathbf{co-NP} \subseteq \mathbf{PMC}_{TDC(2)}$.

By using the simulation technique, it is proved that only problems in class **P** can be solved in polynomial-time by families of tissue P systems with cell separation when using communication rules of length at most 2 [35].

Theorem 5. $\mathbf{P} = \mathbf{PMC}_{TSC(2)}$.

If we consider tissue P systems with cell separation and communication rules of length at most 3, it is shown that the SAT problem can be efficiently solved in polynomial-time by such systems [50]. Hence we have:

Theorem 6. $\mathtt{SAT} \in \mathbf{PMC}_{TSC(3)}$.

Theorem 7. $\mathbf{NP} \cup \mathbf{co-NP} \subseteq \mathbf{PMC}_{TSC(3)}$.

(3) *Tissue P systems with cell division (or cell separation) and without environment*

Now we consider tissue P systems with cell division (or cell separation) and without environment.

By using the algorithmic technique, it is shown that families of tissue P systems with cell separation and without environment can only solve problems in class **P** [26]. Hence we have:

Theorem 8. $\mathbf{P} = \mathbf{PMC}_{\widehat{TSC}}$.

By using the simulation technique, it is shown that each family of recognizer tissue P systems with cell division when using communication rules of length at most $k \geq 1$ and solve a decision problem X in polynomial-time, can be efficiently simulated by a family of recognizer tissue P systems with cell division and without environment when using communication rules of length at most $k \geq 1$, solving X in polynomial-time [48].

Theorem 9. *For each $k \geq 1$ we have:* $\mathbf{PMC}_{\widehat{TDC}(k)} = \mathbf{PMC}_{TDC(k)}$.

3.3. Efficiency of tissue P systems with evolutional symport/antiport rules and cell division or cell separation

Evolutional symport/antiport rules were considered in tissue P systems in [56], and also cell division rules were introduced into such P systems. In [36], tissue P systems evolutional symport/antiport rules and cell separation were proposed, and computational complexity of such P systems was investigated.

Bearing in mind that any classical symport/antiport rule of the form $(i, u/v, j)$ can be considered as a particular case of the evolutional symport/antiport rule $[\, u\,]_i[\, v\,]_j \rightarrow [\, v\,]_i[\, u\,]_j$, the following results are obtained.

Theorem 10. *For $\mathbf{X} \in \{\mathbf{D}, \mathbf{S}\}$, we have $\mathbf{TXC} \subseteq \mathbf{TXEC}$.*

Theorem 11. *For $\mathbf{X} \in \{\mathbf{D}, \mathbf{S}\}$ and for each $k \geq 1$, we have*

$$\mathbf{TXC}(k) \subseteq \mathbf{TXEC}(k, k) \subseteq \mathbf{TXEC}(2k).$$

Theorem 12. *For $\mathbf{X} \in \{\mathbf{D}, \mathbf{S}\}$ and for each $k_1, k_2 \geq 1$, we have*

$$\mathbf{TXEC}(k_1, k_2) \subseteq \mathbf{TXEC}(k_1 + k_2).$$

In [56], it is shown that only tractable problems can be efficiently solved by families of systems from $TDEC(2)$, but the SAT problem can be solved by a family of systems from $TDEC(4)$.

Theorem 13. $\mathbf{PMC}_{TDEC(1)} = \mathbf{PMC}_{TDEC(2)} = \mathbf{P}$.

Theorem 14. $\mathtt{SAT} \in \mathbf{PMC}_{TDEC(4)}$.

In [36], it is shown that only tractable problems can be efficiently solved by families of systems from $TSEC(n, 1)$ or from $TSEC(1, n)$, for each natural number $n \geq 1$; moreover, the SAT problem can be solved in polynomial time by a family of systems from $TSEC(3, 2)$.

Theorem 15. *For each natural number $n \geq 1$, we have*

$$\mathbf{PMC}_{TSEC(n,1)} = \mathbf{PMC}_{TSEC(1,n)} = \mathbf{P}.$$

Theorem 16. $\mathtt{SAT} \in \mathbf{PMC}_{TSEC(3,2)}$.

4. Conclusions and remarks

In this work, a survey of tissue-like P systems has been presented, including several variants of such systems. Additionally, some results about Turing universality and computational efficiency have been recalled. Moreover, a computational complexity theory within the framework of tissue P systems with symport/antiport rules (resp., with evolutional symport/antiport rules), with or without environment and using cell division or cell separation has been recalled. Additionally, polynomial complexity classes associated with several variants of tissue P systems are defined and some relevant results have been defined. Finally, different borderlines between efficiency and non-efficiency on the basis of the length of communication rules have been presented.

In subsection 2.2, many variants of tissue P systems have been introduced, several of them are inspired by some basic features of biological membranes or other biological processes. An important research line is to consider new variants of tissue P systems and investigate the computational property of such P systems.

From subsection 3.2, we see that many problems remain open about tissue P systems with evolutional symport/antiport rules and cell division or cell separation. For instance, can **NP**-complete problems be solved by a family of systems from $TDEC(3)$? What is the computational efficiency of a family of systems from $TSEC(2,2)$?

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References

[1] ALHAZOV A., FREUND R., LEPORATI A., OSWALD M., ZANDRON C., (Tissue) *P Systems with Unit Rules and Energy Assigned to Membranes*, Fund. Informa. **74**(4), 391–408, 2006.

[2] ALHAZOV A., FREUND R., OSWALD M., *Tissue P Systems with Antiport Rules and Small Numbers of Symbols and Cells*, Lect. Notes Comput. Sci. 3572, 100–111, 2005.

[3] ARDELEAN I., DÍAZ-PERNIL D., GUTIÉRREZ-NARANJO M. A., PEÑA-CANTILLANA F., REINA-MOLINA R., SARCHIZIAN I., *Counting Cells with Tissue-Like P Systems*, In Proceedings of the Tenth Brainstorming Week on Membrane Computing, pp. 69–78. Fénix Editora, Sevilla, 2012.

[4] Bernardini, F., Freund, R.: Tissue P Systems with Communication Modes. Lect. Notes Comput. Sci. 4361, 170–182, 2006.

[5] BERNARDINI F., GHEORGHE M., *Cell Communication in Tissue P Systems: Universality Results*, Soft Comput. 9, 640–649, 2005.

[6] BESOZZI D., CAZZANIGA P., PESCINI D., MAURI G., *Modelling Metapopulations with Stochastic Membrane Systems*. BioSystems **91**(3), 499–514, 2008.

[7] CAVALIERE M., *Evolution-Communication P Systems*, Lect. Notes Comput. Sci. 2597, 134–145, 2003.

[8] CHRISTINA A. H., DÍAZ-PERNIL D., MATHU T., *A Uniform Family of Tissue P Systems with Protein on Cells Solving 3-Coloring in Linear Time*, Nat. Comput. **17**(2), 311–319, 2018.

[9] CIOBANU G., PĂUN Gh., PÉREZ-JIMÉNEZ M. J., Applications of Membrane Computing. Springer-Verlag, Heidelberg, 2006.

[10] COLOMER M. A., MARGALIDA A., SANUY D., PÉREZ-JIMÉNEZ M. J., *A Bio-Inspired Computing Model as a New Tool for Modeling Ecosystems: The Avian Scavengers as a Case Study*, Ecol. Model. **222**(1), 33–47, 2011.

[11] CSUHAJ-VARJÚ E., VASZIL G., VERLAN S., *On Generalized Communicating P Systems with One Symbol*, Lect. Notes Comput. Sci. 6501, 160–174, 2010.

[12] CSUHAJ-VARJÚ E., VERLAN S., *On Generalized Communicating P Systems with Minimal Interaction Rules*. Theor. Comput. Sci. 412, 124–135, 2011.

[13] DÍAZ-PERNIL D., GUTIÉRREZ-NARANJO M. A., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., *Solving Subset Sum in Linear Time by Using Tissue P System with Cell Division*, Lect. Notes Comput. Sci. 4527, 170–179, 2007.

[14] DÍAZ-PERNIL D., GUTIÉRREZ-NARANJO M. A., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., *A Uniform Family of Tissue P System with Cell Division Solving 3-Col in A Linear Time*, Theor. Comput. Sci. **404**(1), 76–87, 2008.

[15] DÍAZ-PERNIL D., GUTIÉRREZ-NARANJO M. A., PÉREZ-JIMÉNEZ Romero-Jiménez, Á., *Efficient Simulation of Tissue-Like P Systems by Transition Cell-Like P Systems*. Nat. Comput. **8**(4), 797–806, 2009.

[16] DÍAZ-PERNIL D., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., ROMERO-JIMÉNEZ Á., *Computational Efficiency of Cellular Division in Tissue-like Membrane Systems*, Rom. J. Inf. Sci. Tech. **11**(3), 229–241, 2008.

[17] FREUND R., PĂUN Gh., PÉREZ-JIMÉNEZ M. J., *Tissue P Systems with Channel States*, Theor. Comput. Sci. **330**(1), 101–116, 2005.

[18] FREUND R., VERLAN S., (Tissue) *P Systems Working in the k-Restricted Minimally or Maximally Parallel Transition Mode*, Nat. Comput. 10, 821–833, 2011.

[19] Frisco, P., Gheorghe, M., Pérez-Jiménez, M.J.: Applications of Membrane Computing in Systems and Synthetic Biology. Springer International Publishing, Switzerland, 2014.

[20] GAREY M. R., JOHNSON D. J., *Computers and Intractability: A Guide to the Theory of NP-Completeness*, W. H. Freeman, San Francisco, 1979.

[21] GUTIÉRREZ-ESCUDERO R., PÉREZ-JIMÉNEZ M. J., RIUS-FONT M., *Characterizing Tractability by Tissue-Like P Systems*, Lect. Notes Comput. Sci. 5957, 289–300, 2010.

[22] GUTIÉRREZ-NARANJO M. A., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., ROMERO-CAMPERO F. J., ROMERO-JIMÉNEZ Á., *Characterizing Tractability by Cell-Like Membrane Systems*, In K.G. Subramanian, K. Rangarajan, M. Mukund (eds.) Formal Models, Languages and Applications, World Scientific, Singapore, pp. 137–154. 2006.

[23] IONESCU M., PĂUN Gh., YOKOMORI T., *Spiking Neural P Systems*, Fund. Informa. **71**(2-3), 279–308, 2006.

[24] KRISHNA S. N., GHEORGHE M., IPATE F., CSUHAJ-VARJÚ E., CETERCHI R., *Further Results on Generalised Communicating P Systems*, Theor. Comput. Sci. 701 146–160, 2017.

[25] KRISHNA S. N., LAKSHMANAN K., RAMA R., *Tissue P Systems with Contextual and Rewriting Rules*, Lect. Notes Comput. Sci. 2597, 339–351, 2003.

[26] MACÍAS L. F., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., RIUS M., VALENCIA-CABRERA L., *The Efficiency of Tissue P Systems with Cell Separation Relies on the Environment*, Lect. Notes Comput. Sci. 7762, 243–256, 2013.

[27] MADHU M., PRAKASH V. J., KRITHIVASAN K., *Rewriting Tissue P Systems*, J. Univ. Computer Sci., **10**(9), 1250–1271, 2004.

[28] MANCA V., BIANCO L., *Biological Networks in Metabolic P Systems*, BioSystems, **91**(3), 489–498, 2008.

[29] MARTÍN-VIDE C., PAZOS J., PĂUN Gh., RODRIGUEZ-PATON A., *Tissue P Systems*, Theor. Comput. Sci. **296**(2), 295–326, 2003.

[30] MUTYAM M., KRITHIVASAN K., *P Systems with Membrane Creation: Universality and Efficiency*, Lect. Notes Comput. Sci. 2055, 276–287, 2001.

[31] NAGY B., SZEGEDI L., *Membrane Computing and Graphical Operating Systems*, J. Univers. Comput. Sci. **12**(9), 1312–1331, 2006.

[32] PAN L., ISHDORJ T.-O., **P Systems with Active Membranes and Separation Rules**, J. Univ. Computer Sci., 10, 630–649, 2004.

[33] PAN L., PĂUN Gh., SONG B., *Flat Maximal Parallelism in P Systems with Promoters*, Theor. Comput. Sci. 623, 83–91, 2016.

[34] PAN L., PÉREZ-JIMÉNEZ M. J., *Computational Complexity of Tissue-Like P Systems*, J. Complexity **26**(3), 296–315, 2010.

[35] PAN, L., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., RIUS M., *New Frontiers of the Efficiency in Tissue P Systems*, In Pan, L., Păun, Gh., Song, T. (eds.) Pre-proceedings of Asian Conference on Membrane Computing (ACMC 2012), Huazhong University of Science and Technology, Wuhan, China, October 15-18, pp. 61–73, 2012.

[36] PAN L., SONG B., VALENCIA-CABRERA L., PÉREZ-JIMÉNEZ M. J., *The Computational Complexity of Tissue P Systems with Evolutional Symport/Antiport Rules*, Complexity, Article ID 3745210, 21 pages, 2018.

[37] PAN L., WANG Y., JIANG S., SONG B., *Flat Maximal Parallelism in Tissue P Systems with Promoters*, Rom. J. Inf. Sci. Tech. **20**(1), 42–56, 2017.

[38] PĂUN A., PĂUN Gh., *The Power of Communication: P Systems with Symport/Antiport*, New Generat. Comput. **20**(3), 295–305, 2002.

[39] PĂUN A., PĂUN Gh., ROZENBERG G., *Computing by Communication in Networks of Membranes*, Int. J. Found. Comput. S. 13, 779–798, 2002.

[40] PĂUN Gh., *Computing with Membranes*, J. Comput. Syst. Sci. **61**(1), 108–143, 2000.

[41] PĂUN Gh., *P Systems with Active Membranes: Attacking NP-Complete Problems*, J. Auto. Lang. Comb. **6**(1), 75–90, 2001.

[42] PĂUN Gh., *Membrane Computing: An Introduction*, Springer-Verlag, Berlin, 2002.

[43] PĂUN Gh., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., *Tissue P Systems with Cell Division*, Int. J. Comput. Commun. **3**(3), 295–303, 2008.

[44] PĂUN Gh., ROZENBERG G. SALOMAA A.(Eds.), *The Oxford Handbook of Membrane Computing*, Oxford University Press, New York, 2010.

[45] PENG H., WANG J., SHI P., PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., *Fault Diagnosis of Power Systems Using Fuzzy Tissue-Like P Systems*, Integr. Comput-Aid. E. **24**(4),401–411, 2017.

[46] PÉREZ-JIMÉNEZ M. J., *An Approach to Computational Complexity in Membrane Computing*, Lect. Notes Comput. Sci. 3365, 85–109, 2005.

[47] PÉREZ-JIMÉNEZ M. J., GRACIANI C., ORELLANA-MARTIN D., RISCOS-NÚÑEZ A., ROMERO-JIMÉNEZ Á., VALENCIA-CABRERA L., *Fuzzy Reasoning Spiking Neural P Systems Revisited: A Formalization*, Theor. Comput. Sci. 701, 216–225, 2017.

[48] PÉREZ-JIMÉNEZ M. J., RISCOS-NÚÑEZ A., RIUS-FONT M., ROMERO-CAMPERO F. J., *The Role of the Environment in Tissue P Systems with Cell Division*, In García-Quismondo M., Macías-Ramos L. F., Păun Gh., Valencia-Cabrera L. (eds.) Proceedings of the Tenth Brainstorming Week on Membrane Computing, Volume II, Seville, Spain, January 30-February 3, 2012, Report RGNC 01/2012, Fénix Editora, pp. 89-104, 2012.

[49] PÉREZ-JIMÉNEZ M. J., ROMERO-JIMÉNEZ Á., SANCHO-CAPARRINI F., *Complexity Classes in Models of Cellular Computing with Membranes*, Nat. Comput. **2**(3), 265–285, 2003.

[50] PÉREZ-JIMÉNEZ M. J., SOSÍK P., *An Optimal Frontier of the Efficiency of Tissue P Systems with Cell Separation*, Fund. Informa. **138**(1-2), 45–60, 2015.

[51] PORRECA A. E., MURPHY N., PÉREZ-JIMÉNEZ M. J., *An Optimal Frontier of the Efficiency of Tissue P Systems with Cell Division*, In Garcí-Quismondo M., Macías-Ramos L. F., Păun Gh., Pérez-Hurtado I., Valencia-Cabrera L. (eds.) Proceedings of the Tenth Brainstorming Week on Membrane Computing, Volume II, Seville, Spain, January 30-February 3, 2012, Report RGNC 01/2012, Fénix Editora, pp. 141–166, 2012.

[52] SONG B., PAN L., *Computational Efficiency and Universality of Timed P Systems with Active Membranes*, Theor. Comput. Sci. 567, 74–86, 2015.

[53] SON B., PAN L., *The Computational Power of Tissue-Like P Systems with Promoters*, Theor. Comput. Sci. 641, 43–52, 2016.

[54] SONG B., PAN L., PÉREZ-JIMÉNEZ M. J., *Tissue P Systems with Protein on Cells*, Fundam. Inform. 144, 77–107, 2016.

[55] SONG B., PÉREZ-JIMÉNEZ M. J., PĂUN Gh., PAN L., *Tissue P Systems with Channel States Working in the Flat Maximally Parallel Way*, IEEE Trans. NanoBiosci. **15**(7), 645–656, 2016.

[56] SONG B., ZHANG C., PAN L., *Tissue-Like P Systems with Evolutional Symport/Antiport Rules*, Inf. Sci. 378, 177–193, 2017.

[57] VERLAN S., BERNARDINI F., GHEORGHE M., MARGENSTERN M., *Computational Completeness of Tissue P Systems with Conditional Uniport*, Lect. Notes Comput. Sci. 4361, 521–535, 2006.

[58] VERLAN S., BERNARDINI F., GHEORGHE M., MARGENSTERN M., *Generalized Communicating P Systems*, Theor. Comput. Sci. 404, 170–184, 2008.

[59] ZHANG G., PÉREZ-JIMÉNEZ M. J., GHEORGHE M., *Real-Life Applications with Membrane Computing*, Springer International Publishing AG, Switzerland, 2017.

[60] ZHANG G., RONG H., NERI F., PÉREZ-JIMÉNEZ M. J., *An Optimization Spiking Neural P System for Approximately Solving Combinatorial Optimization Problems*. Int. J. Neural Syst. **24**(5), 1–16, 2014.