P Systems with Active Membranes Working in Sublinear Space

Claudio Zandron, Alberto Leporati, Luca Manzoni, Giancarlo Mauri, Antonio E. Porreca

Dipartimento di Informatica, Sistemistica e Comunicazione Università degli Studi di Milano-Bicocca Viale Sarca 336/14, 20126 Milano, Italy

zandron/leporati/luca.manzoni/mauri/porreca@disco.unimib.it

Abstract. P systems with active membranes are a variant of P systems where the membranes can be created during the computation by division of existing ones. Using this feature, one can create an exponential number of membranes in a polynomial time, and use them in parallel to solve computationally hard problems, such as problems in NP or even in PSPACE. This possibility raises many interesting questions concerning the trade-off between time and space needed to solve various classes of computational problems by means of membrane systems. In this paper we concentrate on P systems with active membranes working in sublinear space, with a survey on recent research results concerning such systems.

1 Introduction

P systems with active membranes have been introduced in [7] as a variant of P systems where the membranes play an active role in the computation: an electrical charge, that can be positive (+), neutral (0), or negative (-), is associated with each membrane; the application of the evolution rules can be controlled by means of these electrical charges. Moreover, new membranes can be created during the computation by division of existing ones. A very interesting feature of such systems is that, using these operations, one can create an exponential number of membranes in polynomial time, and use them in parallel to solve computationally hard problems, such as problems in **NP** or even in **PSPACE**.

This possibility raises many interesting questions concerning the trade-off between time and space needed to solve various classes of computational problems by means of membrane systems. In order to clarify such relations, a definition of space complexity for P systems has been proposed [9], on the basis of an hypothetical implementation of P systems by means of real biochemical materials: every single object and every single membrane requires some constant physical space. Research on the space complexity of P systems with active membranes has shown that these devices, when using a polynomial amount of space, exactly characterize the complexity class **PSPACE** [10], [11]. The result has then been generalized, showing that any Turing machine working in space $\Omega(n)$ can be simulated with a polynomial space overhead [1].

In this paper we concentrate on P systems with active membranes that work in *sublinear* space, with a survey on recent research results. The first natural approach, when considering the use of sublinear space in the framework of membrane systems, is to compare logarithmic space P systems Turing machines using the same amount of space. In Section 3 we present a result from [13] showing that **DLOGTIME**—uniform P systems with active membranes, using a logarithmic amount of space, are able to simulate logarithmic-space deterministic Turing machines, and thus to solve all problems in the class **L**.

In [3] it is pointed out that, while logarithmic-space Turing machines can only generate a polynomial number of distinct configurations, P systems working in logarithmic space have *exponentially* many potential ones, and thus they can be exploited to solve computational problems that are harder than those in **L**. In particular, polynomial-space Turing machines can be simulated by means of P systems with active membranes using only logarithmic auxiliary space, thus obtaining a characterization of **PSPACE**.

We present then a result concerning P systems using only a *constant* amount of space; it turned out [4] that, quite surprisingly, a constant amount of space is sufficient (and trivially necessary) to solve all problems in **PSPACE**. This result challenges our intuition of space, formalized in the definition of space complexity for P systems adopted so far. Thus, a more accurate estimate of the space required by a configuration of a P system was proposed. Using the new space definition, all the results involving at least a polynomial amount of space, according to the first definition, still hold. The difference appears only when P systems with severely tight bounds on the amount of space used during computations are considered.

Finally we present a result, also from [4], that highlights the importance of rewriting input symbols for P systems when a sub-logarithmic number of membrane labels is used. Under this last condition, if we only allow the use of rules that move the input objects in the membrane hierarchy (i.e. send-in, send-out, and dissolution rules), then it is even impossible to correctly distinguish two input strings of the same length (unless the ordering of the symbols is not taken into account), even when no bound on the amount of space is present. In other words, P systems having such limitations and accepting (resp., rejecting) a long enough string x also accept (resp., reject) any other string obtained by swapping two symbols of x.

2 Basic Notions

For a comprehensive introduction to P systems we refer the reader to *The Oxford Handbook of Membrane Computing* [8]. The definition of space complexity for P systems can be found in [9].

In order to consider sublinear space in the framework of P systems, we need to define a meaningful notion of sublinear space inspired by sublinear space definition for Turing machines: we consider two distinct alphabets, an *INPUT* alphabet and a *WORK* alphabet, in the definition of a P system. The input

objects cannot be rewritten and do not contribute to the size of the configuration of a P system. The size of a configuration is defined as the sum of the number of membranes in the current membrane structure and the total number of working objects they contain. We recall here the basic definitions related to P systems with active membranes with an input alphabet [13]:

Definition 1. A P system with (elementary) active membranes having initial degree $d \ge 1$ is a tuple $\Pi = (\Gamma, \Delta, \Lambda, \mu, w_{h_1}, \dots, w_{h_d}, R)$, where:

- Γ is an alphabet, i.e., a finite non-empty set of symbols, usually called objects;
- $-\Delta$ is another alphabet, disjoint from Γ , called the input alphabet;
- Λ is a finite set of labels for the membranes;
- μ is a membrane structure (i.e., a rooted unordered tree, usually represented by nested brackets) consisting of d membranes labelled by elements of Λ in a one-to-one way;
- $-w_{h_1}, \ldots, w_{h_d}$, with $h_1, \ldots, h_d \in \Lambda$, are strings over Γ describing the initial multisets of objects placed in the d regions of μ ;
- R is a finite set of rules over $\Gamma \cup \Delta$.

Each membrane possesses, besides its label and position in μ , another attribute called *electrical charge*, which can be either neutral (0), positive (+) or negative (-) and is always neutral before the beginning of the computation.

A description of the available kinds of rule follows. This description differs from the original definition [7] only in that new input objects may not be created during the computation.

- Object evolution rules, of the form $[a \to w]^{\alpha}_h$ They can be applied inside a membrane labelled by h, having charge α and containing an occurrence of the object a; the object a is rewritten into the multiset w (i.e., a is removed from the multiset in h and replaced by the objects in w). At most one input object $b \in \Delta$ may appear in w, and only if it also appears on the left-hand side of the rule (i.e., if b = a).
- Send-in communication rules, of the form $a \ [\]_h^{\alpha} \to [b]_h^{\beta}$ They can be applied to a membrane labelled by h, having charge α and such that the external region contains an occurrence of the object a; the object a is sent into h becoming b and, simultaneously, the charge of h is changed to β . If $b \in \Delta$ then a = b must hold.
- Send-out communication rules, of the form $[a]_h^{\alpha} \to [\]_h^{\beta} b$ They can be applied to a membrane labelled by h, having charge α and containing an occurrence of the object a; the object a is sent out from h to the outside region becoming b and, simultaneously, the charge of h is changed to β . If $b \in \Delta$ then a = b must hold.
- Dissolution rules, of the form $[a]_h^{\alpha} \to b$ They can be applied to a membrane labelled by h, having charge α and containing an occurrence of the object a; the membrane h is dissolved and its contents are left in the surrounding region unaltered, except that an occurrence of a becomes b. If $b \in \Delta$ then a = b must hold.

- Elementary division rules, of the form $[a]_h^{\alpha} \to [b]_h^{\beta} [c]_h^{\gamma}$ They can be applied to a membrane labelled by h, having charge α , containing an occurrence of the object a but having no other membrane inside (an elementary membrane); the membrane is divided into two membranes having label h and charges β and γ ; the object a is replaced, respectively, by b and c while the other objects in the initial multiset are copied to both membranes. If $b \in \Delta$ (resp., $c \in \Delta$) then a = b and $c \notin \Delta$ (resp., a = c and $b \notin \Delta$) must hold.

Each instantaneous configuration of a P system with active membranes is described by the current membrane structure, including the electrical charges, together with the multisets located in the corresponding regions. A computation step changes the current configuration according to the following set of principles:

- Each object and membrane can be subject to at most one rule per step, except for object evolution rules (inside each membrane several evolution rules can be applied simultaneously).
- The application of rules is maximally parallel: each object appearing on the left-hand side of evolution, communication, dissolution or elementary division rules must be subject to exactly one of them (unless the current charge of the membrane prohibits it). The same principle applies to each membrane that can be involved in communication, dissolution, or elementary division rules. In other words, the only objects and membranes that do not evolve are those associated with no rule, or only to rules that are not applicable due to the electrical charges.
- When several conflicting rules can be applied at the same time, a nondeterministic choice is performed; this implies that, in general, multiple possible configurations can be reached after a computation step.
- In each computation step, all the chosen rules are applied simultaneously (in an atomic way). However, in order to clarify the operational semantics, each computation step is conventionally described as a sequence of microsteps as follows. First, all evolution rules are applied inside the elementary membranes, followed by all communication, dissolution and division rules involving the membranes themselves; this process is then repeated to the membranes containing them, and so on towards the root (outermost membrane). In other words, the membranes evolve only after their internal configuration has been updated. For instance, before a membrane division occurs, all chosen object evolution rules must be applied inside it; this way, the objects that are duplicated during the division are already the final ones.
- The outermost membrane cannot be divided or dissolved, and any object sent out from it cannot re-enter the system again.

A halting computation of the P system Π is a finite sequence of configurations $\mathcal{C} = (\mathcal{C}_0, \dots, \mathcal{C}_k)$, where \mathcal{C}_0 is the initial configuration, every \mathcal{C}_{i+1} is reachable from \mathcal{C}_i via a single computation step, and no rules of Π are applicable in \mathcal{C}_k . A non-halting computation $\mathcal{C} = (\mathcal{C}_i : i \in \mathbb{N})$ consists of infinitely many

configurations, again starting from the initial one and generated by successive computation steps, where the applicable rules are never exhausted.

P systems can be used as language recognisers (see, e.g. [2]) by employing two distinguished objects yes and no; exactly one of these must be sent out from the outermost membrane, and only in the last step of each computation, in order to signal acceptance or rejection, respectively; we also assume that all computations are halting. If all computations starting from the same initial configuration are accepting, or all are rejecting, the P system is said to be confluent. If this is not necessarily the case, then we have a non-confluent P system, and the overall result is established as for nondeterministic Turing machines: it is acceptance iff an accepting computation exists. Unless otherwise specified, the P systems in this paper are to be considered confluent.

In order to solve decision problems (i.e., decide languages over an alphabet Σ), we use *families* of recogniser P systems $\Pi = \{\Pi_x : x \in \Sigma^*\}$. Each input x is associated with a P system Π_x that decides the membership of x in the language $L \subseteq \Sigma^*$ by accepting or rejecting. The mapping $x \mapsto \Pi_x$ must be efficiently computable for each input length [6].

Definition 2. Let \mathcal{E} and \mathcal{F} be classes of functions. A family of P systems $\mathbf{\Pi} = \{\Pi_x : x \in \Sigma^*\}$ is said to be (E, F)-uniform if and only if

- There exists a function $f \in F$ such that $f(1^n) = \Pi_n$, i.e., mapping the unary representation of each natural number to an encoding of the P system processing all inputs of length n, and defining a specific membrane as the input membrane.
- There exists a function $e \in E$ mapping each string $x \in \Sigma^*$ to a multiset $e(x) = w_x$ (represented as a string) over the input alphabet of Π_n , where n = |x|.
- For each $x \in \Sigma^*$ we have $\Pi_x = \Pi_n(w_x)$, i.e., Π_x is Π_n with the multiset encoding x placed inside the input membrane.

Generally, the above mentioned classes of functions \mathcal{E} and \mathcal{F} are complexity classes; in the most common uniformity condition \mathcal{E} and \mathcal{F} denote polynomial-time computable functions.

Any explicit encoding of Π_x is allowed as output of the construction, as long as the number of membranes and objects represented by it does not exceed the length of the whole description, and the rules are listed one by one. This restriction is enforced in order to mimic a (hypothetical) realistic process of construction of the P systems, where membranes and objects are presumably placed in a constant amount during each construction step, and require actual physical space proportional to their number; see also [6] for further details on the encoding of P systems.

Finally, we describe how space complexity for families of recogniser P systems is measured, and the related complexity classes [9, 13].

Definition 3. Let C be a configuration of a recogniser P system Π . The size |C| of C is defined as the sum of the number of membranes in the current membrane

structure and the total number of objects from Γ (i.e, the non-input objects) they contain. If $\mathcal{C} = (\mathcal{C}_0, \dots, \mathcal{C}_k)$ is a computation of Π , then the space required by \mathcal{C} is defined as

$$|\mathcal{C}| = \max\{|\mathcal{C}_0|, \dots, |\mathcal{C}_k|\}.$$

The space required by Π itself is then obtained by computing the space required by all computations of Π and taking the supremum:

$$|\Pi| = \sup\{|\mathcal{C}| : \mathcal{C} \text{ is a computation of } \Pi\}.$$

Finally, let $\Pi = \{\Pi_x : x \in \Sigma^*\}$ be a family of recogniser P systems, and let $s : \mathbb{N} \to \mathbb{N}$. We say that Π operates within space bound s iff $|\Pi_x| \leq s(|x|)$ for each $x \in \Sigma^*$.

By (E,F)-MCSPACE $_{\mathcal{D}}(f(n))$ we denote the class of languages which can be decided by (E,F)-uniform families of confluent P systems of type \mathcal{D} (in the following we will mainly refer to P systems with active membranes, and we denote this by setting $\mathcal{D}=\mathcal{AM}$), where each $\Pi_x\in\mathbf{\Pi}$ operates within space bound f(|x|). The class of problems solvable in (E,F)-logarithmic (resp. polynomial) space is denoted by (E,F)-LMCSPACE $_{\mathcal{D}}$ (resp. (E,F)-PMCSPACE $_{\mathcal{D}}$).

3 Simulating Logarithmic-space Turing Machines

In this section we recall a result from [13] showing that P systems with active membranes, using a logarithmic amount of space, are able to simulate logarithmic-space deterministic Turing machines, and thus to solve all problems in the class L.

In order to consider such systems, we need to define a uniformity condition for the families of P systems that is weaker than the usual P uniformity, to avoid the possibility to solve a problem directly by using the Turing machine that builds the P systems we use to compute. One such possibility is to consider **DLOGTIME**-uniformity, defined on the basis of **DLOGTIME** Turing machines [5]. We refer the reader to [13] for formal definitions.

The efficient simulation of logarithmic space Turing machines (or other equivalent models) has to face two main problems: we cannot use a polynomial number of working objects (to avoid violating the logarithmic space condition) and we cannot use a polynomial number of rewriting rules (to avoid violating the uniformity condition). It has been shown in [13] that such problems can be avoided by a simulation that uses membrane polarization both to communicate objects through membranes as well as to store some information.

Theorem 1. Let M be a deterministic Turing machine with an input tape (of length n) and a work tape of length $O(\log n)$. Then, there exists a (**DLT**, **DLT**)-uniform family $\mathbf{\Pi}$ of confluent recogniser P systems with active membranes working in logarithmic space such that $L(M) = L(\mathbf{\Pi})$.

Proof. (sketch) Consider a Turing machine M working in logarithmic space. The P system Π_n that simulates M on input of length n is composed of:

- A skin membrane containing a *state object* object $q_{i,w}$ to indicate that M is currently in state q and its tape heads are on the i-th and w-th symbols of the input and work tape, respectively.
- $O(\log n)$ nested membranes (INPUT tape membranes) containing, in the innermost one, the input symbols of M, and $O(\log(n))$ membranes to store the work tape of M (WORK tape membranes).
- Two sets of membranes, whose size depend on the dimensions of the input and the working alphabet of M (SYMBOL membranes), respectively.

To simulate a computation step of M, the state object enters the INPUT membranes, storing the bits corresponding to the actual position of the INPUT head of M in their polarizations. Only one object (corresponding to the INPUT symbol actually read) can travel to the outermost membrane. Then, the state object identifies the symbol actually under the WORK head (using the WORK tape membranes) and proceeds to simulate the transition of M using the SYMBOLS membranes.

Each P system H_x (simulating each M(x) such that |x|=n) only requires $O(\log |x|)$ membranes and objects besides the input objects; moreover, the family \boldsymbol{H} is (**DLT**, **DLT**)-uniform. The time required by the simulation is $O(n \cdot t(n))$, where t(n) is the maximum number of steps performed by M on inputs of length n.

An immediate corollary of Theorem 1 is that the class of problems solved by logarithmic-space Turing machines is contained in the class of problems solved by (**DLT**, **DLT**)-uniform, logarithmic-space P systems with active membranes.

Corollary 1. L
$$\subseteq$$
 (DLT, DLT)-LMCSPACE $_{4M}$.

4 Simulating Polynomial-Space Turing Machines

The result presented in the previous section only represents a lower bound for the power of logarithmic-space P systems; as a matter of fact, already in [13] it was conjectured that it could be improved, as P systems working in logarithmic space have an *exponential* number of different configurations, which could possibly be used to efficiently solve harder problems than those in the class **L**. It turned out [3] that this is the case, and that polynomial-space deterministic Turing machines can be simulated by means of P systems with active membranes using only logarithmic auxiliary space, thus characterising **PSPACE**.

The simulation was based on two key ideas. First, input objects (of the form τ_i) are distributed, during the computation, in various substructures. Apart from an initial phase, the value of τ is disregarded: the symbol σ written on the i-th tape cell of the Turing machine being simulated can be inferred from the label of the substructure that contains τ_i . The second idea is applied when querying the symbol under the tape head: the position i of the head is written in binary in the electrical charges of the membranes composing the substructure where the object τ_i is placed, so that the only input object having the correct subscript

can leave the substructure corresponding to the sought symbol, and reach the skin membrane. The depth of each substructure is logarithmic, thus allowing to represent a polynomial number of possible head positions. As a result, we can simulate any polynomial space computation of a deterministic Turing machine with only a logarithmic number of symbols (plus a polynomial number of read-only input symbols) and membranes.

Theorem 2. Let M be a single-tape deterministic Turing machine working in polynomial space s(n) and time t(n). Then, there exists an (\mathbf{L}, \mathbf{L}) -uniform family $\mathbf{\Pi}$ of P systems with active membranes using object evolution and communication rules that simulates M in space $O(\log n)$ and time O(t(n)s(n)).

Proof. (sketch) Let $x \in \Sigma^n$ be an input string, and let $m = \lceil \log s(n) \rceil$ be the minimum number of bits needed in order to represent the tape cell indices $0, \ldots, s(n) - 1$ in binary notation. The P system Π_n , associated with the input length n, has a membrane structure consisting of an external skin membrane that contains, for each symbol of the tape alphabet of M, the following set of membranes, linearly nested and listed from the outside in:

- a symbol-membrane;
- a query-membrane;
- for each $j \in \{0, \ldots, m-1\}$, a membrane labelled by j_{σ} .

An arbitrary configuration of M on input x is encoded by a configuration of Π_x as follows:

- the outermost membrane contains the *state-object* q_i , (where q is the current state of M, and i is the current tape head position);
- if membrane $(m-1)_{\sigma}$ contains the input object τ_i , then the *i*-th tape cell of M contains the symbol σ .

The symbol written on the *i*-th tape cell of M can be inferred from the label of the substructure which contains the corresponding input symbol τ_i . Notice that a logarithmic depth membrane structure allows to represent a polynomial number of possible head positions.

The state-object q_i queries each membrane substructure, by encoding in binary the tape position i on the electrical charges of the membranes. Only the symbol whose subscript is i can reach the skin membrane and be used to conclude the simulation of a computation step.

The family $\mathbf{\Pi}$ described above is (\mathbf{L}, \mathbf{L}) -uniform, and each P system Π_x uses only a logarithmic number of membranes and a constant number of objects per configuration, besides the input objects, which are never rewritten. Π_x works in space $O(\log n)$ and in time O(t(n)s(n)).

As a consequence, we have the following:

Theorem 3. For each class $\mathcal{D} \subseteq \mathcal{AM}$ of P systems with active membranes using object evolution and communication among their rules we have

$$(L, L)$$
-LMCSPACE_D = (L, L) -PMCSPACE_D = PSPACE.

Proof. The inclusion **PSPACE** \subseteq (**L**, **L**)-**LMCSPACE**_{\mathcal{D}} follows immediately from Theorem 2. By definition, the class (**L**, **L**)-**LMCSPACE**_{\mathcal{D}} is included in (**L**, **L**)-**PMCSPACE**_{\mathcal{D}}. Finally, to prove the inclusion of (**L**, **L**)-**PMCSPACE**_{\mathcal{D}} in **PSPACE** it suffices to simulate P systems by means of Turing machines, which can be carried out with just a polynomial space overhead, as shown in [10, 1]. \square

This was the first case where the space complexity of P systems and that of Turing machines differ by an exponential amount. Since, as previously said, **PSPACE** had already been proved to be characterised by *polynomial*-space P systems, these results also highlight a gap in the hierarchy of space complexity classes for P systems: super-polynomial space is required in order to exceed the computational power of logarithmic space.

5 Constant-space P systems

After considering P systems with active membranes working in logarithmic space, a natural question arises concerning the power of such systems using only a constant amount of space. Surprisingly it turned out that constant space is sufficient to simulate polynomial-space bounded deterministic Turing machines, as proved in [4]:

Theorem 4. (L, L)-MCSPACE_{AM}(O(1)) = PSPACE.

Proof. (sketch) Let $L \in \mathbf{PSPACE}$, and let M be a Turing machine deciding L in space p(n). We can construct a family of P systems $\mathbf{\Pi} = \{\Pi_x : x \in \Sigma^*\}$ such that $L(\mathbf{\Pi}) = L$ by letting $F(1^n) = \Pi_n$, where Π_n is the P system simulating M on inputs of length n, and

$$E(x_0 \cdots x_{n-1}) = x_{1,1} \cdots x_{n-1,n-1} \sqcup_n \cdots \sqcup_{p(n)-1},$$

i.e. by padding the input string x with p(n) - n blank symbols \sqcup before indexing the result with the positions of the symbols on the tape.

The simulation relies on two main ideas. As in the previous proof of Theorem 2, input objects of the form τ_i are distributed in substructures, and the symbol written on the *i*-th tape cell of M can be inferred from the label of the substructure where the corresponding input symbol τ_i is placed. The second idea is that it is possible to "read" a subscript of an input object τ_i without rewriting it and by using only a constant number of additional objects and membranes: in particular, a timer object is used to change the charge of a membrane after a requested amount of steps. Any other object that was counting together with the timer is able to observe the charge of the membrane, and thus obtain the designed value.

Since at each computation step only a constant number of working objects and membranes are present, then the simulation requires, according to definition 3, a constant amount of space. Moreover, both F and E can be computed in logarithmic space by Turing machines, since they only require adding subscripts

having a logarithmic number of bits to rules or strings having a fixed structure, and the membrane structure is fixed for all Π_n . This proves the inclusion of **PSPACE** in (\mathbf{L}, \mathbf{L}) -**MCSPACE**_{\mathcal{AM}}(O(1)), while the reverse inclusion is proved in [10].

6 Rethinking the Definition of Space

The result of Theorem 4 shows that all problems in **PSPACE** can be solved by constant-space P systems with active membranes. This rises some natural questions about the definition of space complexity for P systems adopted until now [9]. Does counting each non-input object and each membrane as unitary space really capture an intuitive notion of the amount of space used by a P system during a computation? Is it fair to allow a polynomial padding of the input string when encoding it as a multiset?

In [4], it was highlighted that the constant number of non-input objects appearing in each configuration of the simulation actually encode $\Theta(\log n)$ bits of information, since they are taken from an alphabet Γ of polynomial size. According to the original definition of space recalled in Section 2, each of these objects would only require unitary space, whereas the binary representation of the subscript i requires $\log p(n) = \Theta(\log n)$ bits. It may be argued that this amount of information needs a proportional amount of physical storage space. Similarly, each membrane label contains $\Theta(\log |\Lambda|)$ bits of information, which must also have a physical counterpart.

The information stored in the *positions* of the objects within the membrane structure is also not taken into account by Definition 3. However, the information on the location of the objects is part of the system and it is *not* stored elsewhere, exactly as the information on the location of the tape head in a Turing machine, which is not counted as space.

Due to the above considerations, in [4] an alternative definition of space was proposed:

Definition 4. Let C be a configuration of a P system Π . The size |C| of C is defined as the number of membranes in the current membrane structure multiplied by $\log |\Lambda|$, plus the total number of objects from Γ (i.e, the non-input objects) they contain multiplied by $\log |\Gamma|$.

Adopting this stricter definition does not significantly change space complexity results involving polynomial or larger upper bounds, i.e., the complexity classes $\mathbf{PMCSPACE}_{\mathcal{AM}}$, $\mathbf{EXPMCSPACE}_{\mathcal{AM}}$, and larger ones remain unchanged.

As for padding the input string, one may argue that this operation provides the P system with some "free" storage, since input objects are not counted by Definition 3. The proof of Theorem 4 exploits the ability to encode an input string of length n as a polynomially larger multiset in a substantial way, as allowed by the most common uniformity conditions, including **P** and **LOGSPACE**-uniformity, but also weaker ones such as \mathbf{AC}^0 or **DLOGTIME**-uniformity.

The simulation described in the previous section would require logarithmic space according to Definition 4. Also the space bounds of the simulation of polynomial-space Turing machines by means of logarithmic-space P systems with active membranes described in Section 4 also increase to $\Theta(\log n \log \log n)$, since in that case each configuration of the P systems contains $\Theta(\log n)$ membranes with distinct labels and O(1) non-input objects. Both simulations would be limited to linear-space Turing machines, rather than polynomial-space ones, if input padding were disallowed.

7 Computing without Rewriting Input Objects

In this section we present another result from [4] showing that if input objects are only moved around the membrane structure (without rewriting them into other objects), then evolution rules involving the input objects are essential in order to perform a simulation of a Turing machine using less than a logarithmic number of membrane labels. In fact, if only non-rewriting send-in, send-out, and dissolution rules are applied to input symbols, and the number of membrane labels is $o(\log n)$, then it is even impossible to correctly distinguish two input strings of the same length. This happens independently of the space used by the P systems, as long as the function E encoding the input $x \in \mathcal{L}^*$ as a multiset w_x is "simple":

Definition 5. Let A be an alphabet containing Σ , and let

$$s \colon A^* \to \{\sigma_i : \sigma \in A, i \in \mathbb{N}\}^*$$

be the function defined by $s(x_0 \cdots x_{n-1}) = x_{0,0} \cdots x_{n-1,n-1}$, i.e. the function subscripting each symbol with its position in the string.

An encoding E of Σ^* is "simple" if there exists a function $g \colon \mathbb{N} \to A^*$ such that $E(x) = s(x \cdot g(|x|))$ for all $x \in \Sigma^*$, i.e. E(x) is the original input string x, concatenated with a string depending only on the length of x, and indexed with the positions of its symbols.

Notice that the encoding employed in Theorem 4 is indeed simple.

When the encoding is simple and the input alphabet is at least binary, P systems with the limitations described above accepting (resp., rejecting) a long enough string x also accept (resp., reject) another string obtained by swapping two symbols of x.

Theorem 5. Let Π be a family of $(\mathcal{E}, \mathcal{F})$ -uniform, possibly non-confluent recogniser P systems with active membranes, where \mathcal{F} is unrestricted, and \mathcal{E} is a class of simple encodings. Suppose that the only rules involving input symbols are send-in, send-out and membrane dissolution, that these rules never rewrite the input symbols, and that the family uses $o(\log n)$ membrane labels. Then, there exists $n_0 \in \mathbb{N}$ such that, for each string $x = x_0 \cdots x_{n-1} \in \mathcal{E}^*$ with $|x| = n \geq n_0$, there exist i < j < n such that x can be written as $u \cdot x_i \cdot v \cdot x_j \cdot w$ with $u, v, w \in \mathcal{E}^*$, and $x \in L(\Pi)$ if and only if $u \cdot x_j \cdot v \cdot x_i \cdot w \in L(\Pi)$.

Proof. (sketch) Let Π be a family of P systems as defined in the statement of the theorem, let $F \in \mathcal{F}$ be its "family" function, and let

$$F(1^n) = \Pi_n = (\Gamma, \Delta, \Lambda, \mu, w_{h_1}, \dots, w_{h_d}, R).$$

Assume that the objects in Δ are subject, in R, only to rules of type send-in, send-out, and dissolution not rewriting them. On the other hand, we impose no restriction on rules involving objects in Γ . If we consider the possible rules applicable to a fixed object $a \in \Delta$ and respecting the imposed restrictions, we notice that there are 21|A| possible rules per input object and hence $2^{21|A|}$ possible sets of rules involving each input object. Since the encoding of the input string is simple, each input object has the form σ_i for some $\sigma \in A$; hence, for each position i in the input multiset there are $(2^{21|A|})^{|A|} = 2^{21|A||A|}$ possible sets of rules.

A necessary condition to distinguish two input objects $a, b \in \Delta$ is that the set of rules involving b cannot be simply obtained by replacing a with b in the set of rules involving a (i.e. their sets of rules are not isomorphic); otherwise, replacing a with b in the input multiset would not change the result of the computation of Π_x . In particular, this holds for the first n input objects $x_{0,0}, \ldots, x_{n-1,n-1}$, obtained by indexing $x = x_0 \cdots x_{n-1} \in \Sigma^n$. In order to be able to distinguish these n input objects it is thus necessary that

$$2^{21|A||\varSigma|} > n$$

that is, that the sets of rules associated with the first n objects are pairwise non-isomorphic. This means that

$$|\varLambda| \ge \frac{\log n}{21|\varSigma|}$$

However, since |A| is $o(\log n)$, the inequality does not hold for large enough n. Instead, there exists n_0 such that, for each $n \geq n_0$, there are two indistinguishable positions i and j with $0 \leq i < j < n$: for each $x = u \cdot x_i \cdot v \cdot x_j \cdot w \in \Sigma^n$, either x and $u \cdot x_j \cdot v \cdot x_i \cdot w$ are both accepted, or they are both rejected.

8 Final Remarks

In this paper we survey recent results concerning P systems with active membranes working in sublinear space. We showed that such systems characterize **PSPACE** either when using logarithmic space, as well as when using only a constant amount of space.

A new definition of space has thus been proposed, which considers also the number of bits necessary to encode the non-input objects and the labels of the membranes. While the new definition does not change any result involving an amount of space which is polynomial or larger, it changes the result for sublinear space. In particular, according to the new definition the simulation used to prove

that constant space P systems with active membranes characterize **PSPACE** would now require logarithmic space.

We also recalled a result showing that rewriting input objects is essential when less than a logarithmic number of membrane labels is present; in this case, it is not possible to distinguishing two different input strings when the input objects are only moved around in the membrane structure, even when no restrictions on the amount of space are present.

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