


# A Logarithmic Bound for Solving Subset Sum with P Systems

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**Abstract.** The aim of our paper is twofold. On one hand we prove the ability of polarizationless P systems with dissolution and with division rules for non-elementary membranes to solve NP-complete problems in a polynomial number of steps, and we do this by presenting a solution to the Subset Sum problem. On the other hand, we improve some similar results obtained for different models of P systems by reducing the number of steps and the necessary resources to be of a logarithmic order with respect to  $k$  (recall that  $n$  and  $k$  are the two parameters used to indicate the size of an instance of the Subset Sum problem).

As the model we work with does not allow cooperative rules and does not consider the membranes to have an associated polarization, the strategy that we will follow consists on using objects to represent the weights of the subsets through their multiplicities, and comparing the number of objects against a fixed number of membranes. More precisely, we will generate  $k$  membranes in  $\log k$  steps.

## 1 Introduction

This paper is the continuation of a series of results on Complexity Classes in Membrane Computing that are trying to establish the relevance, in terms of computing power, of each one of the possible features of a P system (see [3]).

The Subset Sum problem is a well-known NP-complete problem which can be formulated as follows: *Given a finite set  $A$ , a weight function,  $w : A \rightarrow \mathbb{N}$ , and a constant  $k \in \mathbb{N}$ , determine whether or not there exists a subset  $B \subseteq A$  such that  $w(B) = k$ .* It has been a matter of study in Membrane Computing several times, being mainly used to prove the ability of different P system models in order to solve problems from the NP class in a polynomial time.

This speed-up is achieved by trading space for time, in the sense that the considered models allow that an exponential amount of membranes can be produced by a P system in a polynomial number of steps. For example, solutions to the Subset Sum problem working in a number of steps which is linear with respect to the parameters  $n$  and  $k$  have been designed using P systems with active membranes [9], using tissue P systems with cell division [2], and using P systems with membrane creation [4].

In this paper we work with P systems using division of non-elementary membranes and dissolution rules. Our aim goes beyond adding this P system model to the above mentioned list; we improve previous complexity results by solving the Subset Sum problem in a linear number of steps with respect to  $n$  and  $\log k$ . We also improve the pre-computation process, as the initial resources are also bounded by  $\log k$ .

The paper is structured as follows: in the next section we present the formal framework, i.e., we recall the definition of recognizing P systems, the P system model used along the paper is settled and the class  $\mathbf{PMC}_{\mathcal{AM}^0(+d,+ne)}$  is presented. In Section 3, our design of the solution of the Subset Sum problem is presented and some conclusions are given in the last section.

## 2 Formal Framework

In this paper we are using cellular systems for attacking the resolution of decision problems. This means that for each instance of a problem that we try to solve, we are only interested in obtaining a Boolean answer (*Yes* or *No*). Therefore, the P system can behave as a *black box* to which the user supplies an input and from which an affirmative or negative answer is received. This is indeed the motivation for defining the concept of *recognizing P systems* (introduced in [13]).

### 2.1 Recognizing P Systems

Let us recall that a decision problem,  $X$ , is a pair  $(I_X, \theta_X)$  where  $I_X$  is a language over an alphabet whose elements are called *instances* and  $\theta_X$  is a total Boolean function over  $I_X$ . If  $u$  is an instance of the problem  $X$  such that  $\theta_X(u) = 1$  (respectively,  $\theta_X(u) = 0$ ), then we say that the answer to the problem for the instance considered is *Yes* (respectively, *No*).

Keeping this in mind, recognizing P systems are defined as a special class of membrane systems that will be used to solve decision problems, in the framework of the complexity classes theory. Note that this definition is stated informally, and it can be adapted for any kind of membrane system paradigm.

A recognizing P system is a P system with input and with external output having two distinguished objects **yes** and **no** in its working alphabet such that:

- All computations halt.
- If  $\mathcal{C}$  is a computation of  $\Pi$ , then either the object **yes** or the object **no** (but not both) must have been released into the environment, and only in the last step of the computation.

### 2.2 The P System Model

The power of membrane division as a tool for efficiently solving **NP** problems in Membrane Computing has been widely proved. Many examples of designs of P systems solving **NP**-complete problems have been proposed in the framework of P systems with active membranes with two polarizations and three polarizations

and in the framework of P systems with non-elementary membrane division. The key of such solutions is the creation of an exponential amount of workspace (membranes) in a polynomial time.

In the literature, one can find two quite different rules for performing membrane division. On the one hand, in [7], P systems with active membranes were presented. In this model new membranes were obtained through the process of *mitosis* (membrane division). In these devices membranes have polarizations, one of the “electrical charges” 0, −, +, and several times the problem was formulated whether or not these polarizations are necessary in order to obtain polynomial solutions to NP-complete problems. The last result is that from [1], where one proves that two polarizations suffice.

P systems with active membranes have been successfully used to design (uniform) solutions to well-known NP-complete problems, such as SAT [13], *Subset Sum* [9], *Knapsack* [10], *Bin Packing* [11], *Partition* [5], and the *Common Algorithmic Problem* [12].

The syntactic representation of membrane division rule is

$$[a]_h^{e_1} \rightarrow [b]_h^{e_2} [c]_h^{e_3} \quad (1)$$

where  $h$  is a label,  $e_1, e_2$  and  $e_3$  are electrical charges and  $a, b$  and  $c$  are objects. The interpretation is well-known: An elementary membrane can be divided into two membranes with the same label, possibly transforming some objects and changing the electrical charge. All objects present in the membrane except the object triggering the rule are copied into both new membranes.

In [6], a variant of this rule was used in which the polarization was dropped:

$$[a]_h \rightarrow [b]_h [c]_h. \quad (2)$$

In both cases (with and without polarizations) the key point is that the membranes are always elementary membranes. In the literature, there also exist rules for the division of non-elementary polarizationless membranes, as

$$[[ ]_{h_1} [ ]_{h_2}]_{h_0} \rightarrow [[ ]_{h_1}]_{h_0} [[ ]_{h_2}]_{h_0} \quad (3)$$

where  $h_0, h_1$  and  $h_2$  are labels. There exists an important difference with respect to elementary membrane division: in the case of (3), the rule is not triggered by the occurrence of an object inside a membrane, but by the membrane structure instead. This point has a crucial importance in the design of solutions, since a membrane can be divided by the corresponding rule even if there are no objects inside it.

According to the representation (3), the membrane  $h_0$  divides into two new membranes also with label  $h_0$  and all the information (objects and membranes) different from membranes  $h_1$  and  $h_2$  inside is duplicated.

In this paper we use a type of membrane division which is syntactically equivalent to (2)

$$[a]_h \rightarrow [b]_h [c]_h, \quad (4)$$

but we will consider a semantic difference; the dividing membrane can be elementary or non-elementary and after the division, all the objects and membranes

inside the dividing membrane are duplicated, except the object  $a$  that triggers the rule, which appears in the new membranes possibly modified (represented as objects  $b$  and  $c$ ).

In this paper we work with a variant of P systems with active membranes which we call with weak division, and that does not use polarizations.

**Definition 1.** *A P system with active membranes with weak division is a P system with  $\Gamma$  as working alphabet, with  $H$  as the finite set of labels for membranes, and where the rules are of the following forms:*

- (a)  $[a \rightarrow u]_h$  for  $h \in H$ ,  $a \in \Gamma$ ,  $u \in \Gamma^*$ . This is an object evolution rule, associated with a membrane labelled with  $h$ : an object  $a \in \Gamma$  belonging to that membrane evolves to a multiset  $u \in \Gamma^*$ .
- (b)  $a [ ]_h \rightarrow [b]_h$  for  $h \in H$ ,  $a, b \in \Gamma$ . An object from the region immediately outside a membrane labeled with  $h$  is introduced in this membrane, possibly transformed into another object.
- (c)  $[a]_h \rightarrow b [ ]_h$  for  $h \in H$ ,  $a, b \in \Gamma$ . An object is sent out from membrane labeled with  $h$  to the region immediately outside, possibly transformed into another object.
- (d)  $[a]_h \rightarrow b$  for  $h \in H$ ,  $a, b \in \Gamma$ : A membrane labeled with  $h$  is dissolved in reaction with an object. The skin is never dissolved.
- (e)  $[a]_h \rightarrow [b]_h [c]_h$  for  $h \in H$ ,  $a, b, c \in \Gamma$ . A membrane can be divided into two membranes with the same label, possibly transforming some objects. The content of the membrane is duplicated. The membrane can be elementary or not.

These rules are applied according to the following principles:

- All the rules are applied in parallel and in a maximal manner. In one step, one object of a membrane can be used by only one rule (chosen in a non-deterministic way), but any object which can evolve by one rule of any form, must evolve.
- If at the same time a membrane labeled with  $h$  is divided by a rule of type (e) and there are objects in this membrane which evolve by means of rules of type (a), then we suppose that first the evolution rules of type (a) are used, and then the division is produced. Of course, this process takes only one step.
- The rules associated with membranes labeled with  $h$  are used for all copies of this membrane. At one step, a membrane can be the subject of *only one* rule of types (b)-(e).

Let us note that in this framework we work without cooperation, without priorities, with weak division, and without changing the labels of membranes.

In this paper we work within the model of *polarizationless P systems using weak division of non-elementary membranes and dissolution*. Let  $\mathcal{AM}^0(+d, +ne)$  be the class of such systems.

### 2.3 The Class $\text{PMC}_{\mathcal{AM}^0(+d,+ne)}$

**Definition 2.** We say that a decision problem  $X = (I_X, \theta_X)$  is solvable in polynomial time by a family  $\Pi = \{\Pi(n) : n \in \mathbb{N}\}$  of recognizing P systems from  $\mathcal{AM}^0(+d, +ne)$  if the following holds:

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

In the above definition we have imposed to every P system  $\Pi(n)$  a *confluent* condition, in the following sense: every computation of a system with the *same* input multiset must always give the *same* answer. The pair of functions  $(\text{cod}, s)$  is called a *polynomial encoding* of the problem in the family of P systems.

We denote by  $\text{PMC}_{\mathcal{AM}^0(+d,+ne)}$  the set of all decision problems which can be solved by means of recognizing polarizationless P systems using division of non-elementary membranes and dissolution in polynomial time.

## 3 Designing the Solution to Subset Sum

In this section we address the resolution of the problem following a brute force algorithm, implemented in the framework of recognizing P systems from the  $\mathcal{AM}^0(+d, +ne)$  class. The idea of the design is better understood if we divide the solution to the problem into several stages:

- *Generation stage*: for every subset of  $A$ , a membrane labeled by  $e$  is generated via membrane division.
- *Calculation stage*: in each membrane the weight of the associated subset is calculated (using the auxiliary membranes  $e_0, \dots, e_n$ ).
- *Checking stage*: in each membrane it is checked whether the weight of its associated subset is exactly  $k$  (using the auxiliary membranes  $ch$ ).
- *Output stage*: the system sends out the answer to the environment, according to the result of the checking stage.

Let us now present a family of recognizing P systems from the  $\mathcal{AM}^0(+d, +ne)$  class that solves Subset Sum, according to Definition 2.

We shall use a tuple  $(n, (w_1, \dots, w_n), k)$  to represent an instance of the Subset Sum problem, where  $n$  stands for the size of  $A = \{a_1, \dots, a_n\}$ ,  $w_i = w(a_i)$ , and  $k$  is the constant given as input for the problem. Let  $g : \mathbb{N} \times \mathbb{N} \rightarrow \mathbb{N}$  be a function defined by

$$g(n, k) = \frac{(n+k)(n+k+1)}{2} + n$$

This function is primitive recursive and bijective between  $\mathbb{N} \times \mathbb{N}$  and  $\mathbb{N}$  and computable in polynomial time. We define the polynomially computable function  $s(u) = g(n, k)$ .

We shall provide a family of P systems where each P system solves all the instances of the Subset Sum problem with the same size. Let us consider the binary decomposition of  $k$ ,  $\sum_{i \in I} 2^i = k$ , where the indices  $i \in I$  indicate the positions of the binary expression of  $k$  where a 1 occurs. Let  $I' = \{1, \dots, \lfloor \log k \rfloor\} - I$  be the complementary set, that is, the positions where a 0 occurs. This binary encoding of  $k$ , together with the weight function  $w$  of the concrete instance, will be provided via an input multiset determined by the function  $cod$  as follows:

$$cod(u) = cod_1(u) \cup cod_2(u),$$

$$\text{where } cod_1(u) = \{\{b_i^{w_i} : 1 \leq i \leq n\}\} \text{ and}$$

$$cod_2(u) = \{\{c_j : j \in I\}\} \cup \{\{c'_j : j \in I'\}\}$$

Next, we shall provide a family  $\Pi = \{\Pi(g(n, k)) : n, k \in \mathbb{N}\}$  of recognizing P systems which solve the Subset Sum problem in a number of steps being of  $O(n + \log k)$  order. We shall indicate for each system of the family its initial configuration and its set of rules. We shall present the list of rules divided by groups, and we shall provide for each of them some comments about the way their rules work.

Let us consider an arbitrary pair  $(n, k) \in \mathbb{N} \times \mathbb{N}$ . The system  $\Pi(g(n, k))$  is determined by the tuple  $(\Gamma, \Sigma, \mu, M, \mathcal{R}, i_{in}, i_0)$ , that is described next:

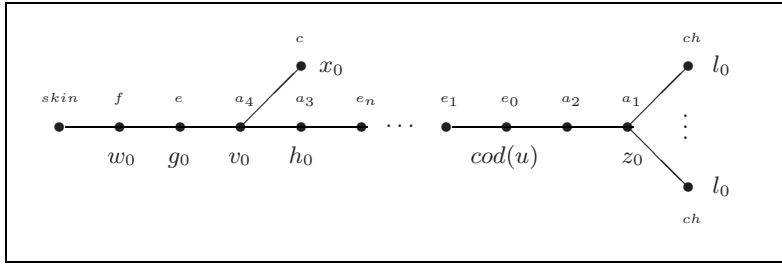
- Alphabet:

$$\begin{aligned} \Gamma = \Sigma \cup & \{b_i^+, b_i^-, b_i^{\bar{-}}, d_i, d_i^+, d_i^{\bar{-}}, p_i, q_i : i = 1, \dots, n\} \\ & \cup \{g_0, \dots, g_{2^{\lfloor \log k \rfloor + 2}}, h_0, \dots, h_{2^{\lfloor \log k \rfloor + 2n + 8}}, l_0, \dots, l_{2^{\lfloor \log k \rfloor + 2n + 10}}\} \\ & \cup \{v_0, \dots, v_{2^{\lfloor \log k \rfloor + 2n + 12}}\} \\ & \cup \{w_0, \dots, w_{2^{\lfloor \log k \rfloor + 2n + 18}}\} \\ & \cup \{x_0, \dots, x_{2^{\lfloor \log k \rfloor + 2n + 15}}, z_0, \dots, z_{2^{\lfloor \log k \rfloor + 2n + 7}}\} \\ & \cup \{s, \text{yes}, \text{no}, \text{Trash}\} \end{aligned}$$

- Input alphabet:  $\Sigma(n, k) = \{b_1, \dots, b_n, c_0, \dots, c_{\lfloor \log k \rfloor}, c'_0, \dots, c'_{\lfloor \log k \rfloor}\}$ .

The initial configuration consists of  $n + \lfloor \log k \rfloor + 9$  membranes, arranged as shown in Figure 1. Formally, the membrane structure  $\mu$  is

$$[[[[[[[ \cdot^n \cdot [ [ [ [ [ ch \dots [ ] ch ]_{a_1} ]_{a_2} ]_{e_0} ]_{e_1} \cdot^n \cdot ]_{e_n} ]_{a_3} [ ] c ]_{a_4} ]_{e'} ]_{f'} ]_{skin}$$



**Fig. 1.** Initial Configuration

where there are exactly  $\lfloor \log k \rfloor + 1$  copies of membrane  $[\ ]_{ch}$ .

Roughly speaking (more precise explanations will be given for the rules), we can classify the membranes according to their role as follows:

- $n+2$  membranes that take care of the generation stage, namely those labeled by  $e_0, e_1, \dots, e_n$  and  $e$ .
- $\lfloor \log k \rfloor + 3$  membranes that take care of preparing and implementing the checking stage, namely those labeled by  $ch, a_1$  and  $a_2$ .
- 4 membranes that take care of the answer stage, handling and synchronizing the results of the checking, namely those labeled by  $a_3, a_4, c$  and  $f$ .

- The initial multisets are:

$$M(f) = \{\{w_0\}\}; M(e) = \{\{g_0\}\}; M(a_4) = \{\{v_0\}\}; M(a_3) = \{\{h_0\}\};$$

$$M(c) = \{\{x_0\}\}; M(a_1) = \{\{z_0\}\}; M(ch) = \{\{l_0\}\}$$

$$M(skin) = M(a_2) = M(e_0) = \dots = M(e_n) = \emptyset$$

- The input membrane is  $i_{in} = e_0$ , and the output region is the environment ( $i_0 = env$ ).

**First task: generate  $k$  membranes  $ch$ .** At the beginning of the computation,  $k$  membranes  $ch$  will be generated inside the innermost region of the structure.

The strategy works as follows:

1. Initially, there are  $\lfloor \log k \rfloor$  membranes  $ch$  in the region  $a_1$ , and the input multiset is located in region  $e_0$  (recall that  $cod_2(u)$  consists of  $\lfloor \log k \rfloor$  objects  $c_i$  or  $c'_i$  representing the binary encoding of  $k$ ).
2. In the first  $\lfloor \log k \rfloor$  steps, the objects from  $cod_2(u)$  get into membrane  $a_2$  (the objects enter one by one membrane  $a_2$ ). Simultaneously, the counter  $z_i$  is evolving inside membrane  $a_1$  and dissolves it at the  $\lfloor \log k \rfloor$  step.
3. Thus, in the next step each element from  $cod_2(u)$  will go inside a membrane  $ch$  (all objects go in parallel into different membranes in a one-to-one manner).

4. Objects  $c'_i$  will dissolve the membranes where they enter, while each object  $c_i$  will generate by division  $2^i$  membranes  $ch$ .
5. After at most  $\lfloor \log k \rfloor$  further steps all divisions have been completed, and the number of membranes  $ch$  is exactly  $k$ .

Membrane  $a_2$  will not be divided until the generation and weight calculation stages have been completed, acting as a separator between objects from  $cod_1(u)$  and membranes  $ch$ .

$$\text{Set (A1).} \quad \left. \begin{array}{l} c_i[]_{a_2} \rightarrow [c_i]_{a_2} \\ c'_i[]_{a_2} \rightarrow [c'_i]_{a_2} \\ \\ c_i[]_{ch} \rightarrow [c_i]_{ch} \\ c'_i[]_{ch} \rightarrow [c'_i]_{ch} \\ [c'_i]_{ch} \rightarrow Trash \end{array} \right\} \text{ for } i \in \{0, \dots, \lfloor \log k \rfloor\}.$$

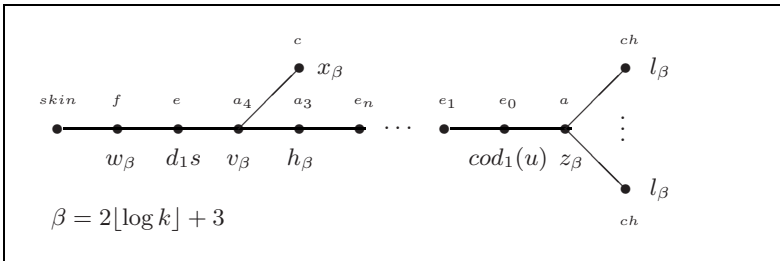
$$\text{Set (A2).} \quad \begin{array}{ll} [c_0 \rightarrow Trash]_{ch} & \\ [c_i]_{ch} \rightarrow [c_{i-1}]_{ch} [c_{i-1}]_{ch} & \text{for } i = 1, \dots, \lfloor \log k \rfloor \\ [z_i \rightarrow z_{i+1}]_{a_1} & \text{for } i = 0, \dots, \lfloor \log k \rfloor - 1 \\ [z_{\lfloor \log k \rfloor}]_{a_1} \rightarrow z_{\lfloor \log k \rfloor + 1} & \\ [g_i \rightarrow g_{i+1}]_e & \text{for } i = 0, \dots, 2\lfloor \log k \rfloor + 1 \\ [g_{2\lfloor \log k \rfloor + 2} \rightarrow d_1 s]_e & \end{array}$$

In the last step of this stage, the counter  $g_i$  produces the objects  $d_1$  and  $s$  which will trigger the beginning of the next stage.

$$\text{Set(B).} \quad \left. \begin{array}{l} [w_i \rightarrow w_{i+1}]_f \\ [v_i \rightarrow v_{i+1}]_{a_4} \\ [h_i \rightarrow h_{i+1}]_{a_3} \\ [x_i \rightarrow x_{i+1}]_c \\ [l_i \rightarrow l_{i+1}]_{ch} \end{array} \right\} \text{ for } i \in \{0, \dots, 2\lfloor \log k \rfloor + 2\}.$$

$$[z_i \rightarrow z_{i+1}]_{a_2} \quad \text{for } i \in \{\lfloor \log k \rfloor + 1, \dots, 2\lfloor \log k \rfloor + 2\}.$$

The rest of the counters simply increase their indices in this stage. (See Fig. 2.)



**Fig. 2.** TIME  $2\lfloor \log k \rfloor + 3$



**Second task: generate  $2^n$  membranes  $e$ .** Objects  $d_i$  residing inside membrane(s)  $e$  will produce  $n$  consecutive divisions, thus yielding  $2^n$  copies of membrane  $e$ . To each one of them, a subset of  $A$  is associated in the following way: after each division, the membranes where object  $p_i$  occurs correspond to subsets of  $A$  containing  $a_i$ , and conversely, membranes where  $q_i$  occurs will be associated with subsets not containing  $a_i$ .

$$\begin{aligned} \text{Set (C). } \quad & [d_i]_e \rightarrow [d_i^+]_e [d_i^-]_e && \text{for } i = 1, \dots, n \\ & [d_i^+] \rightarrow p_i d_{i+1}]_e && \text{for } i = 1, \dots, n-1 \\ & [d_i^- \rightarrow q_i d_{i+1}]_e && \text{for } i = 1, \dots, n-1 \\ & [d_n^+ \rightarrow p_n]_e \\ & [d_n^- \rightarrow q_n]_e \end{aligned}$$

Membrane divisions take place every two steps, so in the  $(2[\log k] + 2n + 2)$ -th step there will be  $2^n$  membranes  $e$ .

$$\begin{aligned} \text{Set (D). } \quad & s []_{a_i} \rightarrow [s]_{a_i} && \text{for } i = 3, 4 \\ & s []_{e_i} \rightarrow [s]_{e_i} && \text{for } i = 0, \dots, n \\ & [s]_{e_0} \rightarrow \text{Trash} \\ & p_j []_{a_i} \rightarrow [p_j]_{a_i} && \text{for } i = 3, 4 \quad j = 1, \dots, n \\ & p_j []_{e_i} \rightarrow [p_j]_{e_i} && \text{for } j = 1, \dots, n \quad i = j, \dots, n \\ & [p_i \rightarrow q_i]_{e_i} && \text{for } i = 1, \dots, n \\ & q_j []_{a_i} \rightarrow [q_j]_{a_i} && \text{for } i = 3, 4 \quad j = 1, \dots, n \\ & q_j []_{e_i} \rightarrow [q_j]_{e_i} && \text{for } j = 1, \dots, n \quad i = j, \dots, n \\ & [q_i]_{e_i} \rightarrow \text{Trash} && \text{for } i = 1, \dots, n \end{aligned}$$

While the divisions are being carried out, objects  $s$ ,  $p_j$  and  $q_j$ , for  $j = 1, \dots, n$ , travel into inner membranes (recall that whenever membrane  $e$  gets divided, the internal nested structure of membranes  $e_i$  is duplicated). In the  $(2[\log k] + n + 2)$ -th step, an object  $s$  arrives to every membrane  $e_0$ . This object dissolves the membrane in the next step, and therefore in the  $(2[\log k] + n + 3)$ -th step we find inside every membrane  $e_1$  the multiset  $\text{cod}_1(u)$ , and in this moment the weight calculation stage begins (see rules in **Set (E)**).

As we said before, objects  $p_j$  and  $q_j$  are traveling into inner membranes, until they reach  $e_j$ . This is done in such a way that in the  $(2[\log k] + n + 3)$ -th step there is in each membrane  $e_1$  either an object  $p_1$  or an object  $q_1$ , in addition to the multiset  $\text{cod}_1(u)$ .

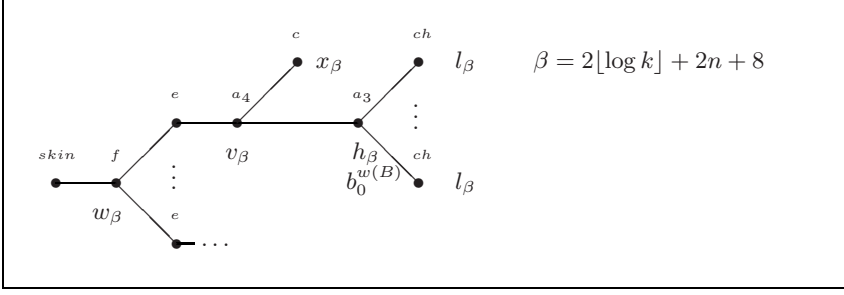
Before going on, let us state two points. First, recall that in the input multiset, introduced in  $e_0$  at the beginning of the computation, there are  $w(a_i)$  copies of  $b_i$ , for  $i = 1, \dots, n$ . Second, let us note that objects  $q_i$  dissolve membrane  $e_i$  immediately after arriving to it, while objects  $p_i$  take two steps to dissolve membrane  $e_i$  (first they are transformed into  $q_i$  and in the next step the dissolution takes place).

$$\begin{aligned}
\text{Set (E). } & [b_1 \rightarrow b_1^+]_{e_1} \\
& [b_{i+1} \rightarrow b_{i+1}^+]_{e_i} \quad \text{for } i = 1, \dots, n-1 \\
& [b_{i+2} \rightarrow b_{i+2}^-]_{e_i} \quad \text{for } i = 1, \dots, n-2 \\
& [b_{i+3} \rightarrow b_{i+3}^-]_{e_i} \quad \text{for } i = 1, \dots, n-3 \\
& [b_i^+ \rightarrow b_0]_{e_i} \quad \text{for } i = 1, \dots, n \\
& [b_i^+ \rightarrow \textit{Trash}]_{e_j} \quad \text{for } i = 1, \dots, n-1, \quad j = i+1 \\
& [b_i^- \rightarrow b_i^+]_{e_i} \quad \text{for } i = 2, \dots, n \\
& [b_{i+1}^- \rightarrow b_{i+1}^+]_{e_i} \quad \text{for } i = 1, \dots, n-1 \\
& [b_i^- \rightarrow b_i^+]_{e_i} \quad \text{for } i = 3, \dots, n \\
& [b_{i+1}^- \rightarrow b_{i+1}^-]_{e_i} \quad \text{for } i = 2, \dots, n-1 \\
& [b_{i+2}^- \rightarrow b_{i+2}^-]_{e_i} \quad \text{for } i = 1, \dots, n-2 \\
& [b_n^+ \rightarrow \textit{Trash}]_{a_3}
\end{aligned}$$

The basic strategy consists on allowing objects  $b_i$  to get transformed into objects  $b_0$  only if the element  $a_i \in A$  belongs to the associated multiset.

Let us summarize informally the evolution of objects  $b_i$  for all possible cases. Recall that in the  $(2\lfloor \log k \rfloor + 2)$ -th step, the counter  $g_i$  produces an object  $s$  in membrane  $e$ :

- At step  $t = 2\lfloor \log k \rfloor + 3$  object  $s$  enters in  $e_n$  and either  $d_1^+$  or  $d_1^-$  appear in each one of the two existing copies of membrane  $e$ .
- At step  $t = 2\lfloor \log k \rfloor + 4$  object  $s$  enters in  $e_{n-1}$  and either  $p_1$  or  $q_1$  appear in membranes  $e$ .
- At step  $t = 2\lfloor \log k \rfloor + 5$ , after the second division has been carried out, there are 4 membranes labeled by  $e$ . Object  $s$  enters in  $e_{n-2}$  (this happens in all 4 copies) and  $p_1$  or  $q_1$  get into  $e_n$  (there are two of each).
- ...
- At step  $t = 2\lfloor \log k \rfloor + n + 3$  object  $s$  arrives into  $e_0$ , and  $p_1$  or  $q_1$  enter in  $e_2$ .
- At step  $t = 2\lfloor \log k \rfloor + n + 4$  object  $s$  dissolves  $e_0$  (and hence objects  $b_i$  are moved to  $e_1$ ), and  $p_1$  or  $q_1$  arrive into  $e_1$ .
- At step  $t = 2\lfloor \log k \rfloor + n + 5$  objects  $b_1$ ,  $b_2$  and  $b_3$  have been transformed in  $b_1^+$ ,  $b_2^-$  and  $b_3^-$ , respectively, and they will be located either in  $e_1$  (if the membrane contained an object  $p_1$ ) or in  $e_2$  (if there was an object  $q_1$  in  $e_1$ ). Besides, in the same step  $p_2$  or  $q_2$  get into  $e_2$ .
- At step  $t = 2\lfloor \log k \rfloor + n + 6$ 
  - Objects  $b_1^+$  evolve to  $b_0$  (if they were in  $e_1$ ) or to *Trash* (if they were in  $e_2$ ).
  - Objects  $b_2^-$  evolve to  $b_2^+$ .
  - Objects  $b_3^-$  have been transformed into  $b_3^-$  (both those that were in  $e_2$  and those in  $e_1$ ).
  - All the objects  $b_i^\alpha$  ( $i = 1, \dots, n$  and  $\alpha \in \{+, -, =\}$ ) will be located either in membrane  $e_2$  (if the latter contained an object  $p_2$ ) or in  $e_3$  (if there was an object  $q_2$  in  $e_2$ ).
  - Besides, in this moment  $p_3$  or  $q_3$  get into  $e_3$ .



**Fig. 3.** TIME  $2\lceil \log k \rceil + 2n + 8$

The design has been adjusted in such a way that in the moment when objects  $p_i$  and  $q_i$  arrive into membranes  $e_i$  it happens that the objects  $b_j^\alpha$  ( $j = i, \dots, n$  and  $\alpha \in \{+, -, =\}$ ) are located in  $e_i$  in half of the membranes or in  $e_{i+1}$  in the rest of membranes. In the next step there will be objects  $b_i^+$  in  $e_i$  only for those cases where there was an object  $p_i$ , and hence the weight of element  $a_i \in A$  should be added to the weight of the associated multiset (that is,  $w(a_i)$  copies of  $b_0$  will be produced in those membranes).

$$\text{Set (F). } \left. \begin{array}{l} [w_i \rightarrow w_{i+1}]_f \\ [v_i \rightarrow v_{i+1}]_{a_4} \\ [h_i \rightarrow h_{i+1}]_{a_3} \\ [x_i \rightarrow x_{i+1}]_c \\ [z_i \rightarrow z_{i+1}]_{a_2} \\ [l_i \rightarrow l_{i+1}]_{ch} \end{array} \right\} \text{ for } i \in \{2\lceil \log k \rceil + 3, \dots, 2\lceil \log k \rceil + 2n + 6\}.$$

$$[z_{2\lceil \log k \rceil + 2n + 7}]_{a_2} \rightarrow \text{Trash}$$

The rest of the counters simply increase their indices during this stage. At the end of the stage, in the  $(2\lceil \log k \rceil + 2n + 7)$ -th step,  $z_i$  will dissolve all membranes  $a_2$ . Therefore, in the next step we have  $2^n$  membranes labeled by  $e$ , and inside them (more precisely, inside membranes  $a_3$ ) we have multisets of objects  $b_0$  encoding the weights of all possible subsets  $B \subseteq A$  (each membrane encodes a different subset) and also exactly  $k$  copies of membrane  $ch$ , see Fig. 3.

**Third task: compare  $k$  to the weight of each subset.** We shall focus next on the checking stage. That is, the system has to check in all membranes  $a_3$  if the number of objects  $b_0$  (encoding the weight of the associated subset) matches or not the parameter  $k$  (represented as the number of membranes  $ch$ ). This task is performed by the following set of rules (for the sake of simplicity, we denote  $\beta = 2\lceil \log k \rceil + 2n + 8$ ):

$$\text{Set (G). } \begin{array}{l} b_0 []_{ch} \rightarrow [c^*]_{ch} \\ [b_0 \rightarrow u_1]_{a_4} \\ [c^*]_{ch} \rightarrow \text{Trash} \\ [h_\beta]_{a_3} \rightarrow \text{Trash} \end{array}$$

At the step  $t = \beta$ , objects  $b_0$  get into membranes  $ch$ , and simultaneously membrane  $a_3$  is dissolved. There are three possible situations:

1. There are exactly  $k$  objects  $b_0$ . In this case at step  $t = \beta + 1$  there will not be any object  $b_0$  remaining, and all membranes  $ch$  have been dissolved.
2. The number of objects  $b_0$  is lower than  $k$ . In this case at step  $t = \beta + 1$  there will not be any object  $b_0$  remaining, but there will be some membranes  $ch$  that have not been dissolved (because no object  $b_0$  entered them).
3. The number of objects  $b_0$  is greater than  $k$ . In this case there are some objects  $b_0$  that could not get inside a membrane  $ch$  (recall that the rules are applied in a maximal parallel way, but for each membrane only one object can cross it at a time).

In the second case, inside each membrane  $ch$  that has not been dissolved the rules  $[l_{\beta+1} \rightarrow l_{\beta+2}]_{ch}$  and  $[l_{\beta+2}]_{ch} \rightarrow u_2$  are applied in the steps  $t = \beta + 1$  and  $t = \beta + 2$ , respectively. Hence at step  $t = \beta + 3$  there will be an object  $u_2$  in  $a_4$ .

In the third case, the exceeding objects  $b_0$  may, nondeterministically, either get into a membrane  $ch$  (avoiding that the dissolution rule is applied to that membrane) or evolve into object  $u_1$ . Irrespectively of the nondeterministic choice, we know that there will be no more objects  $b_0$  in  $a_4$  at step  $t = \beta + 2$ .

Of course, during this stage the rest of the counters continue evolving:

$$\begin{aligned} \text{Set (H).} \quad & [l_{\beta+i-1} \rightarrow l_{\beta+i}]_{ch} \text{ for } i = 0, 1, 2 \\ & [v_{\beta+i-1} \rightarrow v_{\beta+i}]_{a_4} \text{ for } i = 0, \dots, 4 \\ & [x_{\beta+i-1} \rightarrow x_{\beta+i}]_c \text{ for } i = 0, \dots, 7 \\ & [w_{\beta+i-1} \rightarrow w_{\beta+i}]_f \text{ for } i = 0, \dots, 10 \end{aligned}$$

The next set of rules guarantees that in every membrane where the weight of the associated subset was different from  $k$  (and only in such membranes) there will be some objects  $u_3$ .

$$\begin{aligned} \text{Set (I1).} \quad & [u_i \rightarrow u_{i+1}]_{a_4} \text{ for } i = 1, 2 \\ & [l_{\beta+2}]_{ch} \rightarrow u_2 \\ & [l_{\beta+2} \rightarrow u_3]_{a_4} \\ & [c^* \rightarrow u_3]_{a_4} \end{aligned}$$

These objects  $u_3$ , being in membrane  $a_4$ , will go into membranes  $c$  and dissolve them. We have here a similar situation as before, as there may be several objects  $u_3$  willing to go into a membrane  $c$ . The counter  $v_i$  takes care of dissolving membrane  $a_4$  so that any exceeding object  $u_3$  will be moved to membrane  $e$  and subsequently transformed into *Trash*.

$$\begin{aligned} \text{Set (I2).} \quad & u_3 [ ]_c \rightarrow [u_4]_c \\ & [v_{\beta+4}]_{a_4} \rightarrow \text{Trash} \\ & [u_3 \rightarrow \text{Trash}]_e \\ & [u_4 \rightarrow u_5]_c \\ & [u_5]_c \rightarrow \text{Trash} \end{aligned}$$

**Final task: answer stage.** Therefore, only in the branches where the number of objects  $b_0$  were equal to  $k$  we have a membrane  $c$  inside membrane  $e$  at step  $\beta + 7$ . Besides, we also have a counter  $w_i$  evolving in membrane  $f$ :

- If the instance of the Subset Sum problem has an affirmative answer, i.e., if there exists a subset of  $A$  whose weight is  $k$ , then in the step  $\beta + 7$  there will be a membrane  $e$  with a membrane  $c$  inside and an object  $x_{\beta+7}$  in it. This object will produce an object **yes** which will dissolve his way out to the environment.

On the contrary, if the instance has a negative answer, then there will not exist any membrane  $c$  in the system in the step  $\beta + 7$  and the object **yes** will not be produced. Hence, the membrane  $f$  will not be dissolved by **yes** and when the counter  $w_i$  reaches  $w_{\beta+10}$ , an object **no** will appear and will be sent to the environment.

The set of rules is the following one:

**Set (J).**  $[x_{\beta+7}]_c \rightarrow yes$   
 $[yes]_e \rightarrow yes$   
 $[yes]_f \rightarrow yes$   
 $[yes]_{skin} \rightarrow yes []_{skin}$   
 $[w_{\beta+10}]_f \rightarrow no$   
 $[no]_{skin} \rightarrow no []_{skin}$

Consequently, if the answer is affirmative the P system halts after  $\beta + 11$  steps and otherwise after  $\beta + 12$  steps.

## 4 Conclusions

In this paper we have combined different techniques for designing P systems in order to get a uniform family of P systems that solves the Subset Sum problem in the framework of P systems with weak division, with dissolution and without polarization. The main contribution of this paper is related to the Complexity Theory of P systems. The best solution of the **NP**-complete problem Subset Sum in any P system model up to now was linear in both input parameters  $n$  and  $k$ . In this paper we show that the dependency on  $k$  can be significantly reduced, since we show a solution where the resources and the number of steps are of a logarithmic order with respect to  $k$ .

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