
Frequency Membrane Systems

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Summary. We define a model of membrane system where each membrane is clocked independently from the others, in the sense that every derivation step is applied without a global synchronization. The computation is obtained by the execution of a limited amount of rules in each membrane, and only when they are allowed to execute a derivation step. Indeed, each membrane operates with a certain work frequency that could change across the system and during the execution. Simple results show that this model is at least as powerful as the usual one, and a few examples demonstrate that it gives rise to interesting dynamic behaviors.

1 Introduction: Biological Motivation

This work introduces a new class of P systems, where we want to come closer to biological cell's behavior by adopting some new features of membrane computing that could have a higher correspondence in biology. As we known, in general, different chemical reactions can take different time to be executed and moreover the same reaction could take different time depending on some environment conditions (for example concentration, temperature, etc.).

Some models have already adopted different approaches to the timing in P systems. For instance, in [5] maximal parallelism is not enforced, while in [1] a single rule is probabilistically chosen inside each membrane, but all selected rules work in parallel. Interestingly, paper [1] specifically aims at modeling some biological phenomena. In [2,6,4] authors study a model where each rule can take a different time to perform its action, and look for systems where even if timing changes results stay the same. Further results along this line are in [3].

We want to explore other changes to timing inside P systems but, above all, we want to focus the attention on the real asynchronous nature of biological cells. We want to consider every single membrane as a separate domain with a specific clock, where the rules can be applied as often as specified by their membranes' clock frequency. In this behavior, a single derivation step can occur only when the membrane has the right, specified by its own clock and by other constraints,

to carry out one or more rules, so each component of the system, regarding the overall computation, is totally independent from the others, hence the system is partially asynchronous.

As we said before we want, also, to adopt a different approach to the maximal parallel way to execute the rules. We think maximal parallelism is a very strong assumption, so we want to bound the amount of rules that can be applied in each membrane's derivation step. The motivations for this feature come from the fact that, in a living cell, there is a limited amount of energy, hence a limited amount of reactions can take place in a given time.

In this paper we introduce also a decay time for some symbol objects; we have made this assumption thinking that other reactions (here not described) could be modeled by such feature. For instance, symbols could decay because the cell itself uses them to get energy.

One more detail related to clocking is the offset on the starting time of operations in each membrane. This, and the other modeling features are discussed by means of examples and simple formal results in the following sections.

2 Frequency P Systems: Definition

A *frequency P system* is a P system where each rule has a time of execution. This execution's time is expressed in clock steps. Each membrane has its own clock, and a limited amount of rules that can be applied in each clock step (or a fixed amount of energy, if we want to associate different levels of energy to the rules). The clock period is a multiple of the unit time of an external observer.

The system will use symbol objects with evolution rules. We denote by N the set of natural numbers.

A Frequency P system with symbol objects of degree $m \geq 1$, is a construct

$$\Pi = (O, D, T, \mu, \omega_1, \dots, \omega_m, E, t_D, C, R_1, \dots, R_m, i_O)$$

where:

- O is the alphabet of the objects;
- $D \subseteq O$ is the alphabet of decaying symbols;
- $T \subseteq O$ is the alphabet of non-decaying symbols;
- μ is a membrane structure consisting of m membranes labeled with $1, 2, \dots, m$;
- $\omega_i, 1 \leq i \leq m$, specifies the multiset of objects present in the corresponding region i at the beginning of a computation;
- $E \subseteq N^m$ is a set of m numbers indicating the energy value assigned to each membrane at every membrane's clock step, overriding any previous energy level associated to them;
- $t_D \subseteq N^n$ is a set of n numbers indicating the decay time of the n decay symbols in D ;

- $C \subseteq N^m$ is a set of m numbers indicating the clock value (referred to an external observer) assigned on each membrane;
- $R_i, 1 \leq i \leq m$, are finite sets of evolutionary rules over O associated with regions $1, 2, \dots, m$ of μ ; the rules can be either cooperative or non-cooperative rules of the form $A \xrightarrow{s}^k v$, where A is an object from O and v is a string over $\{a_{here}, a_{out}, a_{in} \mid a \in O, 1 \leq j \leq m\}$, if the target is not specified, then it is intended to be *here*; k is an integer representing the energy to consume to apply the rule. Note that k could be a negative number, in this case we assume that the reaction modeled by the rule produces energy for the cell, when k is not specified we assume that $k=1$; s in N is the number of clock's steps necessary to the rules to act (and produce the objects in the right hand side), when s is not specified we assume that $s=0$;
- i_O in $\{0, 1, \dots, m\}$ is the output region (0 for the environment).

A configuration of Π at a given time t is represented by a string of parentheses (the structure μ) and strings over O (contents of the regions). For instance, a possible configuration of the system at time 0 (the starting time) with an alphabet $O=\{A, B\}$ and a structure $\mu = [_1[_2[_3]_3]_1]$ could be:

$$\varsigma(\Pi(0)) = [_1[_2AA]_2[_3BB]_3]_1$$

Given a string ω representing a configuration at time t , then all the strings obtained from ω by taking any permutation of the strings, representing the contents of the regions, represent the same configuration at time t .

We suppose the existence of an external global clock that ticks at uniform intervals, taken as time unit, starting at time 0; we also suppose that each membrane has its own clock that ticks at uniform intervals, taken as multiple of the observer's time unit. In the former example we assume that each membrane starts at same time (time 0 of the observer).

In each membrane of the system we have a finite number of objects from alphabet O , a finite set of evolution rules each one with its own costs (in time and energy) and a finite amount of energy. At each time step of the observer's clock, we have membranes in the system that are allowed to execute their rules according to their own clock ticks and membranes that are not allowed to execute their rules (until their next clock ticks). These membranes could receive object symbols from other membranes if they are target of some rules but they are not allowed to deal with those objects until their next clock ticks. We identify former membranes as active membranes and the latter as passive membranes (in a given observer's time).

When a membrane becomes active we apply as many rules as we can, according to the left hand side of the rules and the energy necessary to carry out the rules. It's important to understand that the rules are NOT applied in maximum parallel manner as in standard P systems, since only one instance of objects on the left hand side of the rule will be consumed and only one instance of the objects on the right hand side of the rule will be produced after a fixed number of time step specified by the rule. During the execution of a rule, the occurrences of symbol

objects in the right hand side are no longer available for other rules. Each time a rule is applied we decrease the energy value of the membrane by the value specified by the rule, in this way a membrane could execute a fixed number of rules for each clock ticks. The energy level of a membrane will be reset to the initial value at the beginning of the next membrane clock ticks.

If two or more rules in an active membrane are allowed to be executed, then possible conflicts for using the occurrences of symbol objects are solved by assigning the objects in a non-deterministic way. The computation halts when at a certain observer's clock step no rule can be applied in any region and there are no rules in execution. The output of a halting computation is the vector of numbers representing the multiplicities of objects present in the output region in the halting configuration.

3 Frequency P Systems: Examples

The following example shows how a frequency P system works:

$$\Pi_0 = (O, D, T, \mu = [1[2]2[3]3[4]4]_1, \omega_1 = \lambda, \omega_2 = A^5, \omega_3 = B^7, \omega_4 = C^7, \\ E, t_D, C, R_1, R_2, R_3, R_4, i_O = 1),$$

where:

$$\begin{aligned} O &= \{A, B, C, a, b, c, e\} ; D = \emptyset ; T = O ; \\ E &= \{2, 1, 1, 1\} \\ t_D(i) &= 1, \forall i \in D \\ C &= \{C_1 = 1, C_2 = 3, C_3 = 2, C_4 = 2\} \\ R_1 &= \{r_1 : abc \rightarrow e, r_2 : bc \rightarrow a, r_3 : aa \rightarrow e\} \\ R_2 &= \{r_4 : A \rightarrow a_{out}\} \\ R_3 &= \{r_5 : B \rightarrow b_{out}\} \\ R_4 &= \{r_6 : C \rightarrow c_{out}\} \end{aligned}$$

The starting configuration of this frequency P system represented by Figure 1.

The configuration of the system at different times is shown in Figure 2.

In this and in the following figures, we focus the attention only to the objects in skin membrane μ_1 , in particular by displaying the availability in there of symbols a, b, c at different times, by marking in the picture the axis labeled as "Symbol object...".

Note that if we set to 0 the time of execution of each rule we get the same result of a computation carried out with a standard P system; the only difference is that we introduce a sort of priority in rules execution. For example, if we introduce a new rule in membrane μ_1 ($r_7: a \rightarrow f$) we force the system to apply this rule before the others at least in t_5 (because in each clock step the membrane could execute at most 2 rules if it can, and in t_5 no other rule can be applied except r_7). In this case we reach the same final configuration of a standard P system also because

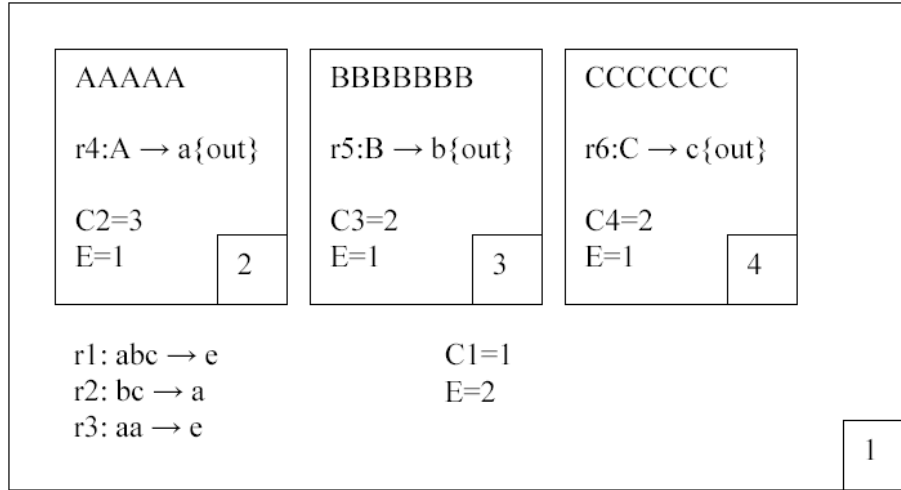


Fig. 1. The starting configuration of Π_0 .

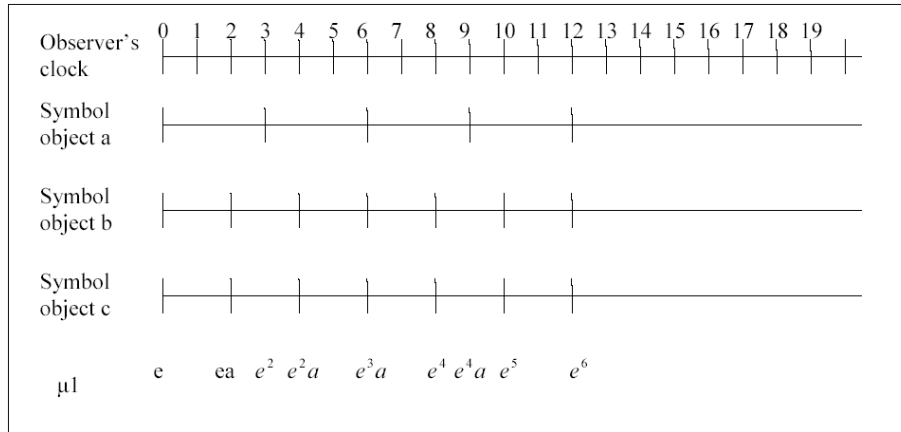


Fig. 2. The evolution of skin membrane in Π_0 .

we set an energy value for the membrane $\mu 1$ to $E=2$. This parameter in the given example enforces maximality because in case of presence of the symbol objects a, b, c in the membrane we could apply either the rule $r1$ or both the rules $r2$ and $r3$ in the same clock step. This behavior produces the same result (the symbol object e) but in the former case it consumes only a single unit of energy indeed, while in the latter, it consumes two energy units.

Note that this sort of “chain reaction” is allowed by the definitions of the system, even though this happens only because we set to 0 the time of execution

of the rules; but, despite of that, this feature will become useful in some further variants of the system (for example we could apply a rule even if the membrane is not active if we have enough energy units left, or we could increase or decrease the clock frequency of the membrane in function of its own energy level).

Note also that if we do not associate decay time to some object symbols we get the same result even if we starts the membranes not at the same time.

In the following example we run the same P system as above, but with the difference that we introduce a delay of one observer's clock step for the membrane μ_4 . The resulting dynamics is shown in Figure 3.

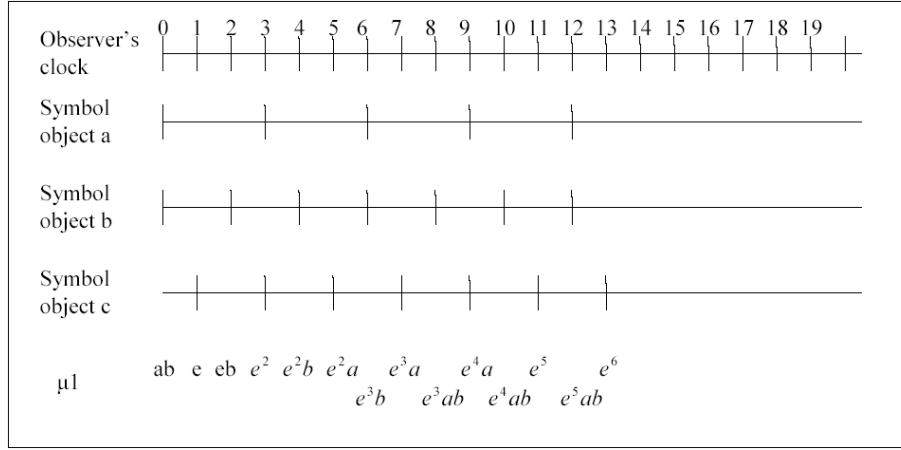


Fig. 3. Dynamics in skin membrane of a system derived from II_0 by introducing a delay for μ_4 .

4 Frequency P Systems with Decay Time: Examples

Now we shows the same example with a delay time 1 for the symbol objects $\{a, b, c\}$.

The following is the definition of the system II_1 .

$$II_1 = (O, D, T, \mu = [1[2]2[3]3[4]4]_1, \omega_1 = \lambda, \omega_2 = A^5, \omega_3 = B^7, \omega_4 = C^7, E, t_D, C, R_1, R_2, R_3, R_4, i_O = 1),$$

where:

$$\begin{aligned} O &= \{A, B, C, a, b, c, e\} ; D = \{a, b, c\} ; T = O - D = \{A, B, C, e\}; \\ E &= \{2, 1, 1, 1\} \\ t_D(i) &= 1, \forall i \in D \\ C &= \{C_1 = 1, C_2 = 3, C_3 = 2, C_4 = 2\} \end{aligned}$$

$$\begin{aligned}
R_1 &= \{r_1 : abc \rightarrow e, r_2 : bc \rightarrow a, r_3 : aa \rightarrow e\} \\
R_2 &= \{r_4 : A \rightarrow a_{out}\} \\
R_3 &= \{r_5 : B \rightarrow b_{out}\} \\
R_4 &= \{r_6 : C \rightarrow c_{out}\}
\end{aligned}$$

As we have done before, the configuration of the system will be showed below. However, before, we want to justify this feature by comparing it with its biological counterpart. We could think of an object produced by a membrane as a sort of bio-chemical stimulus that is a part of a reaction. If this stimulus does not reach a certain concentration the reaction could not take place. We could think this stimulus will be suppressed if it does not match with a proper receptor in a limited period of time.

When we set a decay time for some symbol objects, the system could have a different behavior (and a different final configuration) depending of the starting time of activity of certain membranes.

For the following examples we have set the decay time $t_D()$ equal to 1 for the symbols objects $\{a, b, c\}$; this means that a symbol object i in D produced at time j , could be used by a rule only from time j (included) to time $j+1$ (excluded). The dynamics can be seen in Figure 4.

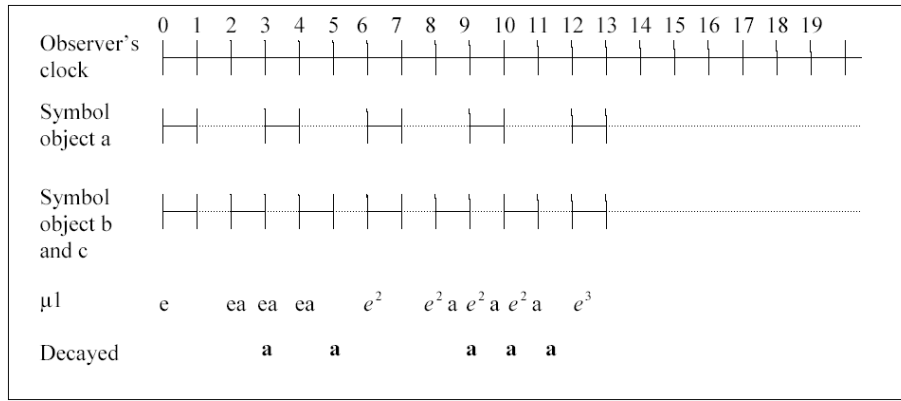


Fig. 4. The dynamics in skin membrane of Π_1 .

As you can see, in this case the same system with decay times produces a different output with respect to a standard P system and moreover, the final configuration could be different if we introduce a random delay in membranes starting.

In the previous example we see that the rule r_1 could be applied only where are present all the three symbol objects $\{a, b, c\}$, and this situation occurs three times: at time t_0 , t_6 and t_{12} .

Also the rule r_2 is applied but the symbol object a decays before another instance of the symbol could reach the membrane, hence the rule r_3 is never carried out.

The following example, described by Figure 5, shows the configuration of the same system, but with a delay of one observer's clock step for the membrane μ_4 .

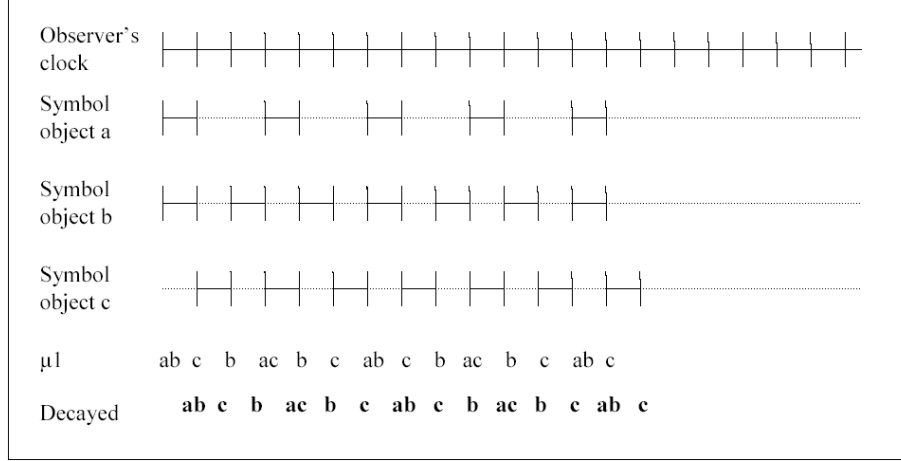


Fig. 5. Dynamics in skin membrane of a system derived from Π_1 by introducing a delay for μ_4 .

Note that no rules of type r_1 or r_3 could be applied during the computation because, due to the time shifting on membrane μ_4 , the symbol objects $\{a, b, c\}$ are never present, at the same time, in the membrane. Hence in this case the halting configuration of the system is \emptyset .

In the last example we want to force the production of the symbol object e by increasing the reactivity frequency of membrane μ_4 . The following is the definition of the system Π_2 .

$$\Pi_2 = (O, D, T, \mu = [1[2]2[3]3[4]4]_1, \omega_1 = \lambda, \omega_2 = A^5, \omega_3 = B^7, \omega_4 = C^7, E, t_D, C, R_1, R_2, R_3, R_4, i_O = 1),$$

where:

$$\begin{aligned} O &= \{A, B, C, a, b, c, e\} ; D = \{a, b, c\} ; T = O - D = \{A, B, C, e\}; \\ E &= \{2, 1, 1, 1\} \\ t_D(i) &= 1, \forall i \in D \\ C &= \{C_1 = 1, C_2 = 3, C_3 = 2, C_4 = 1\} \\ R_1 &= \{r_1 : abc \rightarrow e, r_2 : bc \rightarrow a, r_3 : aa \rightarrow e\} \end{aligned}$$

$$\begin{aligned}
R_2 &= \{r_4 : A \rightarrow a_{out}\} \\
R_3 &= \{r_5 : B \rightarrow b_{out}\} \\
R_4 &= \{r_6 : C \rightarrow c_{out}\}
\end{aligned}$$

The resulting dynamics is shown in Figure 6.

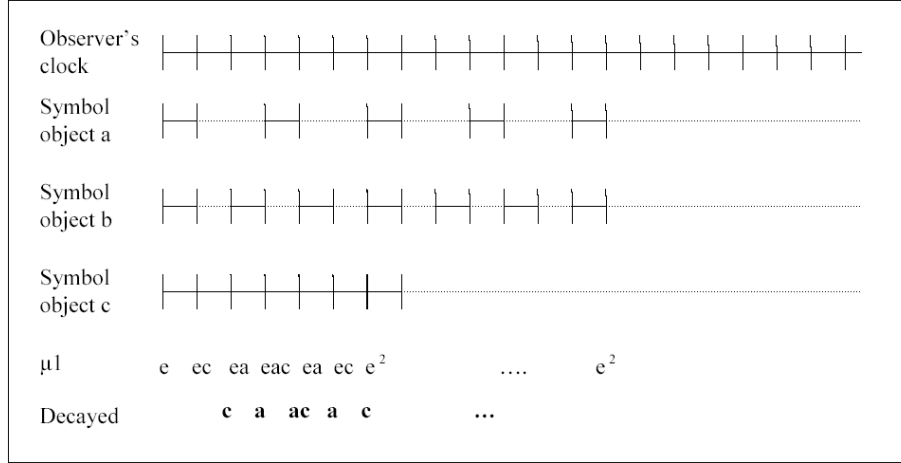


Fig. 6. The evolution of symbols in skin membrane of Π_2 .

This behavior is of interest with respect to the modeling of biological mechanisms. We could think that the presence of symbol object e in the halting configuration models certain gene activation. If we simulate several cells with several P systems, derived from Π_1 but with different shifting of their membranes' starting time, we obtain only a little gene activation depending of the starting configuration of the membranes of each system, but if we increase the concentration of our stimulus (represented by the frequency increasing of membrane μ_4) we force the activation of the gene in every system for every permutation of their membranes' starting time.

5 Some Properties of Frequency P Systems

It is easy to state that the class of frequency P systems includes all usual P systems, since we can: assign 0 to the value of energy consumed by each rule, set to 0 the time required by rules to produce their output, have no decaying symbols, have all membranes' clocks with period equal to the unit time of the observer.

But this remark also leads us to a key aspect: a global clock does exist. It is the clock of the observer, which has a frequency which is a multiple of each

membranes' frequency, and above all, all clocks, in membranes and for the observer, *are* synchronized among themselves, along the grid of time points defined by the observer's clock. Even the eventual offset assigned to membranes is of length equal to an exact multiple of the period of the observer's clock.

This further allows us to state the following:

Proposition: Frequency P systems not consuming energy and without decaying symbols can be simulated by usual P systems with maximal parallelism.

Proof sketch:

We consider observer's clock of simulated frequency P system as the global clock applied in the simulating (usual) P system to each membrane. Membranes of the frequency P system apply rules exactly on (some) ticks of observer's clock. Thus, we could introduce, in the simulating P systems, rules derived from those of the simulated frequency P system, with a left side modified by also requiring the presence a new symbol, associated to the correct (cyclic) counting of global clock's ticks: those new symbols are evolved by specific rules so to represent the waiting of simulated frequency membranes.

(end of Proof sketch)

Nonetheless, our examples show that the dynamics emerging from the behavior of frequency P systems make them an interesting alternative to usual ones as a way to model some basic mechanisms of biological inspiration.

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