

# P Systems: A formalism for computing and for systems biology

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# Introduction (1)

Natural Computing is the study of

- models of computation
- inspired by the functioning of biological systems

Natural Computing is not Bioinformatics

- Bioinformatics is the development and application of Computer Science means to Biology (and Medicine)

A relevant part of Natural Computing exploits methods and means of formal language theory

- Biological mechanisms can be often suitably described by rewrite rules

## Introduction (2)

The main aims of bio-inspired models of computation are:

- to propose new unconventional computing architectures
- (in the context of formal language theory) to study new classes of formal languages
- to propose new programming paradigms

Typical results on bio-inspired models of computation are:

- Universality (that is Turing completeness)
- Existence of polynomial solutions to NP-complete problems (with exponential workspace)
- Connections with other models of computation (Petri Nets, Lambda calculus, etc...)

# Outline of the talk

- 1 Introduction
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- 3 The P Algebra
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- 4 Timed P Automata
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  - An application

# P Systems

P Systems are (a class of) formalisms studied in Membrane Computing

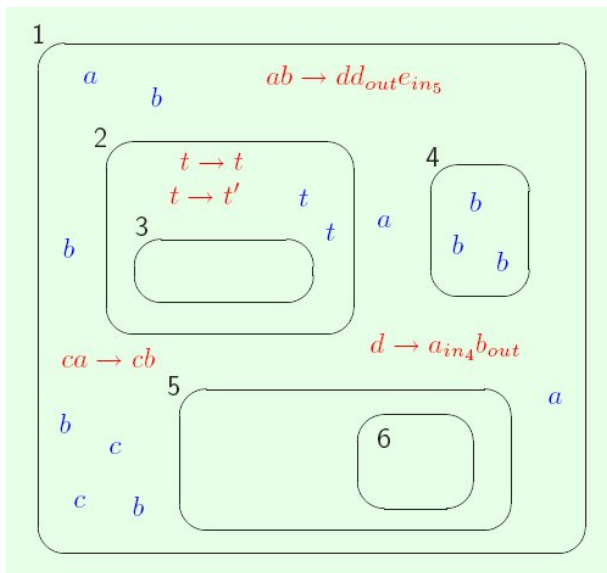
The P Systems web page: <http://ppage.psyste.ms.eu/>

P Systems are distributed computing devices inspired by the structure and the functioning of a living cells.

The key elements of P Systems are:

- Membranes (that create compartments used to distribute computations)
- Multisets (abstractions of chemical solutions that are used as data)
- Evolution (rewriting) rules (abstractions of chemical reactions that are used as programs)

# The simplest P Systems



# Formal definition of P Systems

A *P System*  $\Pi$  is given by

$$\Pi = (V, \mu, w_1, \dots, w_n, R_1, \dots, R_n)$$

where:

- $V$  is an *alphabet* whose elements are called *objects*;
- $\mu \subset \mathbb{N} \times \mathbb{N}$  is a *membrane structure*, such that  $(i, j) \in \mu$  denotes that the membrane labeled by  $j$  is contained in the membrane labeled by  $i$ ;
- $w_i$  with  $1 \leq i \leq n$  are strings from  $V^*$  representing multisets over  $V$  associated with the membranes  $1, 2, \dots, n$  of  $\mu$ ;
- $R_i$  with  $1 \leq i \leq n$  are finite sets of *evolution rules* associated with the membranes  $1, 2, \dots, n$  of  $\mu$ .

## Evolution rules

An evolution rule  $u \rightarrow v$  consists of a multiset of objects  $u$  (representing reactants) and a multiset of messages  $v$  (representing products). A message may have one of the following forms:

- $a_{here}$ , meaning that object  $a$  remains in the same membrane;
- $a_{out}$ , meaning that object  $a$  is sent out of the membrane;
- $a_{in_l}$ , meaning that object  $a$  is sent into the child membrane  $l$ .

The subscript *here* is often omitted.

Evolution rules can be classified into:

- non-cooperative rules: the left-hand side consists of a single object (e.g.  $a \rightarrow b^2 d_{out}$ )
- cooperative rules: the left-hand side can be any multiset of objects (e.g.  $a^2 b \rightarrow b^2 d_{out}$ )
  - ▶ a particular case of cooperative rules are catalytic rules, namely rules of the form  $ca \rightarrow cb^2$  where  $c$  belongs to a special set of objects called catalysts.



# Maximal parallelism

Evolution rules are applied with *maximal parallelism*:

- More than one rule can be applied (on different objects) in the same step
- Each rule can be applied more than once in the same step (on different objects)
- Maximality means that:

*A multiset of instances of evolution rules is chosen non-deterministically such that no other rule can be applied to the system obtained by removing all the objects necessary to apply the chosen instances of rules.*

# Computation of a P System

A sequence of transitions between configurations of a given P System is called a *computation*.

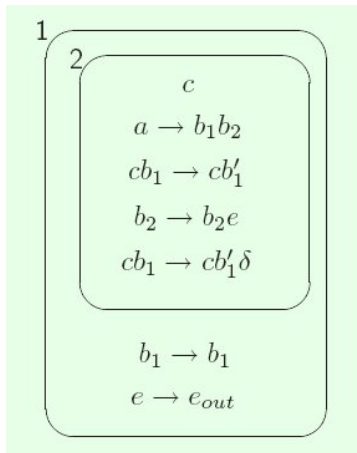
A computation is *successful* if and only if it reaches a configuration in which no rule is applicable.

The result of a successful computation is the multiset of objects sent, during the computation, either out of the skin membrane or into a chosen membrane.

Unsuccessful computations (computations which never halt) yield no result.

## Example of P System

A P System computing  $n^2$  (with a dissolving rule)



INPUT:  $a^n$  inside membrane 2

OUTPUT:  $e^{n^2}$  sent out of membrane 1

# Universality of P Systems

P Systems with cooperative rules are universal,

- actually, catalytic rules are enough

P Systems with non-cooperative rules only are not universal

# Some variants of P Systems

Variants obtained by considering different types of evolution rules:

- extended with priorities;
- with promoters and inhibitors;
- with dissolution of membranes;
- symport/antiport rules;
- with active membranes;
- .....

Variants obtained by considering graphs rather than trees as membrane structures:

- tissue-like systems;
- spiking neural systems.

## P Systems with active membranes

*Active membrane* means that evolution rules can change the membrane structure of a P System

- In particular, there can be membrane division rules
- $[u]_i \rightarrow [v]_j[z]_k$

It has been proved that with membrane division it is possible to solve NP-complete problems in polynomial time (but exponential space).

Roughly, the idea is the following:

- Every possible solution is encoded inside a different membrane in a linear number of steps by means of membrane division rules
- Each membrane checks whether the solution it contains is correct (in polynomial time, by def.)

# Formal semantics of P Systems

Some formal semantics of P Systems have been defined with different aims;

- to develop interpreters proved to be correct (Ciobanu et al.);
- to study causality aspects of P Systems (Busi);

The main difficulty in the definition of a formal semantics is the handling of the maximal parallelism.

# Observable Behavior

In order to define reasonable semantics and behavioral equivalences we have to characterize what it is reasonable to observe of the behavior of a P System

We choose to observe the input/output behavior of membranes:

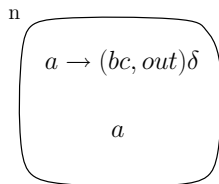
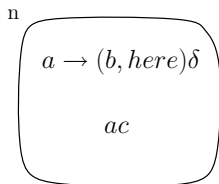
*Two membranes are equivalent if, at each step, they can:*

- *receive the same objects from outer and inner membranes*
- *send the same objects to the outer membrane (or to the external environment)*
- *send the same objects to the same inner membranes*

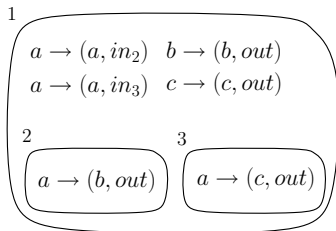
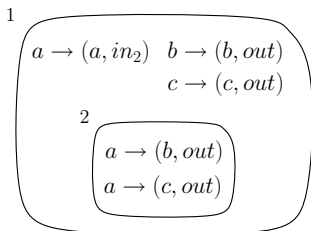


# Examples of Equivalent Membranes

The following membranes could be considered as equivalent:



and also the following two:



# Examples of Equivalent Membrane Contents

A *membrane content* is a pair  $(\mathcal{R}, u)$  where

- $\mathcal{R}$  is a set of evolution rules
- $u$  is a multiset of objects

that can be (a part of) the content of a membrane

These membrane contents should be considered pairwise equivalent:

$$(\mathcal{R}_1, \emptyset) \quad \text{and} \quad (\mathcal{R}_2, \emptyset)$$

$$\text{where } \mathcal{R}_1 = \{ a \rightarrow (b, \text{here}), a \rightarrow (c, \text{here}) \} \text{ and} \\ \mathcal{R}_2 = \mathcal{R}_1 \cup \{ aa \rightarrow (bc, \text{here}) \}.$$

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# The (simplest) P Algebra

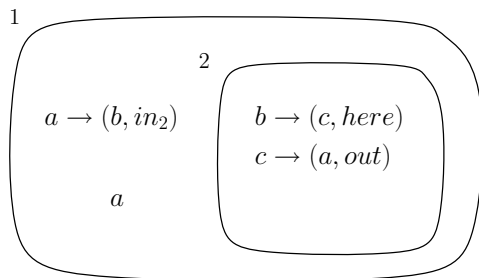
**Def. (P Algebra)** The syntax of *membrane contents*  $c$ , *membranes*  $m$ , and *membrane systems*  $ms$  is given by the following grammar:

$$\begin{aligned} c &::= (\emptyset, \emptyset) \mid (u \rightarrow v_h v_o \{v_{l_i}\}, \emptyset) \mid (\emptyset, a) \mid c \cup c \\ m &::= [{}_l c]_l \qquad ms ::= m \mid ms|ms \mid \mu(m, ms) \end{aligned}$$

where  $l$  and  $l_i$  range over  $\mathbb{N}$  and  $a$  ranges over  $V$ .

- $u \rightarrow v_h v_o \{v_{l_i}\}$  stands for  $u \rightarrow (v_h, \text{here})(h_o, \text{out})(v_{l_1}, in_{l_1}) \dots (v_{l_n}, in_{l_n})$
- $c_1 \cup c_2$  denotes the membrane content obtained by merging the rules and the objects of  $c_1$  and  $c_2$
- $[{}_l c]_l$  denotes a membrane whose content is  $c$  and whose label is  $l$
- $ms|ms$  denotes *juxtaposition* of membranes
- $\mu(m, ms)$  denotes the containment of the membranes  $ms$  in  $m$  (hierarchical composition)

## Example of Term of the P Algebra



corresponds to the term:

$$\mu\left( [1 (a \rightarrow (b, in_2), \emptyset) \cup (\emptyset, a)]_1 , [2 (b \rightarrow (c, here), \emptyset) \cup (c \rightarrow (a, out), \emptyset)]_2 \right)$$

that is (for short):

$$\mu\left( [1 a \rightarrow (b, in_2), a]_1 , [2 b \rightarrow (c, here), c \rightarrow (a, out)]_2 \right)$$

# Semantics of the P Algebra

The semantics of the P Algebra is a Labeled Transition System (LTS)

- states are terms
- transitions are labeled by information about the input/output behavior of the system (observation)

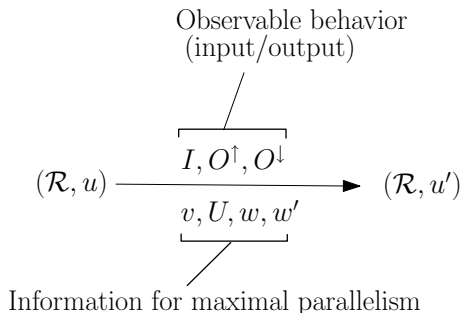
Let's start with membrane contents. We would like to

- define the behavior of individual evolution rules and objects
- infer the behavior of a membrane content from the behaviors of its rules and objects

**Problem:** it is hard to express the concept of maximal parallelism in a compositional way

**Solution:** we enrich transition labels with information concerning the (potential) application and non application of evolution rules

# Transitions of Membrane Contents



In particular:

- $v$  and  $w$  are objects consumed by some evolution rules, as it results from the composition of the transitions of single rules and of single objects, respectively
- $w'$  are objects that are not consumed by any rule
- $U$  contains all left hand sides of rules in  $\mathcal{R}$

## Inference Rules for Membrane Contents

The empty membrane content can only receive input objects:

$$\frac{I \in V^*}{(\emptyset, \emptyset) \xrightarrow[\emptyset, \emptyset, \emptyset, \emptyset]{\emptyset, I, \emptyset, \emptyset} (\emptyset, I)}$$

A single object can either be used by some rule (thus disappearing) or not:

$$\frac{I \in V^*}{(\emptyset, a) \xrightarrow[\emptyset, \emptyset, a, \emptyset]{I, \emptyset, \emptyset} (\emptyset, I)} \qquad \frac{I \in V^*}{(\emptyset, a) \xrightarrow[\emptyset, \emptyset, \emptyset, a]{I, \emptyset, \emptyset} (\emptyset, Ia)}$$

A single rule can be applied  $n$  times (possibly  $n = 0$ ):

$$\frac{I \in V^* \quad n \in \mathbb{N}}{(u \rightarrow v_h v_o \{v_{l_i}\}, \emptyset) \xrightarrow[u^n, \{u\}, \emptyset, \emptyset]{I, v_o^n, \{(l_i, v_{l_i}^n)\}} (u \rightarrow v_h v_o \{v_{l_i}\}, I v_h^n)}$$



# Inference Rules for Unions of Membrane Contents

$$\frac{x_1 \xrightarrow{I_1, O_1^\uparrow, O_1^\downarrow} y_1 \quad x_2 \xrightarrow{I_2, O_2^\uparrow, O_2^\downarrow} y_2 \quad v'_1 v'_2 \not\vdash U_1 \oplus U_2}{x_1 \cup x_2 \xrightarrow{I_1 I_2, O_1^\uparrow O_2^\uparrow, O_1^\downarrow \cup_{\mathbb{N}} O_2^\downarrow} y_1 \cup y_2}$$

This inference rule simply makes the union of each pair of label elements taken from transitions membrane contents  $x_1$  and  $x_2$ .

- $u_1 u_2$  is the union of multisets  $u_1$  and  $u_2$ , whereas  $\cup_{\mathbb{N}}$  and  $\oplus$  are other special union operations

Condition  $v'_1 v'_2 \not\vdash U_1 \oplus U_2$  means that no rule could be applied to the objects left unchanged ( $v'_1 v'_2$ ) must not

- $v \vdash U$  means  $\exists u. (u \subseteq v \wedge u \in U)$

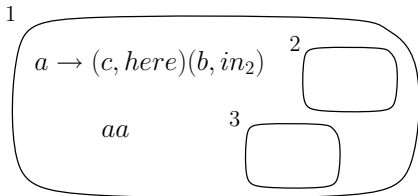
# Inference Rules for Membranes and Membrane Systems

When the  $[ ]_I$  is applied to a membrane content  $x$

- the transition from  $x$  to  $y$  must be *acceptable*
  - ▶ the first and the third label under the arrow must be the same
- information under the arrow is no longer necessary

$$\frac{x \xrightarrow[u, U, u, v']{I, O^\uparrow, O^\downarrow} y}{[ ]_I \xrightarrow{\{(I, I)\}, O^\uparrow, O^\downarrow} [ ]_I}$$

Inference rules for Membrane Systems (i.e. juxtaposition and hierarchical composition operations) are trivial.



$$(a \rightarrow c_{here} b_{in_2}, aa) \xrightarrow[aa, \{a\}, aa, \emptyset]{l, \emptyset, (2, bb)} (a \rightarrow c_{here} b_{in_2}, lcc)$$

$$[1(a \rightarrow c_{here} b_{in_2}, aa)]_1 \xrightarrow{\{(1, l)\}, \emptyset, (2, bb)} [1(a \rightarrow c_{here} b_{in_2}, lcc)]_1$$

$$[2(\emptyset, \emptyset)]_2 \xrightarrow{\{(2, bb)\}, \emptyset, \emptyset} [2(\emptyset, bb)]_2 \quad [3(\emptyset, \emptyset)]_3 \xrightarrow{\{(3, \emptyset)\}, \emptyset, \emptyset} [3(\emptyset, \emptyset)]_3$$

$$[2(\emptyset, \emptyset)]_2 \mid [3(\emptyset, \emptyset)]_3 \xrightarrow{\{(2, bb), (3, \emptyset)\}, \emptyset, \emptyset} [2(\emptyset, bb)]_2 \mid [3(\emptyset, \emptyset)]_3$$

$$\mu([1\dots]_1, [2\dots]_2 \mid [3\dots]_3) \xrightarrow{\{(1, l)\}, \emptyset, \emptyset} \mu([1(-, lcc)]_1, [2(\emptyset, bb)]_2 \mid [3(\emptyset, \emptyset)]_3)$$

# Maximal Parallelism Theorem

The multiset of objects that are left unchanged in an acceptable transition of a membrane content cannot be used to perform an acceptable transition with the same rules

- i.e. there is no rule that can be applied to unused objects

## Theorem (Maximality)

$$(\mathcal{R}, u) \xrightarrow[u', U, u', v']{I, O_1^\uparrow, O_1^\downarrow} x \quad \text{implies} \quad (\mathcal{R}, v') \xrightarrow[u'', U', u'', v'']{I', O_2^\uparrow, O_2^\downarrow} /$$

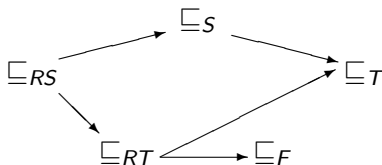
for any  $u'' \neq \emptyset$

# Well-known Behavioral Preorders

We have considered a number of behavioral preorders:

- *simulation*  $\sqsubseteq_S$
- *ready simulation*  $\sqsubseteq_{RS}$
- *ready trace preorder*  $\sqsubseteq_{RT}$
- *failure preorder*  $\sqsubseteq_F$
- *trace preorder*  $\sqsubseteq_T$

It is well-known that the considered preorders are structured as follows (where  $\rightarrow$  is  $\subseteq$ )



In the case of the P Algebra all the inclusions are strict

# Well-known Behavioral Equivalences

The kernels of the preorders (the largest equivalence each of them contains) are well-known behavioral equivalences

- bisimulation  $\approx$  is the kernel of  $\sqsubseteq_S$
- trace equivalence  $\approx_T$  is the kernel of  $\sqsubseteq_T$

The inference rules of the semantics of the P Algebra satisfy *de Simone* format.

**Theorem** All of the considered preorders are precongruences

**Corollary** All of the considered equivalences are congruences

## Diagnosable properties

The presence of a disease in a biological system is usually deduced from observation of markers (e.g. the high/low expression of some proteins, the presence/absence of some substances, etc...)

We have defined a notion of *diagnosability* on the semantics of P systems that allows us to say on a model when a disease (expressed as a logical formula) can be deduced from the observation of specific markers

Diagnosability is defined by exploiting the general systems security concept of *opacity*

# Opacity and Diagnosability

Let  $\mathcal{T}$  be the set of all traces of the semantics of P systems.

**Definition.** Given a set of observables  $\Theta$ , an *observation function* is any function  $\mathcal{O} : \mathcal{T} \rightarrow \Theta^*$ .

**Definition.** A predicate  $\phi$  on system traces is *opaque* w.r.t. the observation function  $\mathcal{O}$  and P system  $P$  if for every trace  $w$  of  $P$  such that  $\phi(w)$  holds, there exists a trace  $w'$  such that  $\neg\phi(w')$  holds and  $\mathcal{O}(w) = \mathcal{O}(w')$ .

**Definition.** A predicate  $\phi$  is *diagnosable* w.r.t. the observation function  $\mathcal{O}$  and P system  $P$  if the predicate  $\phi$  is not opaque w.r.t. the observation function  $\mathcal{O}$  and P system  $P$ .

Diagnosability is in general undecidable, hence the interest of particular classes for which it is decidable



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# Timed P systems

Defined by Cavaliere and Sburlan

Each evolution rule is enriched with a natural number representing the time (number of steps) needed by the rule to be entirely executed

When a rule with time  $n$  is applied

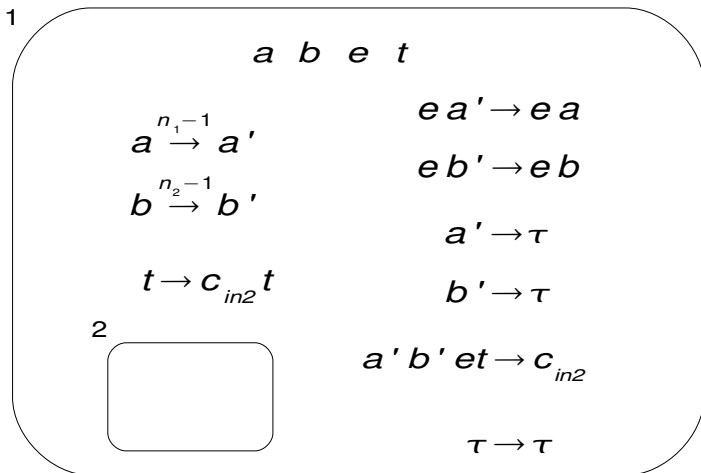
- consumed objects are immediately removed
- produced objects appear after  $n$  steps

Semantically, for each application of an evolution rule  $u \xrightarrow{n} v$  in membrane  $i$ , a *pending rule*  $\xrightarrow{n-1}_i v$  is created. At each step:

- every  $\xrightarrow{k}_i v$  with  $k > 1$  becomes  $\xrightarrow{k-1}_i v$
- every  $\xrightarrow{1}_i v$  is deleted and objects  $v$  are added to the content of membrane  $i$

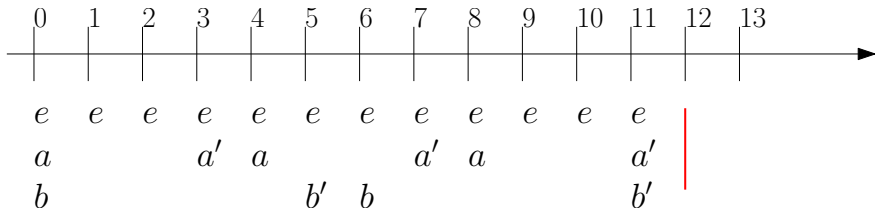
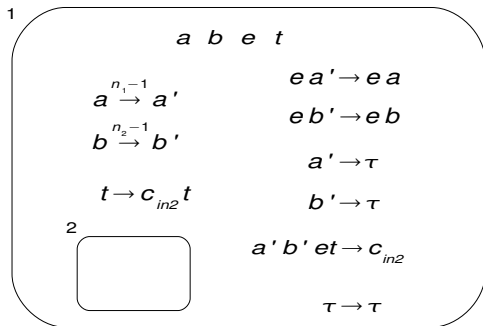
## Example of timed P system

A timed P system computing the least common multiple of  $n_1$  and  $n_2$ .



# Running the example

Let  $n_1 = 4$  and  $n_2 = 6$ ...



## Timed P systems: definition

**Definition** A *timed P system*  $\Pi$  is a tuple

$$\langle V, \mu, w_1, \dots, w_m, R_1, \dots, R_m \rangle$$

where

- $V$  is an alphabet whose elements are called *objects*.
- $\mu$  is a membrane structure consisting of a hierarchy of  $m$  membranes labelled by  $1, 2, \dots, m$ . The skin membrane is labelled by 1.
- $w_i$  ( $i = 1, 2, \dots, m$ ) is a string of  $V^*$  representing a multisets of objects enclosed in membrane  $i$ .
- $R_i$  ( $i = 1, 2, \dots, m$ ) is a finite set of *timed evolution rules* associated with the membrane  $i$ . The rules are of the form  $u \xrightarrow{n} v$ ,  $n \in \mathbb{N}$ ,  $u \in V^+$ , and  $v \in \{a_{\text{here}}, a_{\text{out}}, a_{\text{in}_j} \mid a \in V, 1 \leq j \leq m\}^*$ .

## Timed P systems: definition

**Definition** A multiset of *pending rules*  $\mathcal{U}$  is a multiset of elements of the form  $\xrightarrow{k}_i v$ , with  $k > 0$

**Definition** A *configuration* is a pair  $(\Pi, \mathcal{U})$  where  $\Pi$  is a timed P system and  $\mathcal{U}$  is a multiset of pending rules

A computation performed by a timed P system  $\Pi$  can be described as a sequence of steps between configurations

- the initial configuration is  $(\Pi, \emptyset)$

## A step of a timed P system

**Definition** A configuration  $(\Pi, \mathcal{U})$  can perform a *timed P step*  $\xrightarrow{1}$  to a configuration  $(\Pi', \mathcal{U}')$  if and only if:

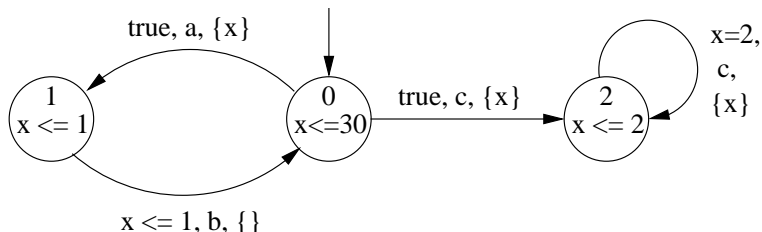
- $\Pi'$  is a timed P system resulting from an evolution step of  $\Pi$  using maximal parallelism, where:
  - ▶ the effects of the rules  $u \xrightarrow{1} v$  are visible in  $\Pi'$ , i.e., the reactants have disappeared and the products of the rules are available
  - ▶ the effects of the rules  $u \xrightarrow{n} v$  with  $n > 1$  are half visible in  $\Pi'$ . More precisely, the reactants have disappeared, but the products are not yet available
  - ▶ for every element  $\xrightarrow{1}_i v$  in  $\mathcal{U}$ , the objects  $v$  are added to membrane  $i$ ;
- $\mathcal{U}'$  is the multiset union of
  - ▶ the multiset of all elements  $\xrightarrow{k-1}_i v$  derived from all elements  $\xrightarrow{k}_i v$ ,  $k > 1$ , in  $\mathcal{U}$ ; and
  - ▶ the multiset of all elements  $\xrightarrow{n-1}_i v$ ,  $n > 1$ , representing that an instance of a timed evolution rule  $u \xrightarrow{n} v \in R_i$ , for some  $i$ , has been fired in the evolution step of  $\Pi$ .

# Timed Automata

We shall extend timed P systems with features from timed automata

A timed automaton is a finite state automaton extended with:

- clocks
- transitions enriched with conditions on the value of clocks and with clock reset actions
- state invariants





## Timed P automata

A timed P automaton is a timed automaton with a discrete time domain in which each location is associated with a timed P system

- all timed P systems must have the same membrane structure

A computation starts in the timed P system associated with the initial location of the automaton

- after each step, clocks are increased by one

When clocks reach values that satisfy the constraint of an outgoing transition, such a transition might be fired

- the computation in the current location is stopped
- objects are moved to the location reached by the transition (in the corresponding membranes)
- some objects might be added to/removed from the skin membrane

## Timed P automata: definition

**Definition** A *timed P automaton* is a tuple

$$T = \langle Q, \Sigma, q_0, \mathcal{E}, \mathcal{X}, F, \mathcal{R}, Inv \rangle$$

where:

- $Q$  is a finite set of locations
- $\Sigma$  is a finite alphabet of symbols
- $q_0$  is the initial location
- $\mathcal{E}$  is a finite set of edges
- $\mathcal{X}$  is a finite set of clocks
- $F = \langle V, \mu \rangle$  is a *timed P frame*: it contains the alphabet and the membrane structure shared by all the timed P systems
- $\mathcal{R}$  is a function assigning to every  $q \in Q$  a set of sets of timed evolution rules
- $Inv$  is a function assigning to every  $q \in Q$  an *invariant*

## Timed P automata: definition

Each edge is a tuple  $(q, \psi, u, \gamma, \sigma, v, q')$  where:

- $q$  is the source location
- $\psi$  is the clock constraint
- $u$  are the objects removed from the skin membrane
- $\gamma$  is the clock reset set
- $\sigma$  is a label (optional – can be used to accept languages)
- $v$  are the objects added to the skin membrane
- $q'$  is the target location

A *state* of execution of a timed P automaton is a tuple  $\langle q, \nu, \Pi, \mathcal{U} \rangle$ , where:

- $q$  is a location
- $\nu$  is a clock valuation
- $\Pi$  is the executing timed P systems
- $\mathcal{U}$  is a multiset of pending rules

## Timed P automata: semantics

The behaviour of a timed P automaton is described by the labelled transition system given by the following rules:

$$\text{T1} \quad \frac{\nu + 1 \models \text{Inv}(q) \quad (\Pi, \mathcal{U}) \xrightarrow{1} (\Pi', \mathcal{U}')}{\langle q, \nu, \Pi, \mathcal{U} \rangle \xrightarrow[TP]{1} \langle q, \nu + 1, \Pi', \mathcal{U}' \rangle}$$

$$\text{T2} \quad \frac{\begin{array}{l} \Pi = \langle V, \mu, w_1, w_2, \dots, w_m, \mathcal{R}(q) \rangle \\ (q, \psi, u, \gamma, \sigma, \nu, q') \in \mathcal{E}, \quad \nu \models \psi, \quad u \subseteq w_1 \quad w'_1 = (w_1 \setminus u) \cup \nu \\ \Pi' = \langle V, \mu, w'_1, w_2, \dots, w_m, \mathcal{R}(q') \rangle \end{array}}{\langle q, \nu, \Pi, \mathcal{U} \rangle \xrightarrow[TP]{\sigma} \langle q', \nu \setminus \gamma, \Pi', \mathcal{U} \rangle}$$

## Timed P automata: results

A computation of a timed P automaton is *valid* (gives an output) only if

- the automaton reaches a location that is never left
- the timed P system associated with such a location halts
- the multiset of pending rules is empty

The output is the multiset of objects left in the skin membrane

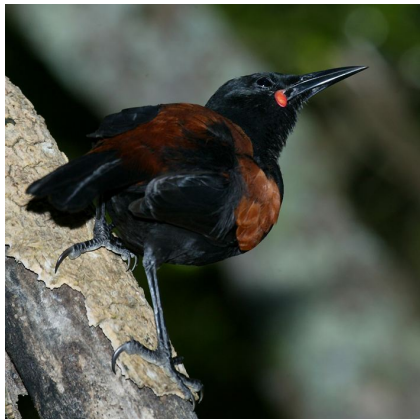
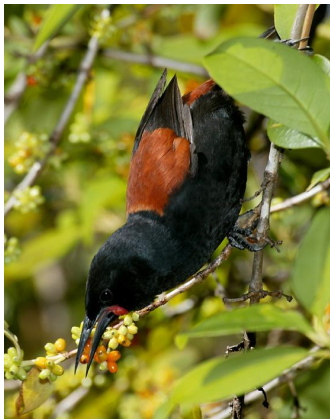
Timed P automata are universal (they allow cooperative rules to be used)

- We have proved that universality holds also with non-cooperative rules

## The saddleback

We have found a model for guiding the reintroduction of extirpated birds in New Zealand mainland.

- The model is derived from the observation of the population of Saddleback birds (*Philesturnus rufusater*) on Mokoia Island

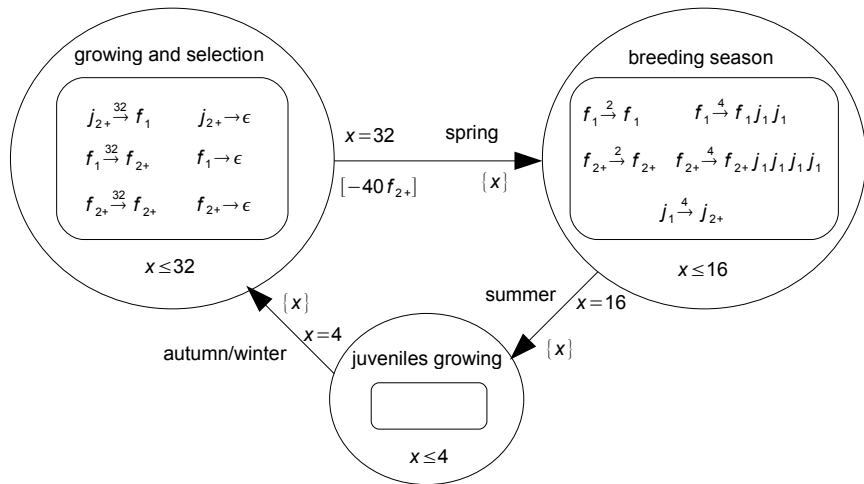


# Description of the model

The model we have found:

- is a stochastic, discrete-time female-only model (the female-only approach assumes that there are sufficient males for all females to be paired)
- females are partitioned in two classes (first-year and older) with different fecundity rates (#fledgings/season)
- an annual harvest of females is scheduled, with harvesting taking place at the start of breeding season.

# A timed P automaton model





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