Membrane Computing at (more than) Twelve Years

Gheorghe Păun Romanian Academy, București, RGNC, Sevilla University, Spain george.paun@imar.ro, gpaun@us.es Everything started 12 years ago, in Turku...



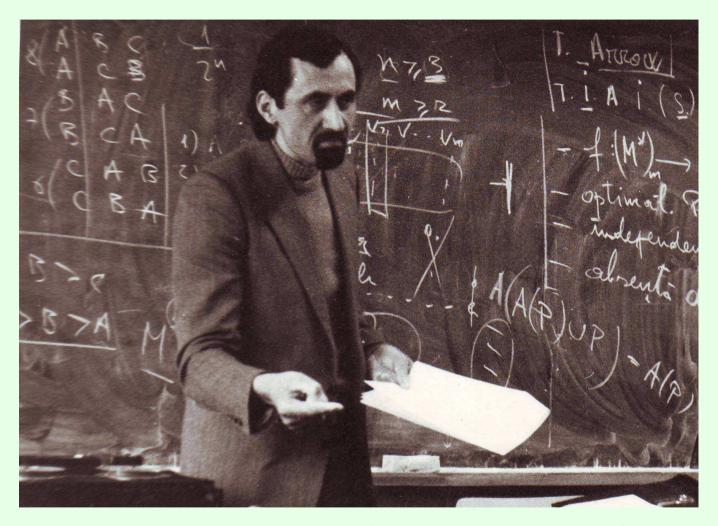
Great environment...



...with really big hats...

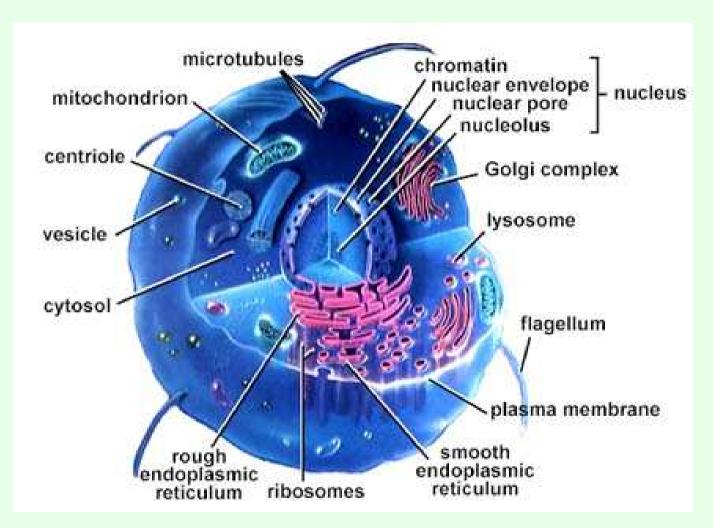


...also the Magician was around



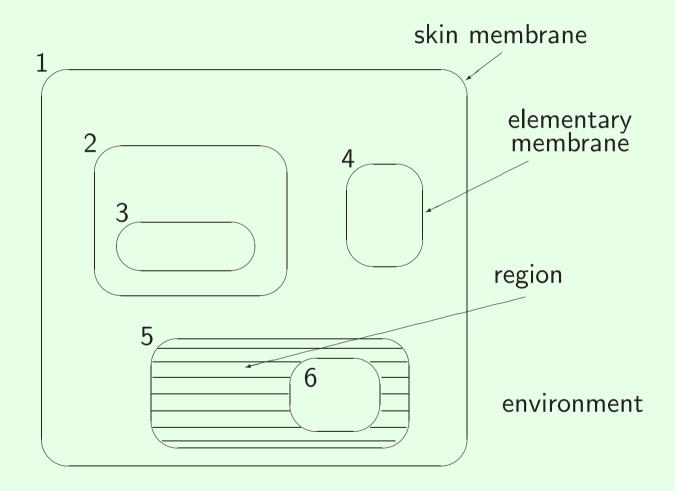
...still, not too satisfied (with DNA computing)

Let's go to the cell!

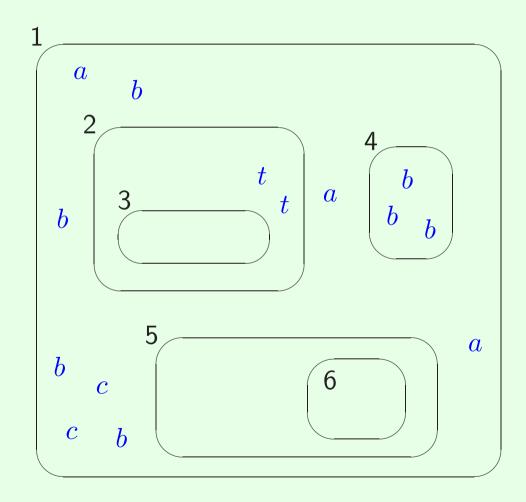


...what a jungle!

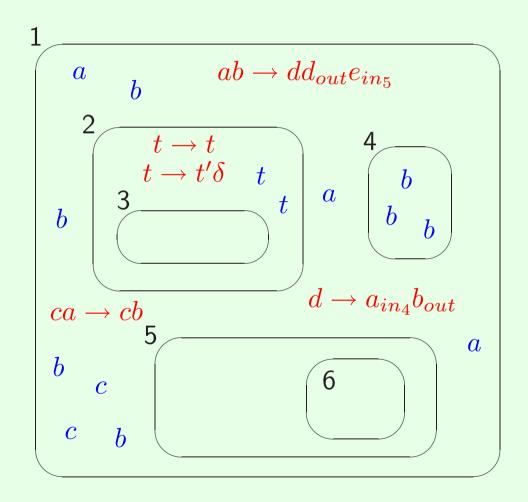
BUT, WE (THE MATHEMATICIANS) CAN SIMPLIFY:



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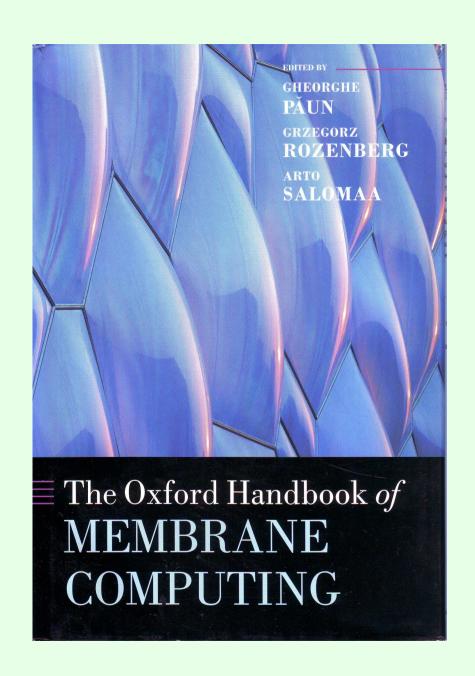
BUT, WE (THE MATHEMATICIANS) CAN SIMPLIFY:



Functioning (basic ingredients):

- nondeterministic choice of rules and objects
- maximal parallelism
- transition, computation, halting
- internal output, external output

Result: Cell-like P system



Handbook of Membrane Computing

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Oxford University Press, 2010

Introducing MC through 12 basic ideas:

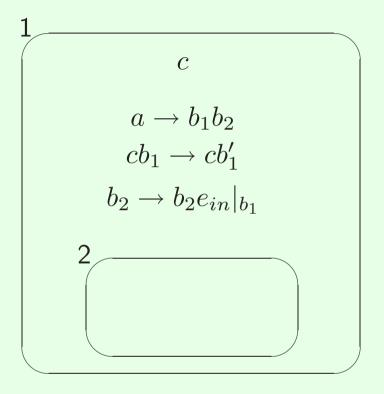
1. Cell-like P system

$$\Pi = (O, \mu, w_1, \dots, w_m, R_1, \dots, R_m, i_o),$$

where:

- O = alphabet of objects
- $\mu =$ (labeled) membrane structure of degree m
- $w_i = \text{strings/multisets over } O$
- R_i = sets of evolution rules typical form $ab \rightarrow (a, here)(c, in_2)(c, out)$
- $i_o =$ the output membrane

EXAMPLE



Computing system: $n \longrightarrow n^2$ (catalyst, promoter, determinism, internal output)

Input (in membrane 1): a^n

Output (in membrane 2): e^{n^2}

Computational power (Universality)

Families $NOP_m(\alpha, tar)$, $\alpha \in \{coo, ncoo, cat\} \cup \{cat_i \mid i \geq 1\}$, $m \geq 1$ or m = *.

Lemma 1. (collapsing hierarchy) $NOP_*(\alpha, tar) = NOP_m(\alpha, tar,)$

for all $\alpha \in \{ncoo, cat, coo\}$ and $m \geq 2$.

Theorem 1. $NOP_*(ncoo, tar) = NOP_1(ncoo) = NCF$.

Proof: use Lemma 1 and CD grammar systems

Theorem 2. $NOP_*(coo, tar) = NOP_m(coo, tar) = NRE$, for all $m \ge 1$.

Theorem 3. [Sosik: 8], [Sosik, Freund: 6], [Freund, Kari, Sosik, Oswald: 2]

$$NOP_2(cat_2, tar) = NRE$$

Conjecture $NRE - NOP_*(cat_1) \neq \emptyset$

2. String objects:

...processed by string operations:

- rewriting
- splicing (DNA computing)
- other DNA-inspired operations

More complex objects, e.g., arrays

3. Computing by communication: symport-antiport

$$(ab, in), (ab, out)$$
 – symport (in general, $(x, in), (x, out)$) $(a, in; b, out)$ – antiport (in general, $(u, in; v, out)$)

$$(\max(|x|,|y|) = \text{weight})$$

System

$$\Pi = (O, \mu, w_1, \dots, w_m, E, R_1, \dots, R_m, i_o),$$

where $E\subseteq O$ is the set of objects which appear in the environment in arbitrarily many copies

Families $NOP_m(sym_p, anti_q)$

Power: (universality)

Theorem 4.

$$NRE = NOP_1(sym_0, anti_2) = NOP_2(sym_2, anti_0) = NOP_1(sym_3, anti_0) = NOP_3(sym_1, anti_1)$$

More general rules:

$$u_i^{\dagger}v \rightarrow u_i^{\dagger}v^{\dagger}$$
 – boundary (Manca, Bernardini) $ab \rightarrow a_{tar_1}b_{tar_2}$ – communication (Sosik) $ab \rightarrow a_{tar_1}b_{tar_2}c_{come}$ $a \rightarrow a_{tar}$

4. Active membranes:

$a[\]_i \rightarrow [b]_i$
$[a]_i \rightarrow b[\]_i$
$[a]_i \to b$
$a \to [b]_i$
$[a]_i \rightarrow [b]_j [c]_k$
$[a]_i[b]_i \to [c]_k$
$[a]_i[\]_j \rightarrow [[b]_i]_j$
$[[a]_i]_j \rightarrow [b]_i[]_j$
$[u]_i \xrightarrow{\circ} []_i [u]_{@i}$
$[Q]_i \to [O - Q]_j[Q]_k$

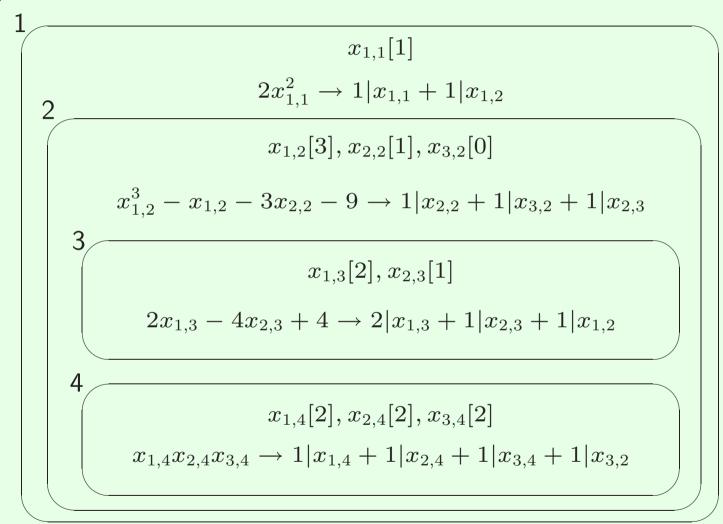
go in
go out
membrane dissolution
membrane creation
membrane division
membrane merging
endocytosis
exocytosis
gemmation
separation

and others

- 5. tissue-like P systems membranes in the nodes of a graph population P systems
- 6. using P systems in the accepting mode P automata
- 7. trace languages
- 8. numerical P systems

Basic idea: numerical variables in regions, evolving by "production functions", whose value is distributed according to "repartition protocols"; dynamical systems approach (sequences of configurations), but also computing device (the set of values of a specified variable).

Example:



Results:

Theorem 5.

$$SLIN_1^+ \subset DSET^+P_*(poly^1(1), nneg, div)$$

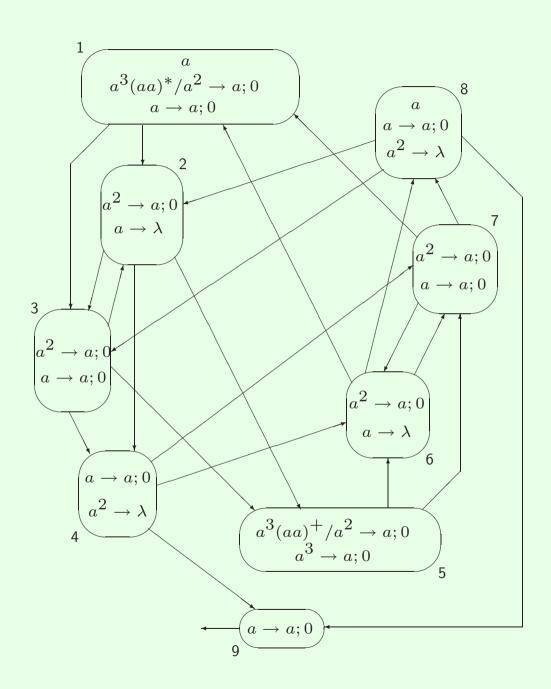
 $N^+RE = SET^+P_8(poly^5(5), div) = SET^+P_7(poly^5(6), div)$

+ many research topics and open problems

- 9. P systems with objects on membranes (brane calculi inspired P systems)
- 10. P colonies (set of cells of a bounded capacity, with minimal object processing rules)
- 11. spiking neural P systems

W. Maass movie about spiking neurons:

http://www.igi.tugraz.at/tnatschl/spike_trains_eng.html



We get

$$st(\Pi) = 0^4 10^3 10^5 10^4 10^6 10^5 10^7 10^6 \dots,$$

that is, an infinite sequence of blocks of the form $0^{2i}10^{2i-1}10^{2i+1}10^{2i}1$ with $i \geq 2$.

For $g: \{0,1\}^* \longrightarrow \{0,1\}^*$ defined by

$$g(0^{i}10^{j}1) = 0^{i+1}10^{j+1}1,$$

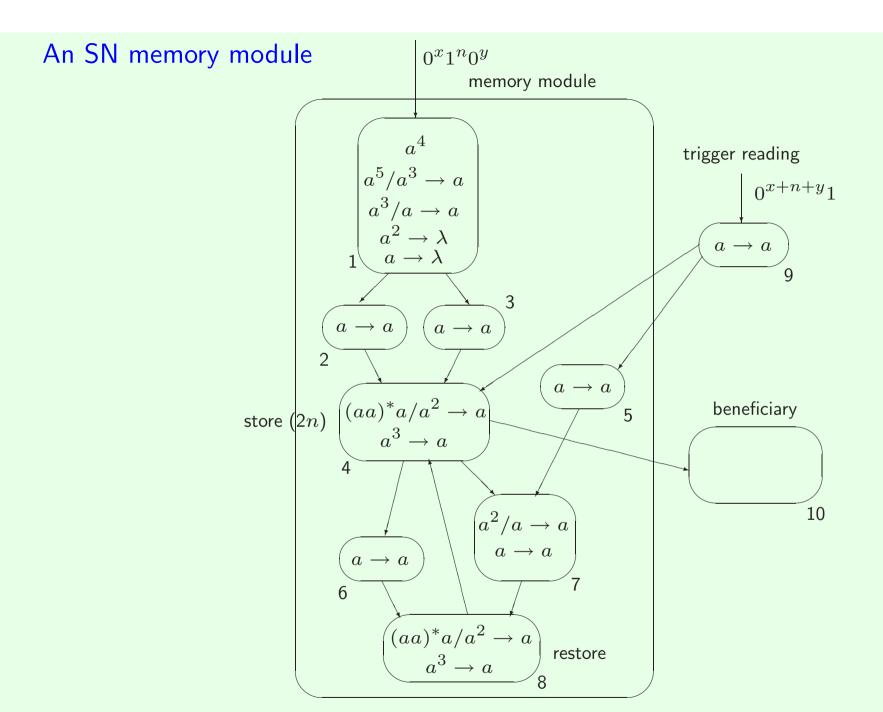
$$g(w10^{i}10^{j}1) = 0^{i+1}10^{j+1}1,$$

for all $w \in \{0,1\}^*$ and $i,j \ge 1$, define the infinite sequence f_{ω} as the limit of the following sequence of strings:

$$f_0 = 0^4 10^3 1,$$

 $f_{n+1} = f_n \ g(f_n), \text{ for } n \ge 0.$

Then $st(\Pi) = f_{\omega}$.



Formal definition:

$$\Pi = (O, \sigma_1, \dots, \sigma_m, syn, \mathbf{in}, \mathbf{out}),$$

where:

- 1. $O = \{a\}$ is the singleton alphabet (a is called spike);
- 2. $\sigma_1, \ldots, \sigma_m$ are *neurons*, of the form

$$\sigma_i = (n_i, R_i), 1 \le i \le m,$$

where:

- a) $n_i \ge 0$ is the *initial number of spikes* contained by the neuron;
- b) R_i is a finite set of rules of the following two forms:

- (1) $E/a^c \rightarrow a; d$, where E is a regular expression with a the only symbol used, $c \ge 1$, and $d \ge 0$;
- (2) $a^s \to \lambda$, for some $s \ge 1$, with the restriction that $a^s \in L(E)$ for no rule $E/a^c \to a; d$ of type (1) from R_i ;
- 3. $syn \subseteq \{1, 2, ..., m\} \times \{1, 2, ..., m\}$ with $(i, i) \notin syn$ for $1 \le i \le m$ (synapses among neurons);
- 4. $in, out \in \{1, 2, ..., m\}$ indicate the input and the output neuron.

only out = generative system
only in = accepting system
both in, out = computing system

Spike trains, types of output

FAMILIES:
$$Spik_{gen}P_m(rule_k, cons_p, forg_q)$$
 – generative
$$Spik_{acc}P_m(rule_k, cons_p, forg_q)$$
 – accepting $(DSpik, if deterministic)$

Theorem 6. $NFIN = Spik_{gen}P_1(rule_*, cons_1, forg_0) = Spik_{gen}P_2(rule_*, cons_*, forg_*).$

Theorem 7. $Spik_{gen}P_*(rule_2, cons_3, forg_3) = Spik_{acc}P_*(rule_2, cons_3, forg_2) = NRE$.

Theorem 8. $SLIN_1 = Spik_{gen}P_*(rule_k, cons_p, forg_q, bound_s)$, for all $k \ge 3$, $q \ge 3$, $p \ge 3$, and $s \ge 3$.

Normal forms, generating languages and infinite sequences, small universal SN P systems, etc.

Extension (spiking requesting rules: $E/\lambda \leftarrow a^r$)

Some results (extended):

Lemma 1. The number of configurations reachable after n steps by an extended SN P system with request rules of degree m is bounded by a polynomial g(n) of degree m.

Theorem 1. If $f: V^+ \longrightarrow V^+$ is an injective function, $card(V) \ge 2$, then there is no extended SN P system Π with request rules such that $L_f(V) = \{x f(x) \mid x \in V^+\} = L_*^g(\Pi)$.

Corollary 1. The following two languages are not in $L_*^gSNP_*$ (in all cases, $card(V) = k \ge 2$):

$$L_1 = \{x \, mi(x) \mid x \in V^+\}, \qquad L_2 = \{xx \mid x \in V^+\}.$$

12: dP systems

A dP scheme (of degree $n \ge 1$) is a construct

$$\Delta = (O, \Pi_1, \dots, \Pi_n, R),$$

where:

- 1. O is an alphabet of objects;
- 2. Π_1, \ldots, Π_n are cell-like P systems with O as the alphabet of objects and the skin membranes labeled with s_1, \ldots, s_n , respectively;
- 3. R is a finite set of rules of the form $(s_i, u/v, s_j)$, where $1 \le i, j \le n$, $i \ne j$, and $u, v \in O^*$, with $uv \ne \lambda$; |uv| is called the weight of the rule $(s_i, u/v, s_j)$.

A dP automaton is a construct

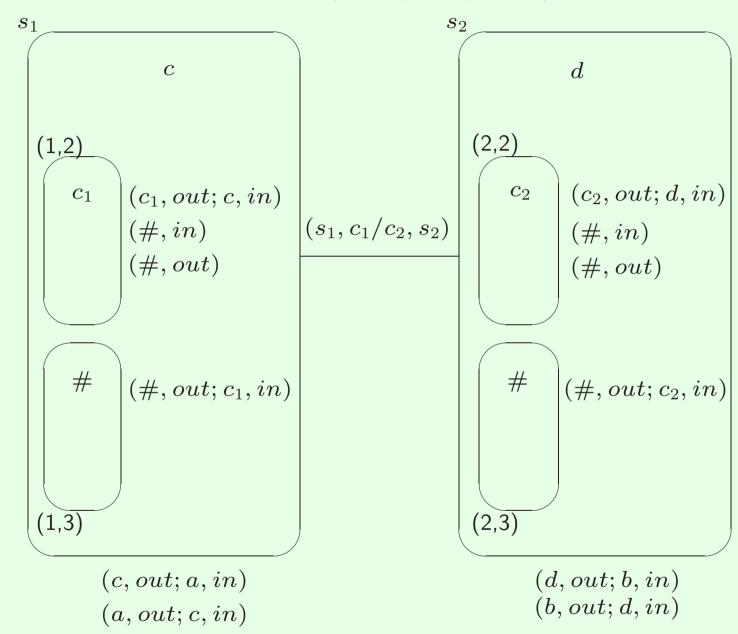
$$\Delta = (O, E, \Pi_1, \dots, \Pi_n, R),$$

where $(O, \Pi_1, \ldots, \Pi_n, R)$ is a dP scheme, $E \subseteq O$ (the objects available in arbitrarily many copies in the environment), $\Pi_i = (O, \mu_i, w_{i,1}, \ldots, w_{i,k_i}, E, R_{i,1}, \ldots, R_{i,k_i})$ is a symport/antiport P system of degree k_i (without an output membrane), with the skin membrane labeled with $(i, 1) = s_i$, for all $i = 1, 2, \ldots, n$.

A halting computation with respect to Δ accepts the string $x=x_1x_2\ldots x_n$ over O if the components Π_1,\ldots,Π_n , starting from their initial configurations, using the symport/antiport rules as well as the inter-components communication rules, in the non-deterministically maximally parallel way, bring from the environment the substrings x_1,\ldots,x_n , respectively, and eventually halts.

Communication complexity, power, [efficiently] parallelizable languages, etc.

A dP system accepting the language $L(\Delta) = \{(ac)^s (bd)^s \mid s \geq 0\}.$



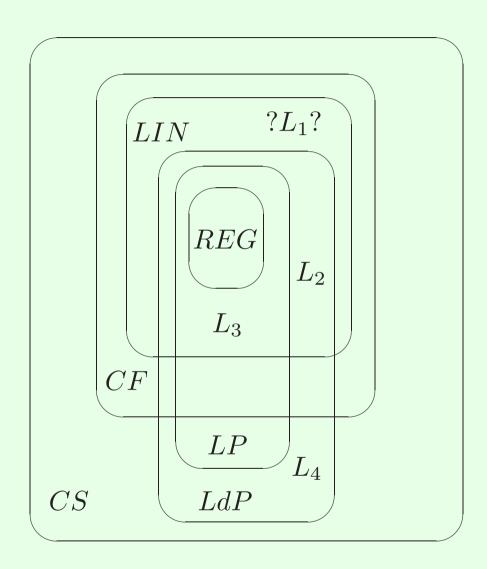


Figure 1: The place of the families LP and LdP in Chomsky hierarchy

SN dP Systems

An $SN\ dP\ system$ is a construct

$$\Delta = (O, \Pi_1, \dots, \Pi_n, esyn),$$
 where:

- 1. $O = \{a\}$ (a = spike),
- 2. $\Pi_i = (O, \sigma_{i,1}, \dots, \sigma_{i,k_i}, syn, in_i)$ is an SN P system with request rules present only in neuron σ_{in_i} problem: relax this $(\sigma_{i,j} = (n_{i,j}, R_{i,j}),$
- 3. esyn is a set of $external\ synapses$, namely between neurons from different systems Π_i , with the restriction that between two systems Π_i , Π_j there exist at most one link from a neuron of Π_i to a neuron of Π_j and at most one link from a neuron of Π_i .

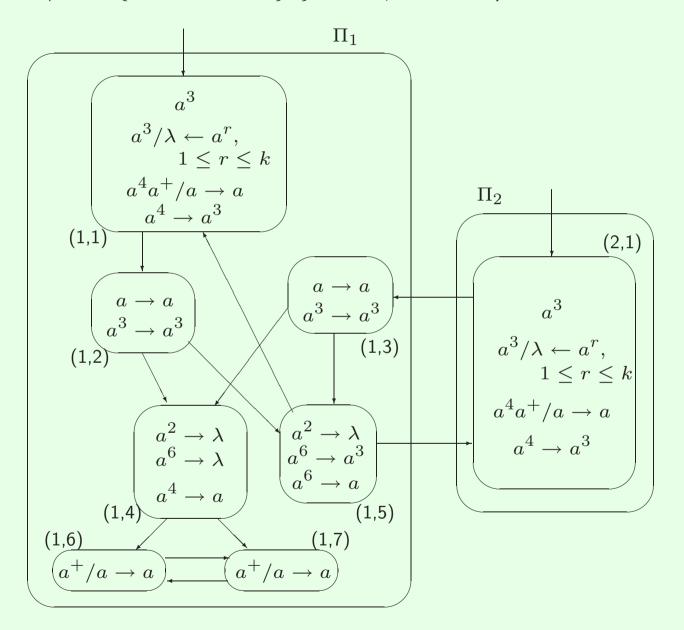
The systems Π_i , $1 \leq i \leq n$, are called *components* (or *modules*) of the system Δ .

Languages, families:

 $L(\Delta)$ is the set of all strings $x \in V^*$ such that we can write $x = x_1 x_2 \dots x_n$, with $||x_i| - |x_j|| \le 1$ for all $1 \le i, j \le n$, each component Π_i of Δ takes as input the string $x_i, 1 \le i \le n$, and the computation halts. Moreover, we can distinguish between considering b_0 as a symbol or not, like above, thus obtaining the languages $L_{\alpha}(\Delta)$, with $\alpha \in \{0, 1, 2, \ldots\} \cup \{\infty, *\}$.

 $L_{\alpha}SNdP_{n}$, the family of languages $L_{\alpha}(\Delta)$, for Δ of degree at most n and $\alpha \in \{0, 1, 2, \ldots\} \cup \{\infty, *\}$.

Example $(\{ww \mid w \in \{b_1, b_2, \dots, b_k\}^*\} \in L_{k+2}SNdP_2)$



Results (in general):

- characterization of Turing computability (RE, NRE, PsRE)
 Examples: by catalytic P systems (2 catalysts) [Sosik, Freund, Kari, Oswald]
 by (small) symport/antiport P systems [many]
- polynomial solutions to NP-complete problems even characterizations of PSPACE (by using an exponential workspace created in a "biological way": membrane division, membrane creation, string replication, etc) [Sevilla team], [Milano team], [Obtulowicz], [Alhazov, Pan], [Madrid team] etc
- other types of mathematical results (normal forms, hierarchies, determinism versus nondeterminism, complexity) [lbarra group]
- connections with ambient calculus, Petri nets, X-machines, quantum computing, lambda calculus, brane calculus, etc. [many]
- simulations and implementations (Adelaide, Sevilla, Madrid)
- applications



The most practical application

Open problems, research topics:

Many: see the P page

- borderlines: universality/non-universality, efficiency/non-efficiency
 (local problems: the power of 1 catalyst, the role of polarizations, dissolution, etc.
 general problems: uniform versus semi-uniform, deterministic-confluent,
 pre-computed resources, etc.)
- semantics (events, causality, etc.)
- neural-like systems (more biology, complexity, applications, etc.)
- user friendly, flexible, efficient (!) software for bio-applications
- MC and economics
- implementations (electronics, bio-lab), dedicated hardware and software (P-lingua)
- finding a killer-app

Applications:

- biology, medicine, ecosystems (continuous versus discrete mathematics) [Sevilla, Verona, Milano, Sheffield, Nottingham, Ruston, etc.]
- computer science (computer graphics, sorting/ranking, 2D languages, cryptography, general model of distributed-parallel computing) [many]
- linguistics (modeling framework, parsing) [Tarragona, Chişinău]
- optimization (membrane algorithms [Nishida, 2004], [many especially in China])
- economics ([Warsaw group], [R. Păun], [Vienna group])

Applications of MC in biology, bio-medicine, ecology – several chapters in Handbook

A typical application in biology/medicine:

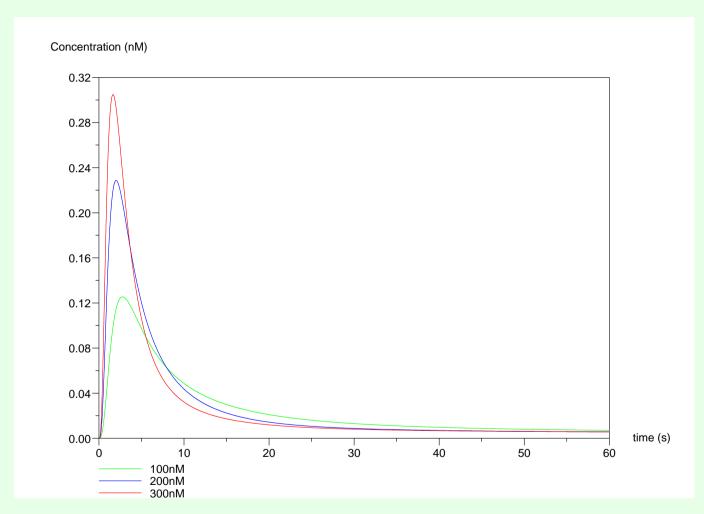
M.J. Pérez–Jiménez, F.J. Romero–Campero:

A Study of the Robustness of the EGFR Signalling Cascade Using Continuous Membrane Systems.

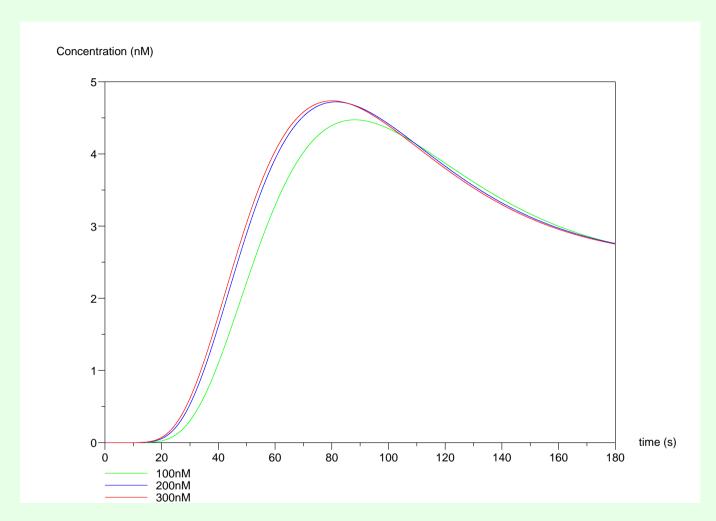
In Mechanisms, Symbols, and Models Underlying Cognition. First International Work-Conference on the Interplay between Natural and Artificial Computation, IWINAC 2005 (J. Mira, J.R. Alvarez, eds.), LNCS 3561, Springer, Berlin, 2005, 268–278.

- 60 proteins, 160 reactions/rules
- reaction rates from literature
- results as in experiments

Typical outputs:



The EGF receptor activation by auto-phosphorylation (with a rapid decay after a high peak in the first 5 seconds)



The evolution of the kinase MEK (proving a surprising robustness of the signalling cascade)

Other bio-applications:

- photosynthesis [Nishida, 2002]
- Brusselator [Suzuki, Verona, Milano]
- quorum sensing in bacteria [Nottingham, Sheffield, Sevilla]
- cancer related pathways [Sevilla, Ruston-Louisiana]
- circadian cycles [Verona]
- apoptosis [Ruston-Lousiana]
- signaling pathways in yeast [Milano]
- HIV infection [Edinburgh, Ruston-Louisiana]
- peripheral proteins [Trento]
- others [Milano, Iași, Bucharest, Sevilla, Verona, etc.]

Modeling ecosystems

Y. Suzuki, H. Tanaka, Artificial life and P systems, WMC1, Curtea de Argeș, 2000 (herbivorous, carnivorous, volatiles)

Lotka-Voltera model (predator-prey) [Verona, Milano]

M. Cardona, M.A. Colomer, M.J. Perez-Jimenez, S. Danuy, A. Margalida, A P system modeling an ecosystem related to the bearded vulture, 6BWMC

(Some) Results:

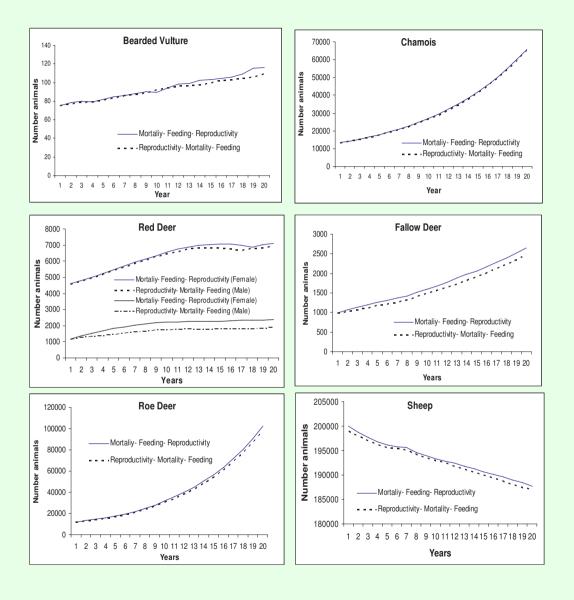


Figure 2: Robustness of the ecosystem

Membrane algorithms – T. Nishida

- candidate solutions in regions, processed locally (local sub-algorithms)
- better solutions go down
- static membrane structure dynamical membrane structure
- two-phases algorithms

Excellent solutions for Travelling Salesman Problem (benchmark instances)

- rapid convergence
- good average and worst solutions (hence reliable method)
- in most cases, better solutions than simulated annealing

Still, many problems remains: check for other problems, compare with subalgorithms, more membrane computing features, parallel implementations (no free lunch theorem)

Recent: L. Huang, N. Wang, J. Tao; G. Ciobanu, D. Zaharie; A. Leporati, D. Pagani; M. Gheorghe et colab.

SOFTWARE AND APPLICATIONS:

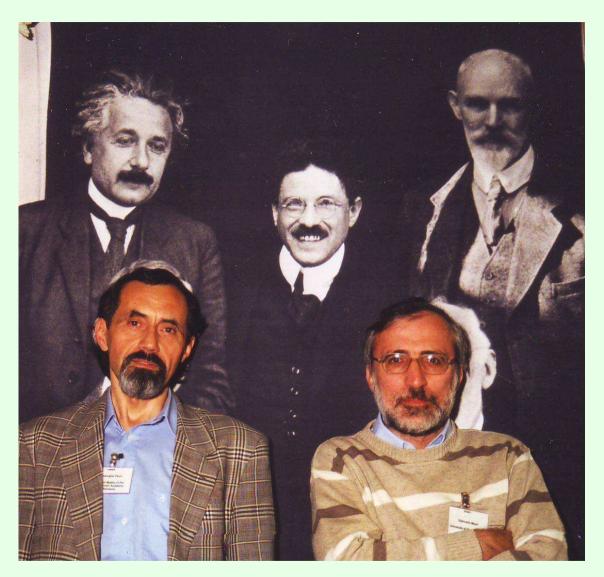
Verona (Vincenzo Manca: vincenzo.manca@univr.it)

Sheffield (Marian Gheorghe: M.Gheorghe@dcs.shef.ac.uk)

Sevilla (Mario Pérez-Jiménez: marper@us.es) - P-lingua!

Milano (Giancarlo Mauri: mauri@disco.unimib.it)

Trento, Nottingham, Leiden/Edinburgh, Vienna, Evry, Iași



Finally, satisfied...

Hypercomputation = passing beyond the Turing barrier

Fypercomputation = passing polynomially beyond the **NP** barrier

So far: membrane division, membrane creation, string replication, pre-computed resources

Further ideas:

- (local) acceleration (membranes, rules, objects)
- oracles
- \bullet ω multiplicity (like in R systems) SAT solved in poly time
- what else?

Thank you!