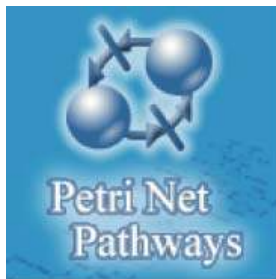


Petri Net Based Descriptions for Systematic Understanding of Biological Pathways



松野浩嗣

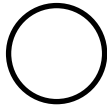


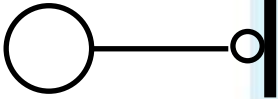
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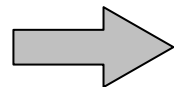
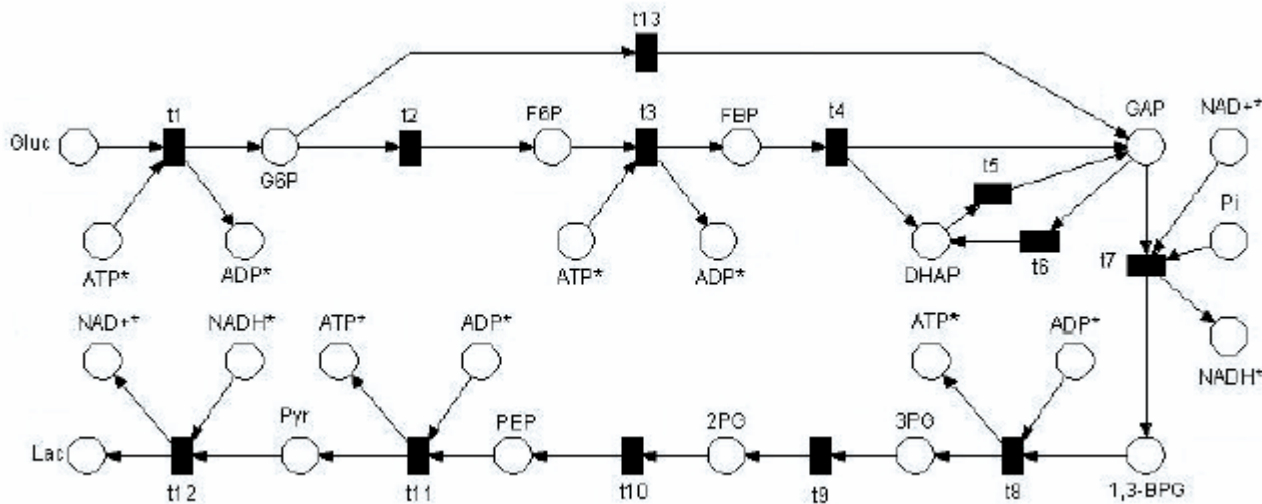


Element assignments

| Biological pathways | Petri net |
|--|---|
| static elements (substances, states ...) |  |
| active elements (chemical reactions, interactions) |  |
| relations, flows |  |
| repression |  |

Metabolic pathway modeling with Petri nets

- Reddy et al. (1993) : The first application paper of Petri net to model biological pathway in 1st ISMB
 - ✓ place – amount of metabolite
 - ✓ transition – speed of enzymic reaction

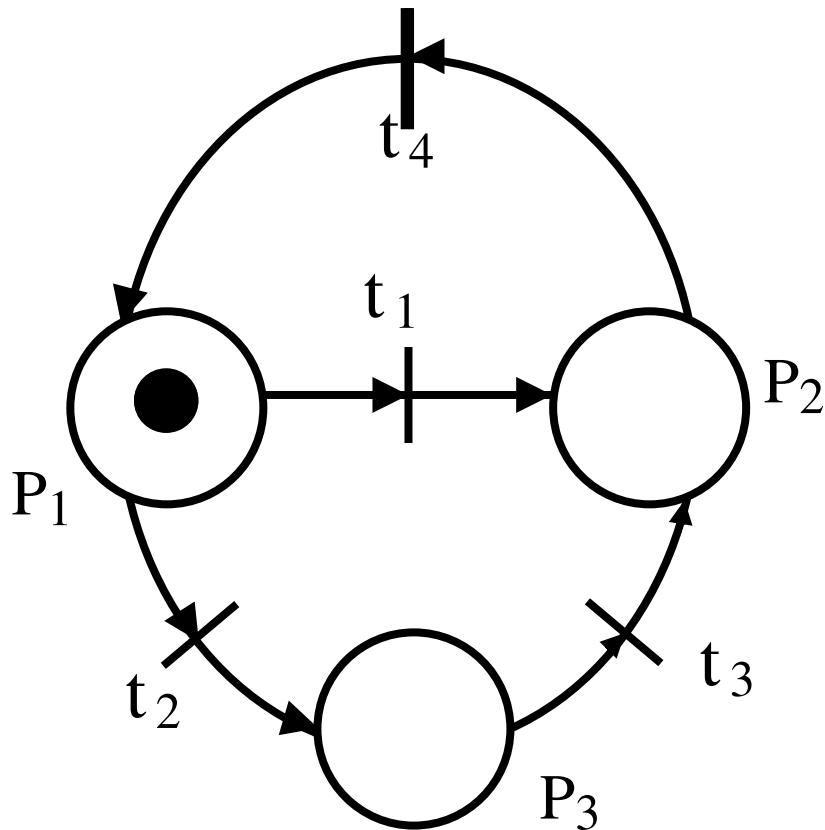


Can be modeled with simple rules

P-T incidence matrix

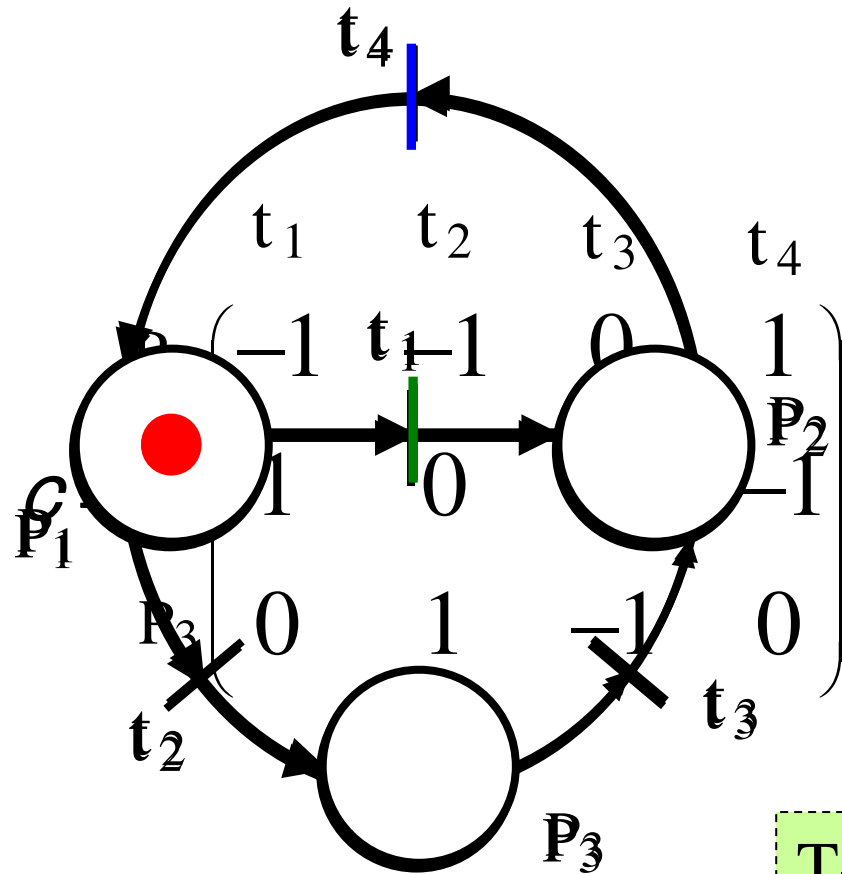
■ P-T incidence matrix

express connections between places and transitions



$$C = \begin{matrix} & t_1 & t_2 & t_3 & t_4 \\ P_1 & \begin{pmatrix} -1 & -1 & 0 & 1 \end{pmatrix} \\ P_2 & \begin{pmatrix} 1 & 0 & 1 & -1 \end{pmatrix} \\ P_3 & \begin{pmatrix} 0 & 1 & -1 & 0 \end{pmatrix} \end{matrix}$$

T-invariant



T-invariant

Non-negative integer vector J satisfying $CJ=0$

| | | | | | |
|---------|-----------------------|-------|-------|----------|--------------------------|
| | t_1 | t_2 | t_3 | t_4 | |
| $J_1 =$ | <u>1</u> | 0 | 0 | <u>1</u> | } elementary T-invariant |
| $J_2 =$ | 0 | 1 | 1 | 1 | |
| $J_3 =$ | $J_1 + J_2$ | | | | |
| | $= (1 \ 1 \ 1 \ 2)^t$ | | | | |

elementary T-invariant

T-invariant that can not be expressed by non-negative rational linear combination of the other T-invariants.

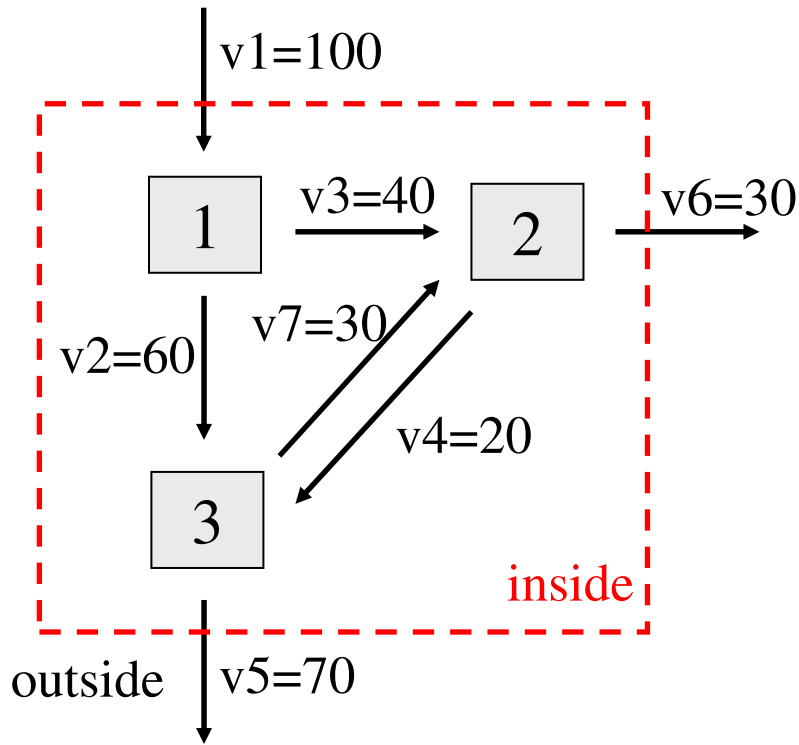
Metabolic pathways and elementary modes

Elementary Mode *

a minimum set of enzymic reaction paths, into which a metabolic pathway is decomposed so that it can keep steady state

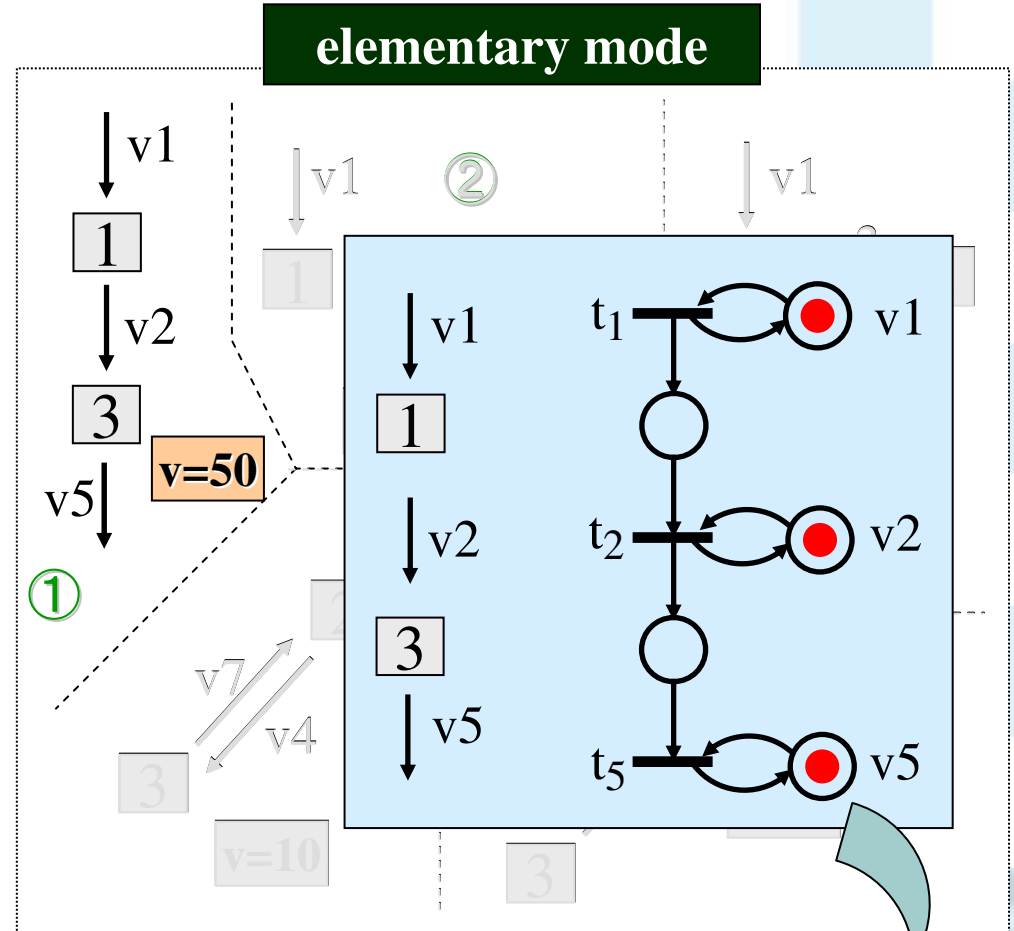
- * S. Schuster, D.A. Fell, and T. Dandekar, “A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks.”, *Nature America Inc.*, vol.18, 2000.

Elementary mode in metabolic pathways



v_N : speed of an enzymic reaction

□ : metabolite

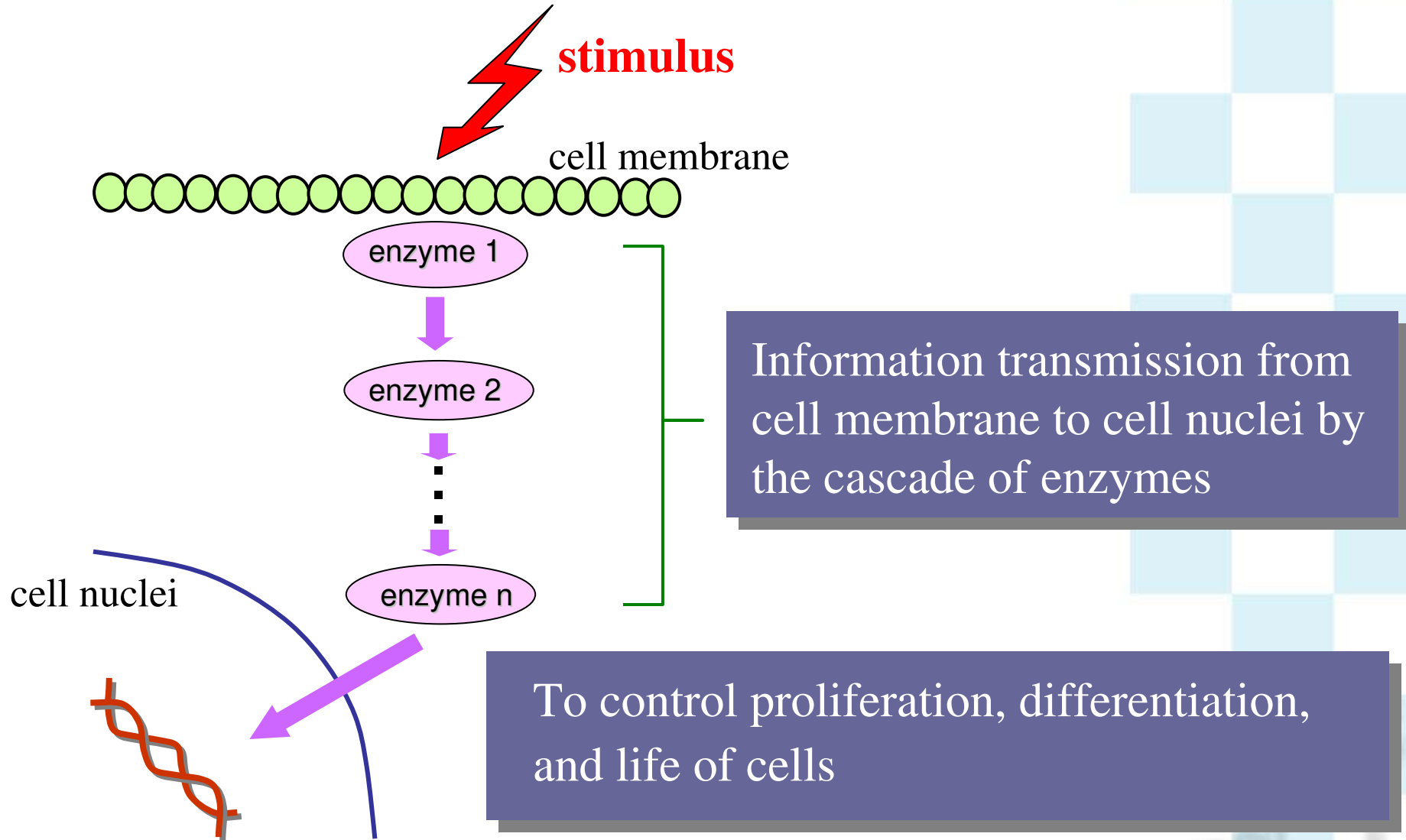


Elementary mode = Elementary T-invariant

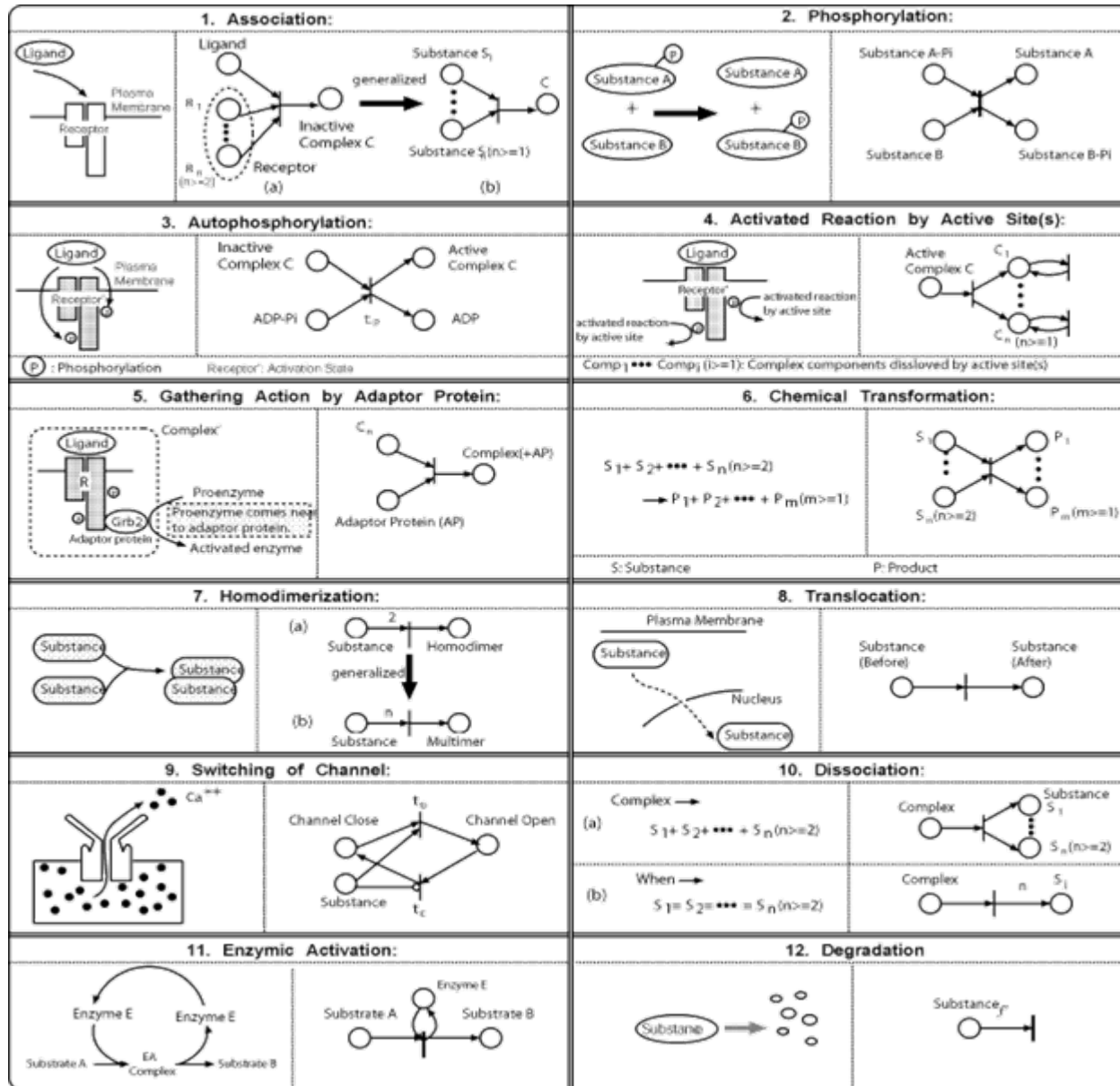
** I. Zevedei-Oancea and S. Schuster,

"Topological analysis of metabolic networks based on Petri net theory," *In Silico Biology*, 3, 2003.

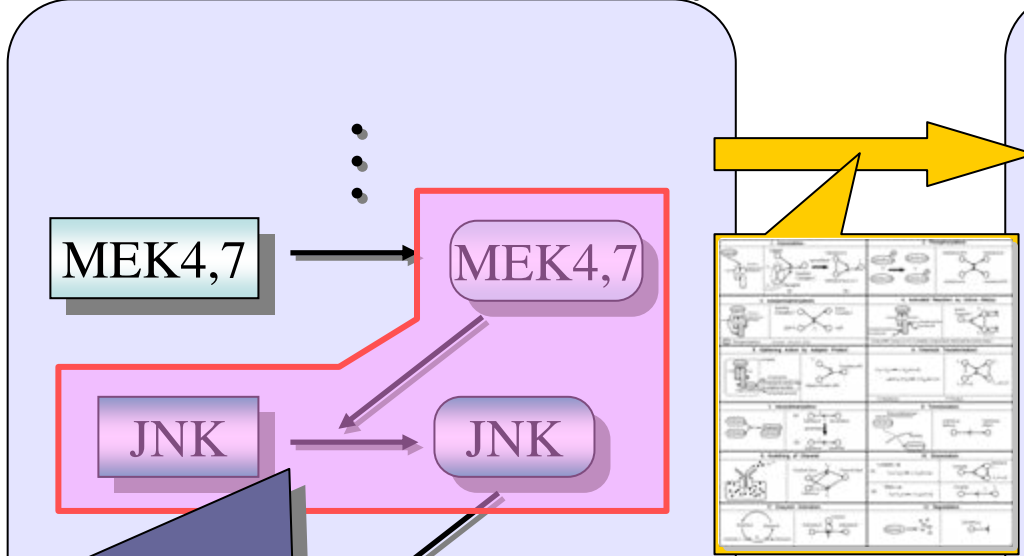
Signaling pathways



signaling pathway components



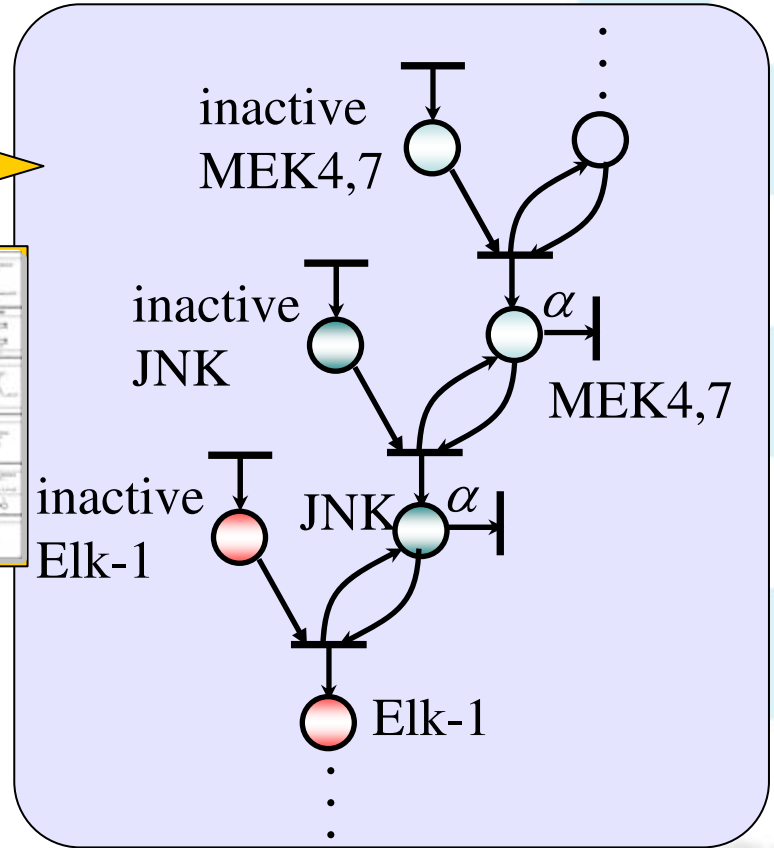
a part of signaling pathway



**Activation Transduction
Component (ATC)**

A range of an activation process
influenced by an enzyme reaction

Petri net model



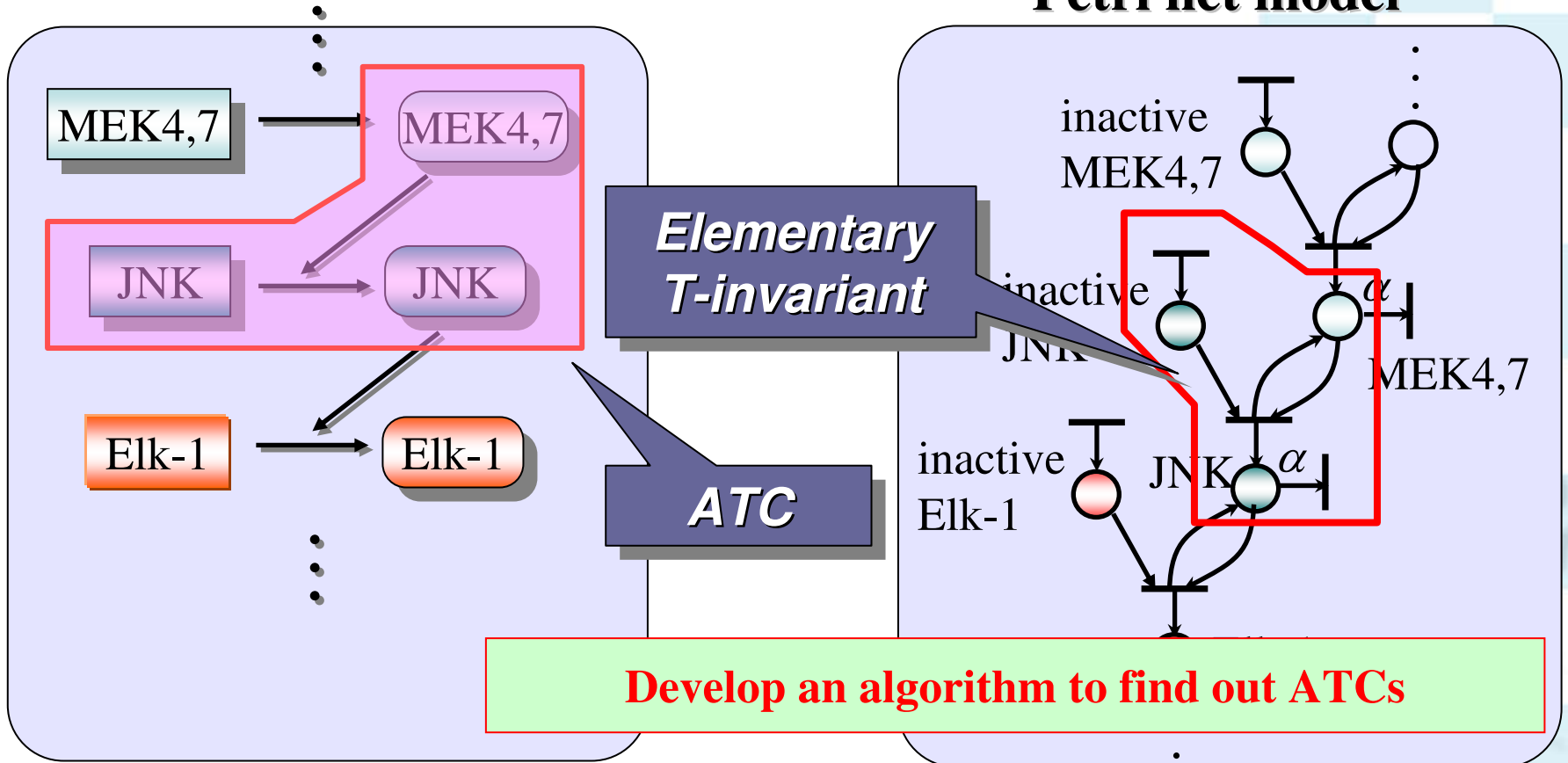
ATC = Elementary T-invariant

Signaling
Pathway
TERM

Petri net
TERM

A part of signaling pathway

Petri net model



Algorithm to find ATC

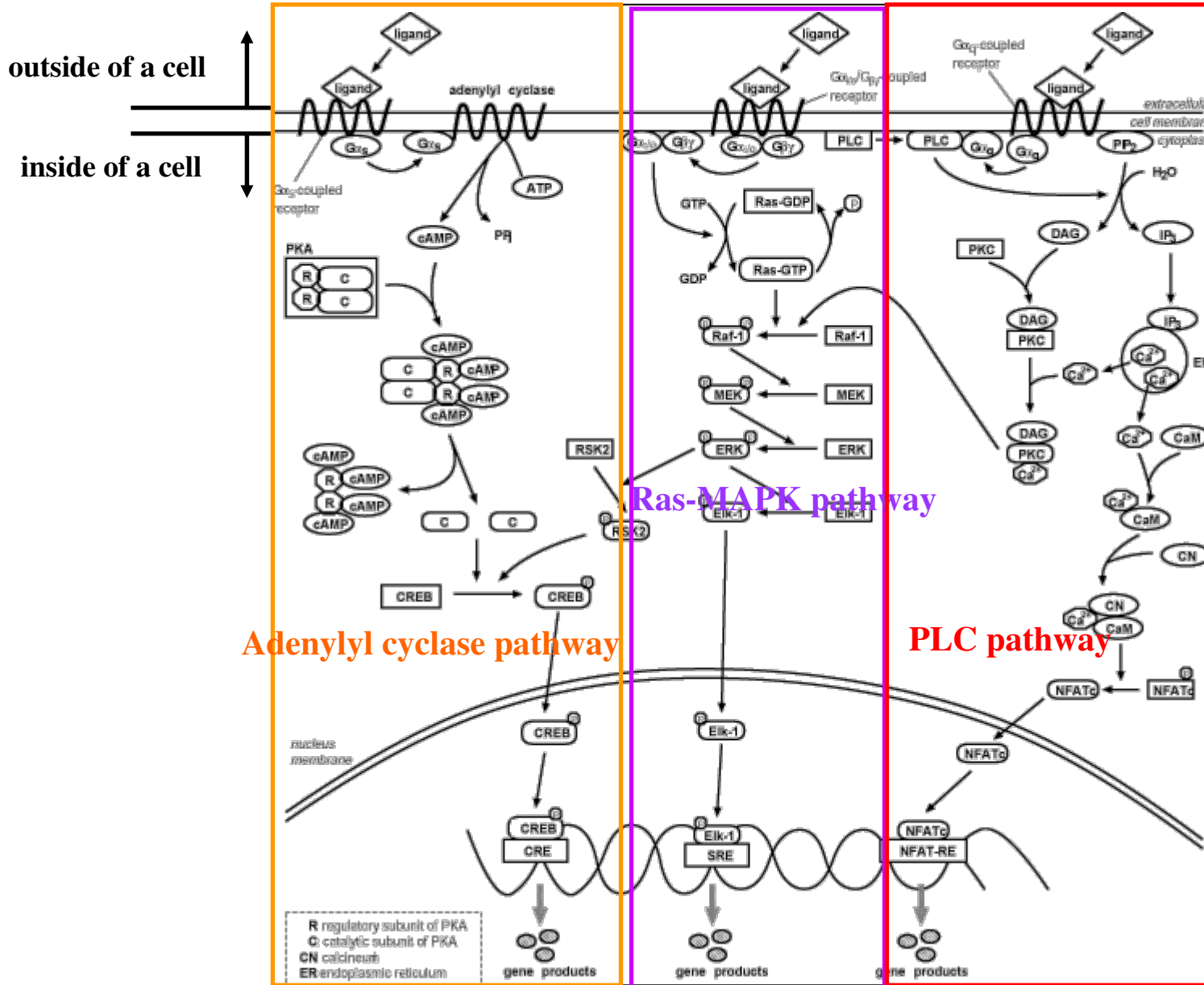
C. Li, S. Suzuki, Q.-W.Ge, M. Nakata, H. Matsuno, S. Miyano, Structural modeling and analysis of signaling pathways based on Petri nets, J. Bioinfo. Comput. Biol. in press. 2006.

«Searching Activation Transduction Components»

- 1° Let PN be a given Petri net, and L_s be a list of sink transitions (except sink output transitions of enzyme places) in PN . Do $SN_J \leftarrow \phi$, $T_{sink} \leftarrow \{t | t \in L_s\}$, $T_{gen} \leftarrow \phi$ and initialize $FIFO$ queue $Q \leftarrow \phi$.
- 2° If $Q \neq \phi$, pull a subnet N_{J_i} from Q and do the followings:
 - (i) let P_e and T_e be a set of enzyme places in N_{J_i} and a set of transitions providing tokens to the places of P_e , respectively;
 - (ii) let L_e be a list of transitions in $T_e - T_{gen}$, and do $L_s \leftarrow L_s \cdot L_e$, $T_{gen} \leftarrow T_{gen} \cup T_e$ and $PROV(N_{J_i}) = \{t | t \in T_e\}$.
- 3° If $L_s = \phi$ go to 4°, otherwise take out a transition t from the beginning of L_s and do $gen(t) \leftarrow \phi$. Obtain all the elementary T-invariants $\{J_i\}$ with $J_i(t) > 0$ by applying «Searching Basic-Feasible Solution with $x_s > 0$ »²³. For each J_i , do the followings:
 - (i) obtain its corresponding subnet N_{J_i} (generated by the support T_{J_i} of J_i);
 - (ii) do $gen(t) \leftarrow gen(t) \cup \{N_{J_i}\}$;
 - (iii) if $N_{J_i} \notin SN_J$ is satisfied, then $SN_J \leftarrow SN_J \cup \{N_{J_i}\}$ and push N_{J_i} to Q .
- 4° If $Q = \phi$ then output T_{gen} , T_{sink} , $gen(t)$ for $t \in T_{gen} \cup T_{sink}$ and $PROV(N_{J_i})$ for $N_{J_i} \in SN_J$, and stop; otherwise go to 2°. □

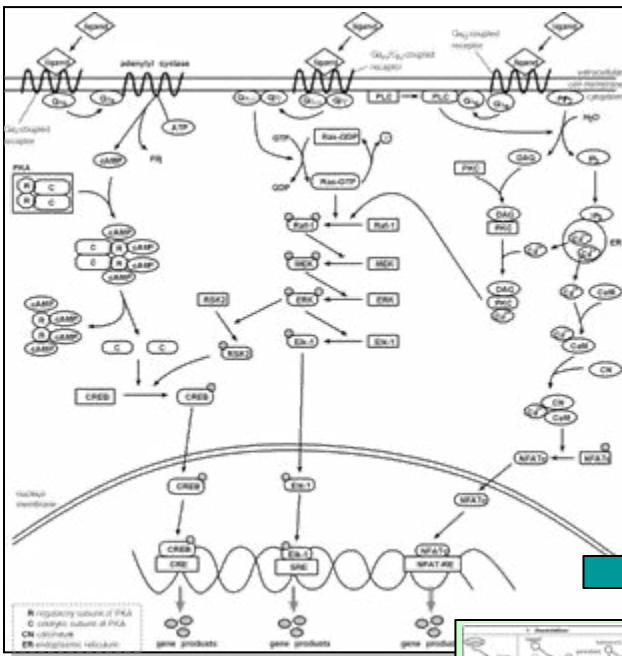
Q.-W.Ge, Fukunaga, T., Nakata, M., On generating elementary T-invariants of Petri nets by linear programming, Proc. ISCA2005, pp.168-171, 2005.

An Example of signaling pathway modeling

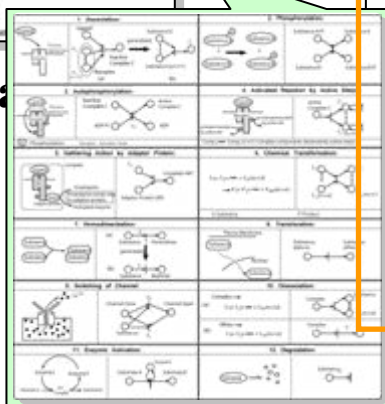


G protein signaling pathways

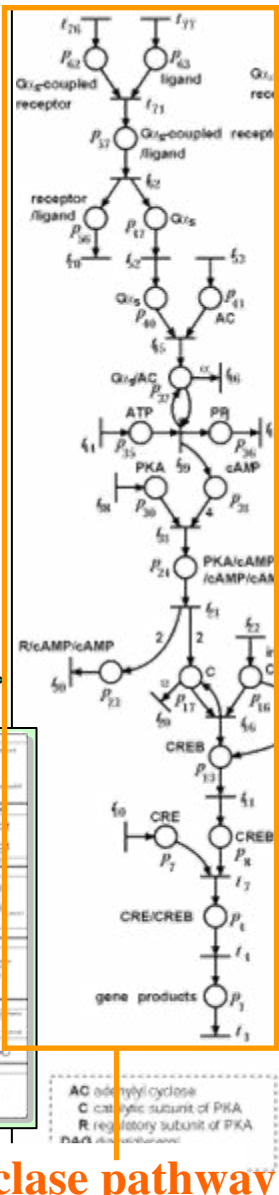
Petri net model of signaling pathway



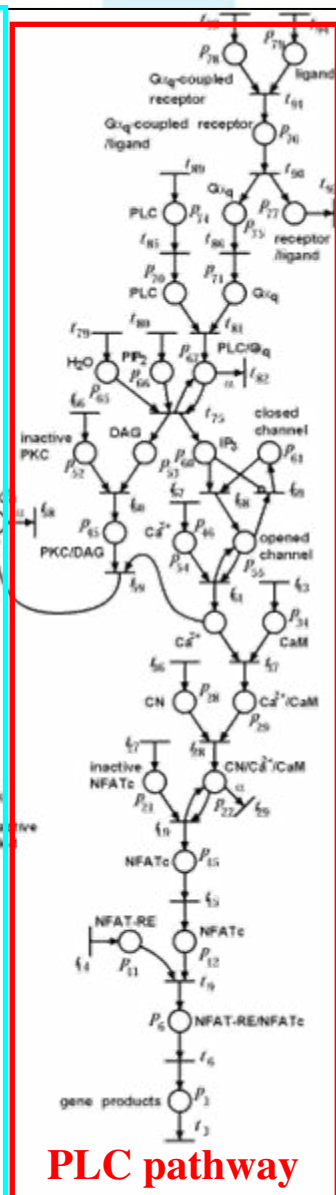
G protein signaling pathway



Adenylyl cyclase pathway



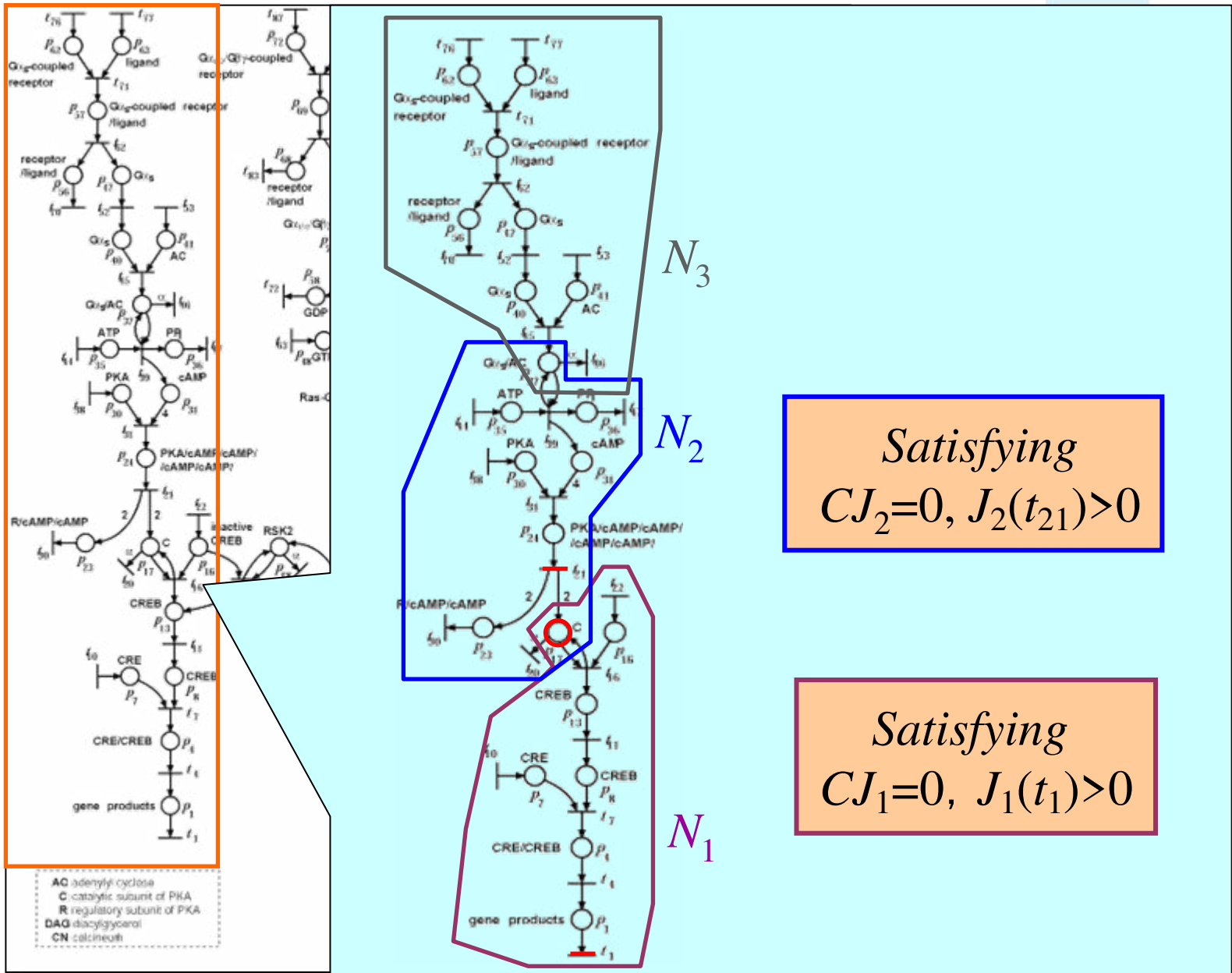
Ras-MAPK pathway



PLC pathway

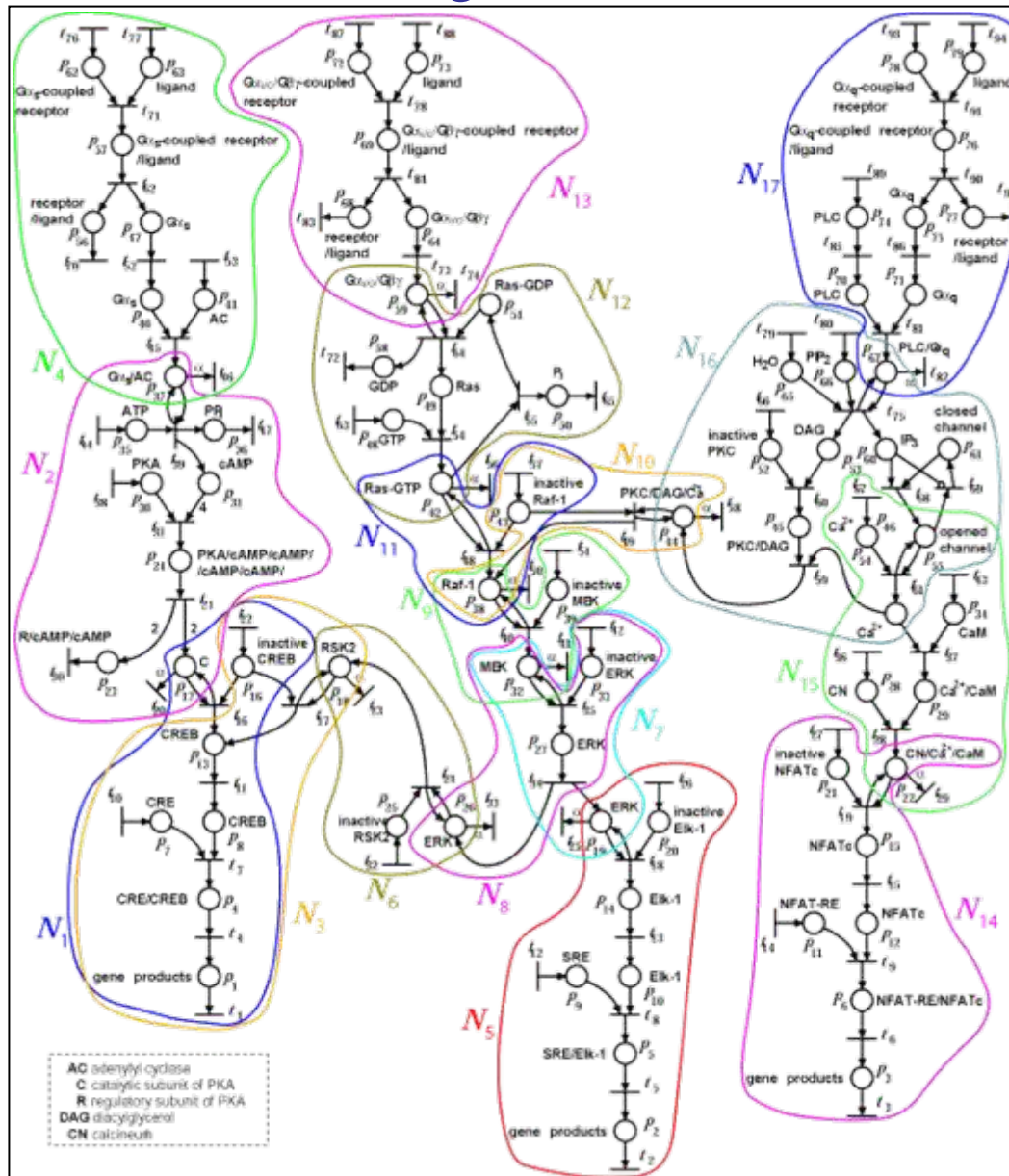
Petri net model of G protein signaling pathway

Searching ATC by the proposed algorithm



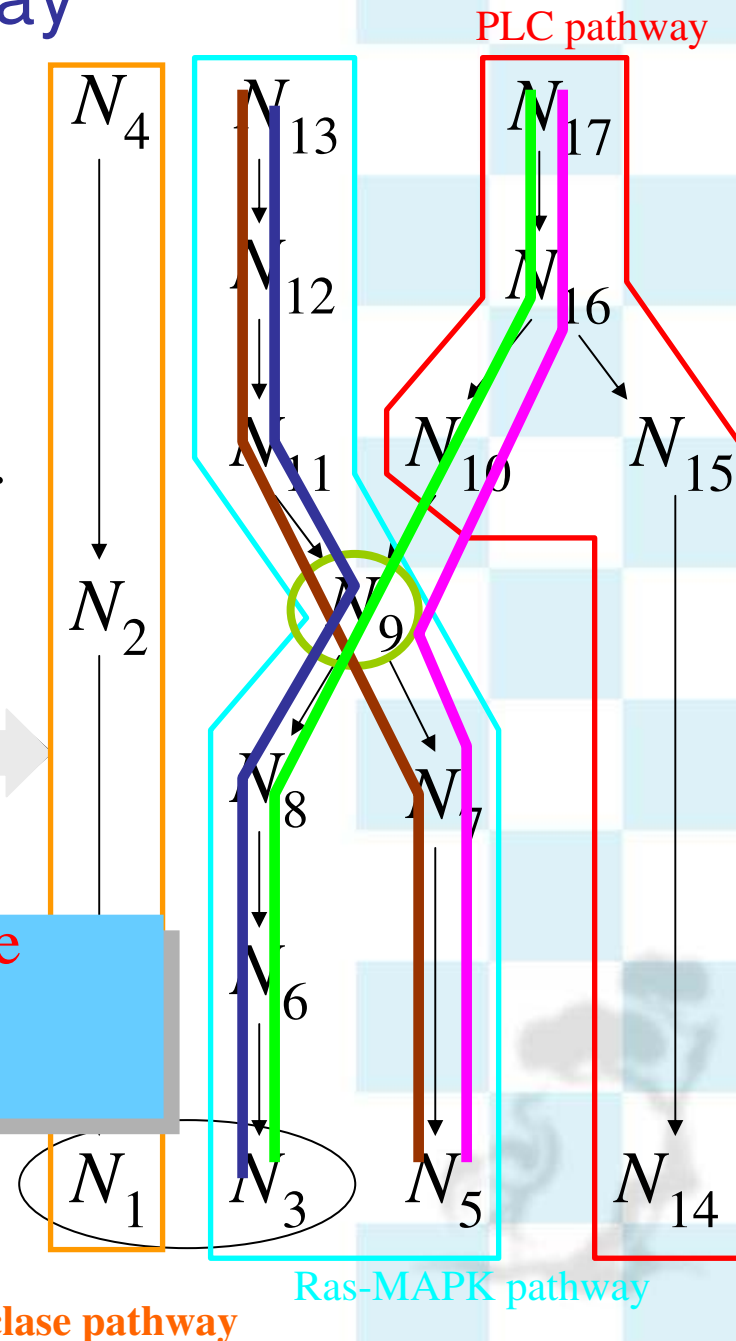
G protein signaling pathway

Result of ATC searching



ATC representation of pathway

- Subnet N_9 (MEK activation by Raf-1) is an important reaction in the pathway.
- More than one pathways are working for producing the same gene product.



Easy to acquire the characteristics on the structure of signaling pathways

Adenylyl cyclase pathway

Ras-MAPK pathway

PLC pathway

Summary

- We present Petri net models of various reactions in cells, with which signaling pathways can be modeled.
 - Modeled pathways are open to the public by the web site “[Petri Net Pathways](#)”.
- We define the new notation “activation transduction component (ATC)” and propose a new algorithm to search ATCs, and show that
 - ATC corresponds to elementary T-invariant in Petri net theory,
 - signaling pathways can be expressed by chains of ATC (=elementary T-invariants), and
 - network representation of signaling pathways with ATC gives a new view for clarifying the characteristics of signaling pathways based on these structures.