

BIOCHEMICALLY INTERPRETED PETRI NETS

- SOME OPEN PROBLEMS -

Monika Heiner
Brandenburg University of Technology Cottbus
Dept. of CS

- **BACKGROUND**

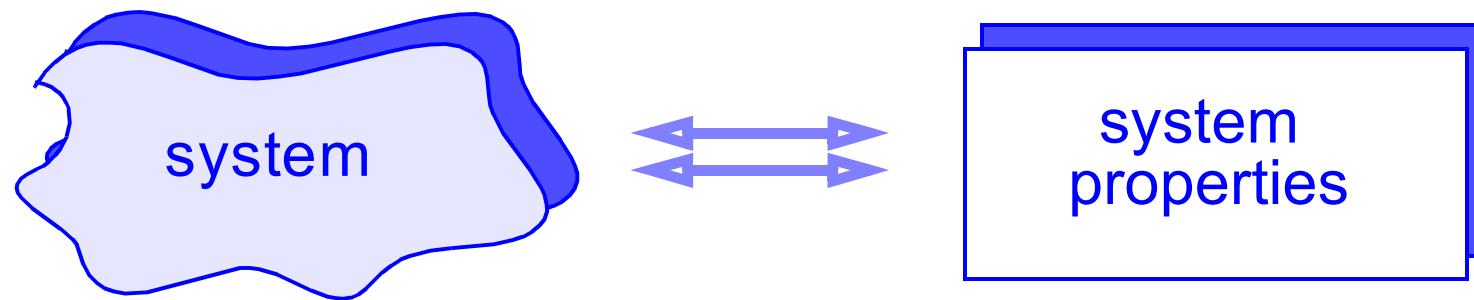
- **How STRUCTURAL ANALYSIS TECHNIQUES CAN CONTRIBUTE**

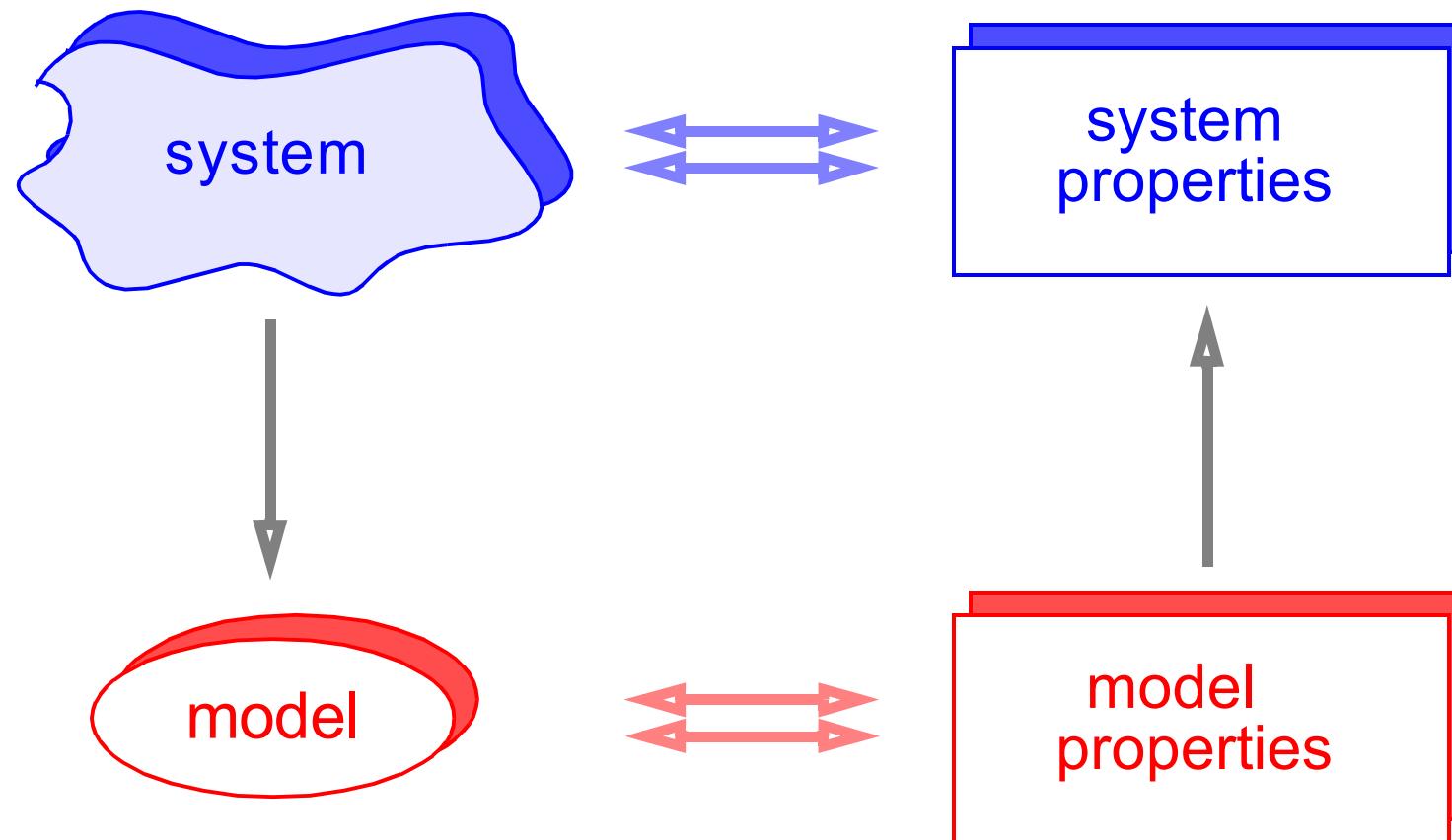
- > modularization approach
- connected ADT sets = flow equivalent server component ?*
- > *identify core network*

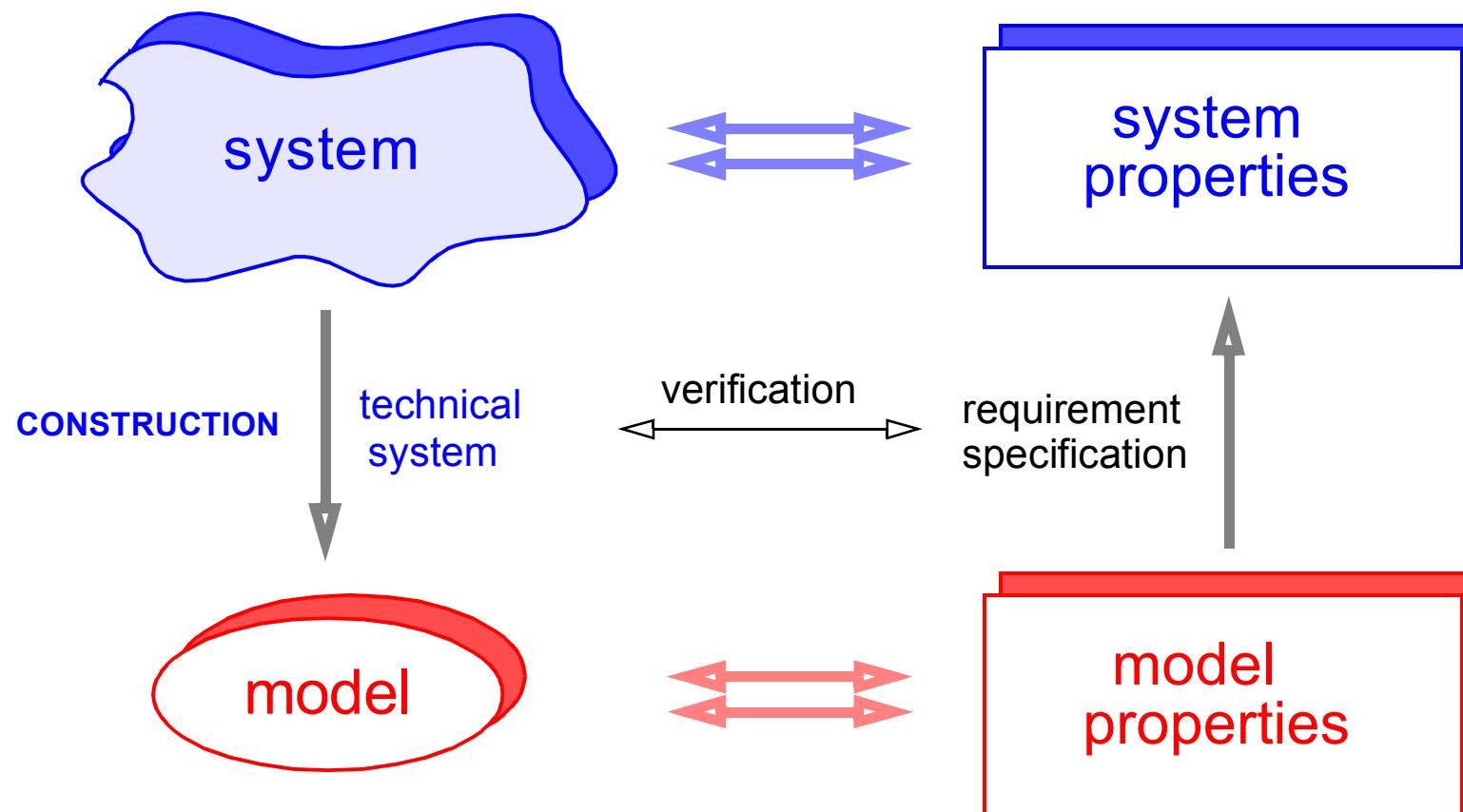
- **LATEST NEWS**

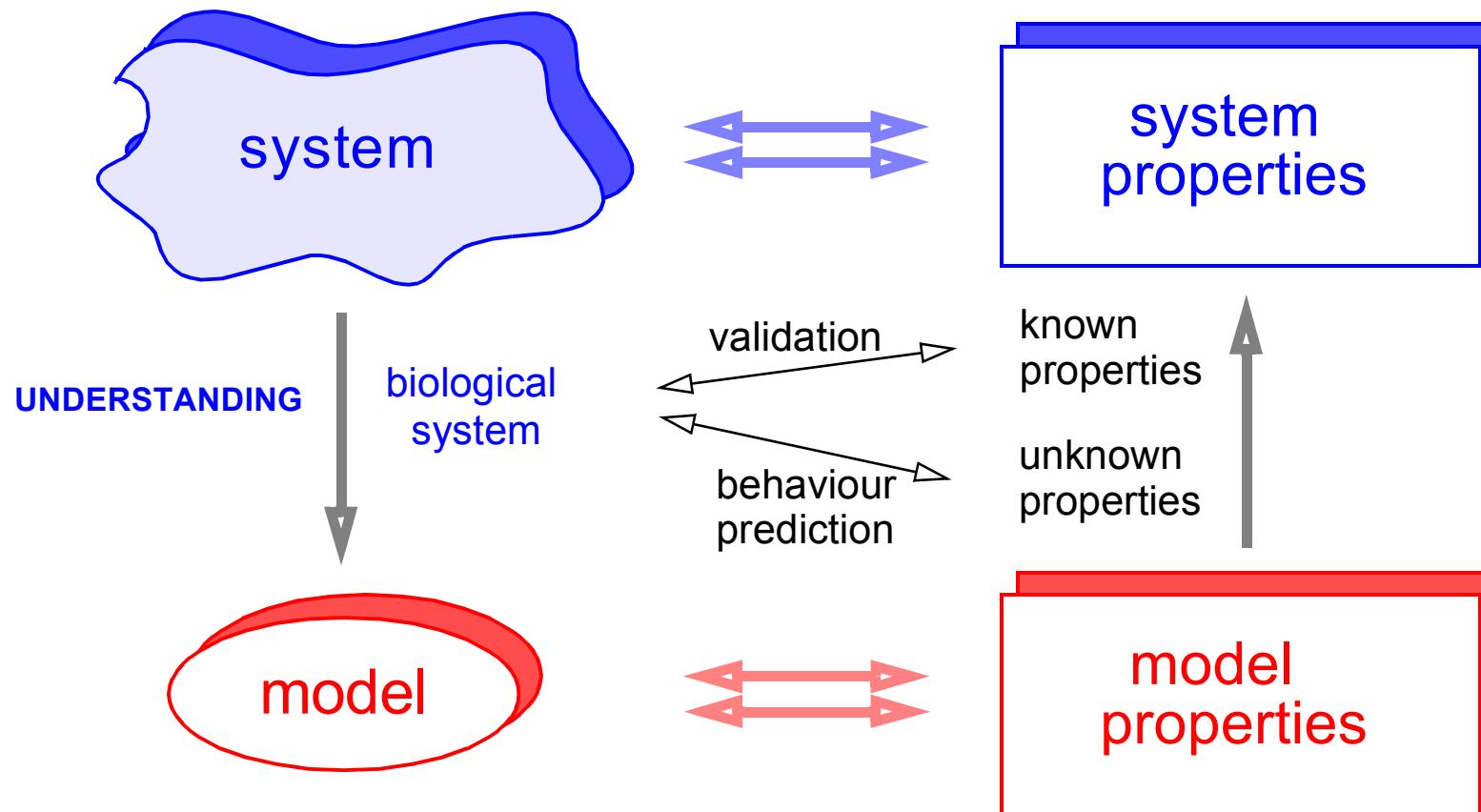
- > *our tool box: Snoopy, Charlie, Marcie*
- > *colored framework*
- > *Generalized Hybrid Petri Nets*

BACKGROUND

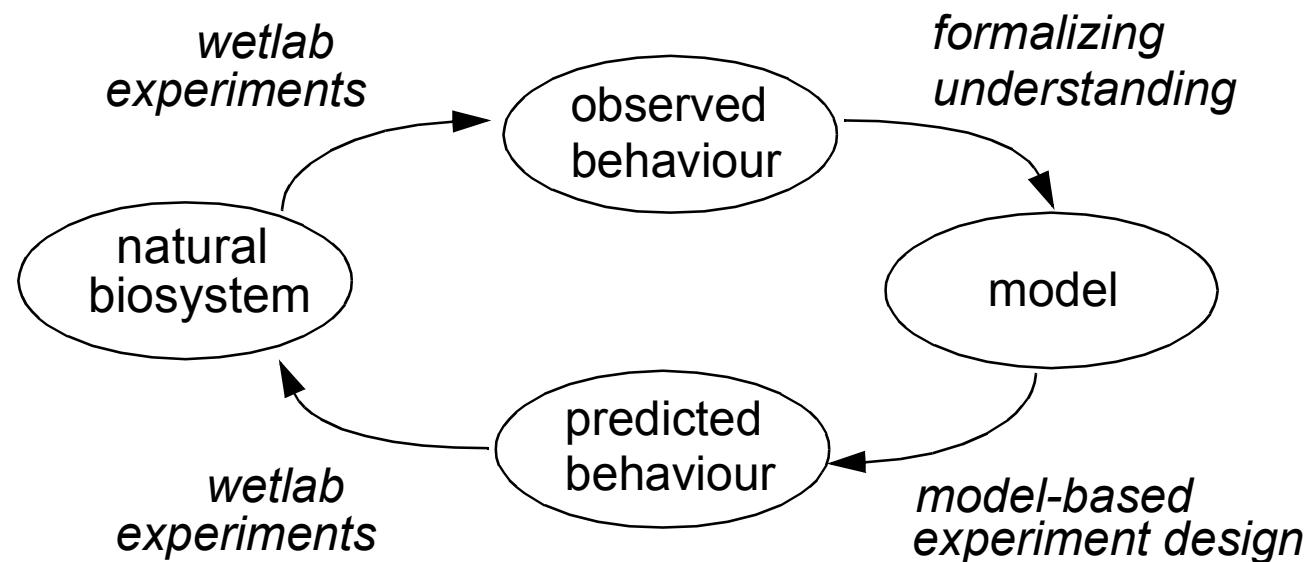




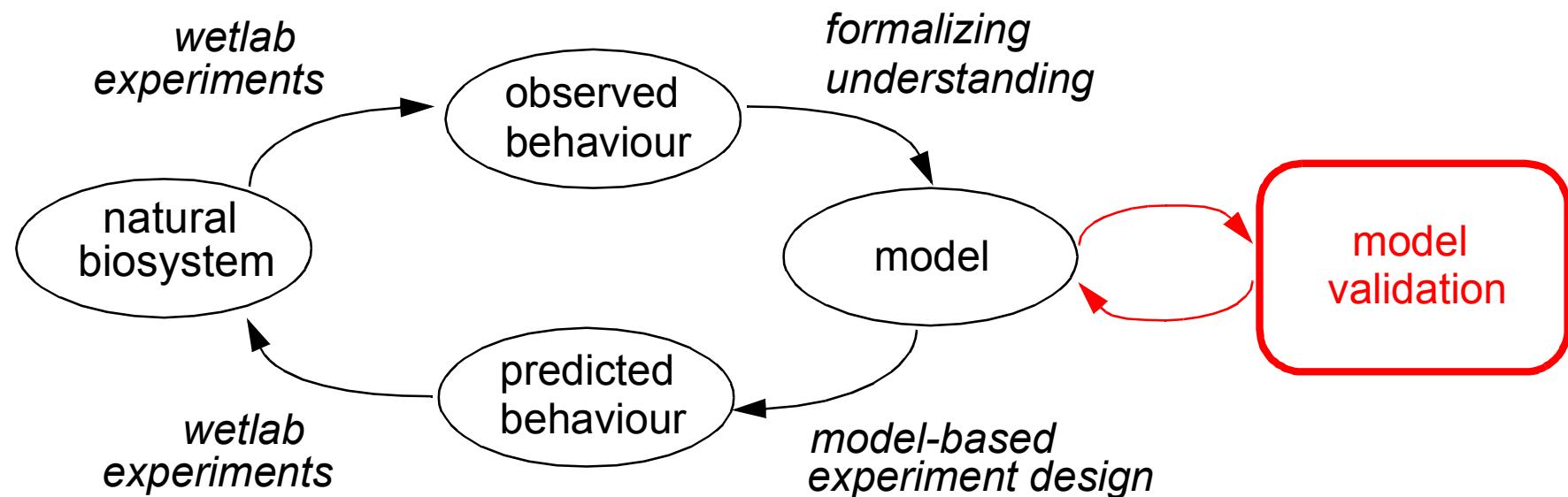




MODELLING = FORMAL KNOWLEDGE REPRESENTATION

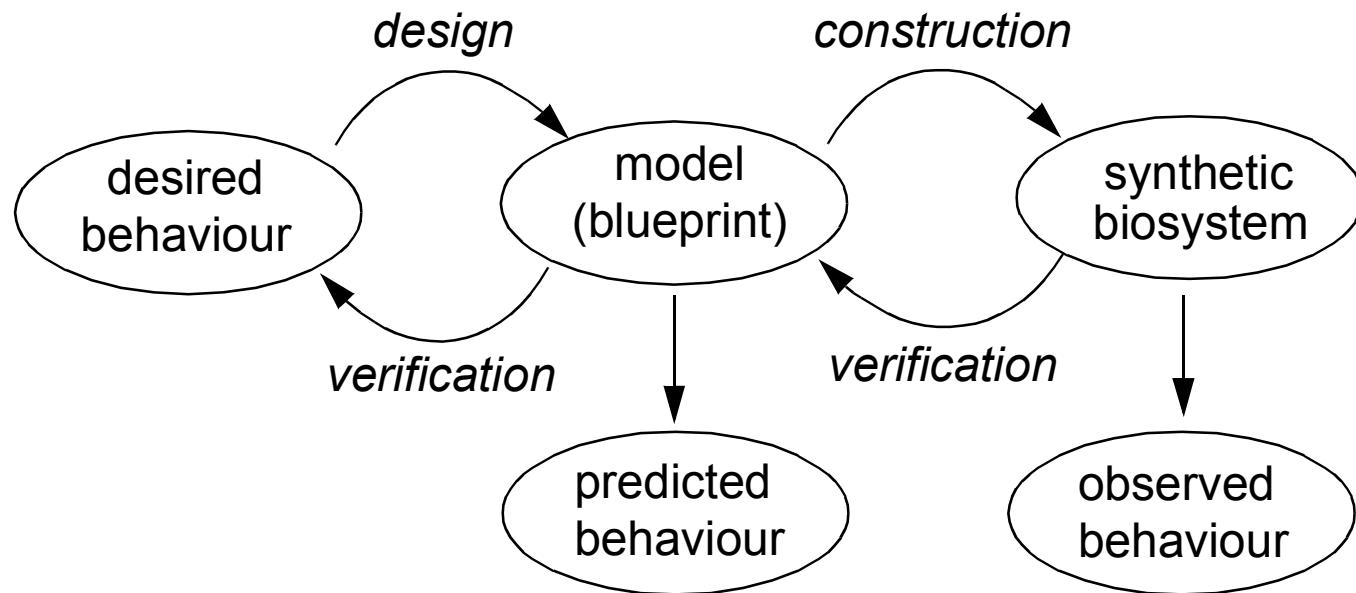


MODELLING = FORMAL KNOWLEDGE REPRESENTATION



MODEL VALIDATION = CONFIDENCE INCREASE

MODELLING = BLUEPRINT FOR SYSTEM CONSTRUCTION



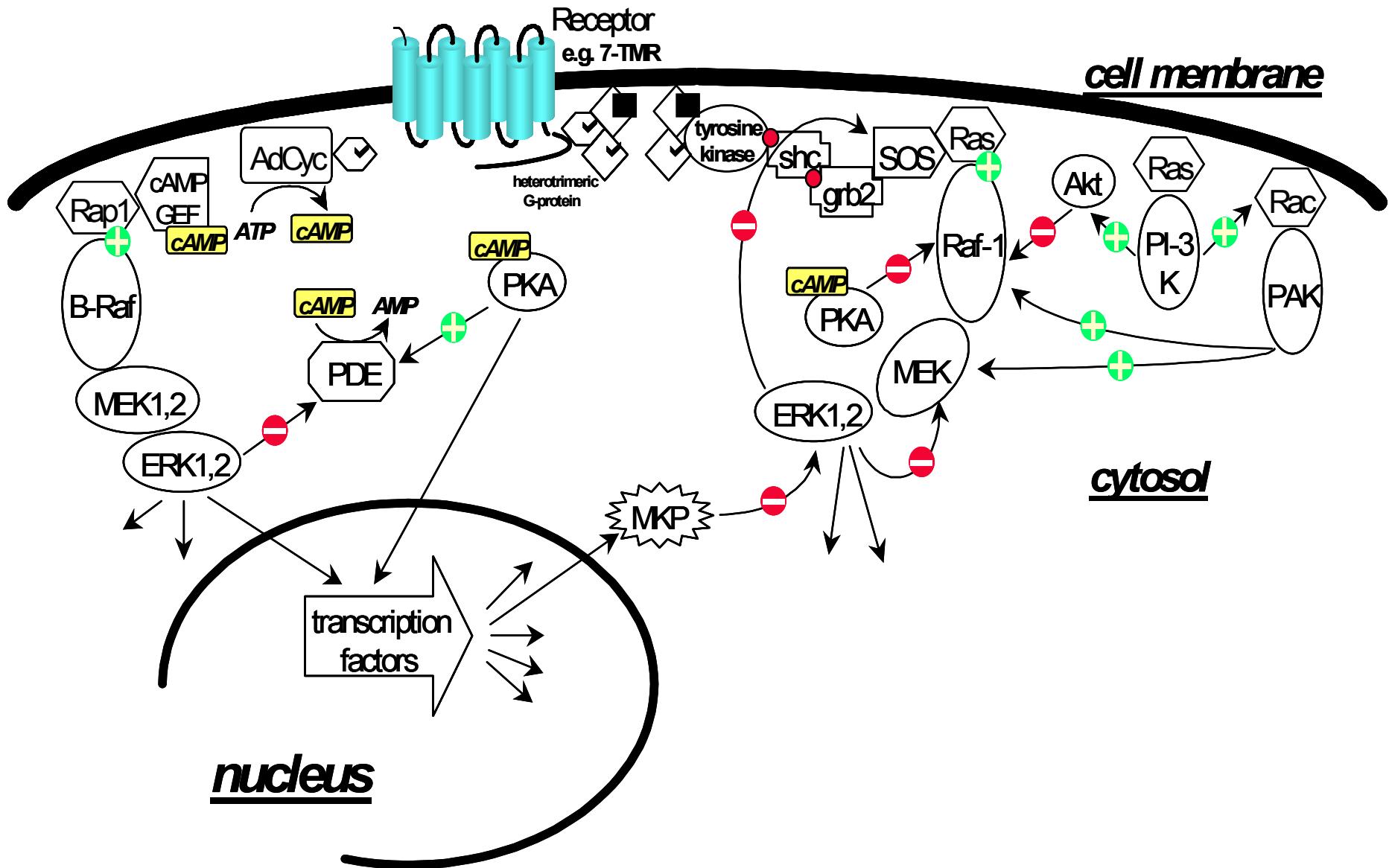
RELIABLE AND ROBUST ENGINEERING REQUIRES VERIFIED MODELS

WHAT KIND OF MODEL SHOULD BE USED?



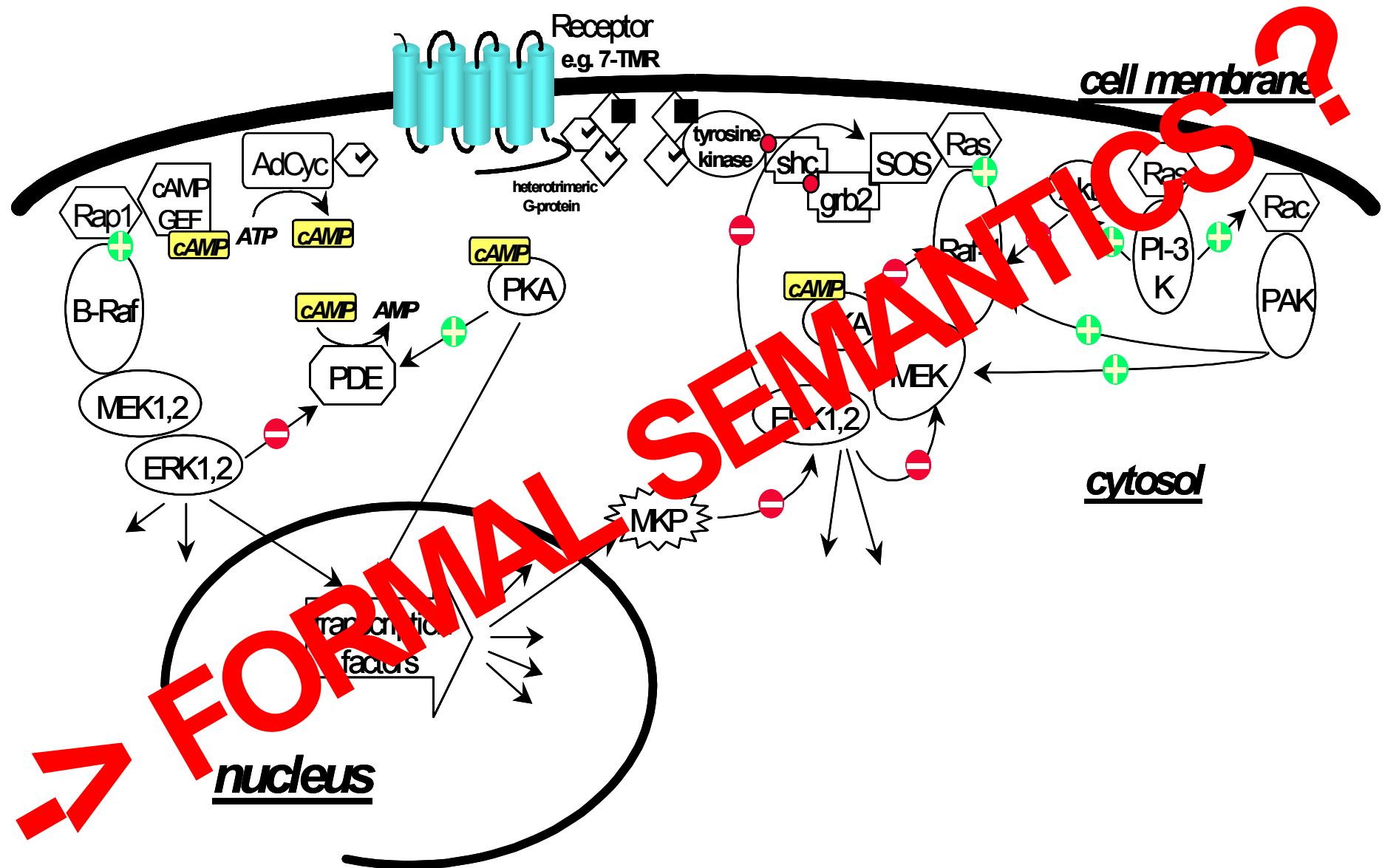
NETWORK REPRESENTATIONS, Ex1

PN & Systems Biology



NETWORK REPRESENTATIONS, Ex1

PN & Systems Biology



NETWORK REPRESENTATIONS, Ex2

PN & Systems Biology

$$\begin{aligned}
 \frac{d\alpha}{dt} &= -v_1 \\
 \frac{d\text{Ste2}}{dt} &= -v_2 + v_3 - v_5 \\
 \frac{d\text{Ste2}_{\text{active}}}{dt} &= v_2 - v_3 - v_4 \\
 \frac{d\text{Sst2}_{\text{active}}}{dt} &= v_{46} - v_{47} \\
 \frac{dG\alpha\beta\gamma}{dt} &= -v_6 + v_9 \\
 \frac{dG\alpha\text{GTP}}{dt} &= v_6 - v_7 - v_8 \\
 \frac{dG\alpha\text{GDP}}{dt} &= v_7 + v_8 - v_9 \\
 \frac{dG\beta\gamma}{dt} &= v_6 - v_9 - v_{10} + v_{11} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32} \\
 &\quad - v_{42} + v_{43} \\
 \frac{d\text{Ste5}}{dt} &= -v_{12} + v_{13} + v_{17} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32} \\
 \frac{d\text{Ste11}}{dt} &= -v_{12} + v_{13} + v_{17} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32} \\
 \frac{d\text{Ste7}}{dt} &= -v_{14} + v_{15} + v_{17} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32} \\
 \frac{d\text{Fus3}}{dt} &= -v_{14} + v_{15} + v_{17} + v_{21} + v_{23} + v_{25} + v_{27} - v_{29} \\
 &\quad + v_{30} + v_{33} \\
 \frac{d\text{Ste20}}{dt} &= -v_{18} + v_{19} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32}
 \end{aligned}$$

$$\begin{aligned}
 v_1 &= \alpha[t] \cdot \text{Bar1}_{\text{active}}[t] \cdot k_1 \\
 v_2 &= \text{Ste2}[t] \cdot \alpha[t] \cdot k_2 \\
 v_3 &= \text{Ste2}_{\text{active}}[t] \cdot k_3 \\
 v_4 &= \text{Ste2}_{\text{active}}[t] \cdot k_4 \\
 v_5 &= \text{Ste2}[t] \cdot k_5 \\
 v_6 &= \text{Ste2}_{\text{active}}[t] \cdot G\alpha\beta\gamma[t] \cdot k_6 \\
 v_7 &= G\alpha\text{GTP}[t] \cdot k_7 \\
 v_8 &= G\alpha\text{GTP}[t] \cdot \text{Sst2}_{\text{active}}[t] \cdot k_8 \\
 v_9 &= G\alpha\text{GDP}[t] \cdot G\beta\gamma[t] \cdot k_9 \\
 v_{10} &= G\beta\gamma[t] \cdot C[t] \cdot k_{10} \\
 v_{11} &= D[t] \cdot k_{11} \\
 v_{12} &= \text{Ste5}[t] \cdot \text{Ste11}[t] \cdot k_{12} \\
 v_{13} &= A[t] \cdot k_{13} \\
 v_{14} &= \text{Ste7}[t] \cdot \text{Fus3}[t] \cdot k_{14} \\
 v_{15} &= B[t] \cdot k_{15} \\
 v_{16} &= A[t] \cdot B[t] \cdot k_{16} \\
 v_{17} &= C[t] \cdot k_{17} \\
 v_{18} &= D[t] \cdot \text{Ste20}[t] \cdot k_{18}
 \end{aligned}$$

NETWORK REPRESENTATIONS, Ex2

PN & Systems Biology

$$\begin{aligned}
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 \frac{d\text{Ste20}}{dt} &= -v_{18} + v_{19} + v_{21} + v_{23} + v_{25} + v_{27} + v_{32}
 \end{aligned}$$

?

$$\begin{aligned}
 v_1 &= \alpha[t] \cdot \text{Bar1}_{\text{active}}[t] \\
 v_2 &= \text{Ste2}[t] \cdot \alpha[t] \cdot k_2 \\
 v_3 &= \text{Ste2}_{\text{active}}[t] \cdot k_3 \\
 v_4 &= \text{Ste2}_{\text{inactive}}[t] \cdot k_4 \\
 v_5 &= \text{Ste2}[t] \cdot k_5 \\
 v_6 &= \text{Ste2}_{\text{active}}[t] \cdot G\alpha\beta\gamma[t] \cdot k_6 \\
 v_7 &= G\alpha\text{GTP}[t] \cdot k_7 \\
 v_8 &= G\alpha\text{GTP}[t] \cdot \text{Sst2}_{\text{active}}[t] \cdot k_8 \\
 v_9 &= G\alpha\text{GDP}[t] \cdot G\beta\gamma[t] \cdot k_9 \\
 v_{10} &= G\beta\gamma[t] \cdot C[t] \cdot k_{10} \\
 v_{11} &= D[t] \cdot k_{11} \\
 v_{12} &= \text{Ste5}[t] \cdot \text{Ste11}[t] \cdot k_{12} \\
 v_{13} &= A[t] \cdot k_{13} \\
 v_{14} &= \text{Ste7}[t] \cdot \text{Fus3}[t] \cdot k_{14} \\
 v_{15} &= B[t] \cdot k_{15} \\
 v_{16} &= A[t] \cdot B[t] \cdot k_{16} \\
 v_{17} &= C[t] \cdot k_{17} \\
 v_{18} &= D[t] \cdot \text{Ste20}[t] \cdot k_{18}
 \end{aligned}$$

knowledge

-> **PROBLEM 1**

-> *uncertain*

-> *growing, changing*

-> *distributed over independent data bases, papers, journals, . . .*

various, mostly ambiguous representations

-> **PROBLEM 2**

-> *verbose descriptions*

-> *diverse graphical representations*

-> *contradictory and / or fuzzy statements*

network structure

-> **PROBLEM 3**

-> *tend to grow fast*

-> *dense, apparently unstructured*

-> *hard to read*

- knowledge -> **PROBLEM 1**
 - > *uncertain*
 - > *growing, changing*
 - > *distributed over independent data bases, papers, journals, . . .*
- various, mostly ambiguous representations -> **PROBLEM 2**
 - > *verbose descriptions*
 - > *diverse graphical representations*
 - > *contradictory and / or fuzzy statements*
- network structure -> **PROBLEM 3**
 - > *tend to grow fast*
 - > *dense, apparently unstructured*
 - > *hard to read*

-> MODELS ARE FULL OF ASSUMPTIONS <-

- readable**

- > *fault avoidance*
 - > *informal = cartoon-like representations ?*

- analysable**

- > *formal = mathematical representations*

- executable**

- > *to experience the model*

- unifying power**

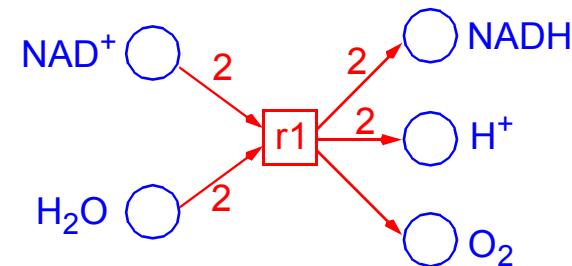
- > *high-level description for various analysis approaches*

... · ·

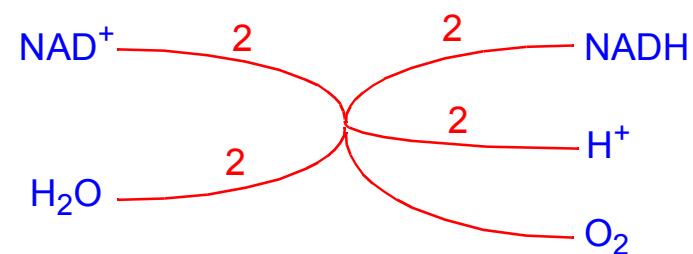
***ARE NETWORKS
OF BIOCHEMICAL
REACTIONS***

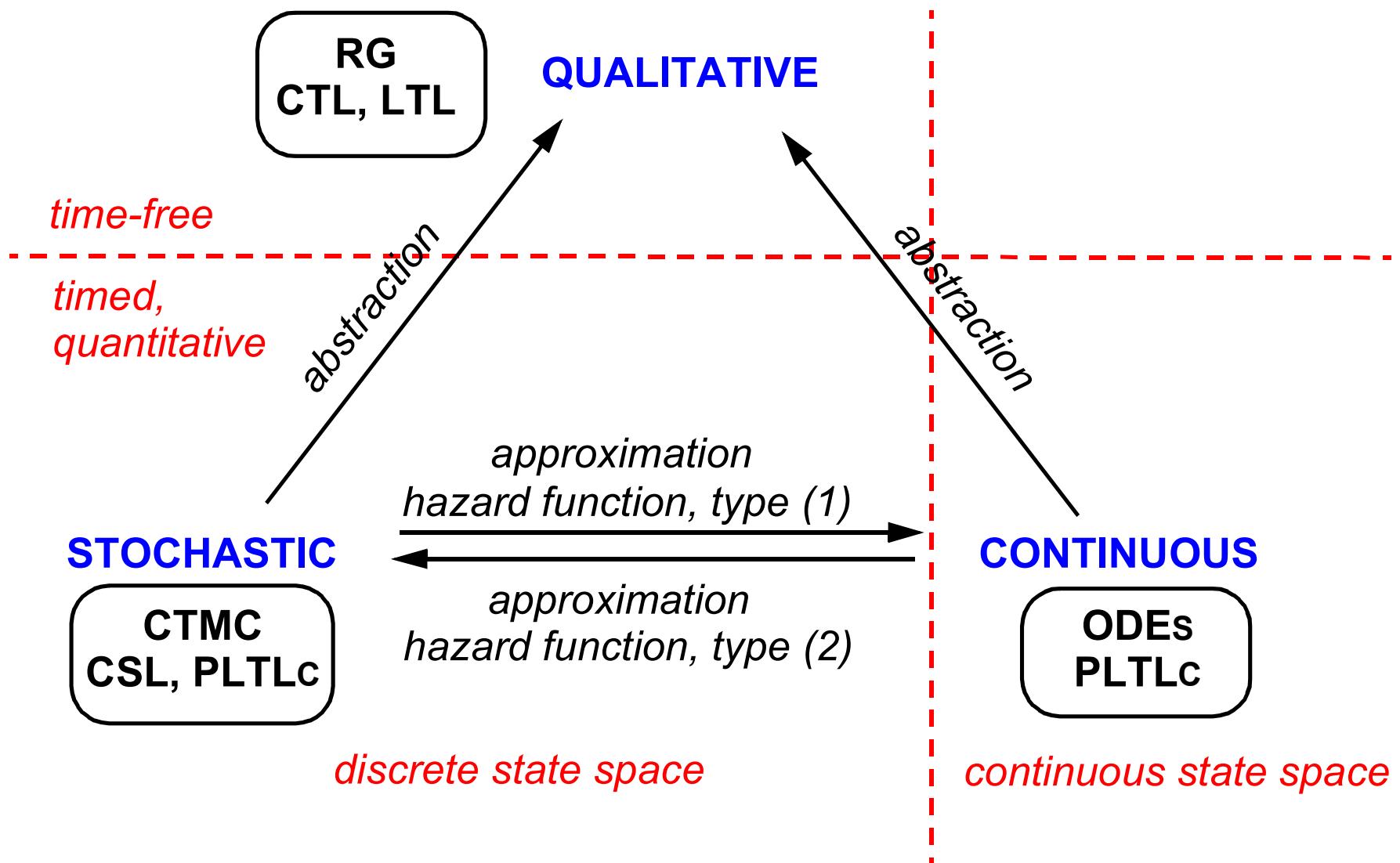
· · ·

***NATURALLY
EXPRESSIBLE AS
PETRI NETS***



hyper-arcs

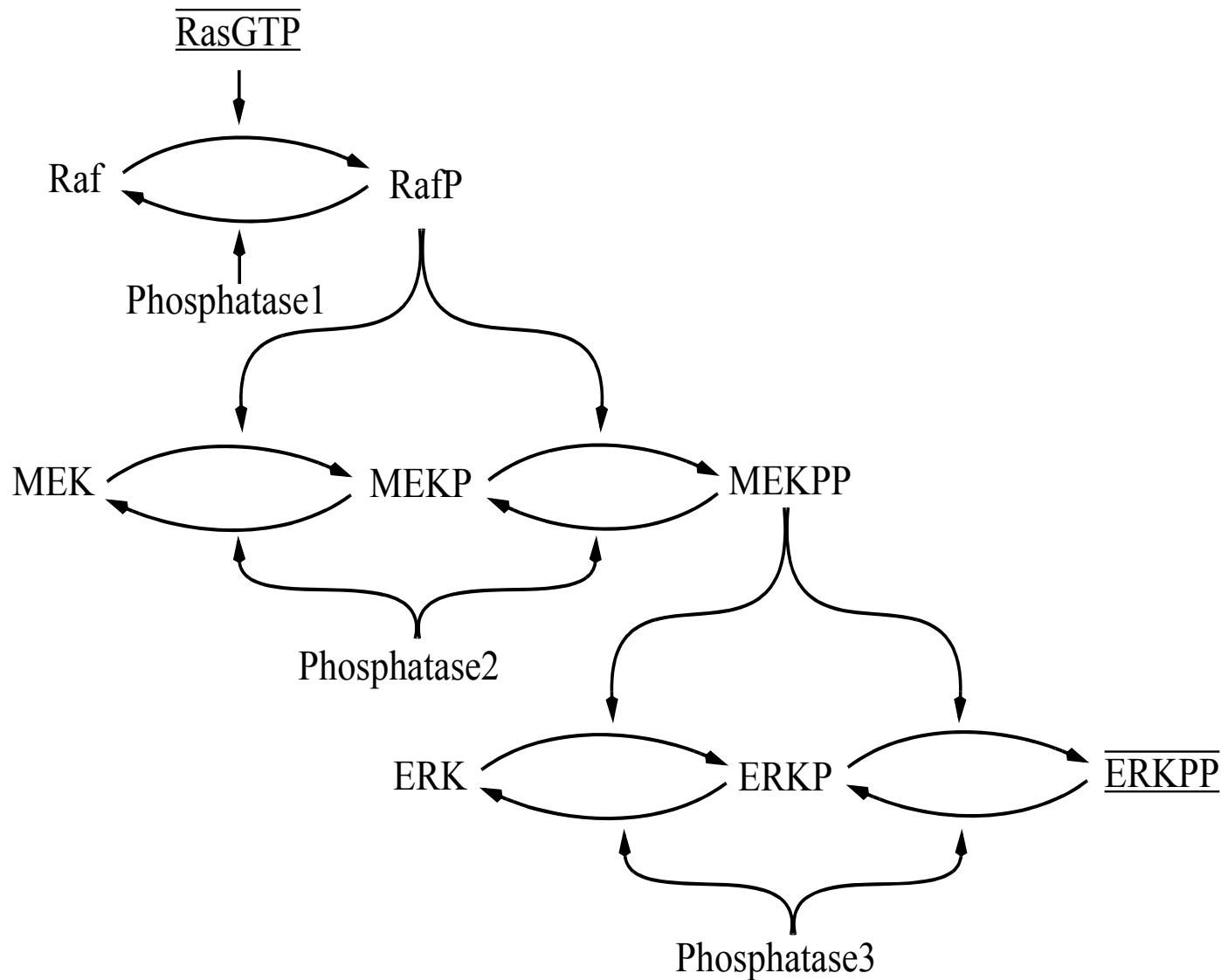




BIO PETRI NETS - SOME EXAMPLES

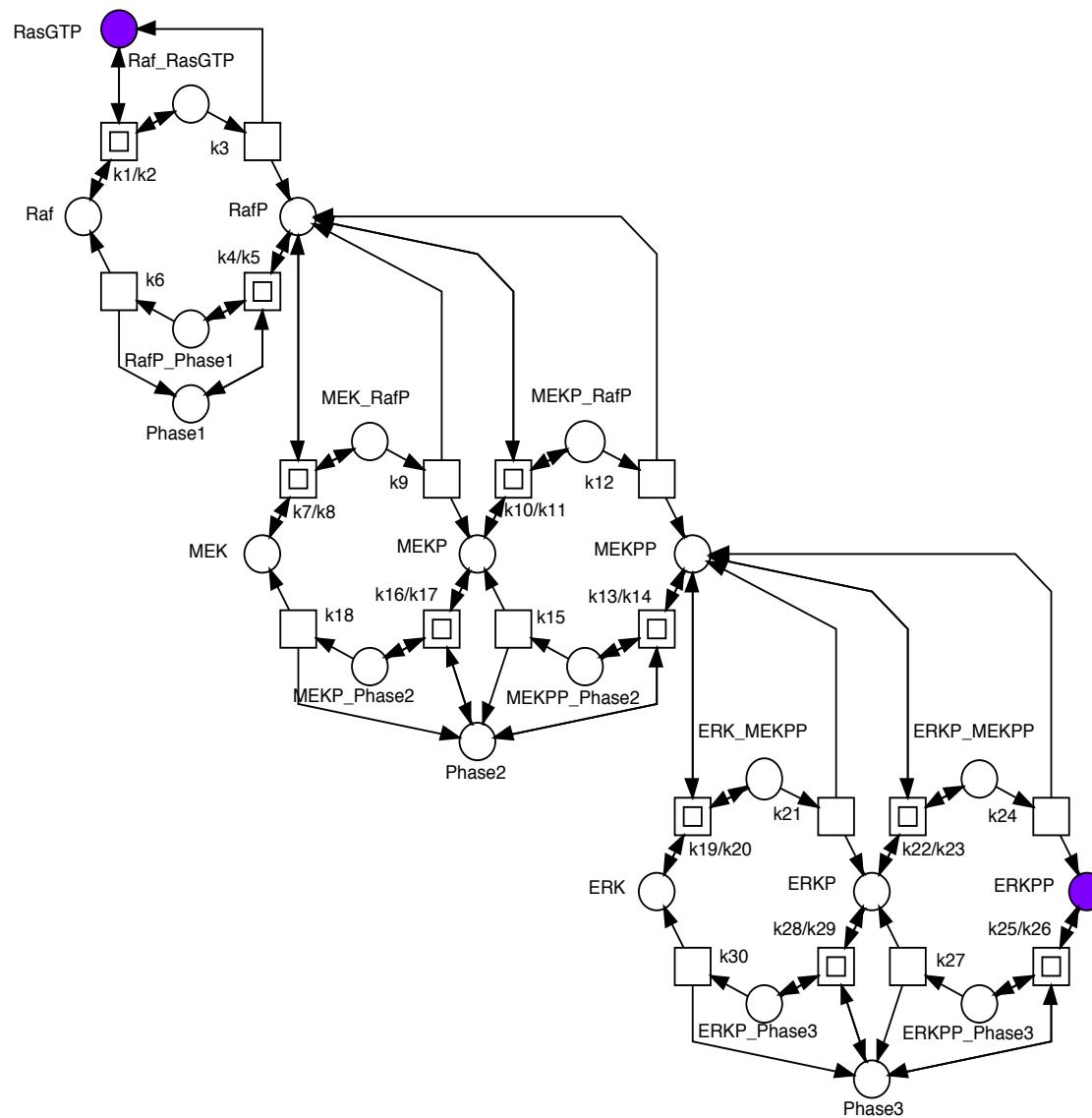
EX1 - SIGNALLING CASCADE

PN & Systems Biology



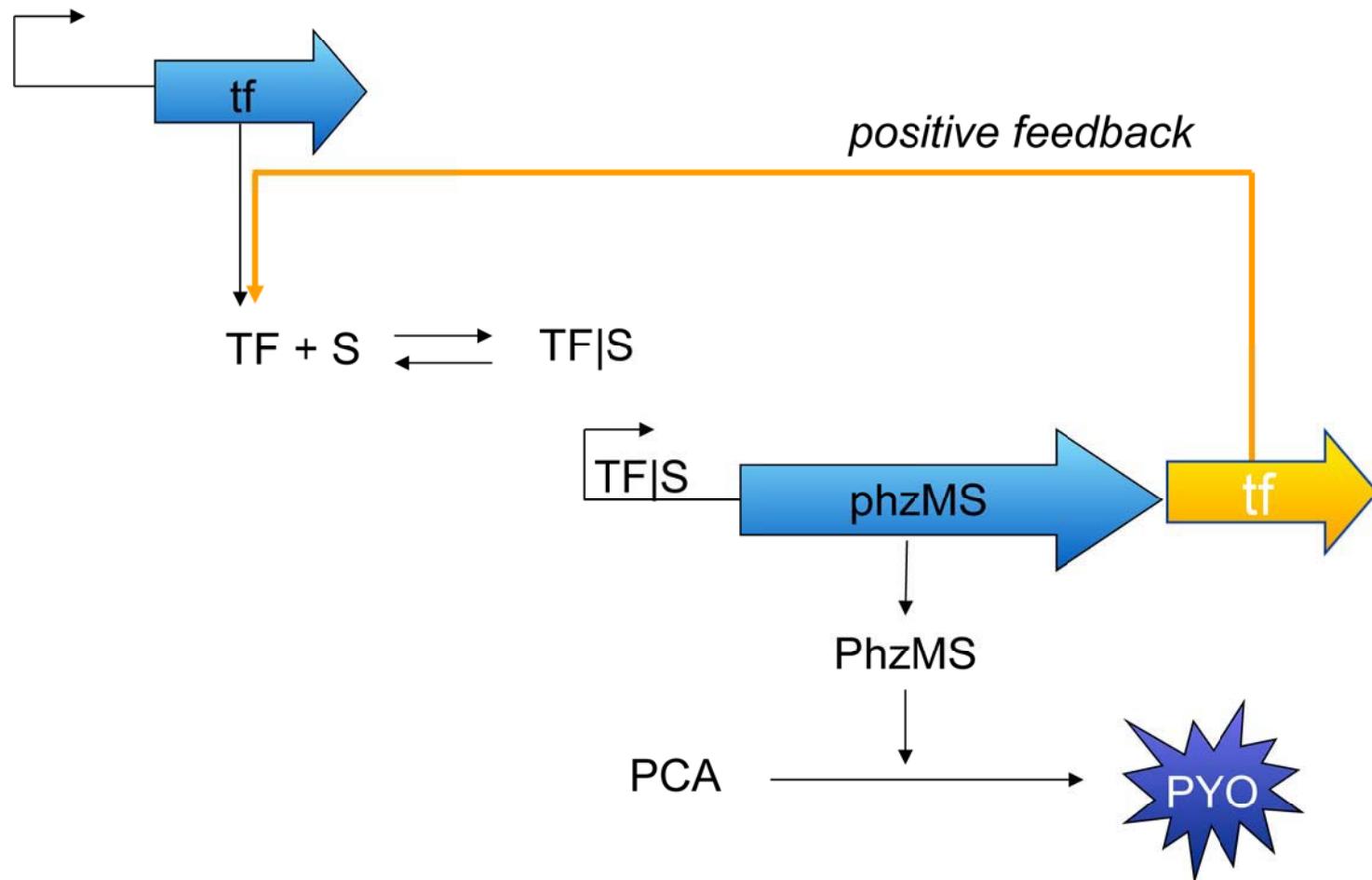
EX1 - SIGNALLING CASCADE

PN & Systems Biology

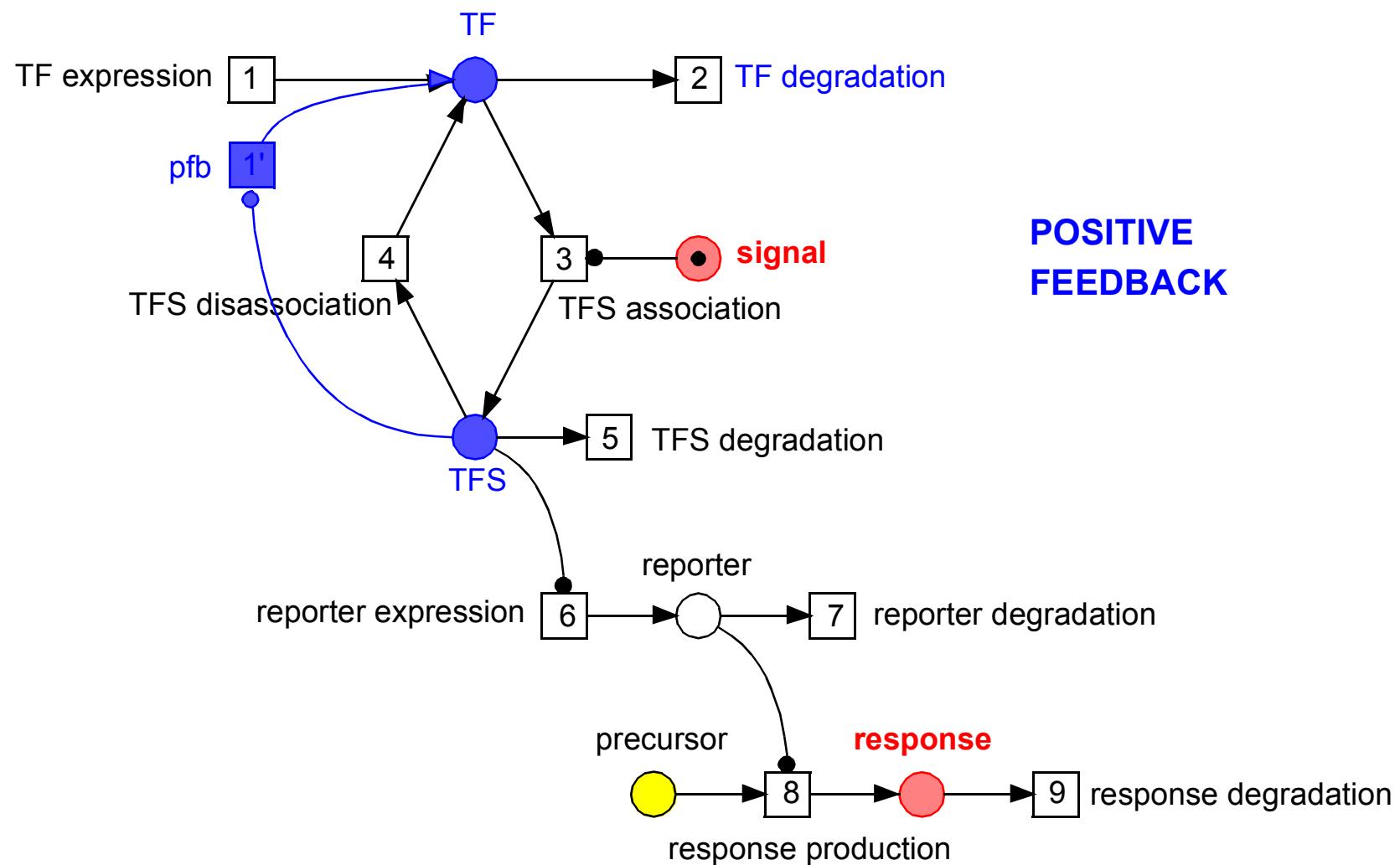


Ex2 - BIOSENSOR

PN & Systems Biology

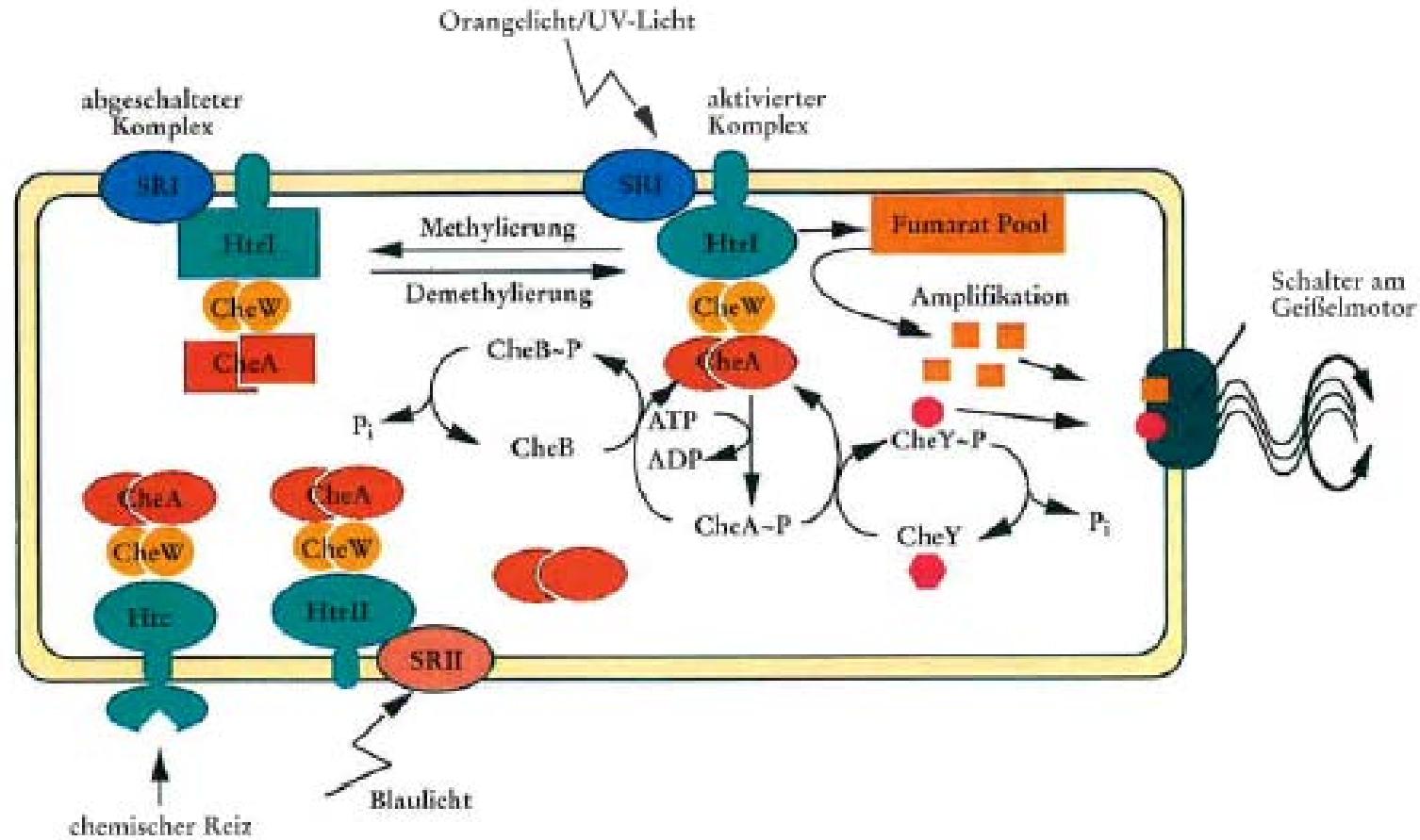


Ex2 - BIOSENSOR



Ex3 - SWITCH CYCLE HALOBACTERIUM SALINARUM

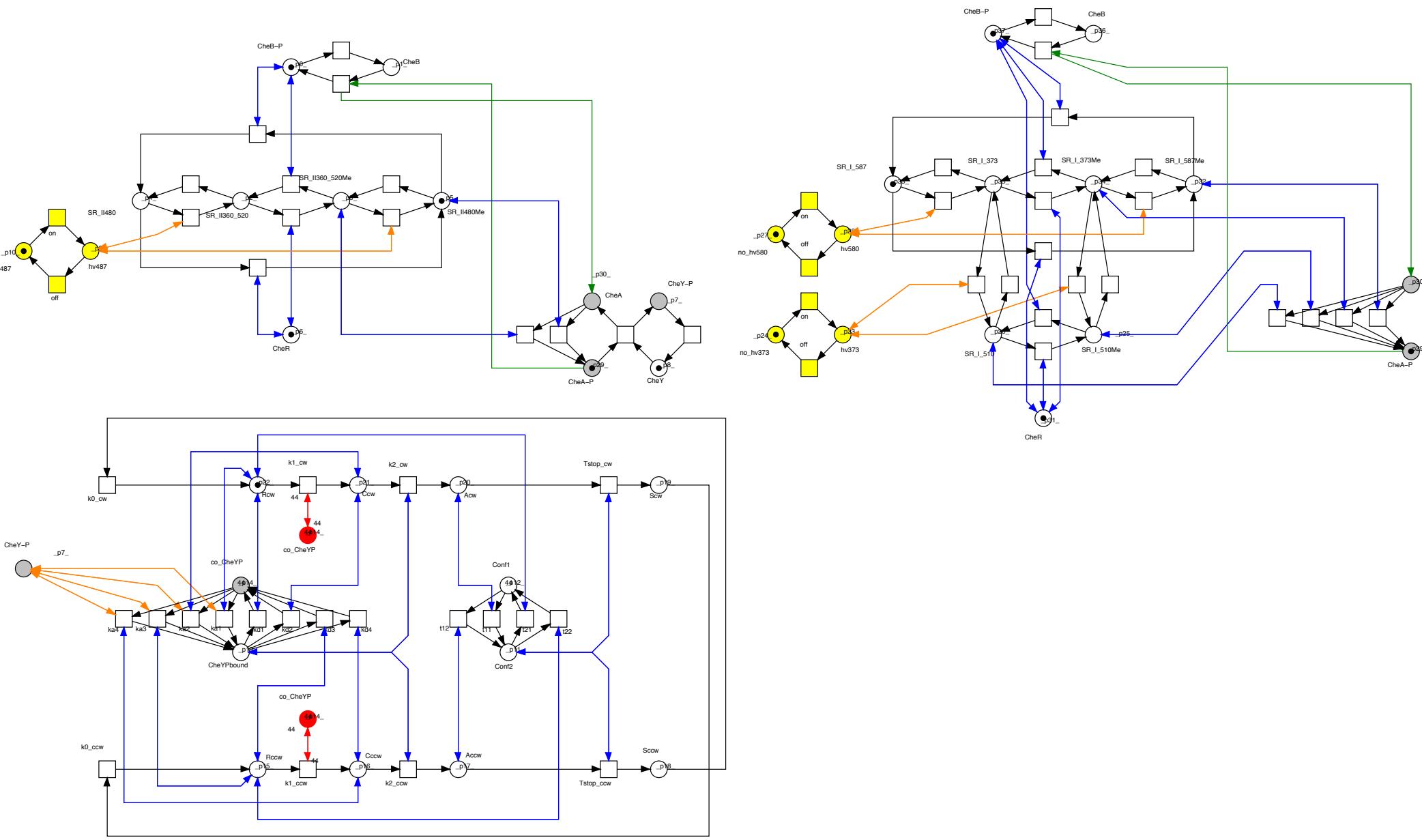
PN & Systems Biology



[Marwan; Oesterhelt 1999]

Ex3 - SWITCH CYCLE HALOBACTERIUM SALINARUM

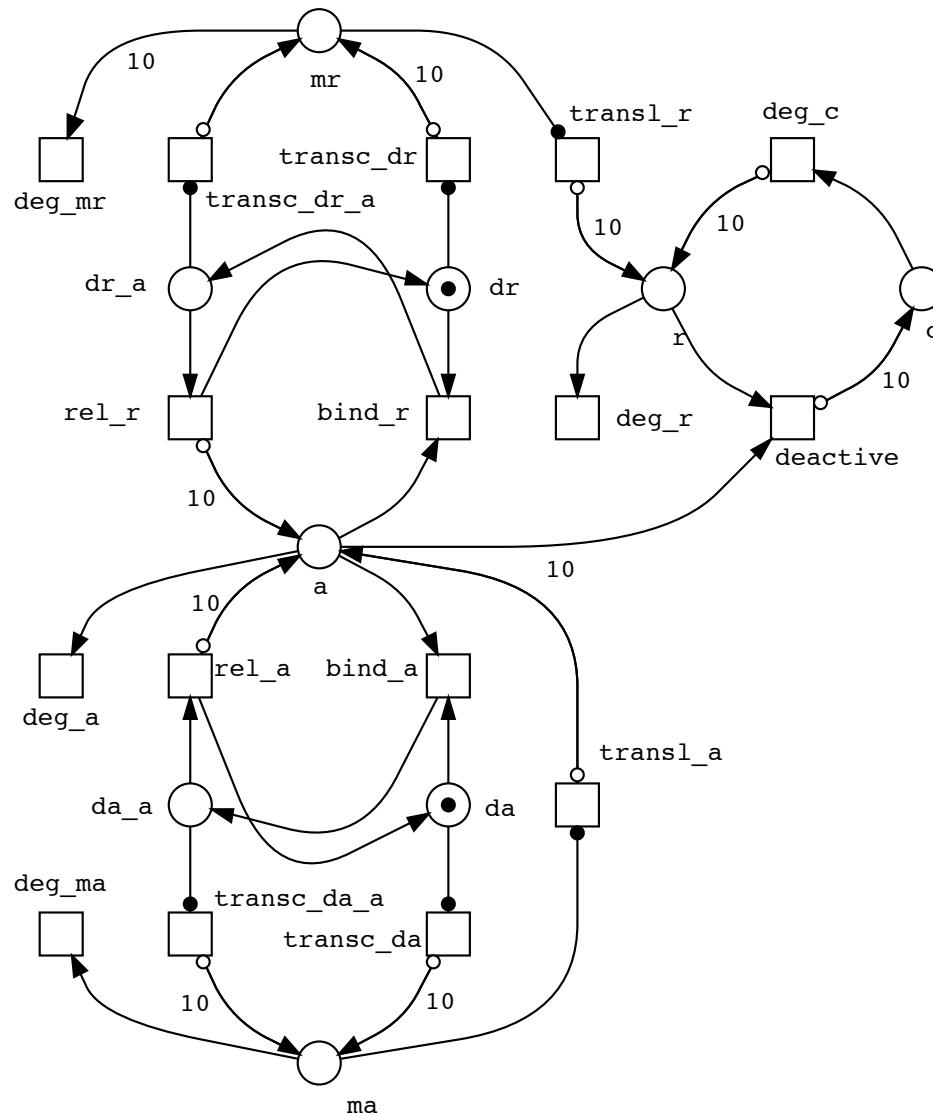
PN & Systems Biology



Ex4 - CIRCADIAN CLOCK

PN & Systems Biology

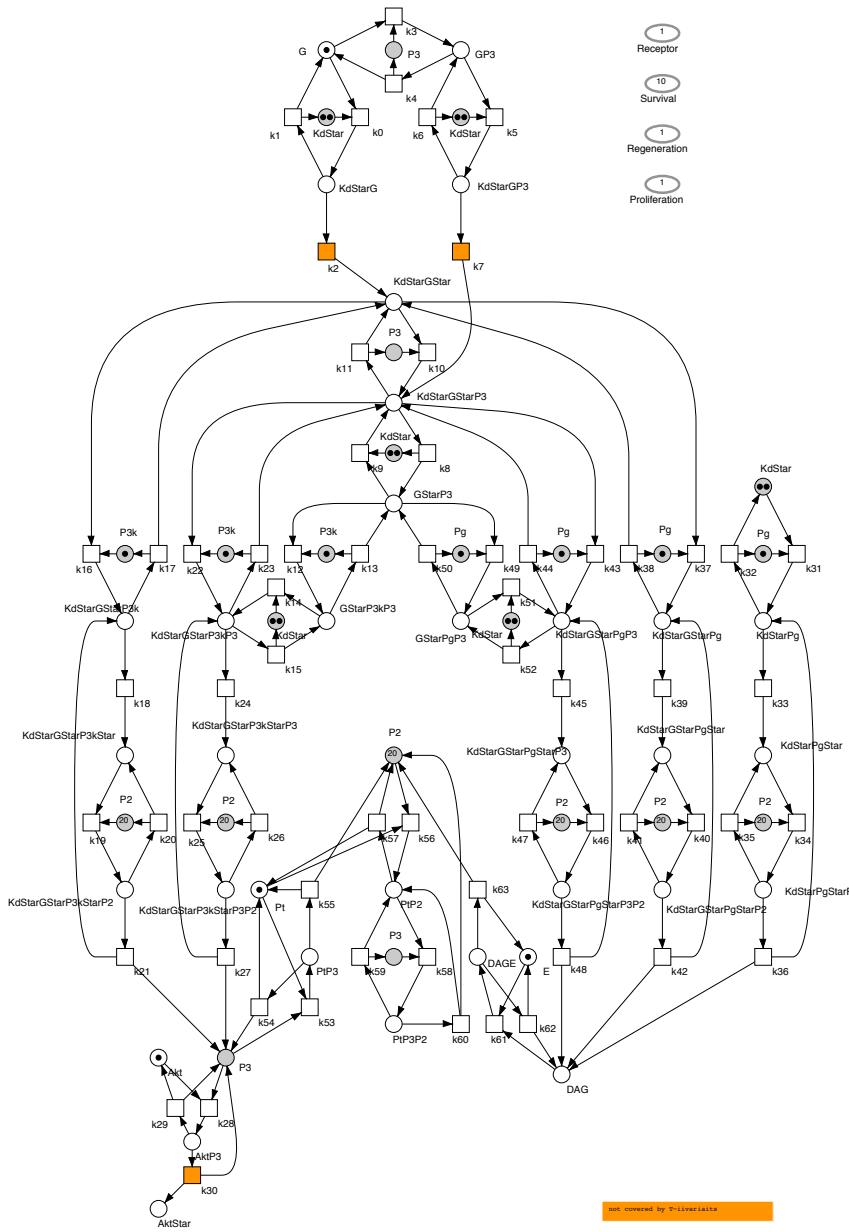
[PRISM website]



Ex5 - ANGIOGENESIS

PN & Systems Biology

[... Balbo ... 2009]



MOULARIZATION BY T-INVARIANTS

$r1: A \rightarrow 2B$

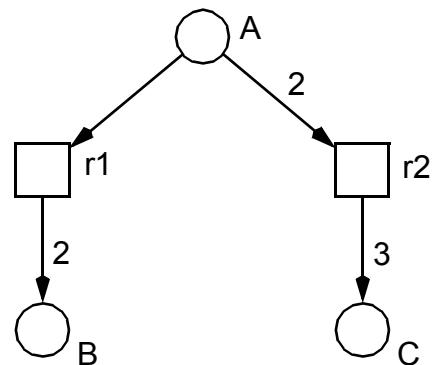
$r2: 2A \rightarrow 3C$

T-INVARIANTS, Ex1

PN & Systems Biology

$r1: A \rightarrow 2B$

$r2: 2A \rightarrow 3C$

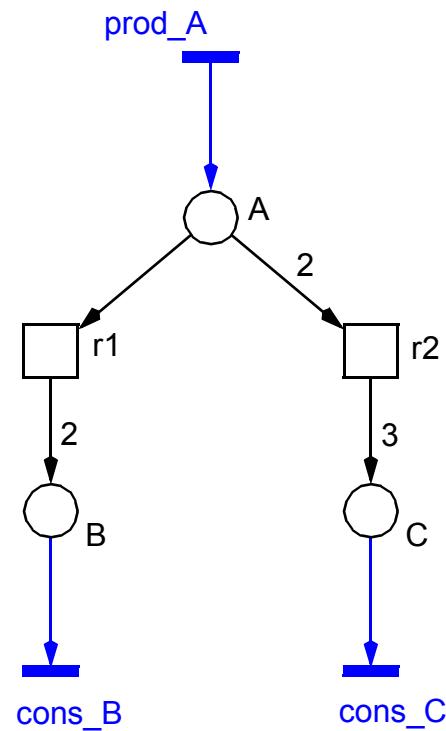
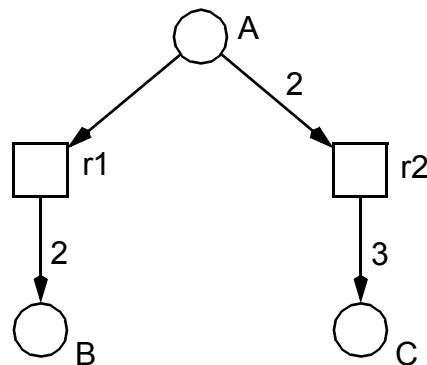


T-INVARIANTS, Ex1

PN & Systems Biology

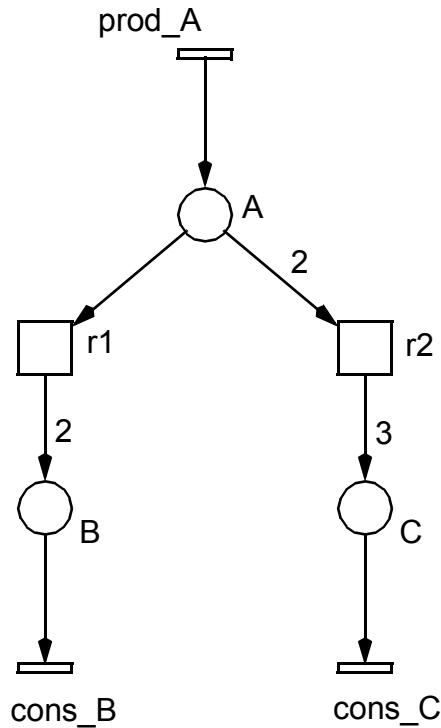
$r1: A \rightarrow 2B$

$r2: 2A \rightarrow 3C$



INCIDENCE MATRIX C, Ex1

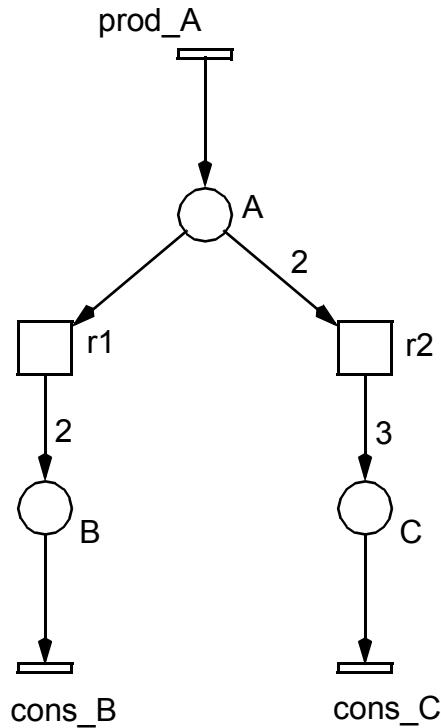
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T P	r1	r2	prod_A	cons_B	cons_C
A					
B					
C					

INCIDENCE MATRIX C, Ex1

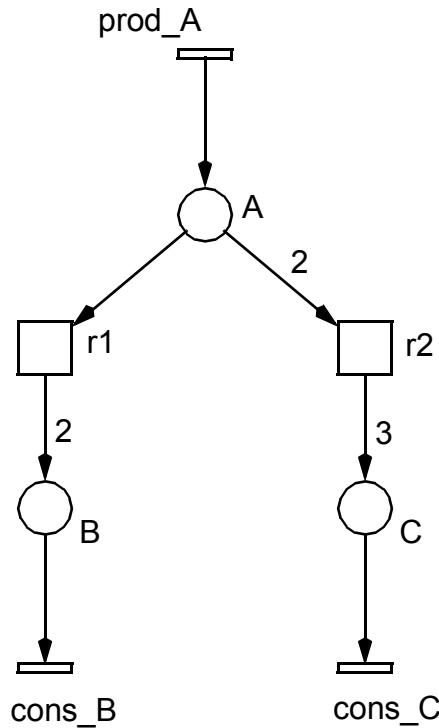
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T P	r1	r2	prod_A	cons_B	cons_C
A	-1	-2	1		
B	2			-1	
C		3			-1

INCIDENCE MATRIX C, Ex1

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T P	r1	r2	prod_A	cons_B	cons_C
A	-1	-2	1		
B	2			-1	
C		3			-1
	1	1	2		

- Lautenbach, 1973 -> Schuster, 1993
 - T-invariants -> *multisets of transitions*
 - > *integer solutions x*
$$Cx = 0, x \neq 0, x \geq 0$$
 - minimal T-invariants
 - > *there is no T-invariant with a smaller support* -> *sets of transitions*
 - > *gcd of all non-zero entries is 1*
 - any T-invariant is a non-negative linear combination of minimal ones
 - > *multiplication with a positive integer*
 - > *addition*
 - > *division by a common divisor*
$$kx = \sum_i a_i x_i$$
 - Covered by T-Invariants (CTI)
 - > *each transition belongs to a T-invariant*

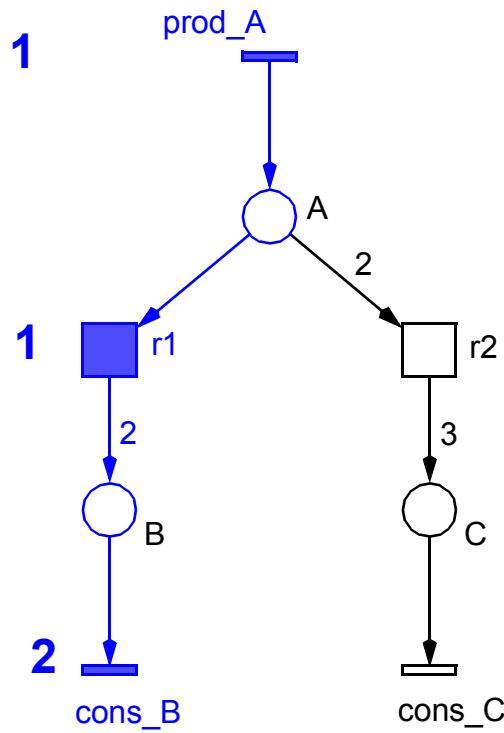
- T-invariants = (multi-) sets of transitions = Parikh vector
 - > zero effect on marking
 - > reproducing a marking / system state
 - two interpretations
 1. *partially ordered transition sequence*
of transitions occurring one after the other
 - > substance / signal flow
 2. *relative transition firing rates*
of transitions occurring permanently & concurrently
 - > steady state behaviour
 - a minimal T-invariant defines a connected subnet
 - > the T-invariant's transitions (the support),
 - + all their pre- and post-places
 - + the arcs in between
 - > pre-set of support = post-set of support

T-INVARIANTS, Ex1

PN & Systems Biology

$r1: A \rightarrow 2 B$

$r2: 2 A \rightarrow 3 C$



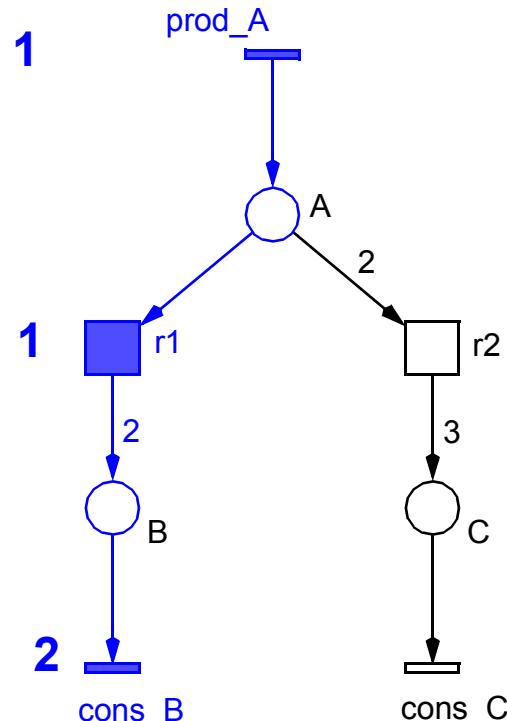
T-INVARIANT 1

T-INVARIANTS, Ex1

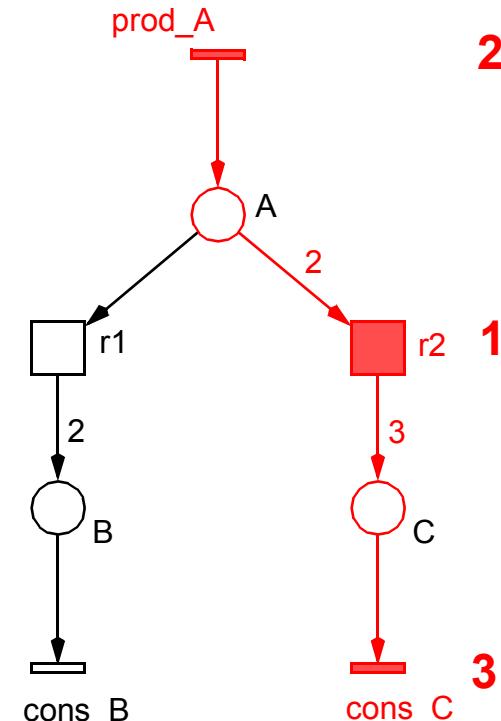
PN & Systems Biology

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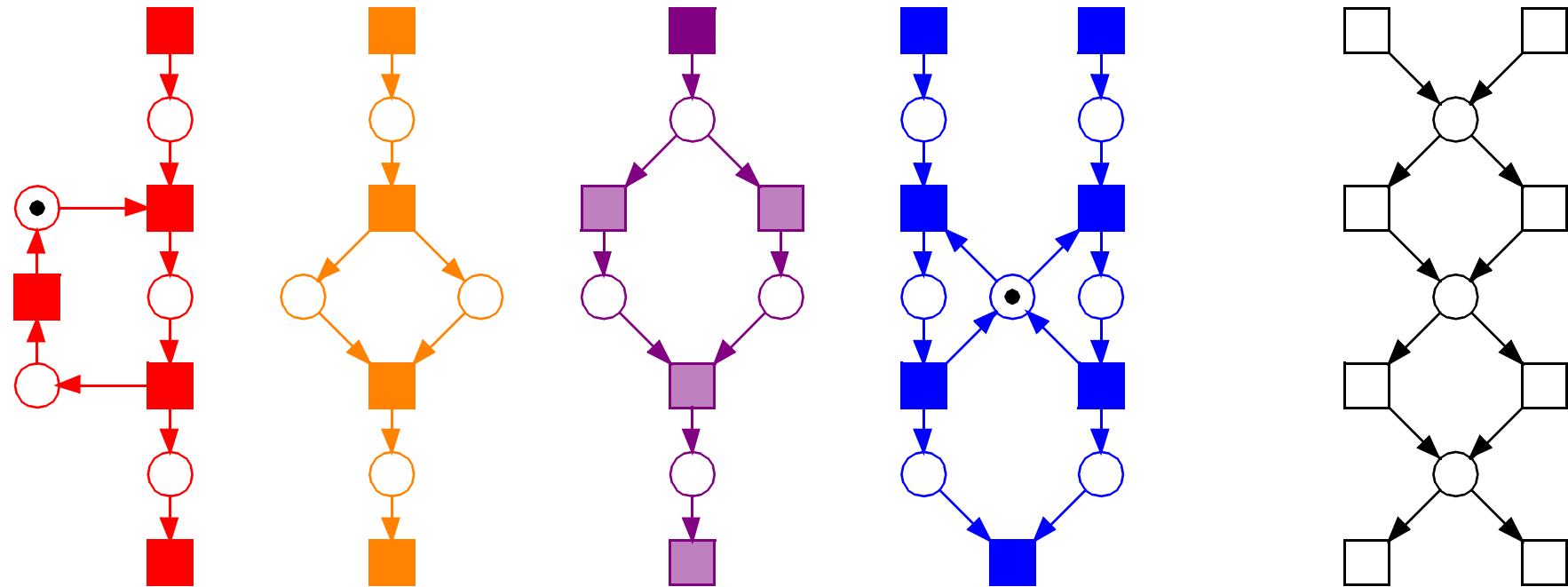


T-INVARIANT 1



T-INVARIANT 2

- T-invariants may contain any structure



- T-invariants generally overlap

-> combinatorial effect brings **explosion** in the number of min. T-invariants (2^4)

- Let X denote a set of (all / non-trivial) minimal T-invariants x of a given PN.
- **dependency relation:**
Two transitions i, j depend on each other,
if they always appear together in all minimal T-invariants x , i.e.

$$\forall x \in X: i \in supp(x) \Leftrightarrow j \in supp(x)$$

- **equivalence relation in the transition set, leading to a partition of T**
 - > *reflexive*
 - > *symmetric*
 - > *transitive*
- **the equivalence classes A represent maximal ADT-sets**

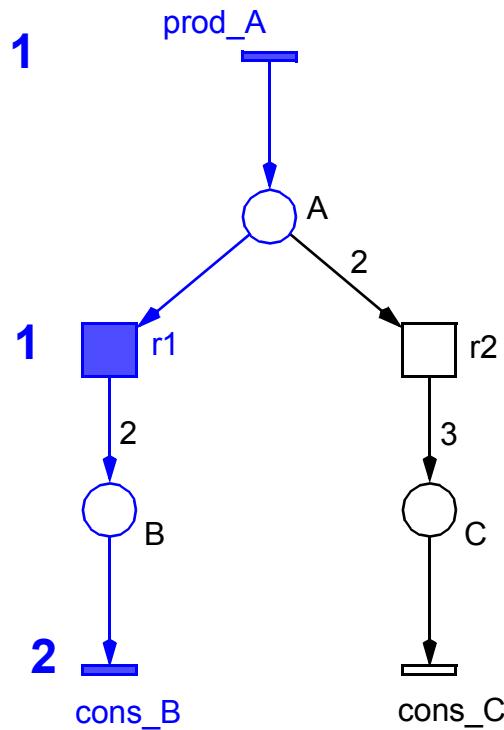
$$\forall x \in X: A \subseteq supp(x) \vee A \cap supp(x) = \emptyset$$

ADT-SETS, Ex1

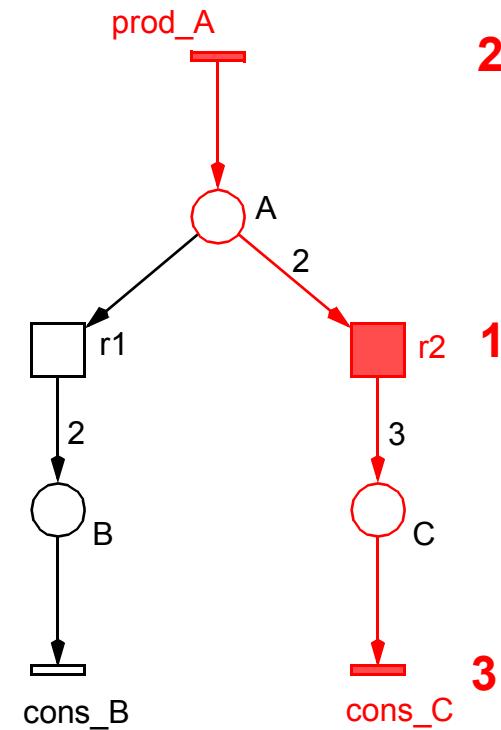
PN & Systems Biology

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T-INVARIANT 1

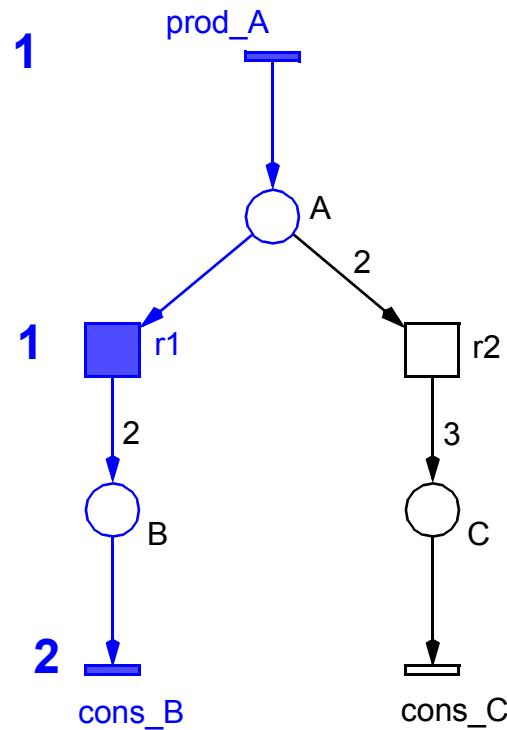


T-INVARIANT 2

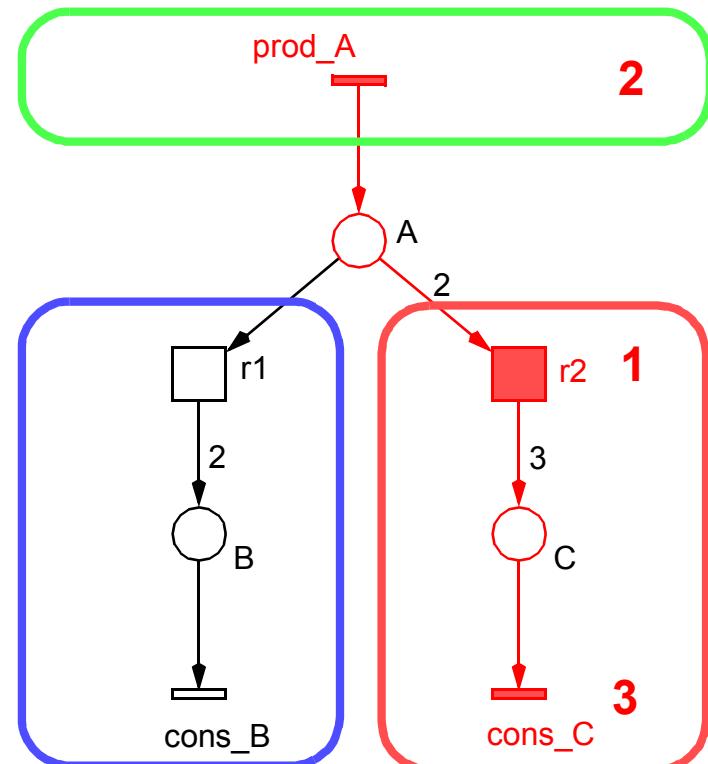
ADT-SETS, Ex1

$r1: A \rightarrow 2 B$

$r2: 2 A \rightarrow 3 C$



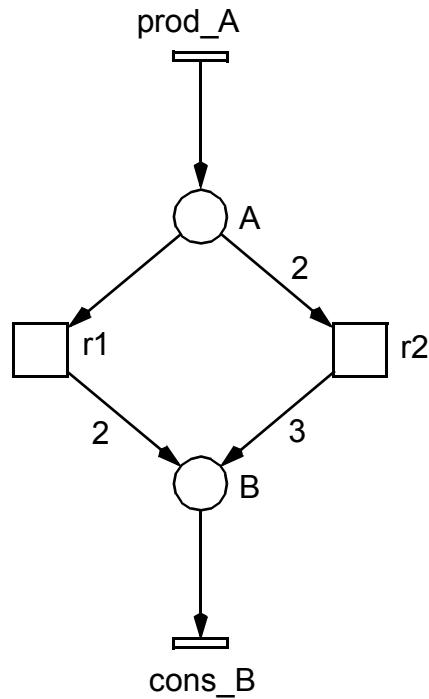
T-INVARIANT 1



T-INVARIANT 2

$r1: A \rightarrow 2B$

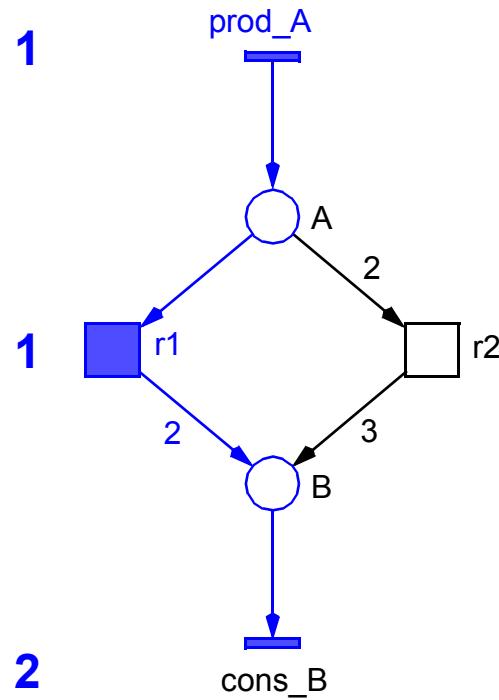
$r2: 2A \rightarrow 3B$



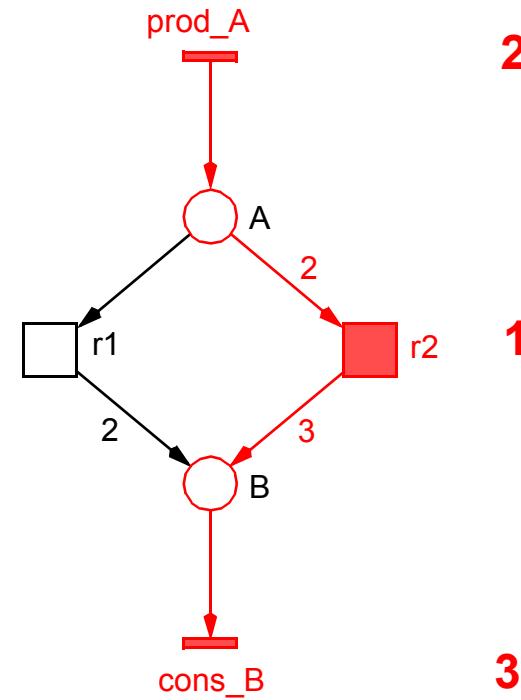
ADT-SETS, Ex2

$r1: A \rightarrow 2 B$

$r2: 2 A \rightarrow 3 B$



T-INVARIANT 1



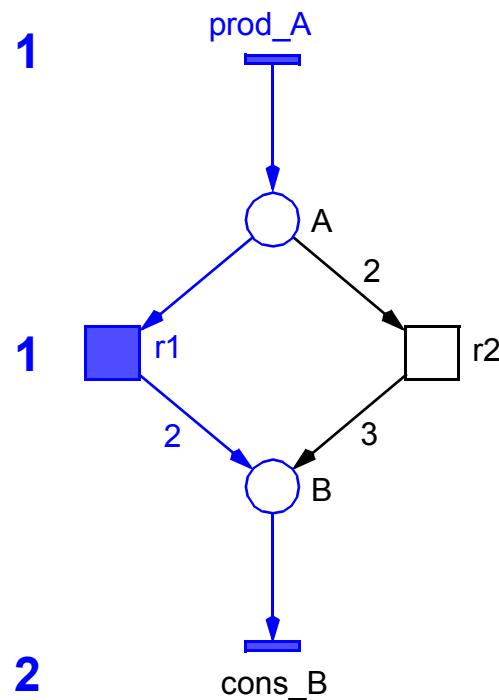
T-INVARIANT 2

ADT-SETS, Ex2

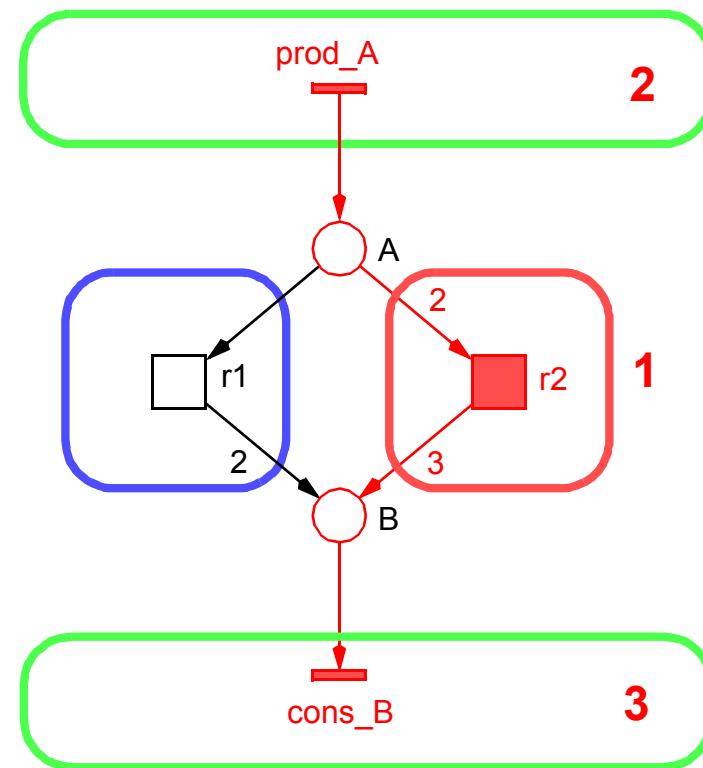
PN & Systems Biology

$r1: A \rightarrow 2 B$

$r2: 2 A \rightarrow 3 B$



T-INVARIANT 1



T-INVARIANT 2

□ maximal ADT-sets

- > *disjunctive subnets*
- > *not necessarily connected*

minimal T-invariants

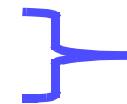
- > *overlapping subnets*
- > *connected*

□ interpretation

- > *structural decomposition into rather small subnets*
- > *smallest biologically meaningful functional units*
- > *building blocks*

□ variations

- > *with / without trivial T-invariants*
- > *whole / partial set of T-invariants*



not necessarily maximal ADT-sets

□ classification of all transitions based on the T-invariants' support

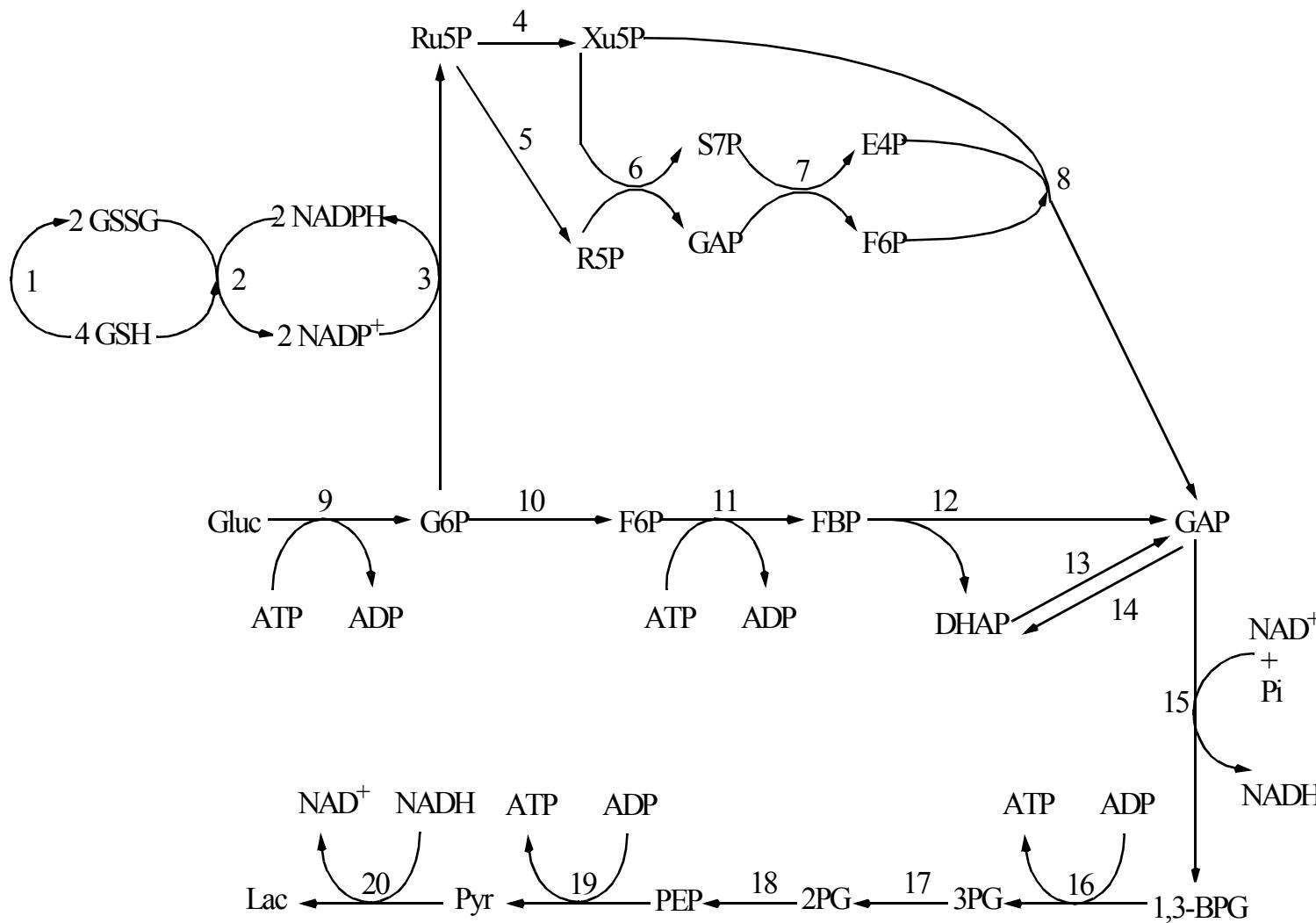
- maximal ADT-sets
 - > *not necessarily connected*
- further decomposition into connected ADT-sets
 - > *possibly according to primary compounds, only,
i.e. neglecting connections by auxiliary compounds*
 - > *non-maximal ADT-sets*
- coarse network structure, definition
 - > *macro transitions* - *abstract from connected ADT-sets*
 - > *places* - *interface between functional units*
- coarse network structure, what for?
 - > *set of T-invariants gets structured*
 - > *better understanding of the net behaviour*
- flow equivalent server component ?

BIO PETRI NETS, SOME EXAMPLES

Ex1 - Glycolysis and Pentose Phosphate Pathway

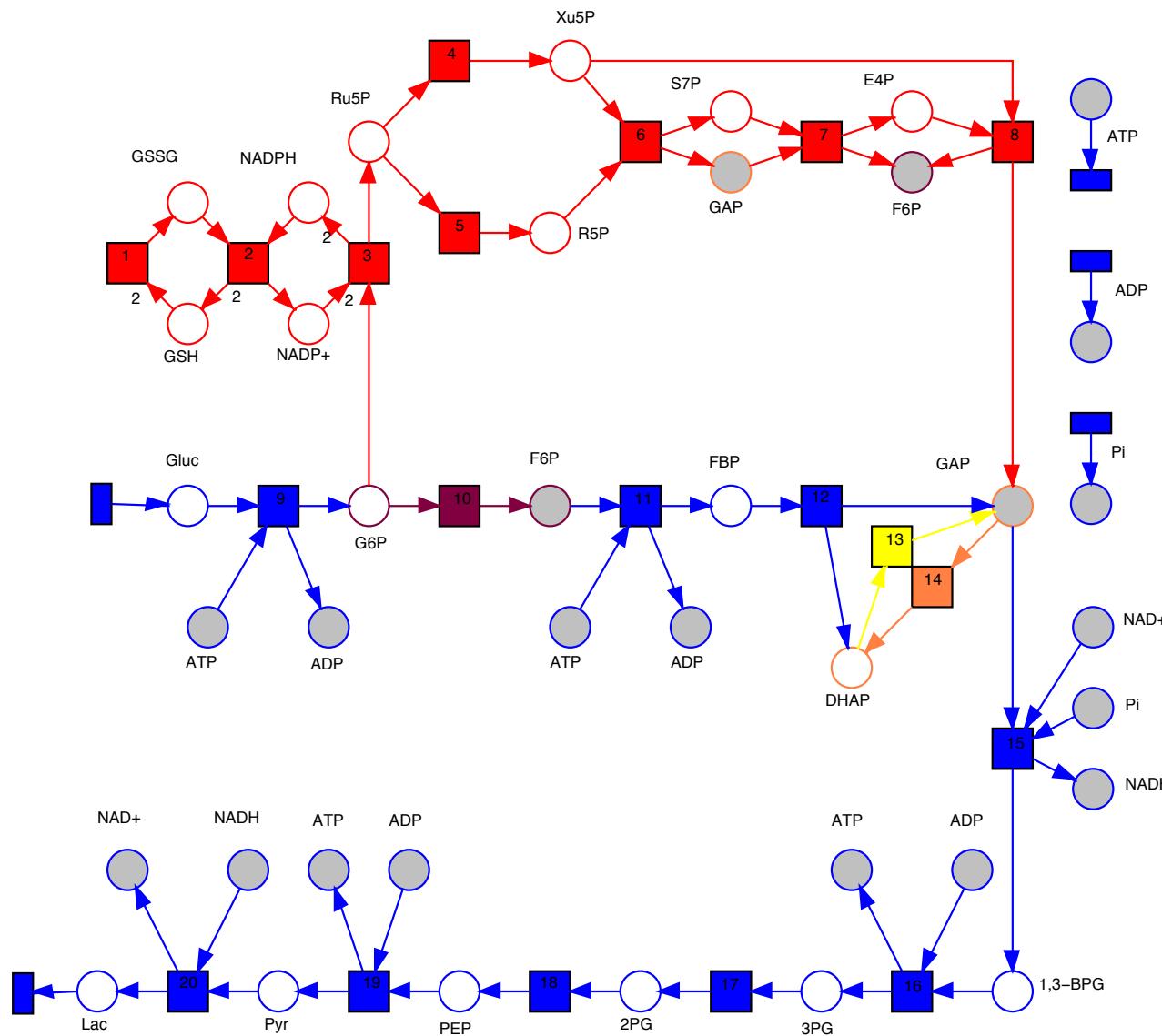
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[Reddy 1993]



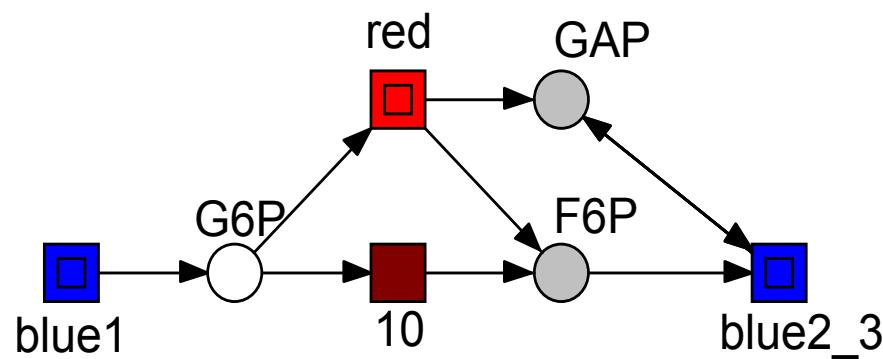
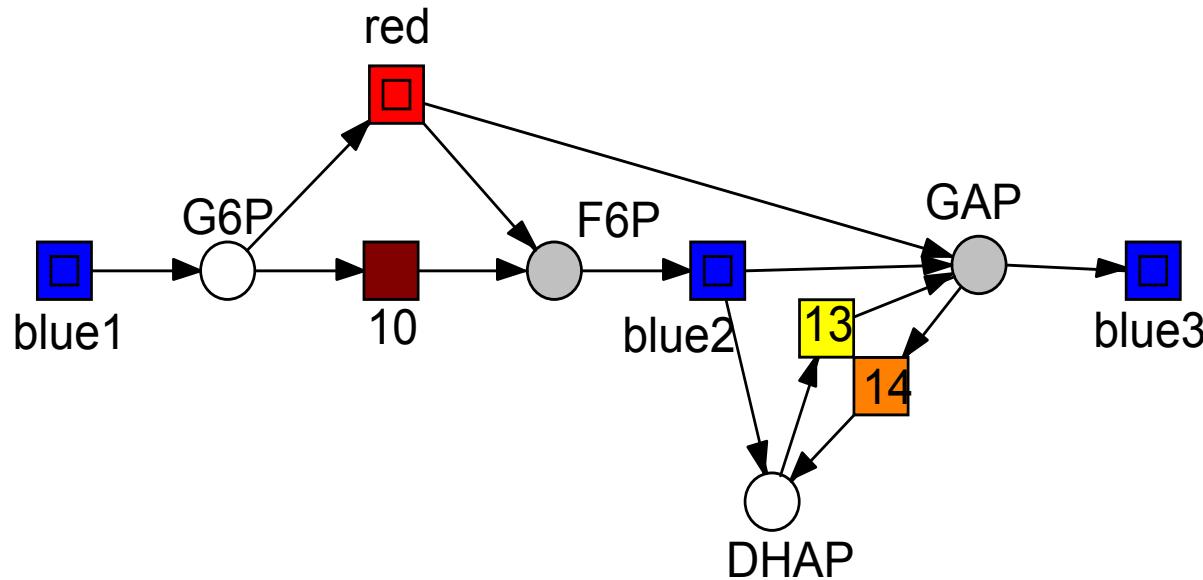
Ex1 - Glycolysis and Pentose Phosphate Pathway

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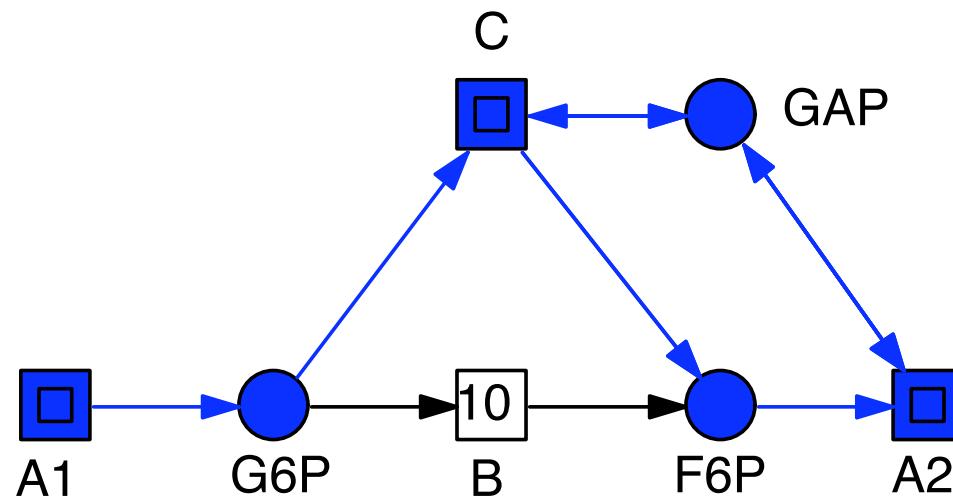
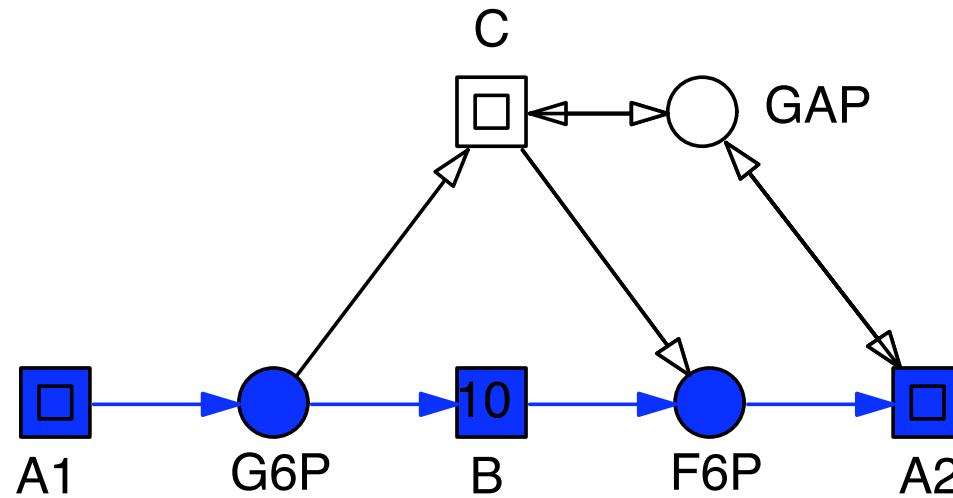
Ex1 - Glycolysis and Pentose Phosphate Pathway

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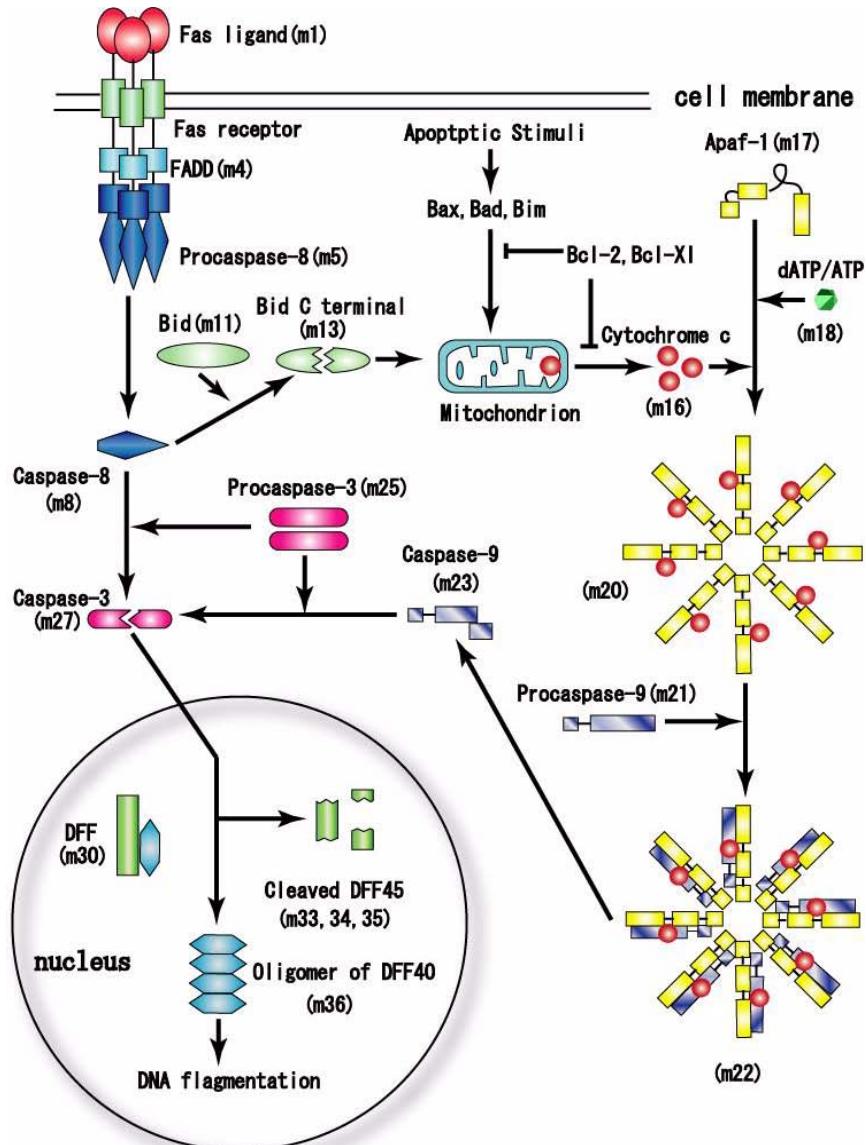
Ex1 - Glycolysis and Pentose Phosphate Pathway

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Ex2: APOPTOSIS IN MAMMALIAN CELLS

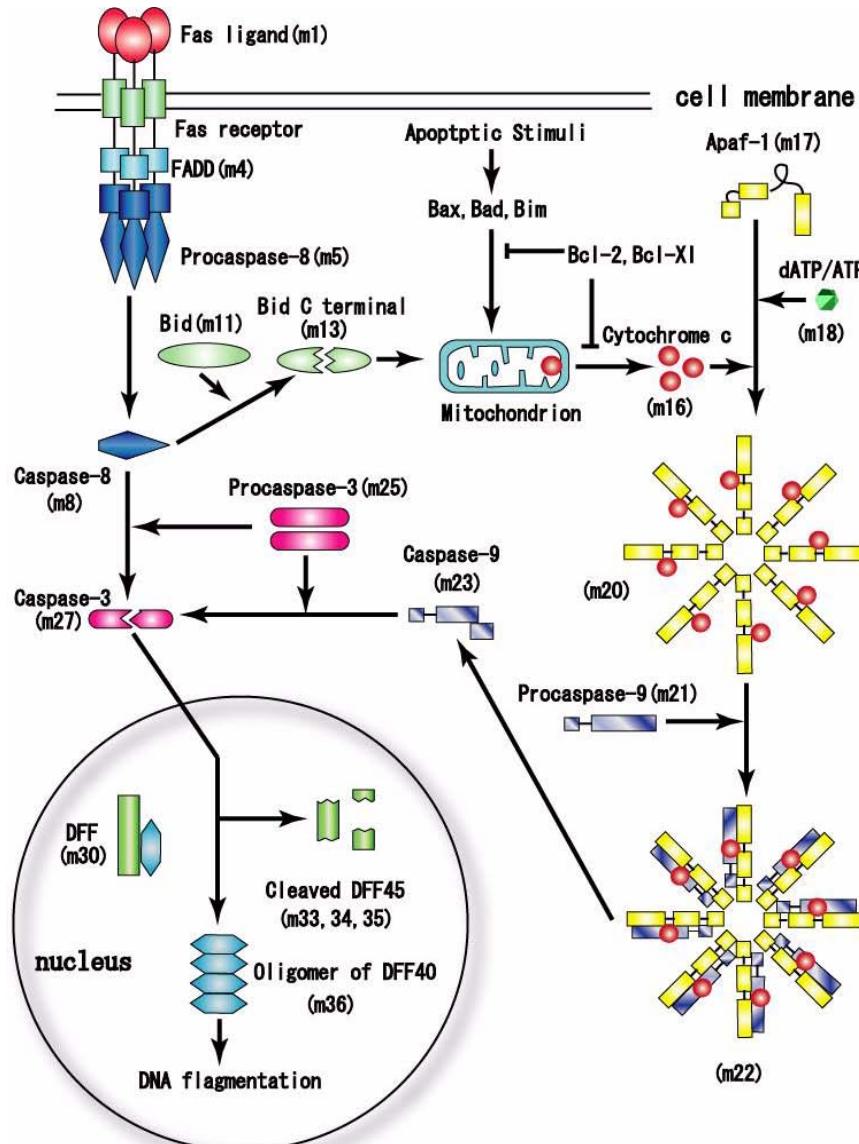
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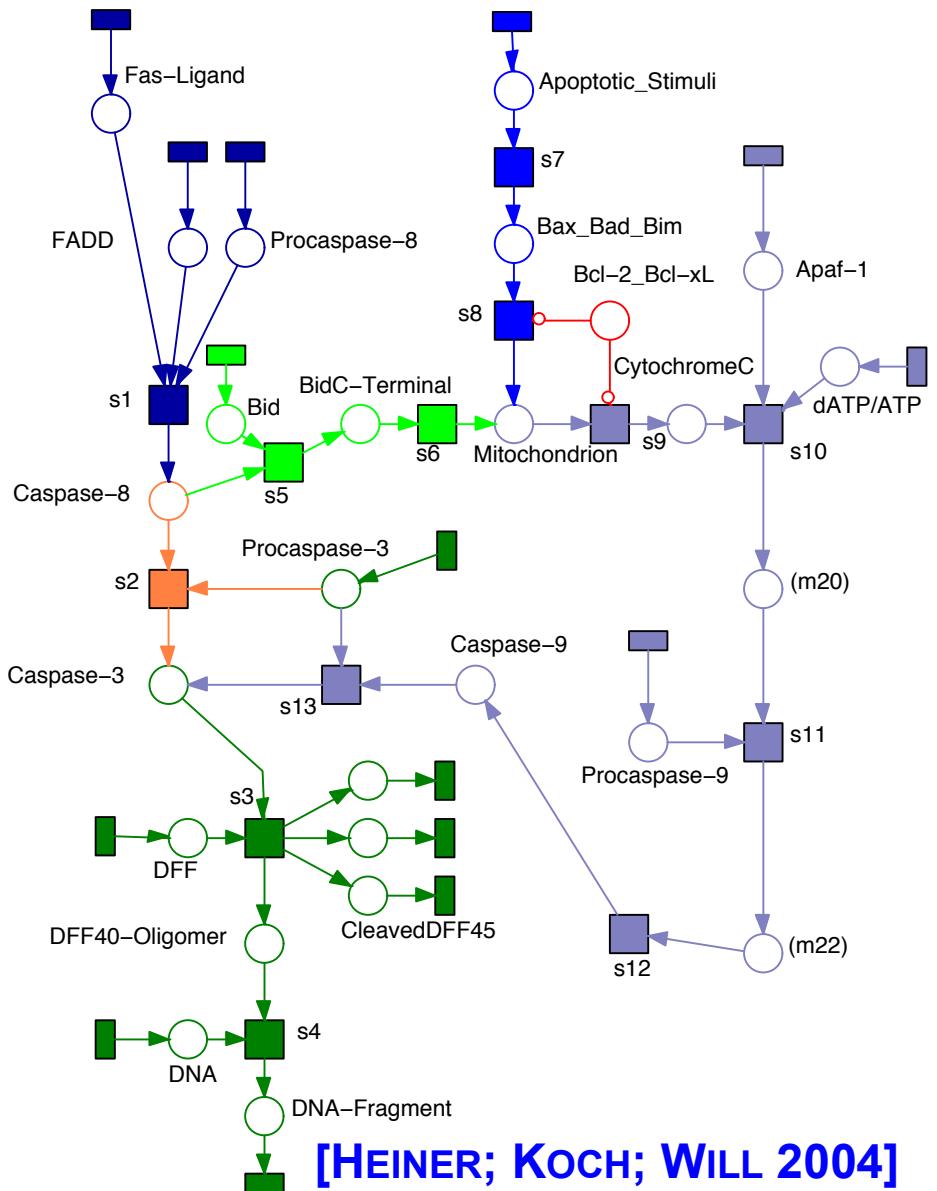
[GON 2003]

Ex2: APOPTOSIS IN MAMMALIAN CELLS

PN & Systems Biology



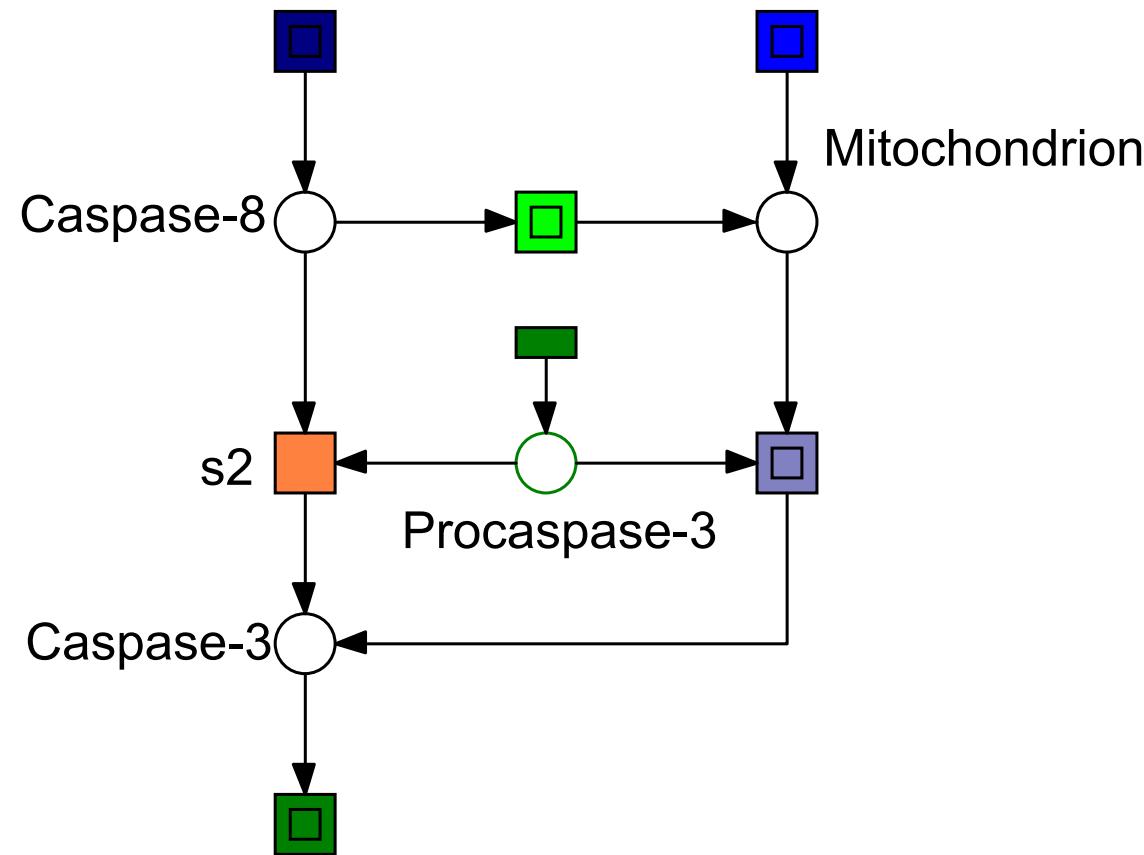
[GON 2003]



[HEINER; KOCH; WILL 2004]

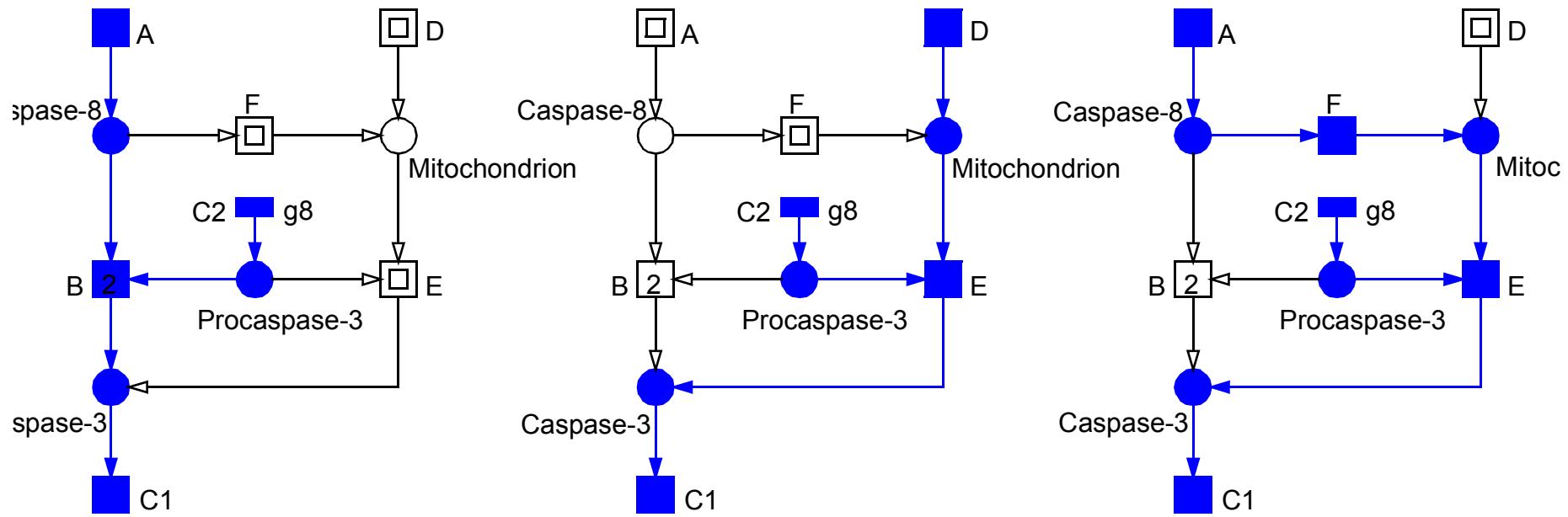
Ex2: APOPTOSIS IN MAMMALIAN CELLS

PN & Systems Biology



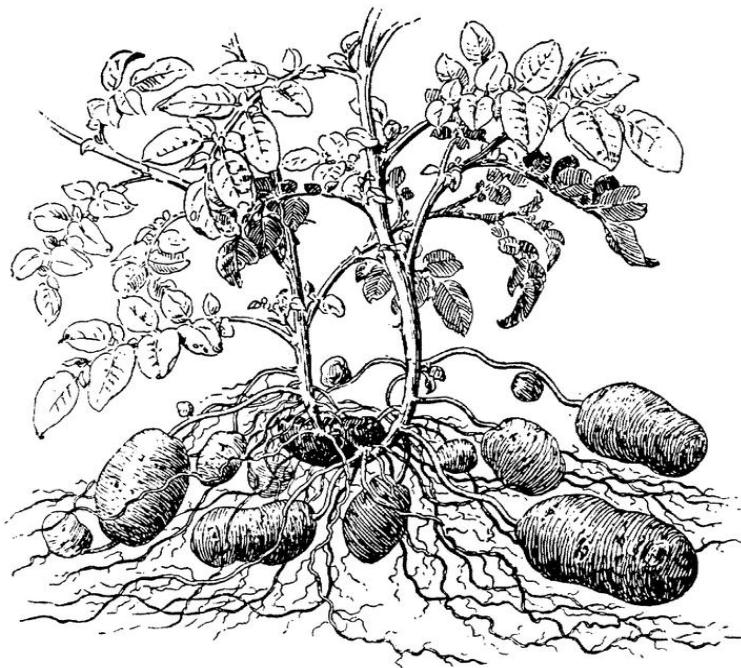
Ex2: APOPTOSIS IN MAMMALIAN CELLS

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Ex3 - Carbon Metabolism in Potato Tuber

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[Koch; JUNKER; HEINER 2005]

ADT-sets without trivial T-invariants

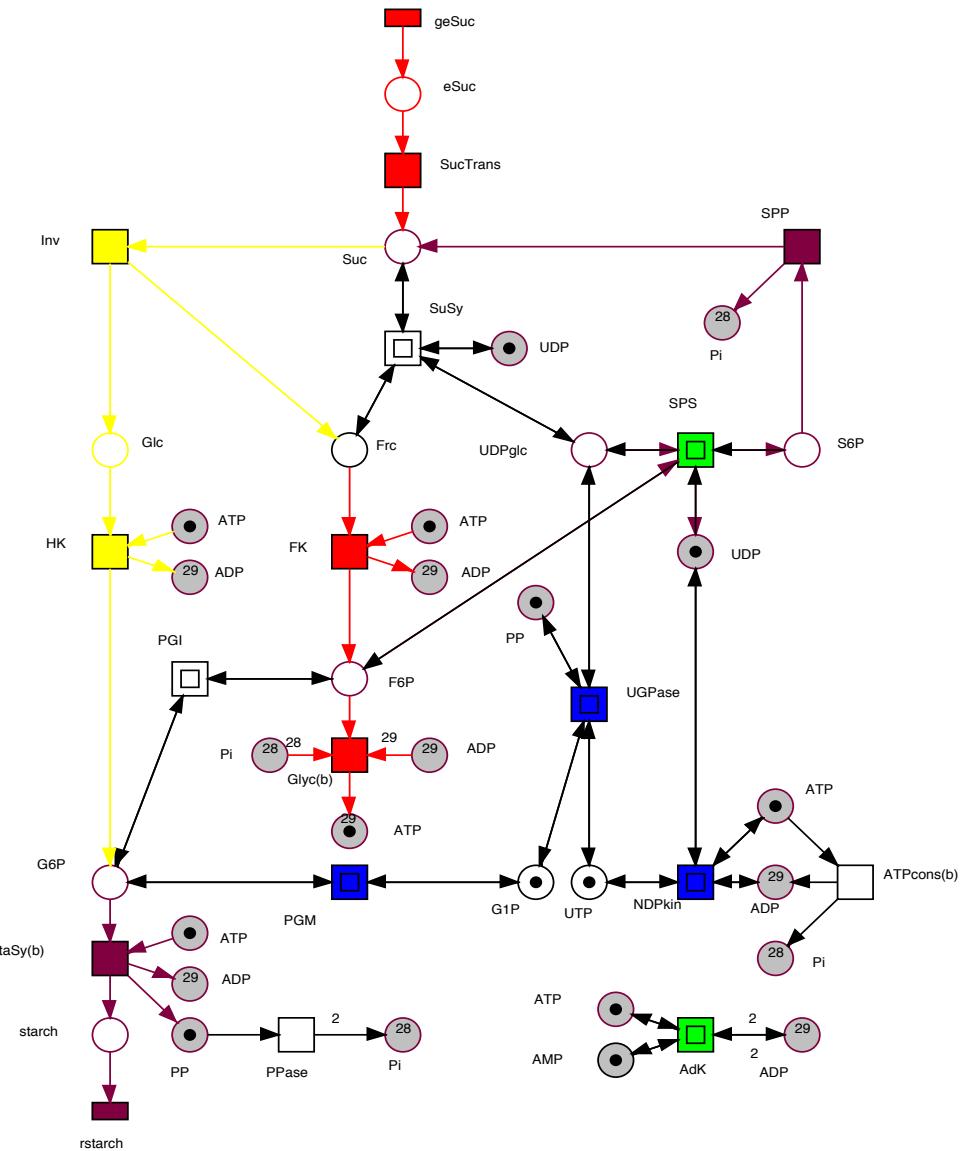
Ex3 - Carbon Metabolism in Potato Tuber

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[KOCHE; JUNKER; HEINER 2005]

ADT-sets without trivial T-invariants



- “promote hierarchical thinking & unbiased modularization”
- structured representation of invariants
 - > *may contribute to a better understandability*
- coarse network structure identifies sensitive net parts
 - > *the knock-off of interface places affects several ADT-sets*
- efficient design of wetlab experiments
 - > *minimal sets of observation points providing coverage of the whole network (one for each ADT-set)*
- support of dedicated layout algorithms

“can include non-obvious groups of reactions and differ from groupings of reactions based on a visual inspection of the network topology”
(Papin, Reed, Palsson 2004)

□ PROS

- > *algorithmically defined*
- > *static analysis technique (state space not constructed), works also for unbounded models*

□ CONS

- > *may be computational expensive*
- > *to avoid computation of all (T-) invariants:*

$$Cx = 0, x \neq 0, x \geq 0, \quad x(i) = 0, x(j) \neq 0, \forall i, j \in T$$

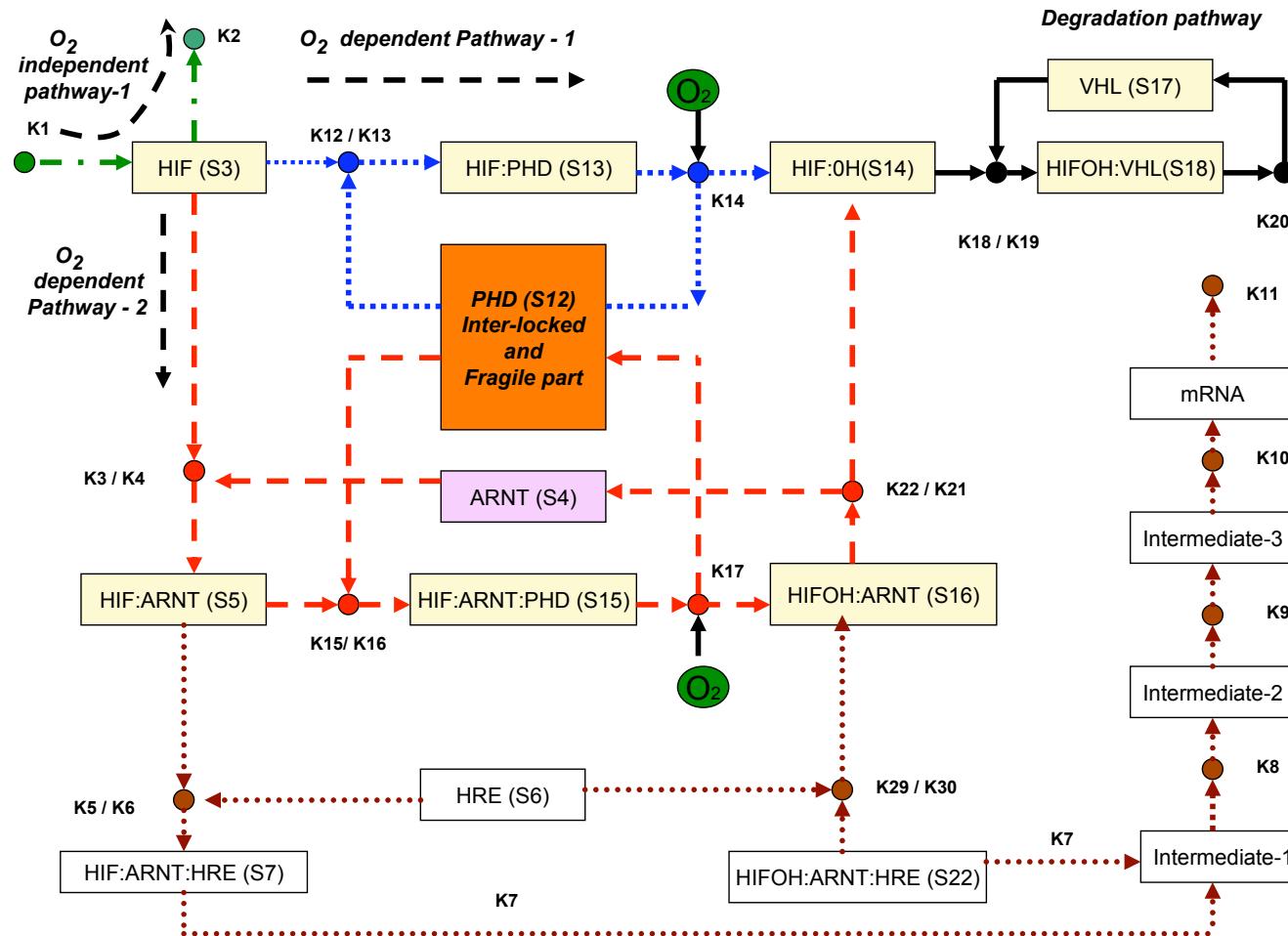
-- especially helpful for analyzing bio Petri nets --

□ related work (T-invariants)

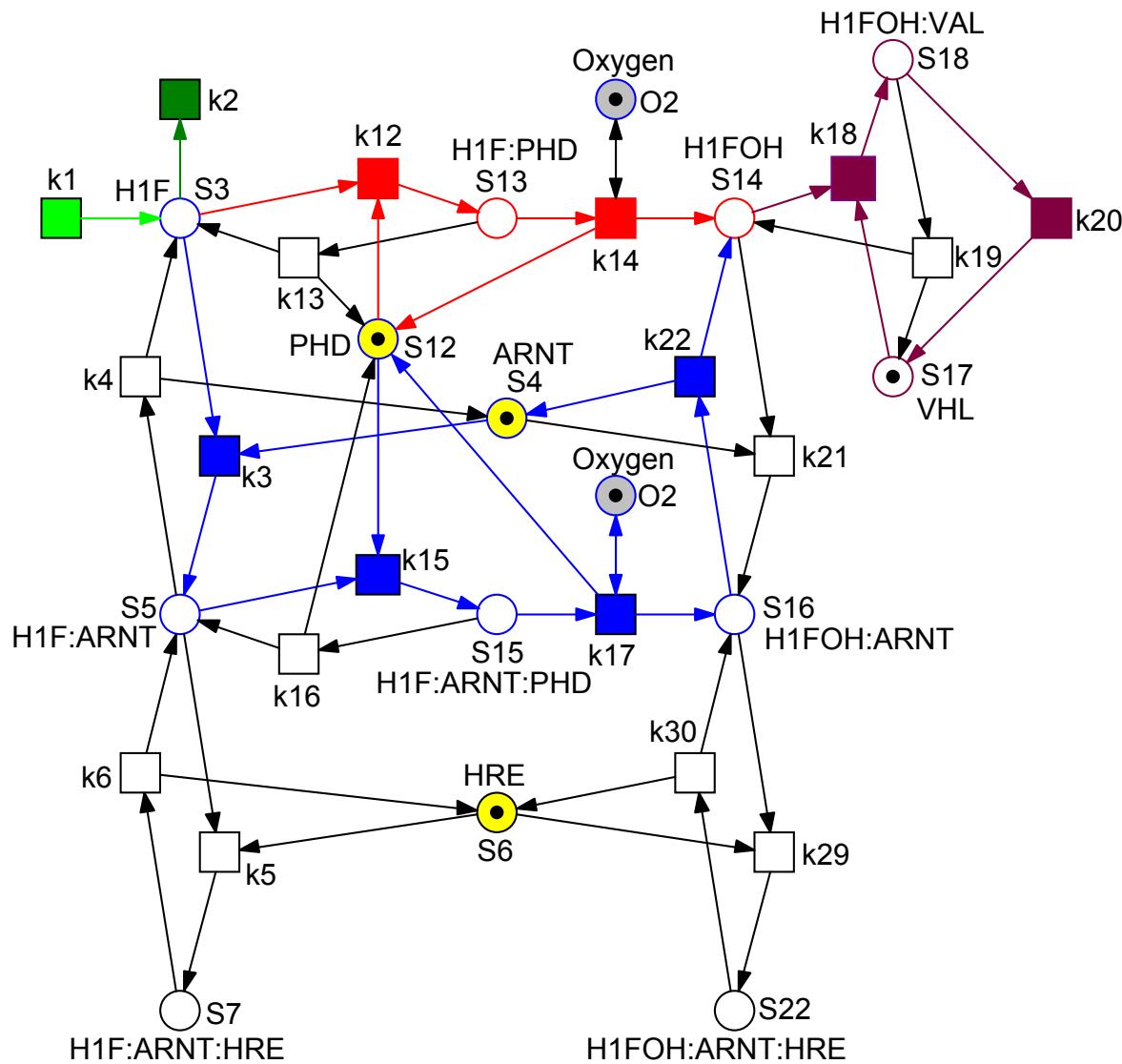
- > *MCT-sets (Sackmann, Heiner, Koch 2006)*
- > *(A)DT-sets (Winder 2006)*
- > *partially correlated reaction sets (Papin, Reed, Palsson 2004)*
- > *Flux coupling analysis (Burgard 2004)*

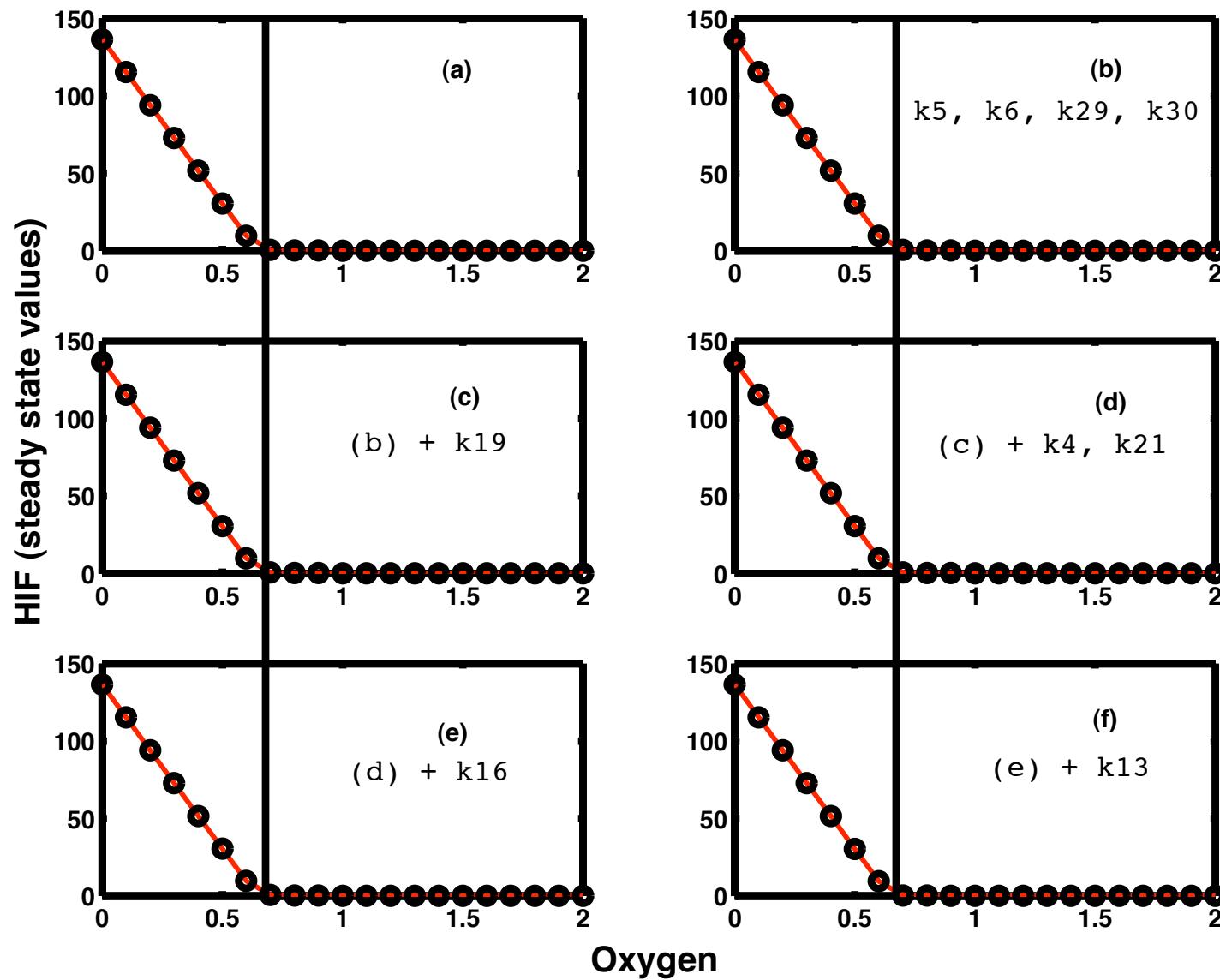
CORE NETWORK IDENTIFICATION

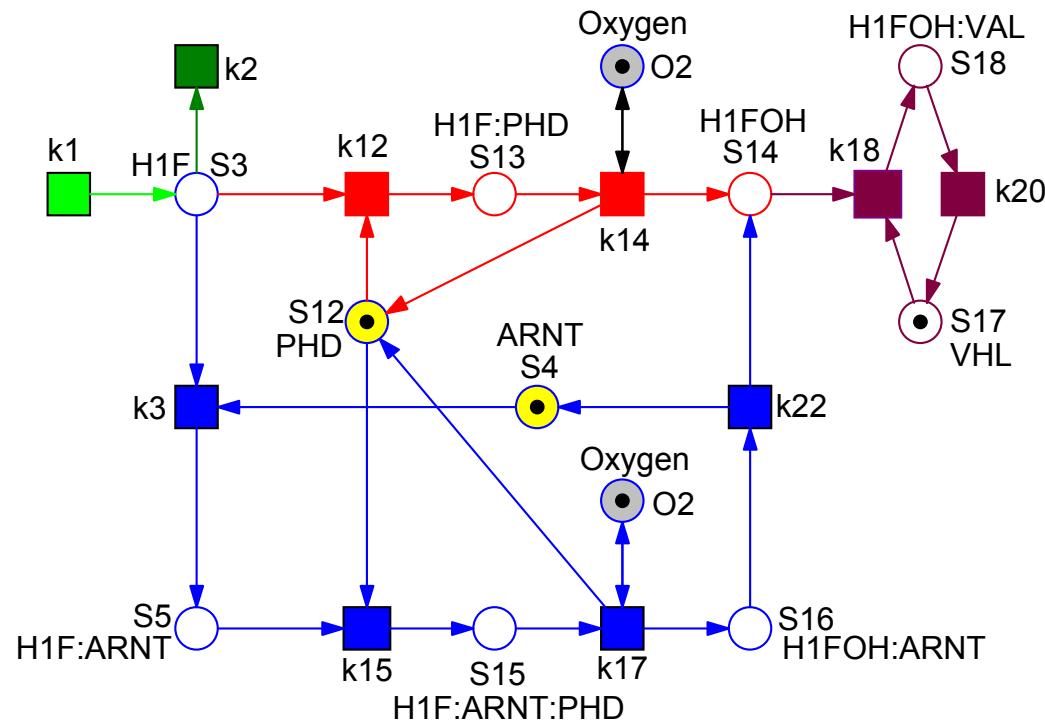
[YU ET AL. 2007]

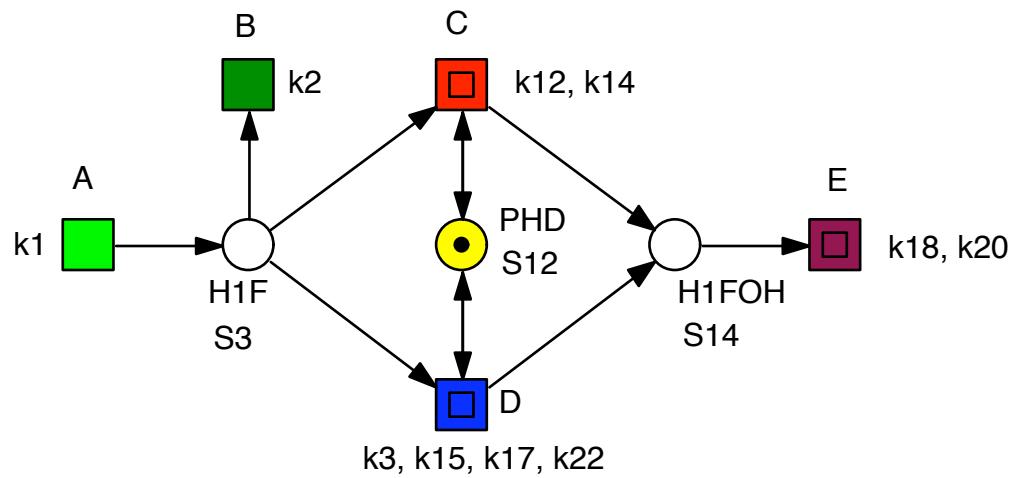


[HEINER; SRIRAM 2010]



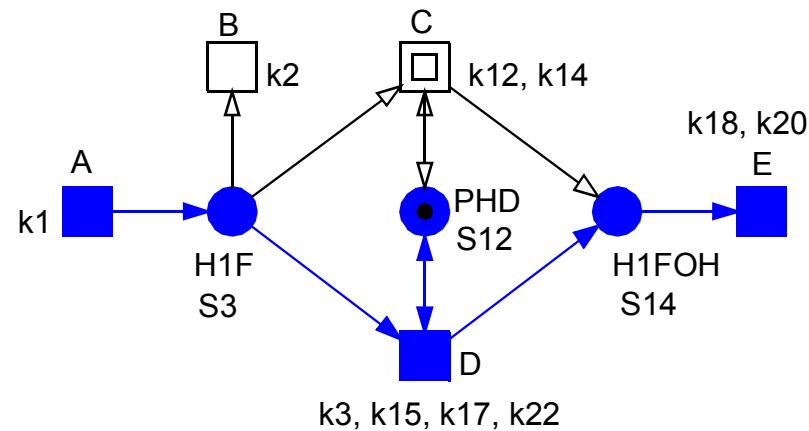
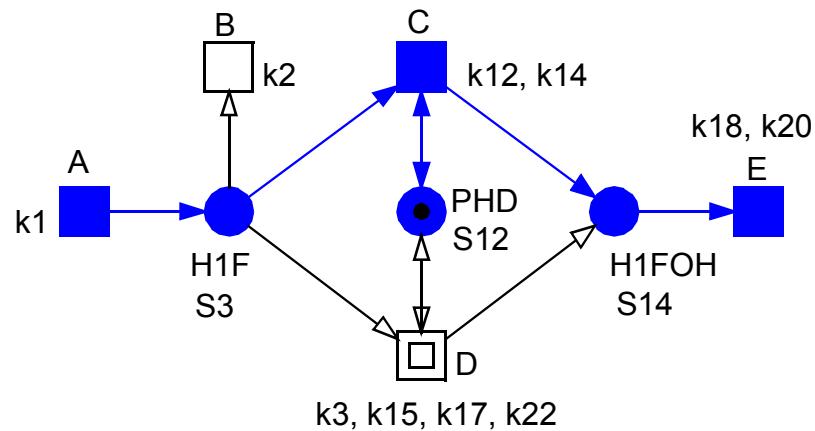
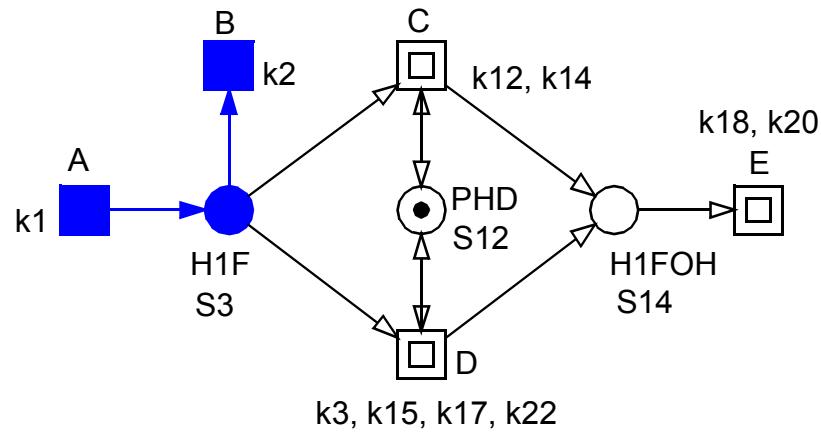






Ex - HYPOXIA

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HOW TO GENERALIZE ?

LATEST NEWS

Snoopy

-> *in collaboration with Wolfgang Marwan, Magdeburg*

Charlie

-> *inspired by INA*

-> *analysis tasks done by threads*

MARCIE

-> **Model checking And Reachability analysis done effiCIEntly of qualitative and stochastic models**

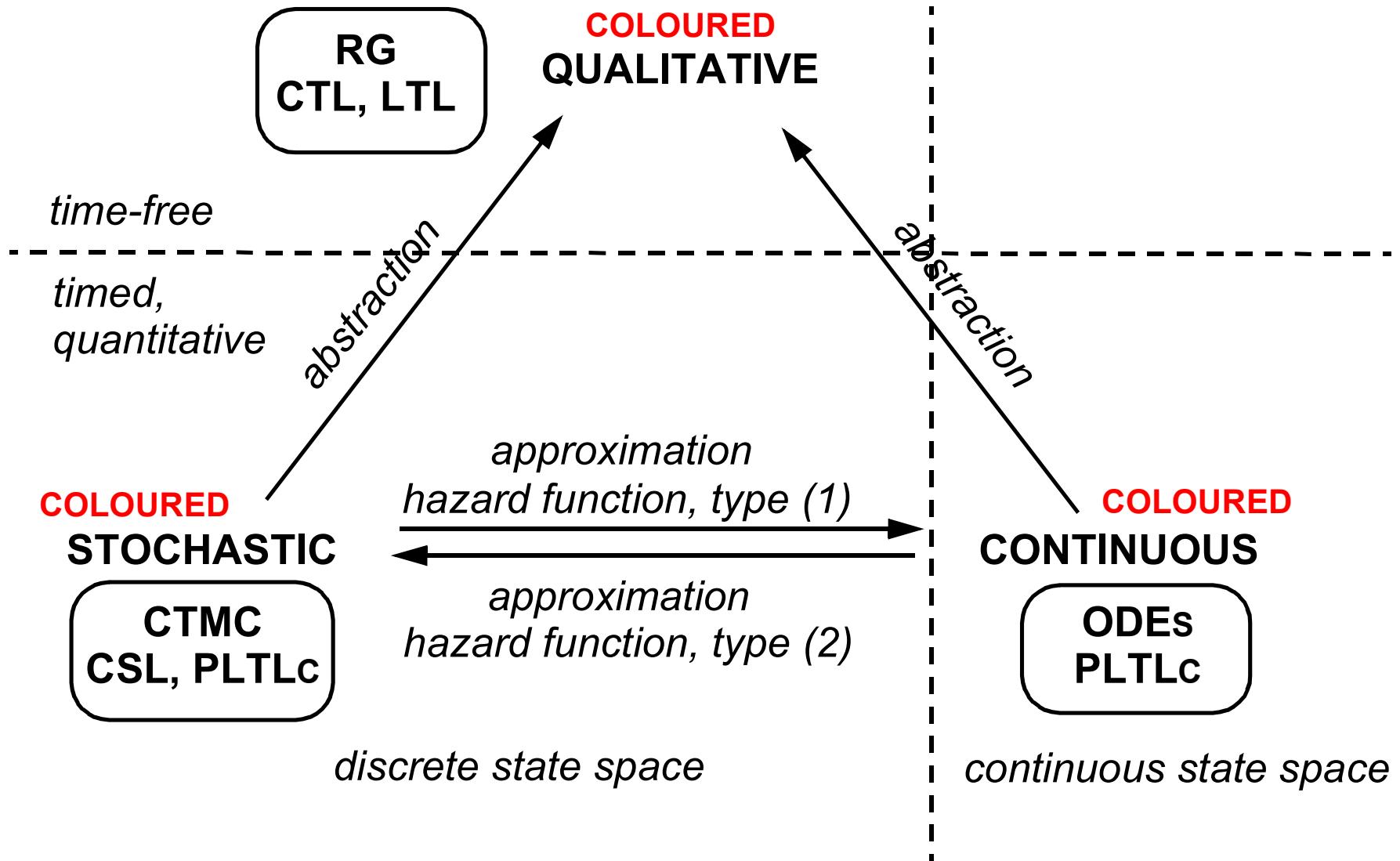
-> *Interval Decision Diagrams*

-> *CTL model checking*

-> *“matrix free” transient and steady state analysis*

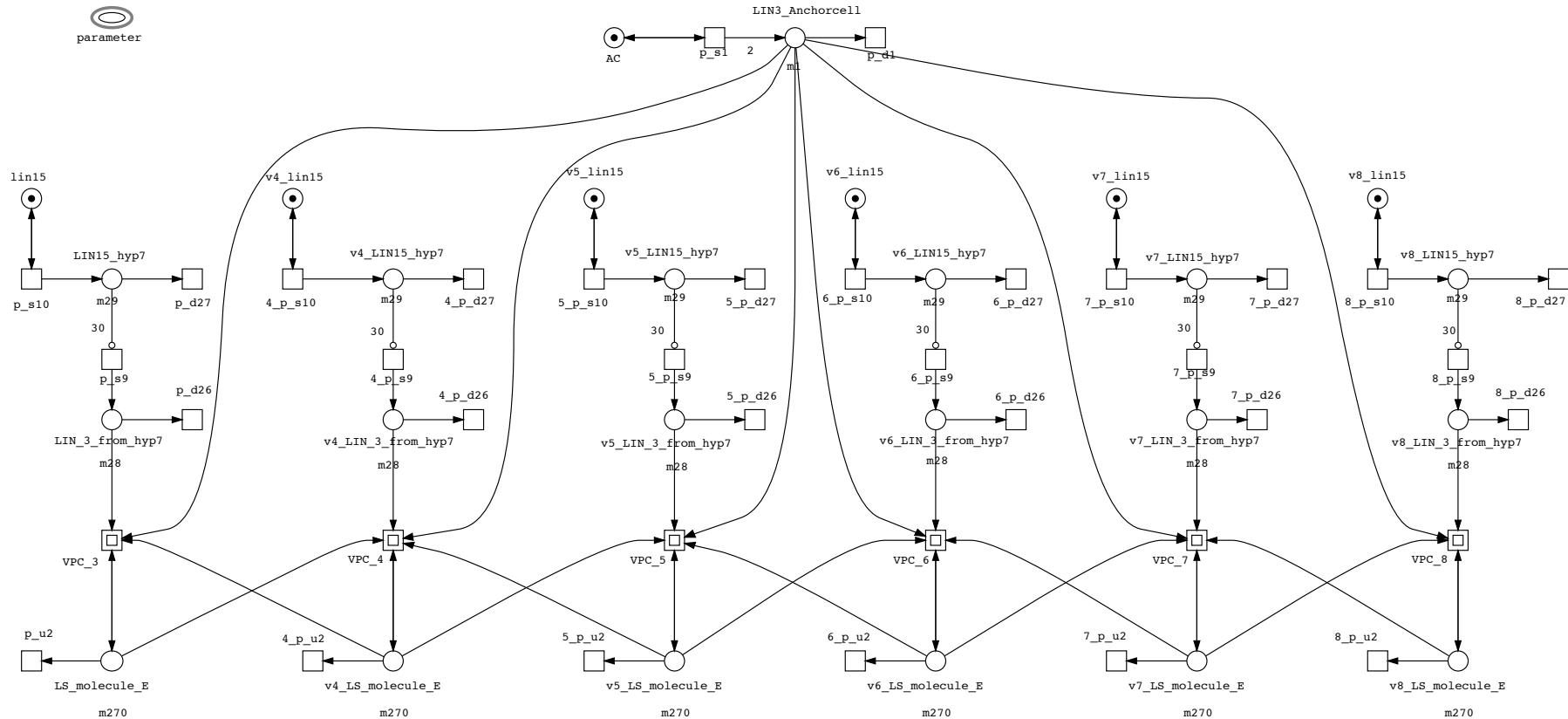
-> **full CSL model checking + rewards**

-> **distributed simulative PLTL model checking (pre-beta-version)**



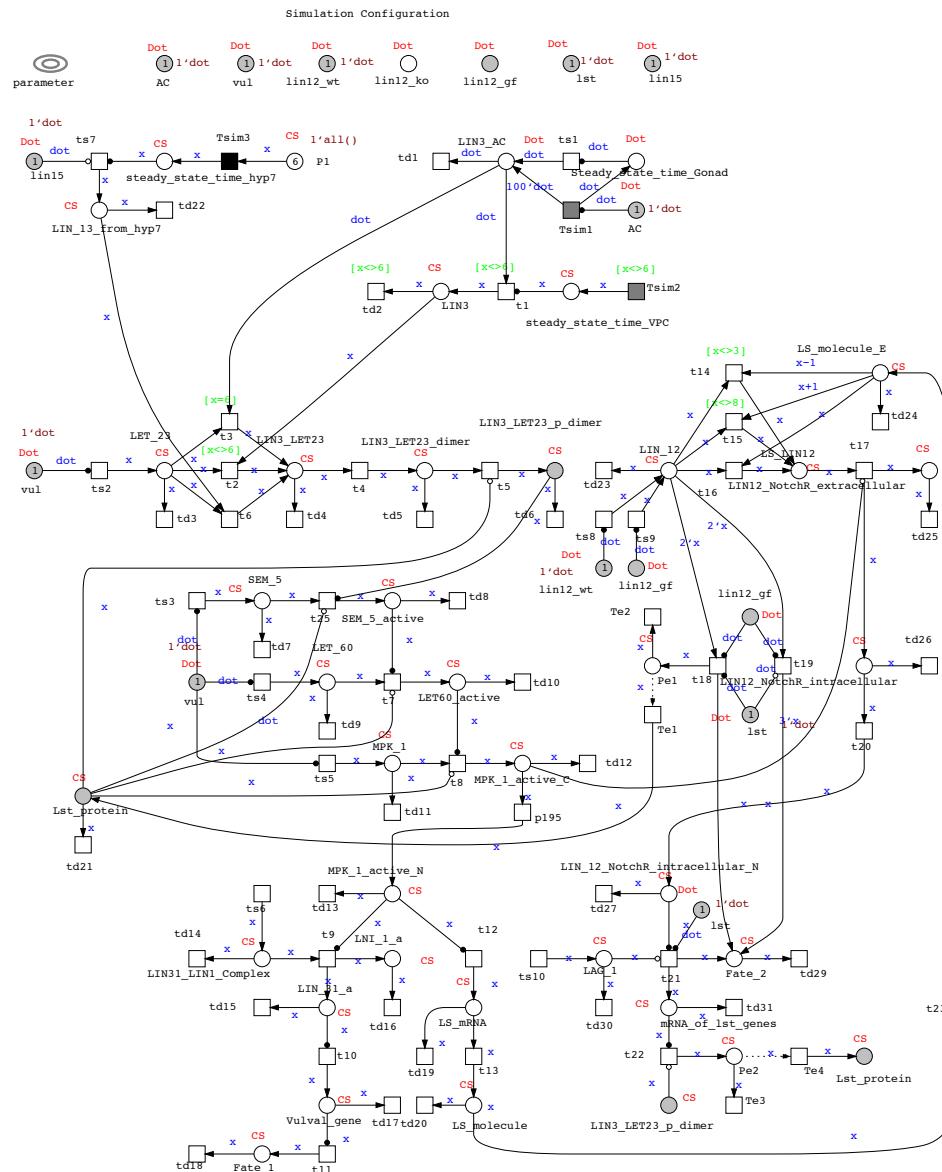
- **get multiple copies of patterns**
 - > *Halo model, new order of net sizes*
- **differentiate between submodels within a master net**
 - > *T-invariants*
 - > *generated models in conformance with wet-lab data*
 - > *mutants*
 - > *algorithmic folding*
- **encode locality**
 - > *Ca channel models*
 - > *agents on a grid*
 - > ...
- **dynamic membrane systems**
- ...

[LI ET AL. 2009]
 [BONZANNI ET AL. 2009]



Ex - C. ELEGANCE

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- **Extended Generalized Stochastic Petri Nets (XSPN)**

- > *discrete places*
- > *discrete transitions: stochastic, immediate, deterministically delayed, scheduled*
- > *special arcs: read, inhibitor, equal, reset*

- **Continuous Petri Nets (CPN)**

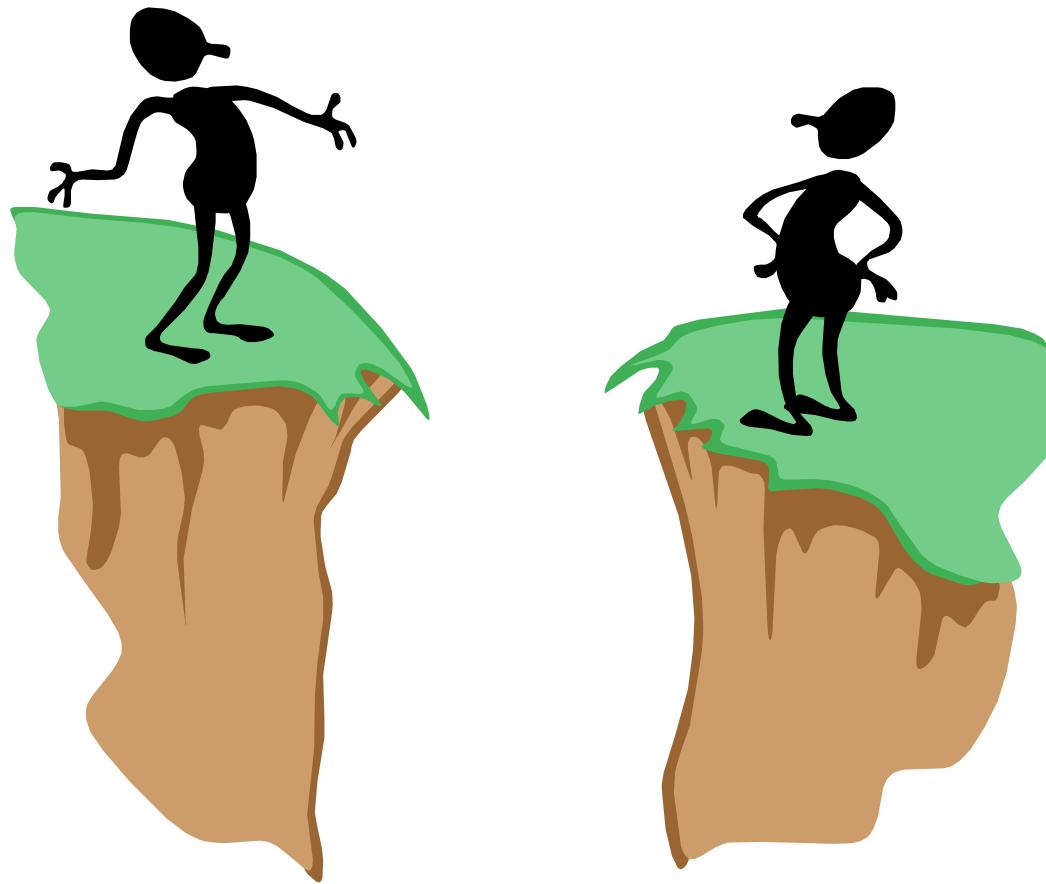
- > *continuous places*
- > *continuous transitions*
- > *special arcs: read, inhibitor*



GHPN = XSPN + CPN

- **hybrid simulation engine**

- **dynamic partitioning**



THANKS !

[HTTP://WWW-DSSZ.INFORMATIK.TU-COTTBUS.DE](http://www-dssz.informatik.tu-cottbus.de)