

(Carl Adam Petri, Petri nets, Concurrency) and Systems Biology:

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Background

Petri nets



Carl Adam Petri



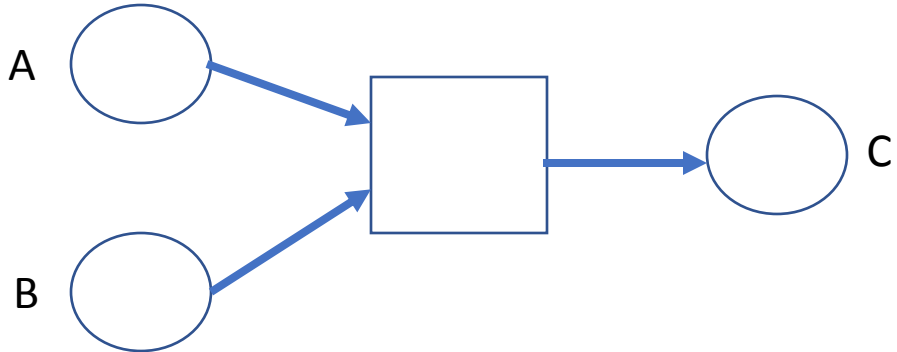
Concurrency
theory



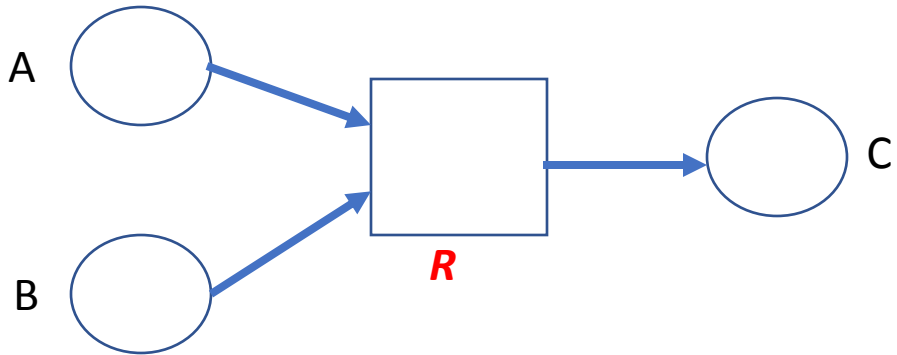
Computational
systems biology

Carl Adam Petri , chemical reactions

- “Started” with chemistry
- places: reactants, products
- transitions: reactions
- $A + B \longrightarrow C$



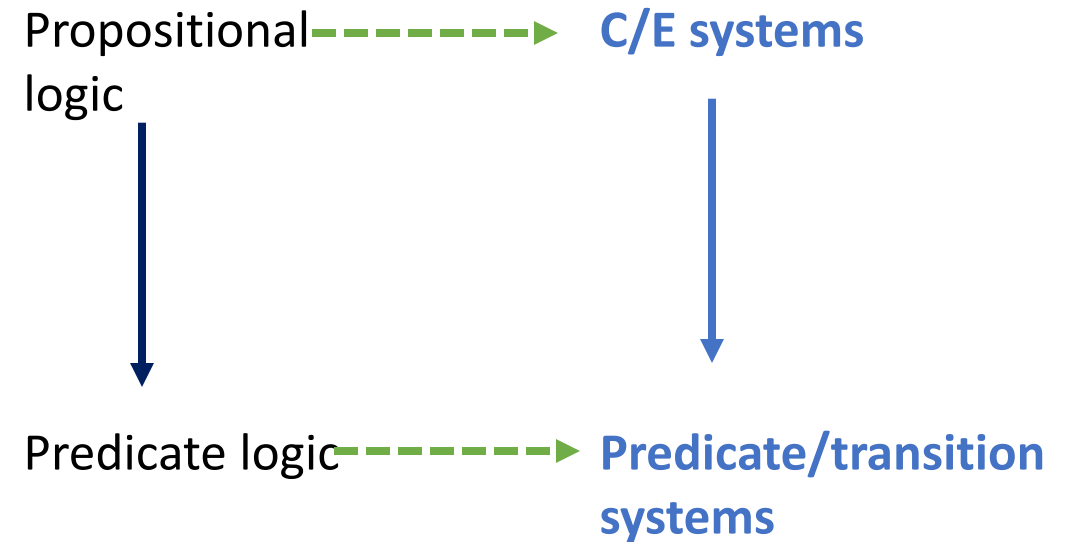
Carl Adam Petri : chemical reactions



Extensions of C/E systems

- Carl Adam Petri “endorsed” two extensions:

- Predicate/transition nets

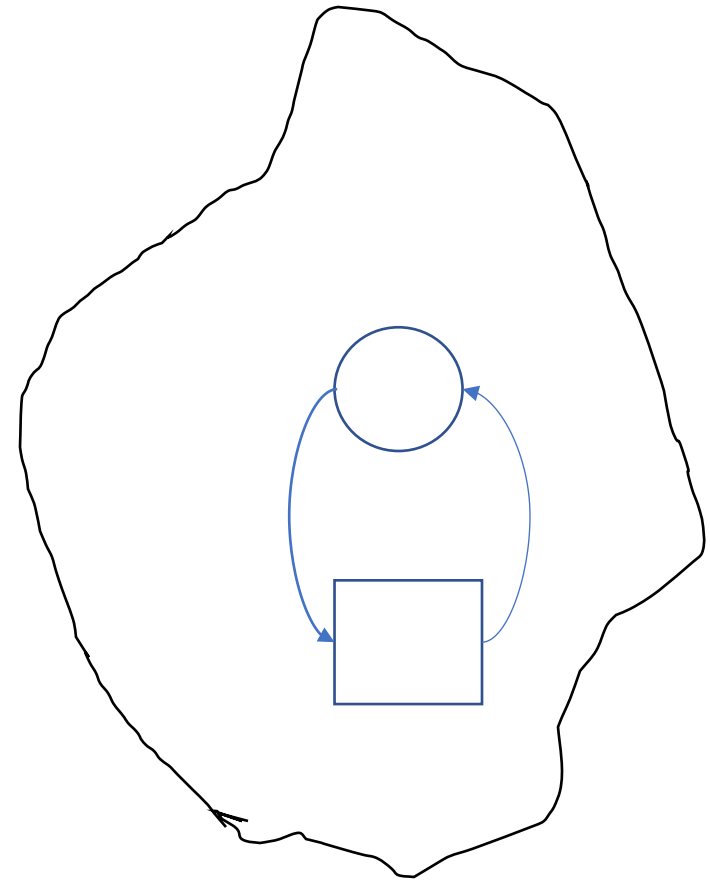


Extensions of C/E systems

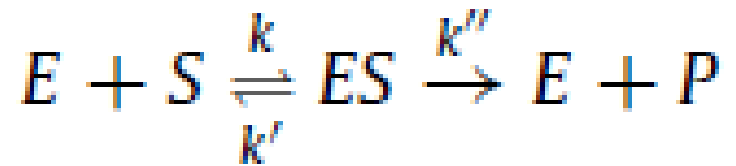
- Carl Adam Petri “endorsed” two extensions:

- (1-safe Petri) nets with *self-loops*

- in C/E systems, events involved in self-loops are dead*

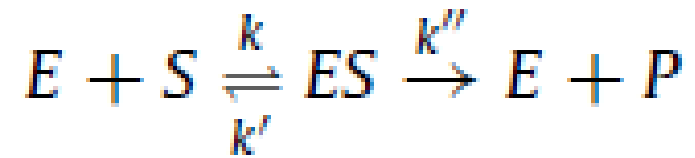


Enzymatic reactions



- *Enzymes speed up reactions*
 - by dramatically lowering the activation energy needed to start the reactions.*
- *S ----> P*
 - will take too long without the enzyme*

Enzymatic reactions



$$\frac{dS}{dt} = -k \cdot S \cdot E + k' \cdot ES$$

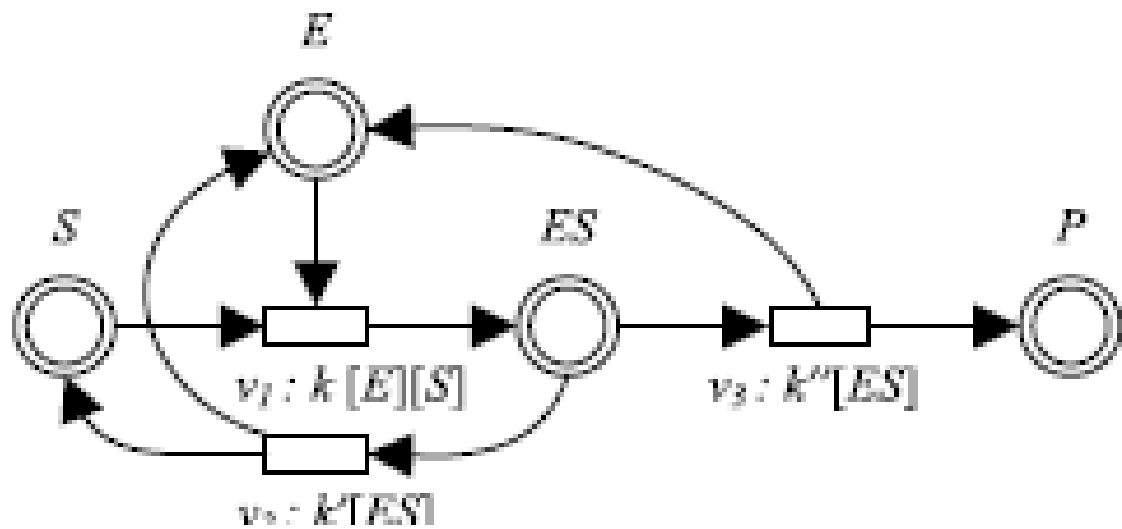
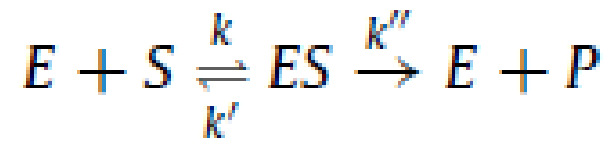
$$\frac{dE}{dt} = -k \cdot S \cdot E + (k' + k'') \cdot ES$$

$$\frac{dES}{dt} = k \cdot S \cdot E - (k' + k'') \cdot ES$$

$$\frac{dP}{dt} = k'' \cdot ES$$

Under mass law

Enzymatic reactions



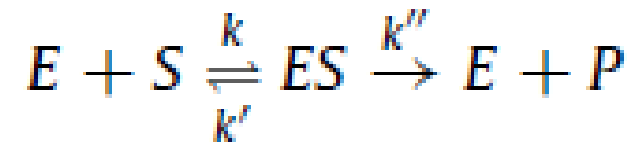
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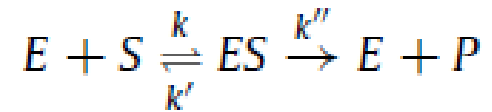
The Michaelis-Menten model



(A1) ES reaches steady state much faster than the rate of product (P) formation.

(A2) [S] >> [E]; all of the enzyme is substrate bound

The Michaelis-Menten model



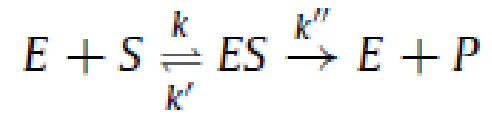
$$dP/dt = V_{\max} [S]/K_M + [S]$$

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(A2) [S] >> [E]; all of the enzyme is substrate bound

Briggs, G. E., and Haldane, J. B. (1925) A Note on the Kinetics of Enzyme Action, Biochem J 19, 338-339

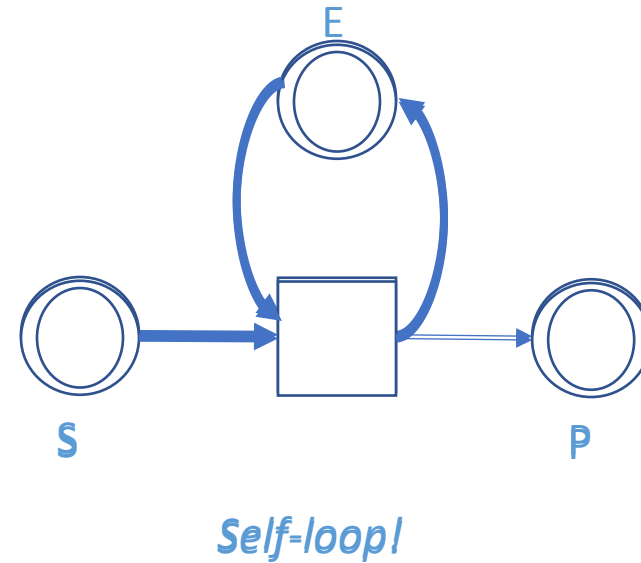
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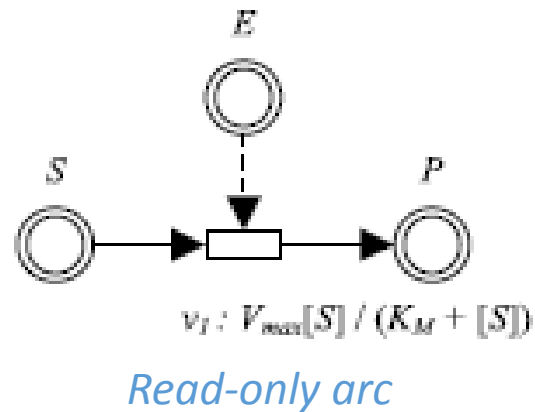
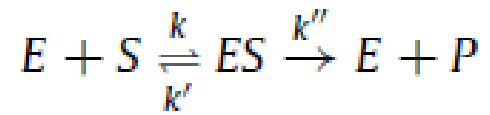
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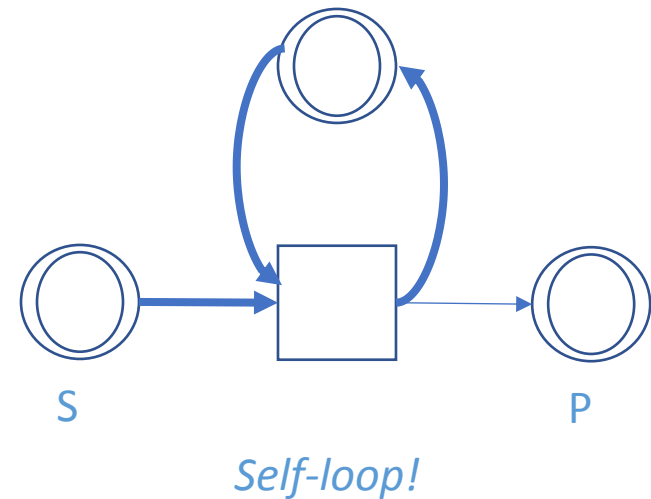
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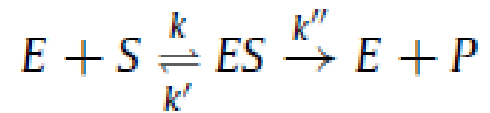
Self-loops or read-only arcs?



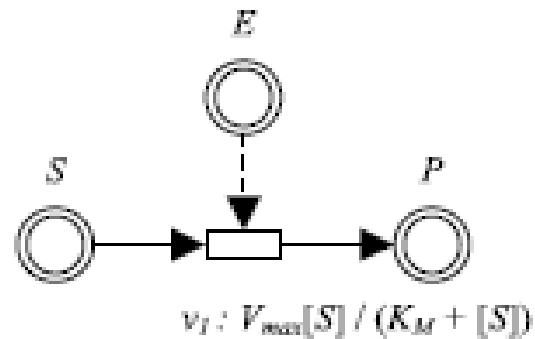
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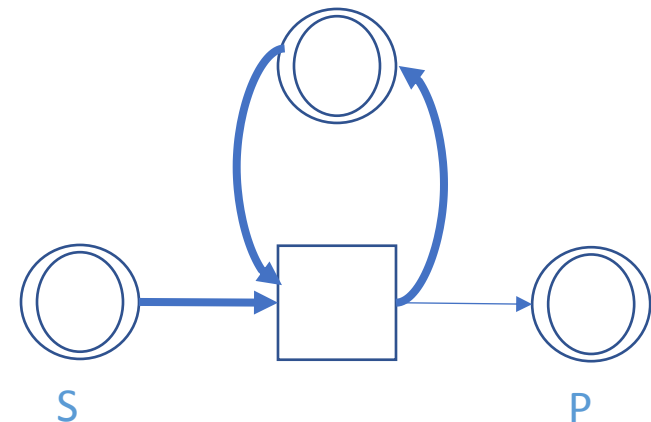
Self-loops or read-only arcs?



$$dP/dt = V_{\max} [S] / K_M + [S]$$



Read-only arc



Self-loop!

The **strongly connected components** of the underlying (bipartite) directed graphs will be different.

Parameter estimation

- The values of rate constants is often not known
 - k, k', k''
- The initial concentrations also may not be known
 - $[S_0], [E_0], [ES_0], [P_0]$
- Must be estimated
 - Using limited experimental data
 - via non-linear optimization techniques
 - evolutionary search procedures

$$\frac{dS}{dt} = -k \cdot S \cdot E + k' \cdot ES$$

$$\frac{dE}{dt} = -k \cdot S \cdot E + (k' + k'') \cdot ES$$

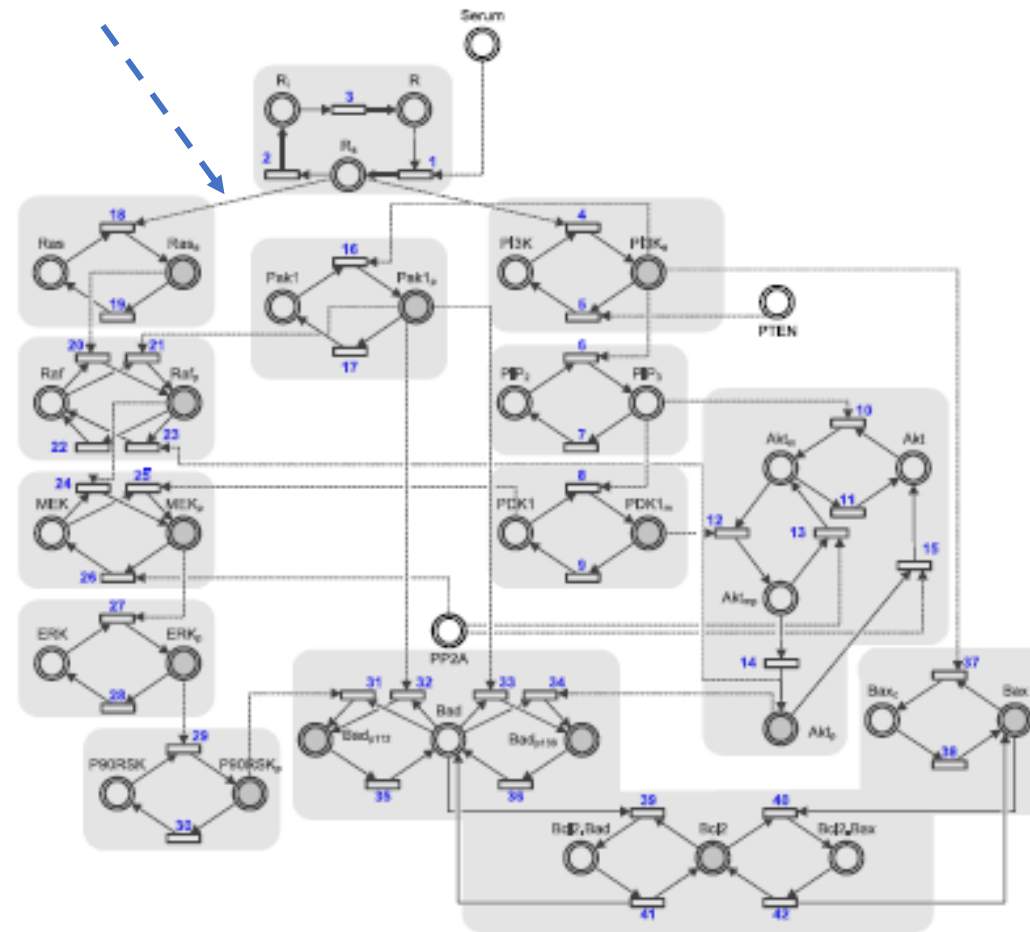
$$\frac{dES}{dt} = k \cdot S \cdot E - (k' + k'') \cdot ES$$

$$\frac{dP}{dt} = k'' \cdot ES$$

Decompositions based parameter estimation

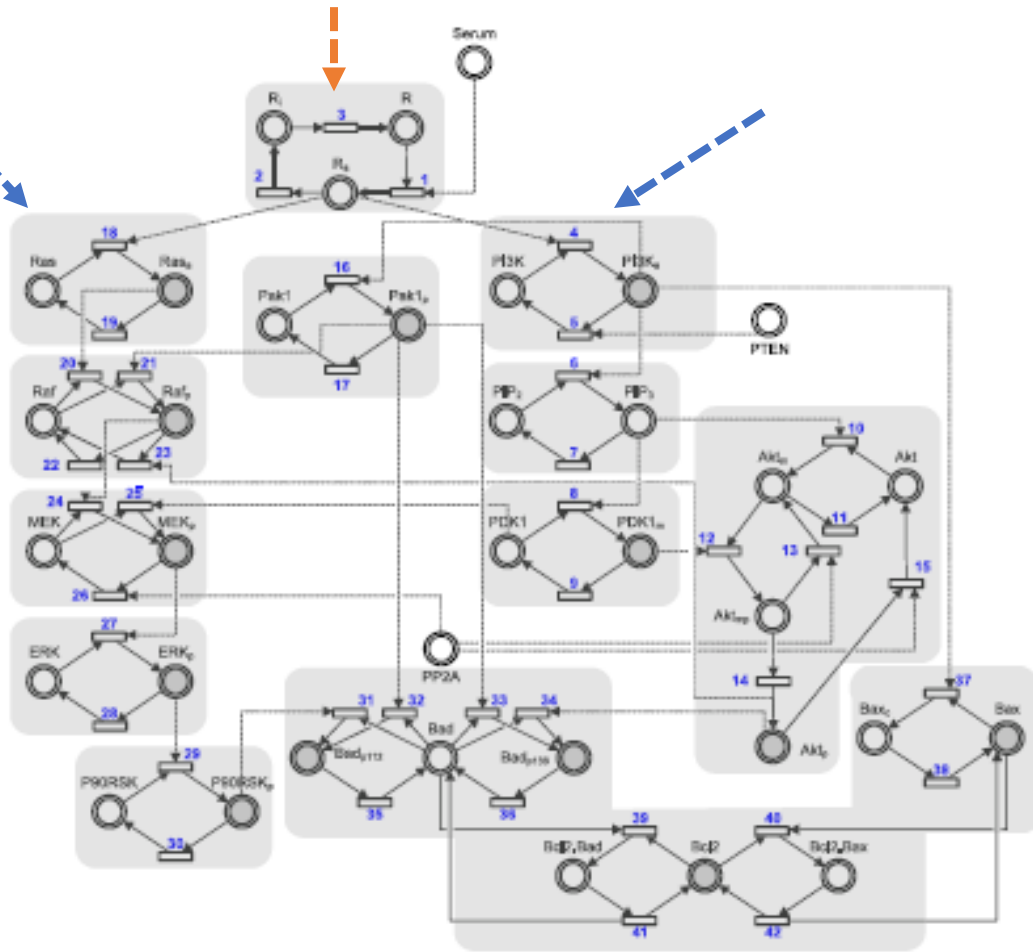
- Derive the net diagram from the ODEs system
- Decompose the net (bipartite digraph) into its maximal strongly connected components.
 - Use *read-only arcs* to model enzymatic reactions.
- Exploit the structure of the DAG of the maximal strongly connected components:
 - break down the parameter estimation problem into smaller ones.

Decompositions based parameter estimation



The decomposed AKT-MAPK signaling pathway

Decompositions based parameter estimation



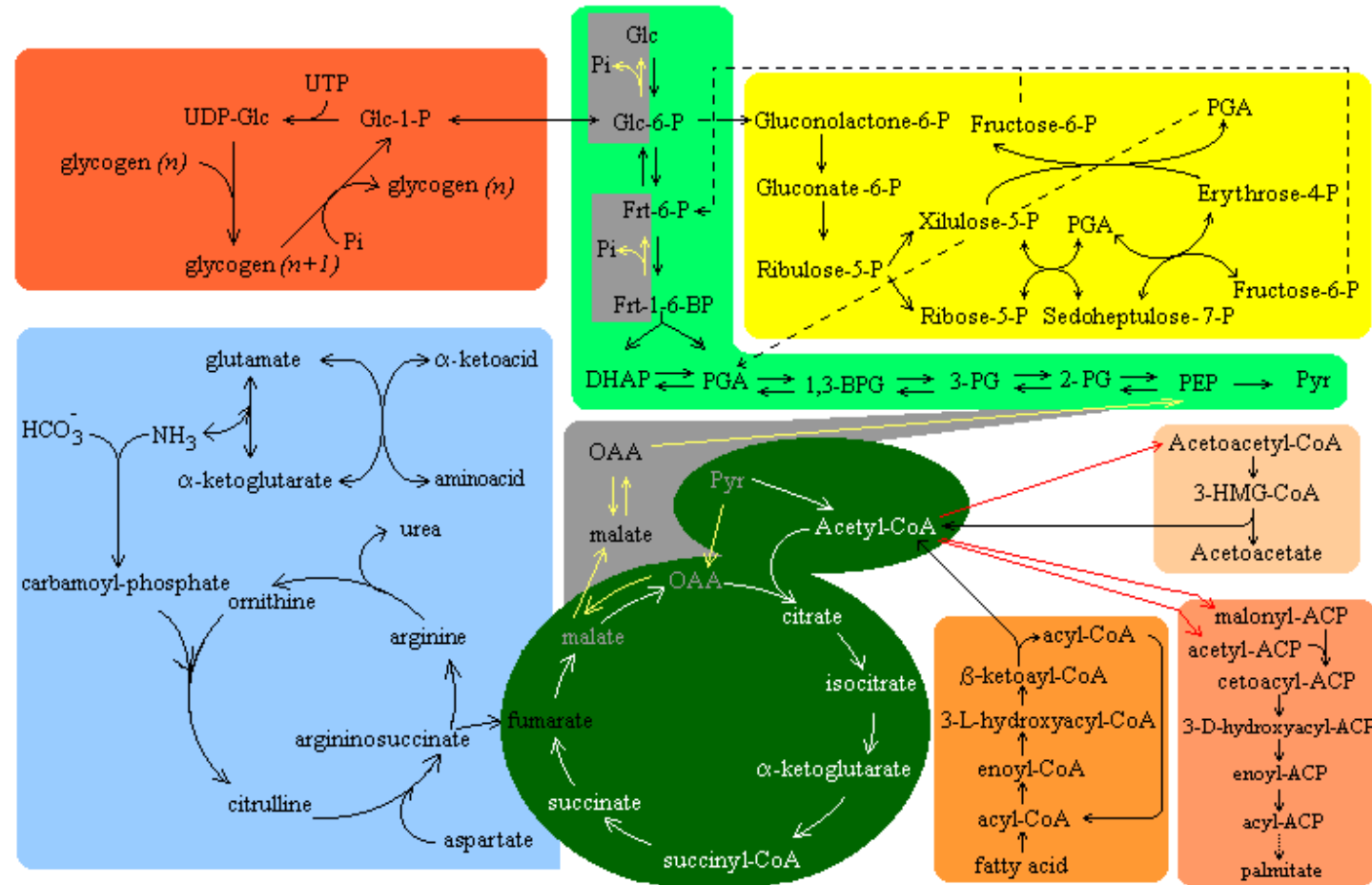
The decomposed AKT-MAPK signaling pathway

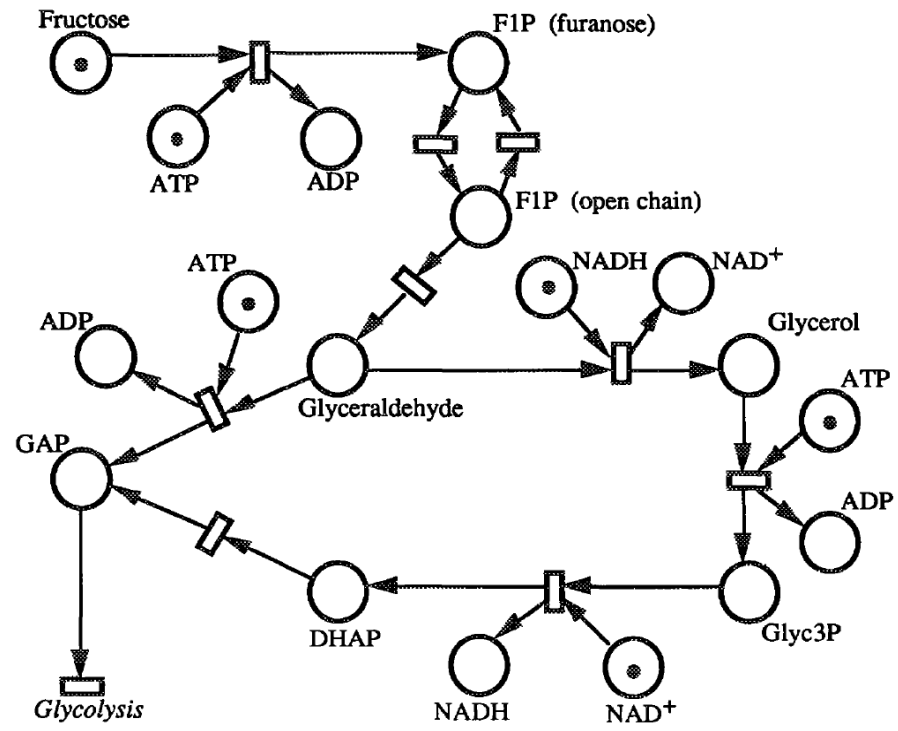
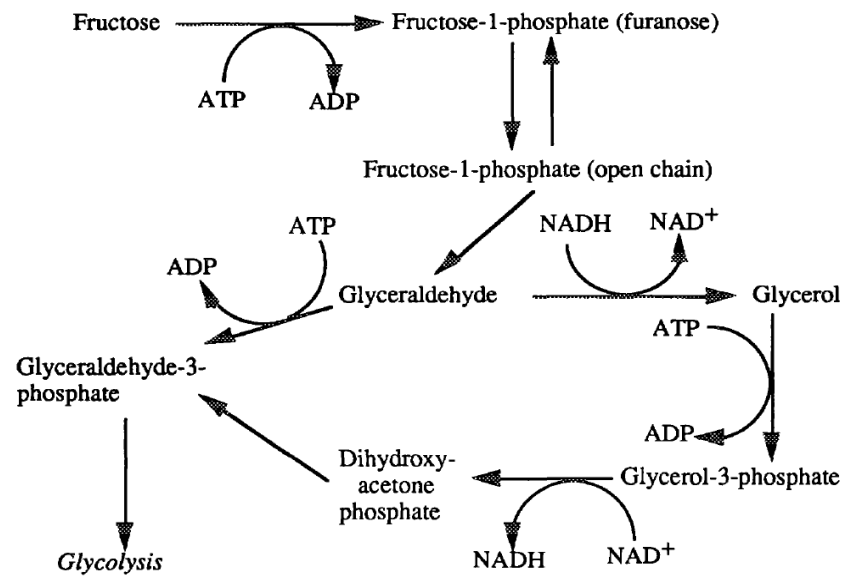
- Estimate the parameters of the upstream components first
- Complications:
 - Distribution of experimental data
 - Computing consistent global estimates from local ones.
 - Belief propagation*

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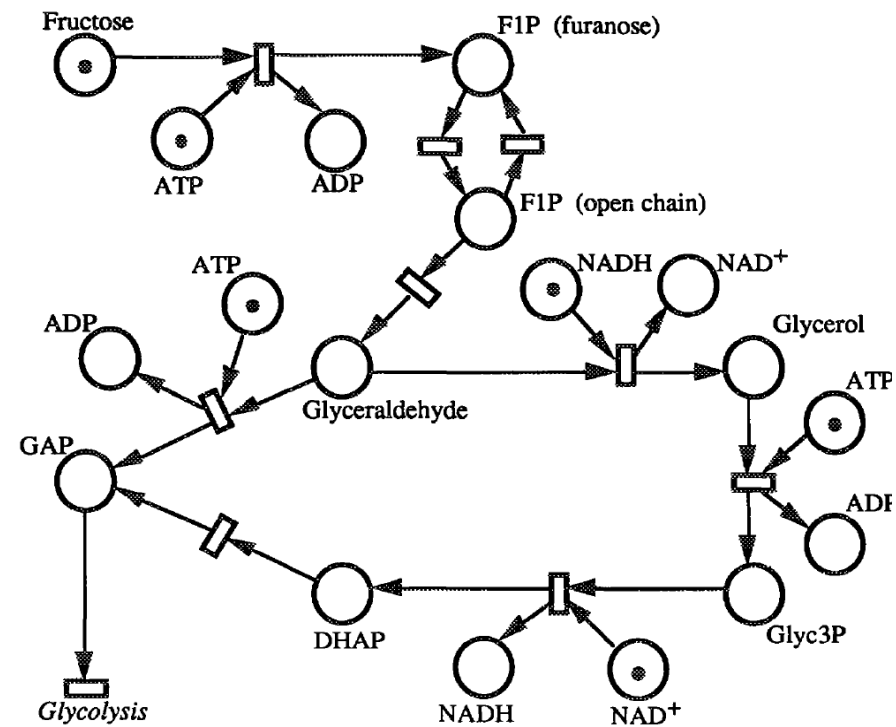
Metabolic pathways:

- Complex biochemical networks that :
 - consume nutrients to obtain –and store- energy (*catabolism*)
 - Produce new cell components by consuming -stored- energy (*anabolism*)
- Vital for living, growing, replenishing





$$\mathbf{N} = \begin{pmatrix}
 1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\
 0 & -1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 1 & 0 \\
 0 & 0 & -1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\
 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & -1 & -1 \\
 0 & 0 & 0 & 0 & -1 & -1 & 0 & 0 & 0 & 0 & 1
 \end{pmatrix}$$



$$N = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 1 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & -1 & -1 \\ 0 & 0 & 0 & 0 & -1 & -1 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

- *T-invariants*
 - *Flux analysis*
- *S-invariants*
 - *Dead cycles*

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- Steady state analysis of metabolic networks :
 - Reddy, V. N., Mavrovouniotis, M. L. and Liebman, M. N. (1993). Petri Net Representation in Metabolic Pathways. In Proc. First Intern. Conf. on Intelligent Systems for Molecular Biology, AAAI Press, Menlo Park, pp. 328-336
 - Schuster S, Hilgetag C (1994) On elementary flux modes in biochemical reaction systems at steady state. J Biol Syst 2:165–182
 - **Heiner M, Koch I**, Schuster S (2000) Using time-dependent Petri nets for the analysis of metabolic networks. In: Hofestadt R, Lautenbach K, Lange, M (eds) Workshop Modellierung und Simulation Metabolischer Netzwerke
 - Heiner M, Koch I, Voss K (2001) Analysis and simulation of steady states in metabolic pathways with Petri nets. In: Workshop and tutorial on practical use of coloured Petri nets and the CPN tools (CPN'01)
 - Colored Petri nets based

Petri net variants in systems biology

- *Many* extensions of Petri nets have been used to model and analyze biopathways.
- Stochastic Petri nets
 - *Goss, P. J. E. and Peccoud, J. (1998). Quantitative modeling of stochastic systems in molecular biology by using stochastic Petri nets. Proc. Natl. Acad. Sci. USA 95, 6750-6755*
- Continuous Petri nets
- Hybrid Petri nets

Tools based on Petri nets

- MonaLisa

- *Jens Einloft Jörg Ackermann Joachim Nöthen Ina Koch: MonaLisa—visualization and analysis of functional modules in biochemical networks. Bioinformatics, Volume 29, Issue 11, 1 June 2013, Pages 1469–1470*

- Snoopy

- *M Heiner, M Herajy, F Liu, C Rohr and M Schwarick:p Snoopy – a unifying Petri net tool; In Proc. PETRI NETS 2012, Hamburg, Springer, LNCS, volume 7347, pp. 398–407*

- **Cell Illustrator (based on hybrid functional Petri nets)**

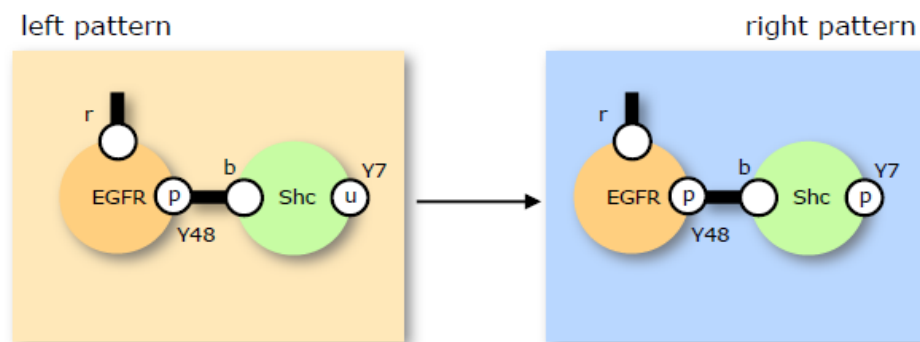
- *Matsuno H, Tanaka Y, Aoshima H, Doi A, Matsui M, **Miyano S**. Biopathways Representation and Simulation on Hybrid Functional Petri Net. In Silico Biology. 2003; 3(3): 389-404*

(~~Carl Adam Petri, Petri nets~~, Concurrency) and systems biology

- Dynamics of biochemical networks:
 - great deal of concurrency
 - studied/exploited *seldom*
- Difficult to obtain a fine grained description that exposes the concurrency present.
- ODEs:
 - must know in advance all the molecular species that can arise
 - can give rise to *huge* blow up in size
 - when the formation and interactions of complex molecules play a role; often the case!

Rule based modelling: kappa, bngl, ..

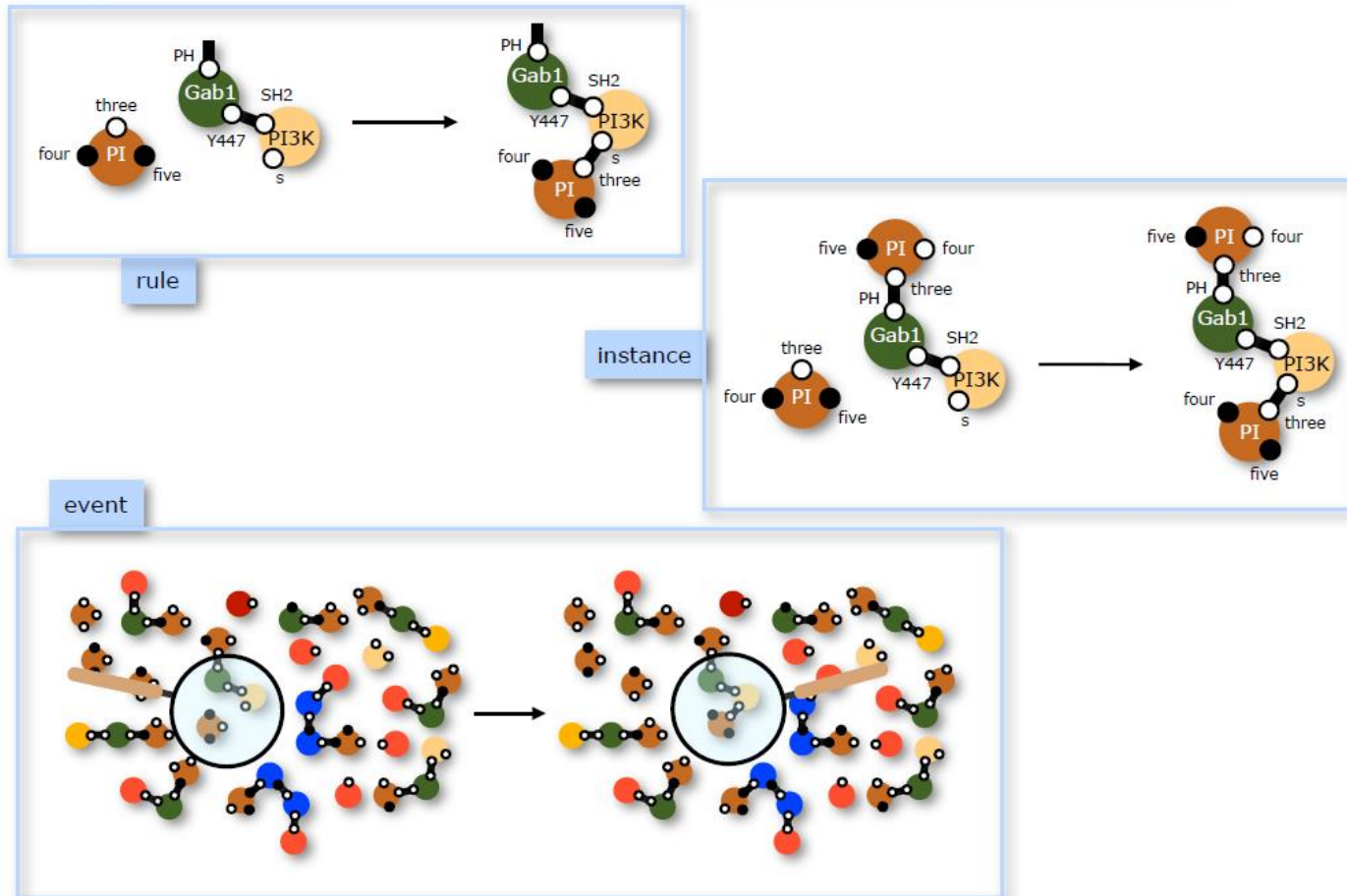
a rule rewrites a pattern:



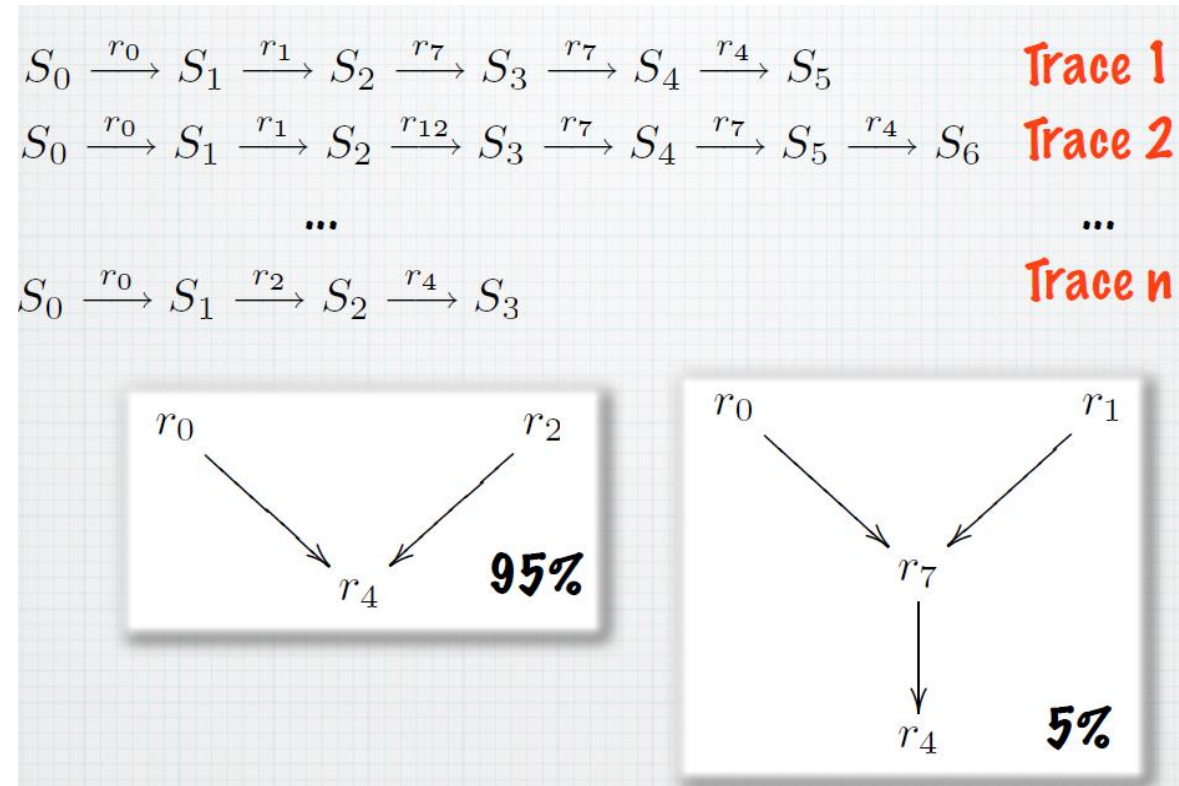
$EGFR(r!-, Y48 \sim p!1), Shc(b!1, Y7 \sim u) \longrightarrow EGFR(r!-, Y48 \sim p!1), Shc(b!1, Y7 \sim p)$

https://www.irif.fr/~jkrivine//homepage/Teaching_files/Partie%201%20-%20Introduction.pdf

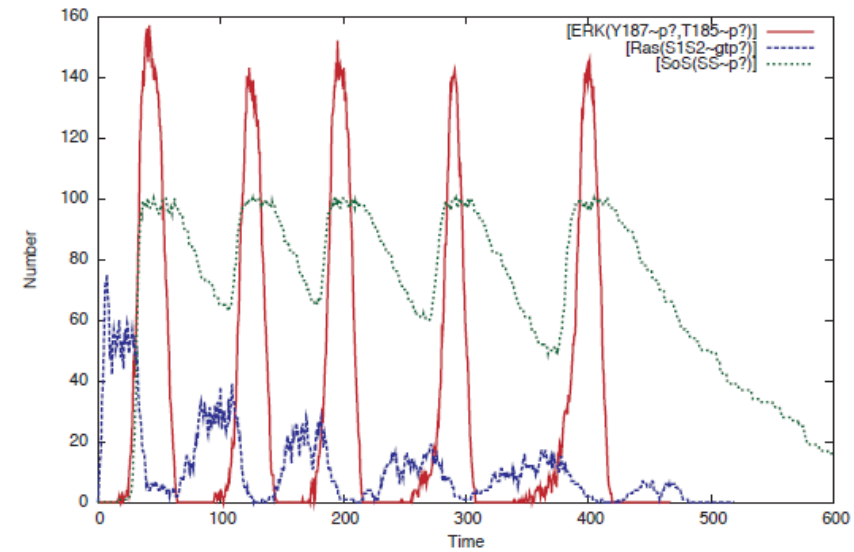
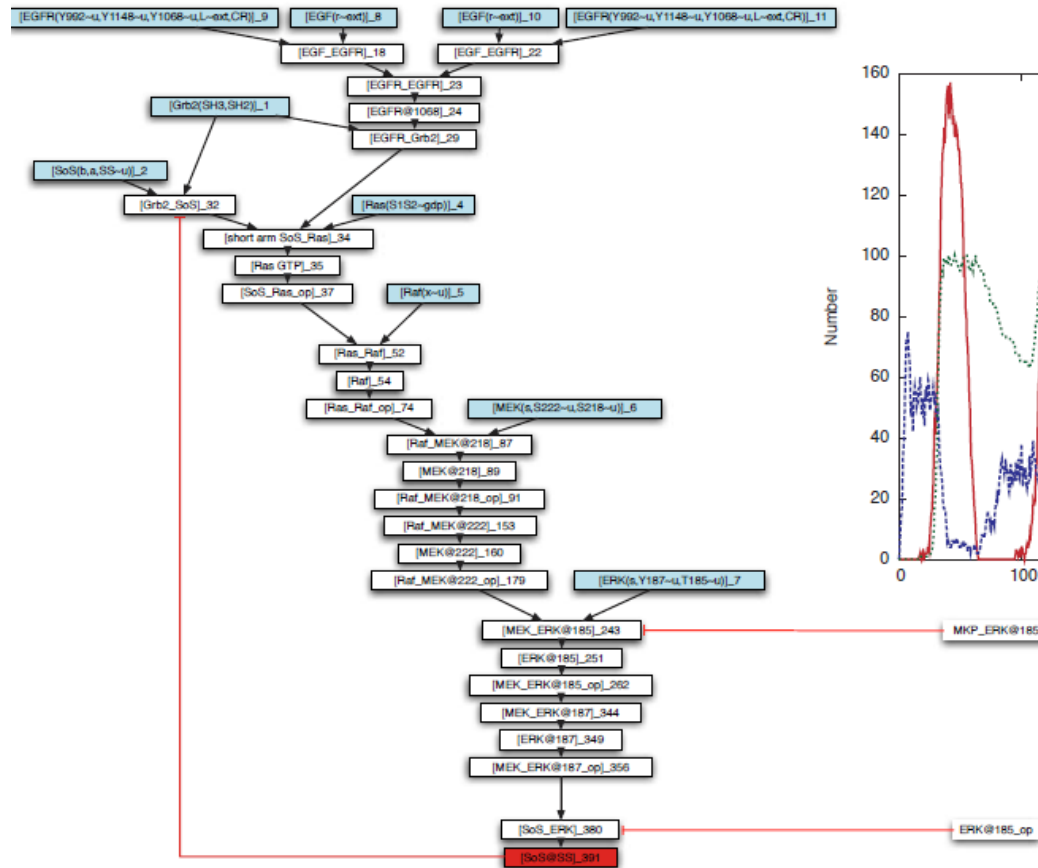
Rules, Instances, events



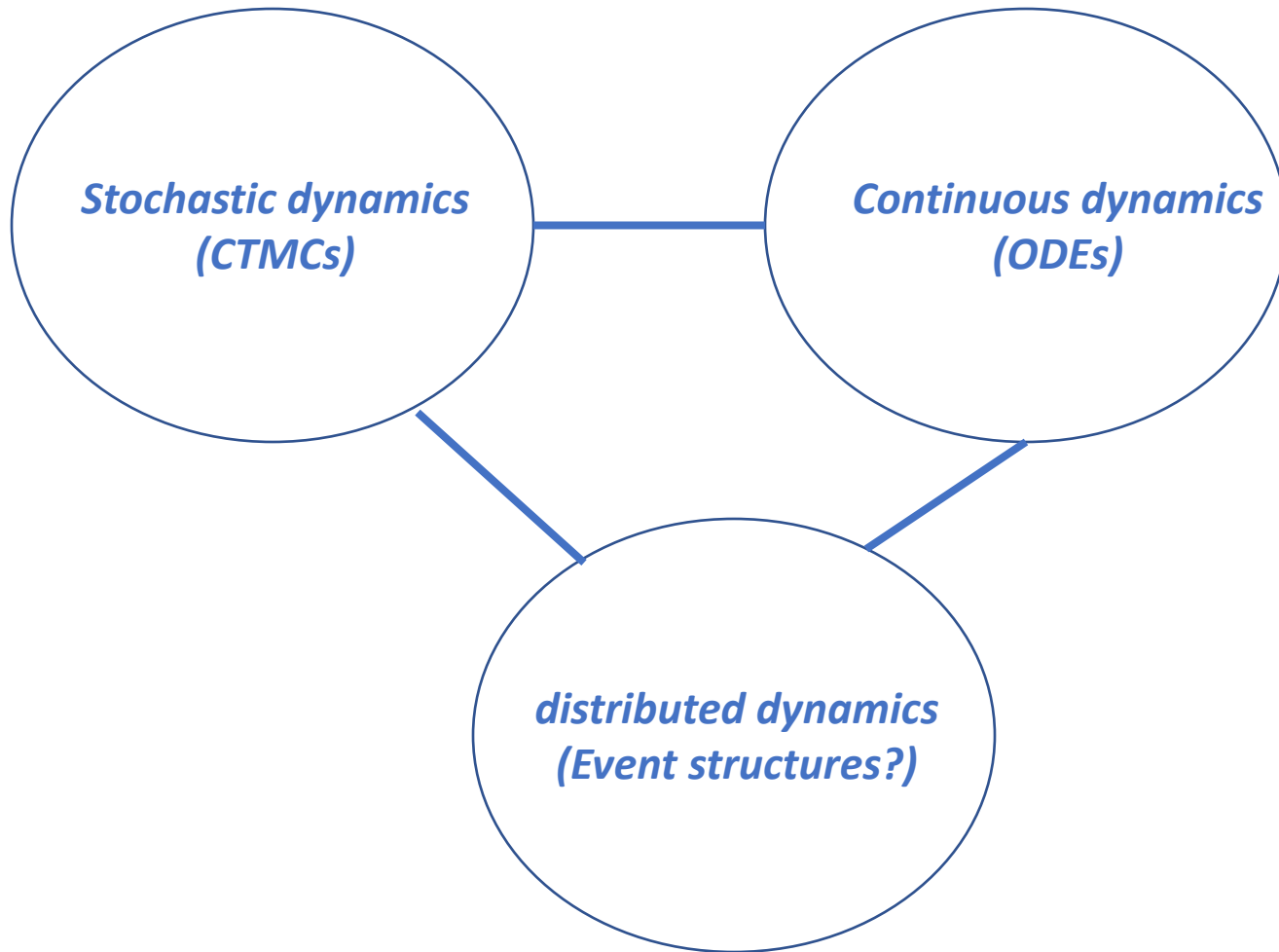
Concurrency



Stories -----> Event structures



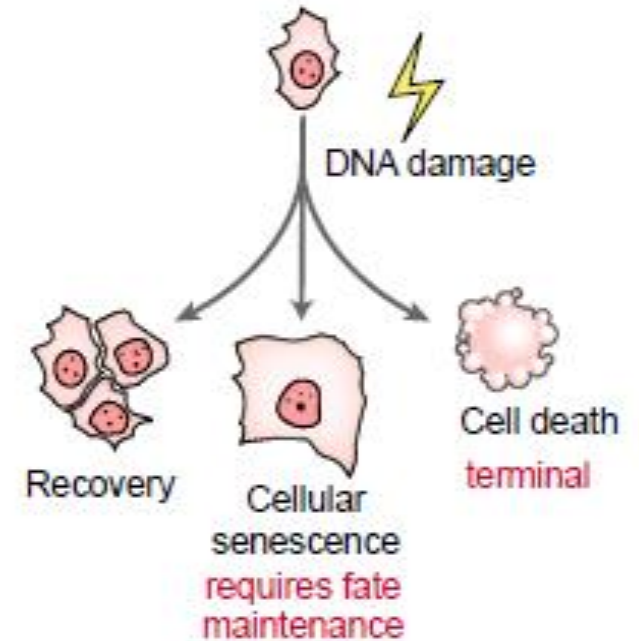
A perspective



- **Not merely descriptive**
- **Must yield a succinct partial order based representation of the state space**
- **Lead to efficient sampling based statistical analysis**

Motivation

- Signaling must be:
 - *robust*: filter out small fluctuations
 - *Sensitive*: respond according to signal strengths/shapes
- Tumor cells rewire their signaling pathways in order to adapt to and resist drug treatments.
 - response to vemurafenib in melanoma patients
- Cell differentiation/proliferation choices in developmental biology



Jose' Reyes, Jia-Yun Chen, Jacob Stewart-Ornstein, Kyle W. Karhohs, Caroline S. Mock and Galit Lahav. Fluctuations in p53 Signaling Allow Escape from Cell-Cycle Arrest. Molecular Cell 71, 581–591

Marie Csete, John Doyle. Bow ties, metabolism and disease. TRENDS in Biotechnology Vol.22 No.9

Returning to Carl Adam Petri

- His research:
 - Uncompromising
 - Commitment to fundamental issues
 - Fit-for-purpose

Returning to Carl Adam Petri

- His research:
 - Uncompromising
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 - Fit-for-purpose
- *Health warning:*
 - Don't try this at home!*