

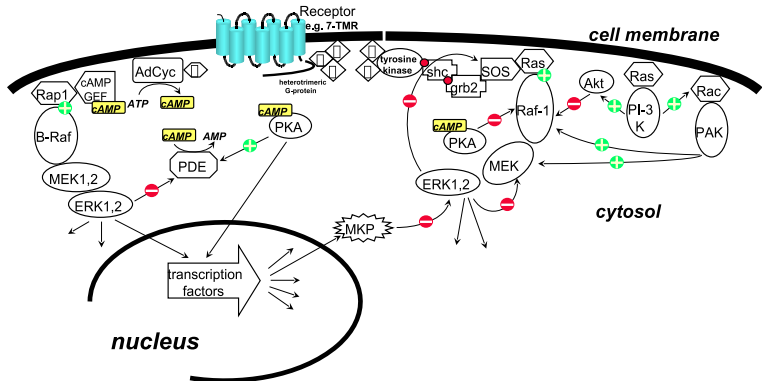
A Unifying Framework for Modelling and Analysing Biochemical Pathways Using Petri Nets

David Gilbert, Monika Heiner, Sebastian Lehrack

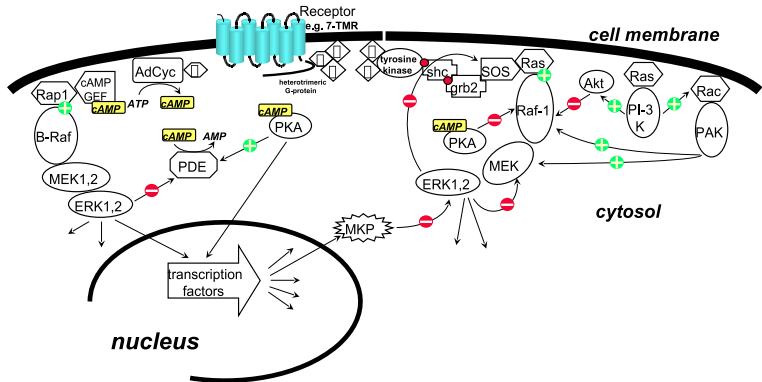
Bioinformatics Research Centre, University of Glasgow,
INRIA Rocquencourt/BTU Cottbus

CMSB 2007, Edinburgh
September 21, 2007

- Biochemical pathways

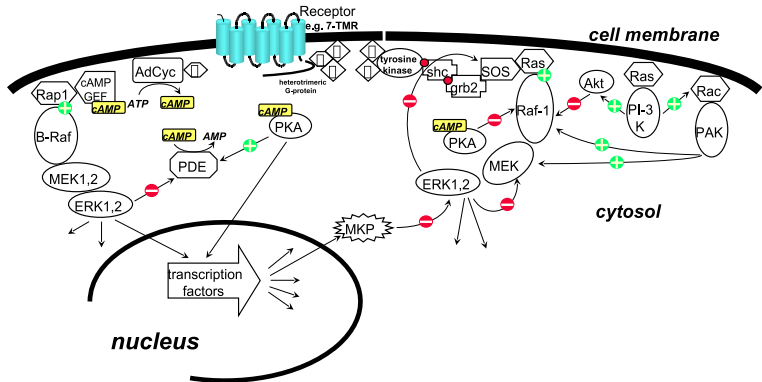


- Biochemical pathways



How to model this?

- Biochemical pathways



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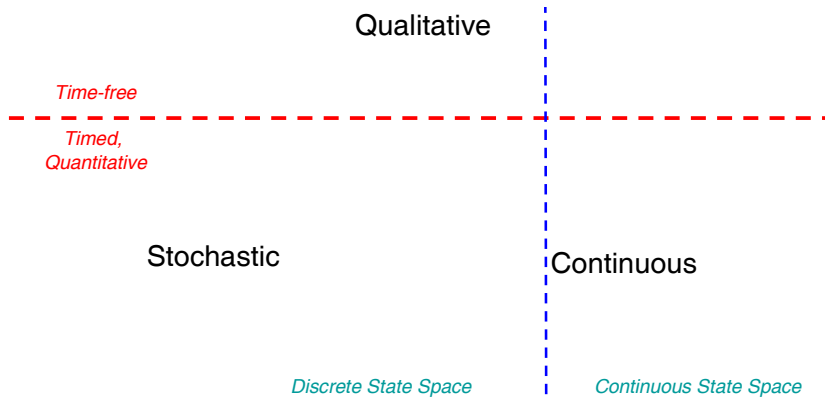
How to analyse this?

Qualitative

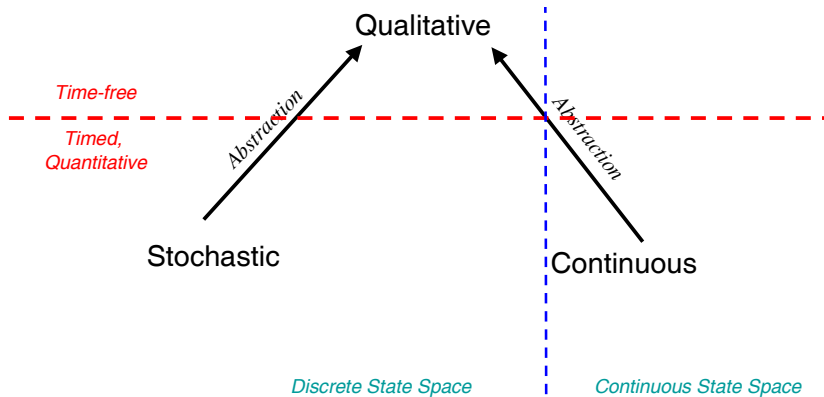
Stochastic

Continuous

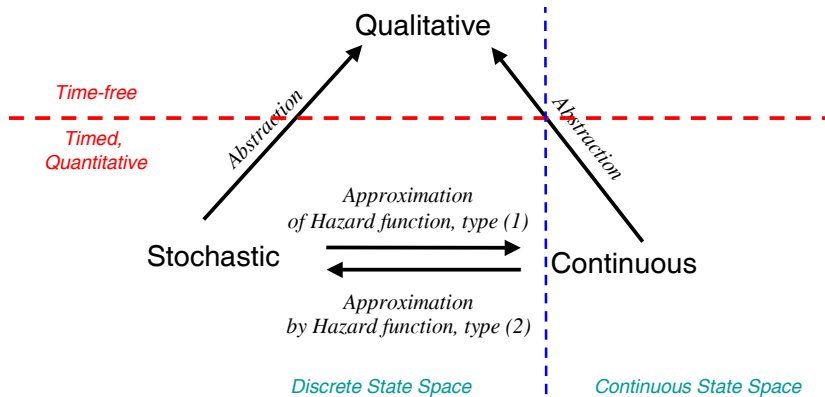
Framework



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Definition :

A **place/transition Petri net** is a quadruple

$\mathcal{PN} = (P, T, f, m_0)$, where

- P, T - finite, non empty, disjoint sets (**places, transitions**)

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Interleaving Semantics : reachability graph / CTL, LTL

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A biochemically interpreted continuous Petri net is a quintuple $\mathcal{CPN}_{Bio} = (P, T, f, v, m_0)$, where

- P, T - finite, non empty, disjoint sets (places, transitions)
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- $v : T \rightarrow H$ (**continuous firing rate functions**) with
 - $H := \bigcup_{t \in T} \{h_t \mid h_t : \mathbb{R}^{|\bullet t|} \rightarrow \mathbb{R}^+\}$
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Semantics : ODEs / LTLc

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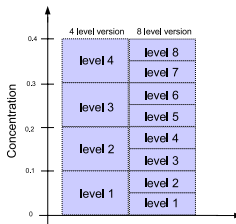
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Semantics : Continuous Time Markov Chain / CSL

Interpretation of tokens :

- *tokens = molecules*
- *tokens = concentration levels* [Calder et al., CMSB 2005]



Specialised stochastic firing rate function, two examples :

- *molecules semantics*

$$h_t := c_t \cdot \prod_{p \in \bullet t} \binom{m(p)}{f(p, t)} \quad (1)$$

- *concentration levels semantics*

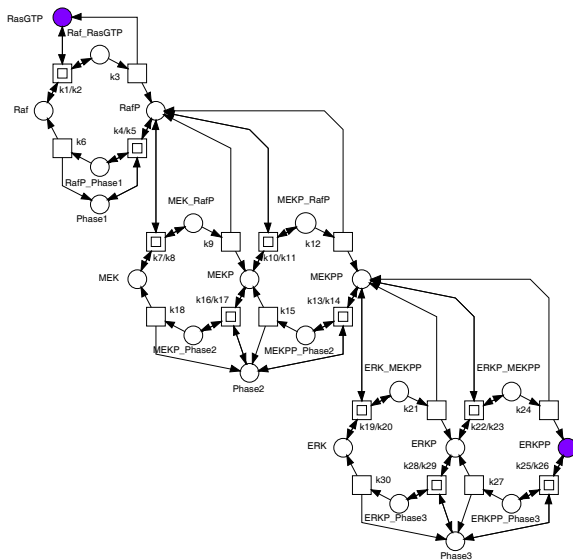
$$h_t := k_t \cdot N \cdot \prod_{p \in \bullet t} \left(\frac{m(p)}{N} \right) \quad (2)$$

Running Case Study - Origin

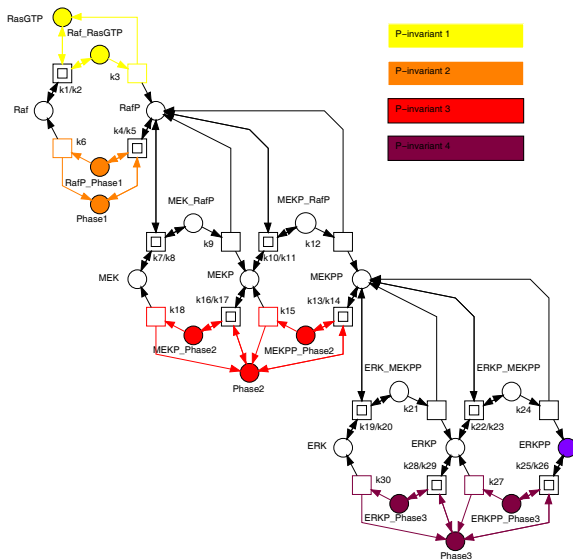
[Levchenko et al. 2000], *Supplemental Material : ODEs*

$$\begin{aligned}dRaf/dt &= k_2 * Raf_RasGTP + k_6 * RafP_Phase1 - k_1 * Raf * RasGTP \\dRasGTP/dt &= k_2 * Raf_RasGTP + k_3 * Raf_RasGTP - k_1 * Raf * RasGTP \\dRaf_RasGTP/dt &= k_1 * Raf * RasGTP - k_2 * Raf_RasGTP - k_3 * Raf_RasGTP \\dRafP/dt &= k_3 * Raf_RasGTP + k_{12} * MEKP_RafP + k_9 * MEK_RafP + \\&\quad k_5 * RafP_Phase1 + k_8 * MEK_RafP + k_{11} * MEKP_RafP - \\&\quad k_7 * RafP * MEK - k_{10} * MEKP * RafP - k_4 * Phase1 * RafP \\dRafP_Phase1/dt &= k_4 * Phase1 * RafP - k_5 * RafP_Phase1 - k_6 * RafP_Phase1 \\dMEK_RafP/dt &= k_7 * RafP * MEK - k_8 * MEK_RafP - k_9 * MEK_RafP \\dMEKP_RafP/dt &= k_{10} * MEKP * RafP - k_{11} * MEKP_RafP - k_{12} * MEKP_RafP \\dMEKP_Phase2/dt &= k_{16} * Phase2 * MEKP - k_{18} * MEKP_Phase2 - k_{17} * MEKP_Phase2 \\dMEKPP_Phase2/dt &= k_{13} * MEKPP * Phase2 - k_{15} * MEKPP_Phase2 - k_{14} * MEKPP_Phase2 \\dERK/dt &= k_{20} * ERK_MEKPP + k_{30} * ERKP_Phase3 - k_{19} * MEKPP * ERK \\dERK_MEKPP/dt &= k_{19} * MEKPP * ERK - k_{20} * ERK_MEKPP - k_{21} * ERK_MEKPP \\dERKP_MEKPP/dt &= k_{22} * MEKPP * ERKP - k_{24} * ERKP_MEKPP - k_{23} * ERKP_MEKPP \\etcetera &= \dots\end{aligned}$$

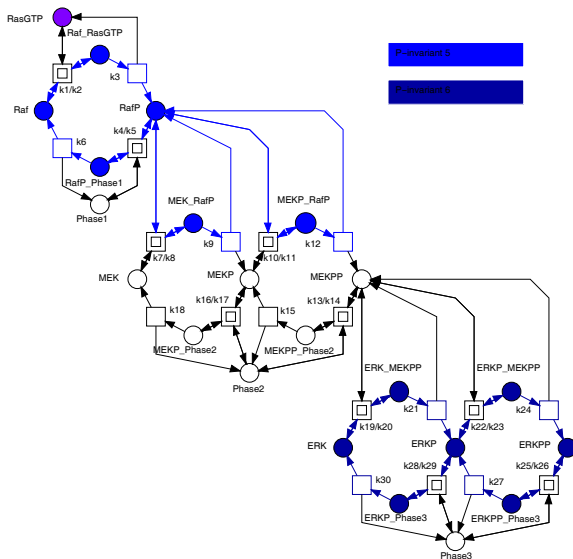
Running Case Study



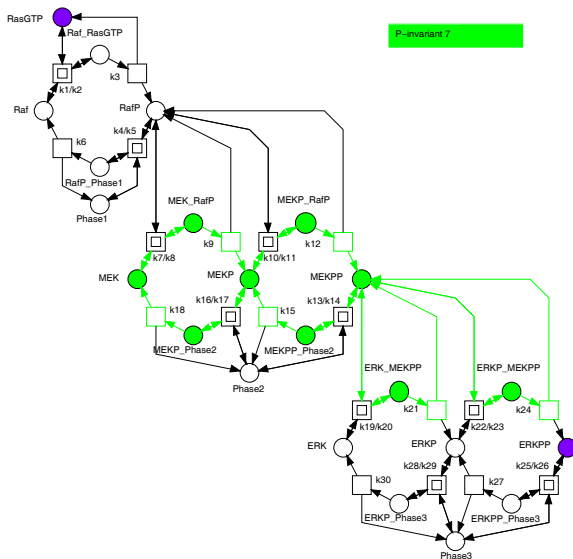
Running Case Study - P-invariants



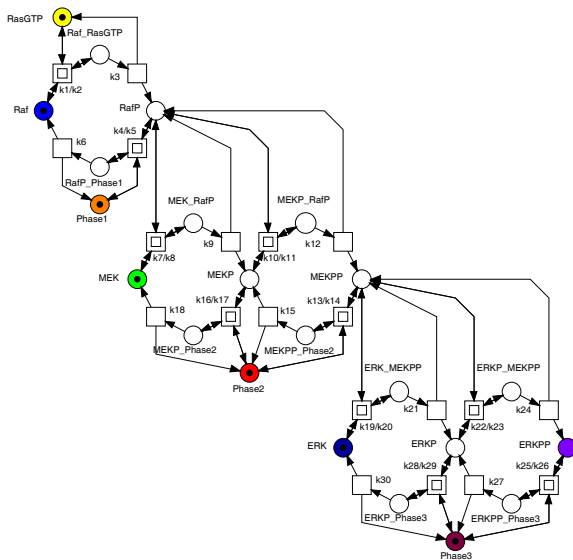
Running Case Study - P-invariants



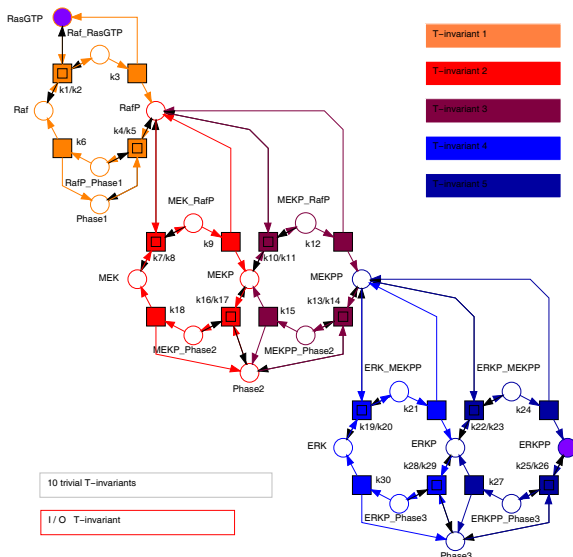
Running Case Study - P-invariants



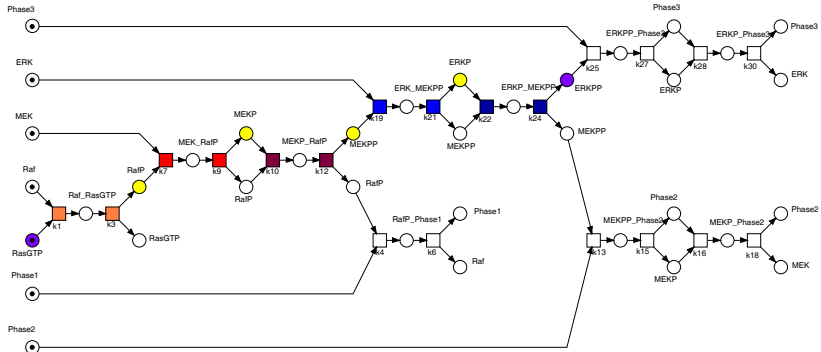
Running Case Study - initial marking



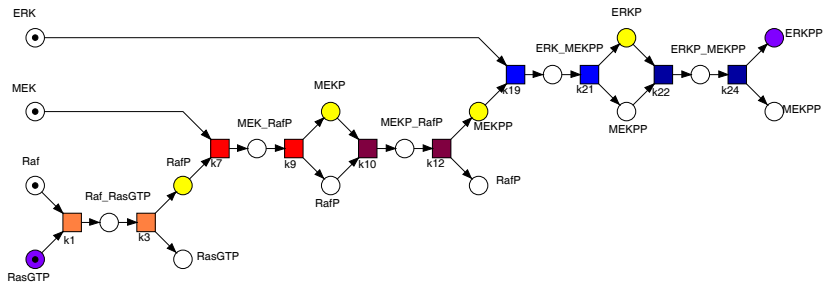
Running Case Study - T-invariants



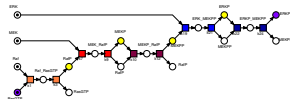
Running Case Study - partial order run of I/O T-invariant



Running Case Study - partial order run of I/O T-invariant



Qualitative Model Checking (CTL)



property Q1 :

The signal sequence predicted by the partial order run of the I/O T-invariant is the only possible one;
i.e., starting at the initial state, it is necessary to pass through RafP, MEKP, MEKPP and ERKP in order to reach ERKPP.

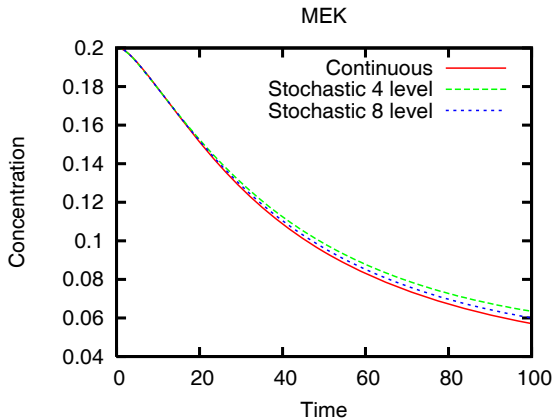
$$\neg [\mathbf{E} (\neg \text{RafP} \mathbf{U} \text{MEKP}) \vee \\ \mathbf{E} (\neg \text{MEKP} \mathbf{U} \text{MEKPP}) \vee \\ \mathbf{E} (\neg \text{MEKPP} \mathbf{U} \text{ERKP}) \vee \\ \mathbf{E} (\neg \text{ERKP} \mathbf{U} \text{ERKPP})]$$

- *isomorphism of reachability graph and CTMC*,
thus all qualitative properties still valid
- *How many levels needed for quantitative evaluation ?*
 - state space(1 levels) = 118 (Boolean interpretation)
 - state space(4 levels) = 24,065
 - state space(8 levels) = 6,110,643
- *equivalence check*

$$C_{RafP}(t) = \frac{0.1}{s} \cdot \underbrace{\sum_{i=1}^{4s} (i \cdot P(L_{RafP}(t) = i))}_{\text{expected value of } L_{RafP}(t)}$$

Stochastic Model Checking - Preparation

- *equivalence check, results, e.g. for MEK :*

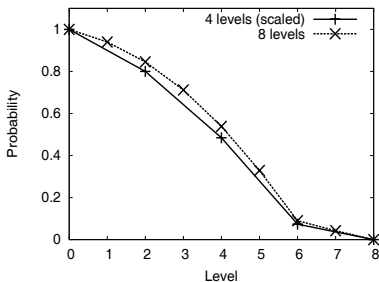


Stochastic Model Checking (CSL)

property S1 :

What is the probability of the concentration of RafP increasing, when starting in a state where the level is already at L ?

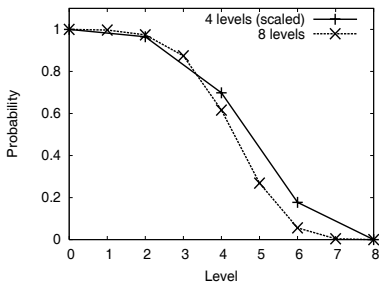
$$P_{=?} [(\text{RafP} = L) \mathbf{U}^{\leq 100} (\text{RafP} > L) \{ \text{RafP} = L \}]$$



property S2 :

What is the probability that RafP is the first species to react?

$$P_{=?} [((\text{MEKPP} = 0) \wedge (\text{ERKPP} = 0)) \mathbf{U}^{\leq 100} (\text{RafP} > L) \\ \{ (\text{MEKPP} = 0) \wedge (\text{ERKPP} = 0) \wedge (\text{RafP} = 0) \}]$$

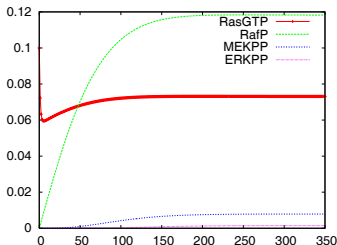


Continuous Model Checking (LTLC)

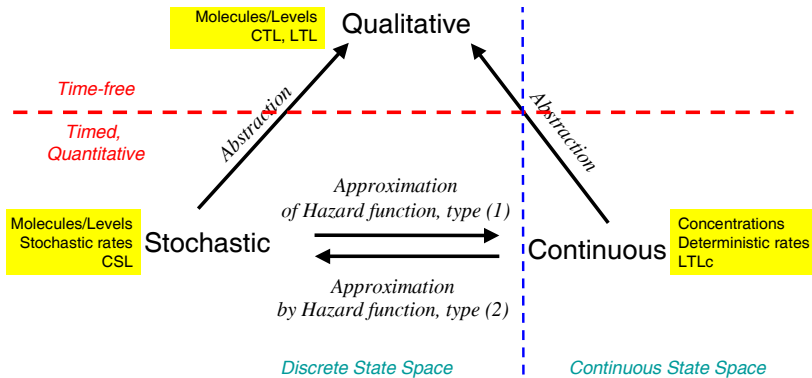
property C1 :

The concentration of RafP rises to a significant level, while the concentrations of MEKPP and ERKPP remain close to zero ;
i.e. RafP is really the first species to react.

$$((MEKPP < 0.001) \wedge (ERKPP < 0.0002)) \text{ U } (RafP > 0.06)$$



Framework



- *model construction*
Snoopy (*Cottbus*)

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- *qualitative analysis*

- INA, Charlie (*Cottbus*)

- Model Checking Kit, CTL (Boolean semantics) (*Cottbus*)

- IDD-based CTL model checker (integer semantics) (*Cottbus*)

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- *continuous analysis*

- BioNessie (*Glasgow*)
- MATLAB
- Biocham, LTLc model checker

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qualitative & stochastic & continuous paradigms

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- **not bound to the Petri net perspective**

Thanks !

all data files and analysis results available at
www-dssz.informatik.tu-cottbus.de/examples/levchenko

laptop demonstration available

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