

The Continuous π -Calculus

An Algebra for Biochemical Modelling

Marek Kwiatkowski

School of Informatics
University of Edinburgh

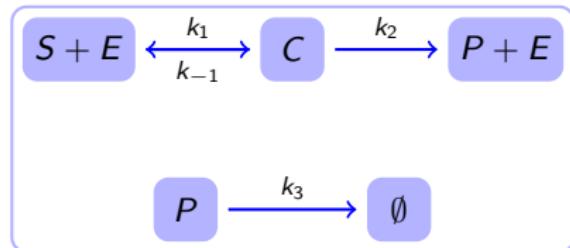
14 Oct 2008, CMSB

joint work with Ian Stark

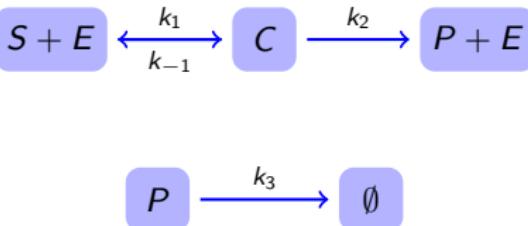
Outline

- 1 Introduction: ODEs and Process Algebras
- 2 The Continuous π -Calculus
- 3 Example: the KaiABC circadian clock
- 4 Future work and conclusions

Ordinary Differential Equations

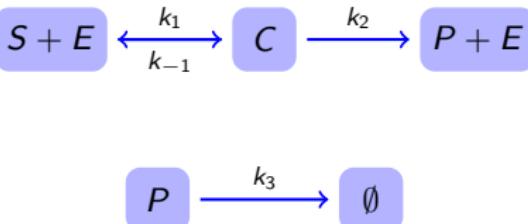


Ordinary Differential Equations

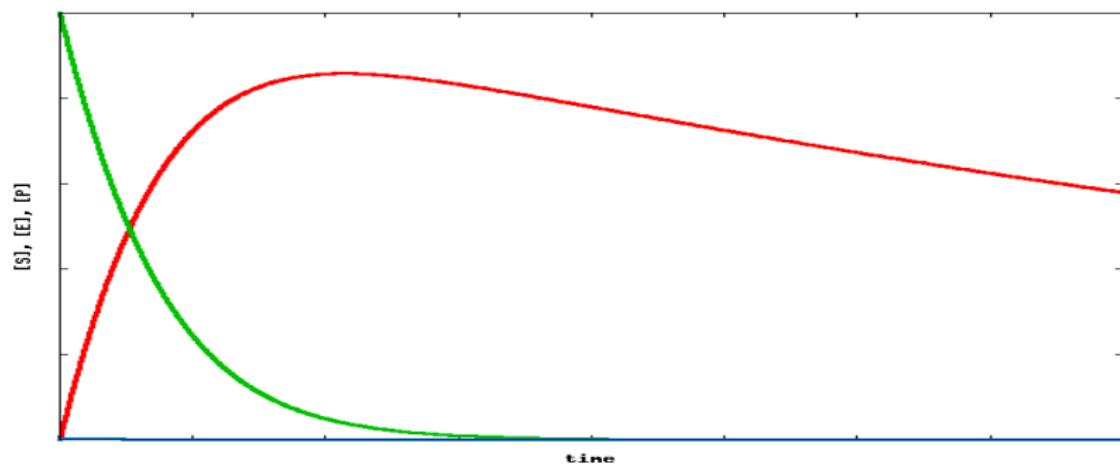


$$\begin{aligned}\frac{d[S]}{dt} &= -k_1[S][E] + k_{-1}[C] \\ \frac{d[E]}{dt} &= -k_1[S][E] + k_{-1}[C] + k_2[C] \\ \frac{d[C]}{dt} &= k_1[S][E] - k_{-1}[C] - k_2[C] \\ \frac{d[P]}{dt} &= k_2[C] - k_3[P]\end{aligned}$$

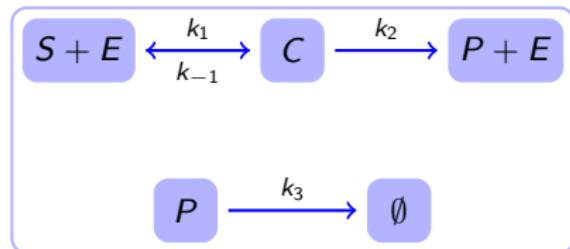
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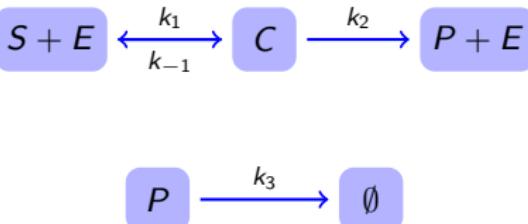
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Process Algebras

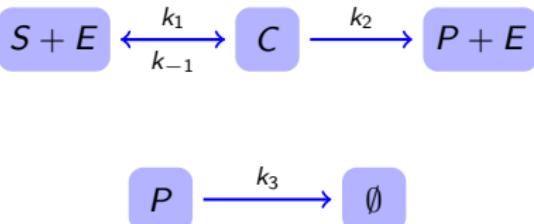


Process Algebras

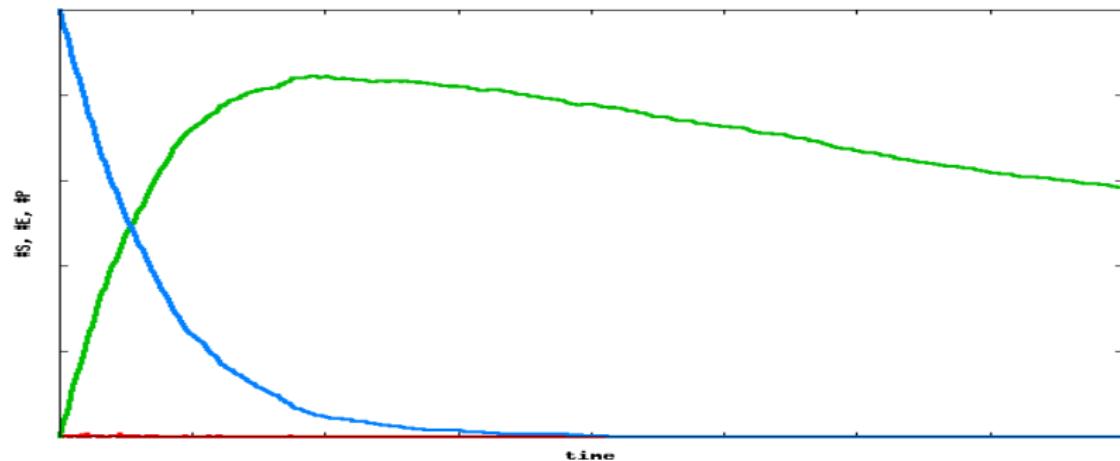


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 S &\stackrel{\Delta}{=} a(x, y).(x.S + y.P) \\
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 P &\stackrel{\Delta}{=} \tau.\mathbf{0} \\
 S \mid \dots \mid S \mid E \mid \dots \mid E
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ODEs vs PAs

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- continuous

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ODEs vs PAs

ODEs:

- continuous
- deterministic
- monolithic
- specify dynamics
- very popular

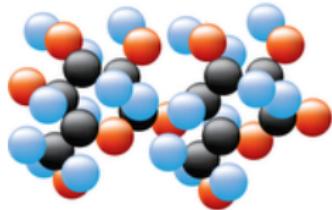
PAs:

- discrete
- non-deterministic/stochastic
- modular (compositional)
- specify interactions
- relatively unknown

Syntax: species and processes

Species:

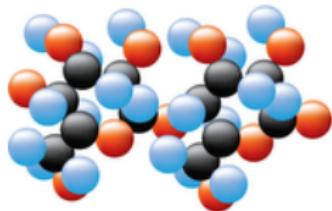
$$A, B ::= \mathbf{0} \mid \pi_1.A_1 + \cdots + \pi_n.A_n \\ D(\vec{a}) \mid A \mid B \mid (\nu M)A$$



Syntax: species and processes

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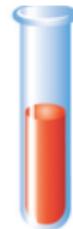
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Processes:

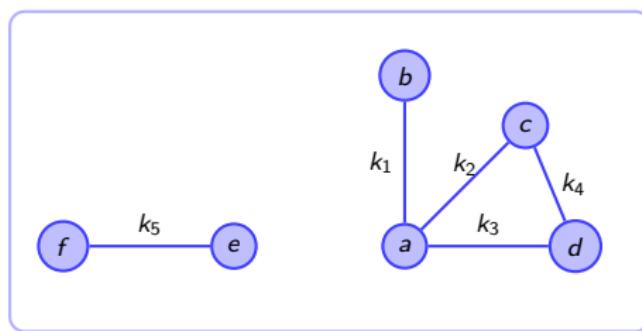
$$P, Q ::= c \cdot A \mid P \parallel Q \quad c \in \mathbb{R}_{\geq 0}$$

(thus P is an element of \mathbb{R}^S)



Syntax: affinity networks

Names represent protein interaction sites.



An affinity network gives their interaction structure.

Semantics

$\frac{dP}{dt}$: immediate behaviour

- element of \mathbb{R}^S
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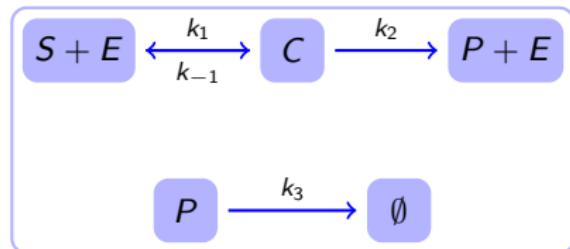
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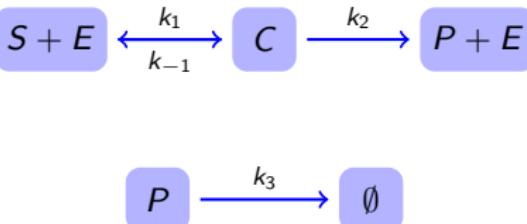
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$$1_{A \xrightarrow{x} F} \odot 1_{B \xrightarrow{y} G} \triangleq Aff(x, y)(\langle F \cdot G \rangle - \langle A \rangle - \langle B \rangle)$$

Example: a simple chemical reaction network

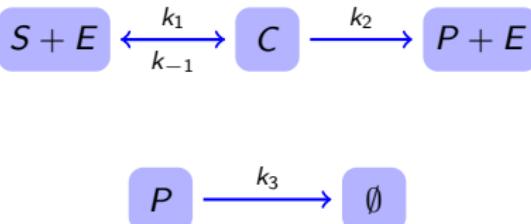


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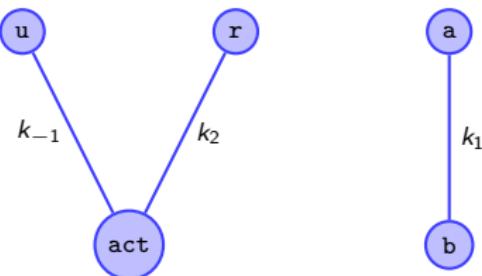


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 P &\stackrel{\Delta}{=} \tau @ k_3. \mathbf{0} \\
 c_E \cdot E &\parallel c_S \cdot S
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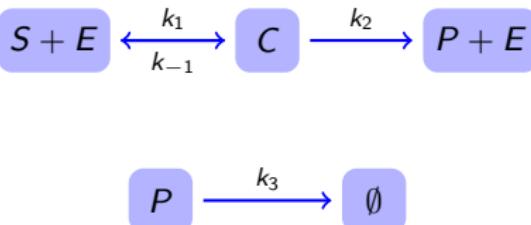
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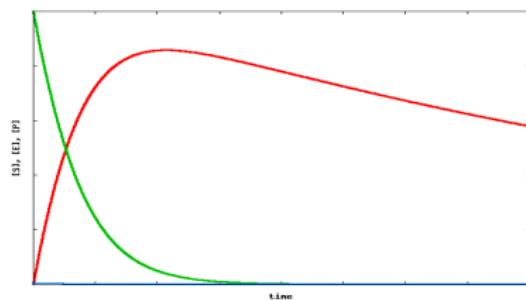
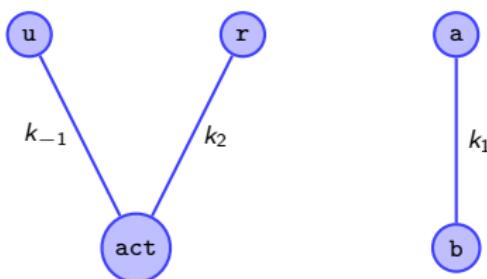
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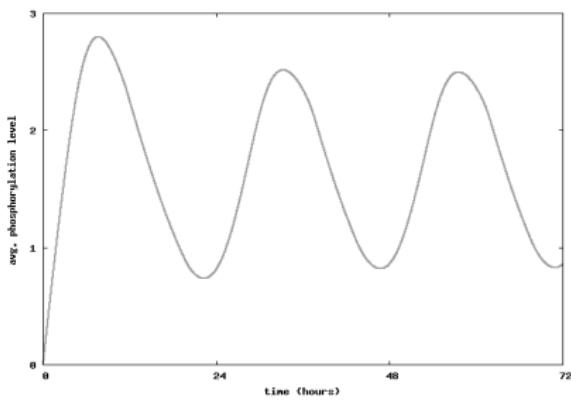
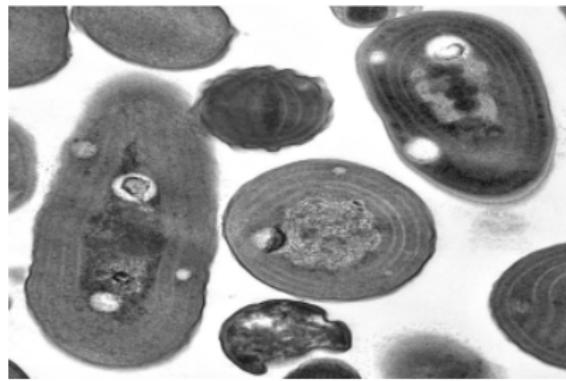
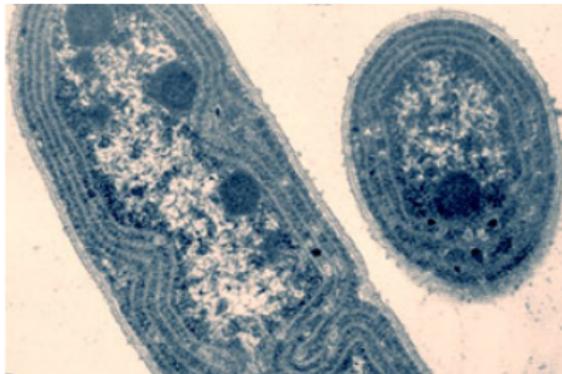
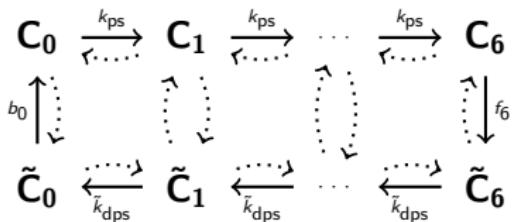
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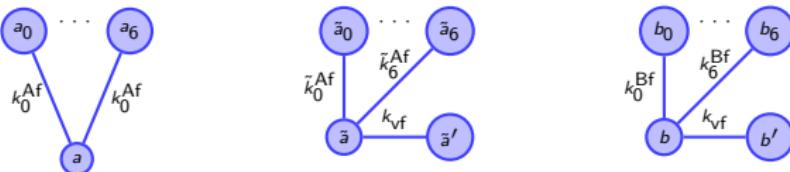


The KaiABC circadian clock of *Synechococcus elongatus*



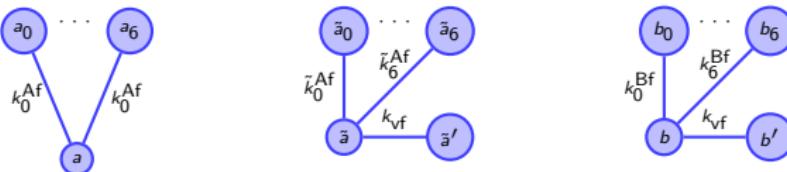
The model

$$\begin{aligned}
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 \tilde{C}_i &\triangleq \tau @ \tilde{k}_{ps}.\tilde{C}_{i+1} + \tau @ b_i.C_i + \tau @ \tilde{k}_{dps}.\tilde{C}_{i-1} + b_i.b'.B\tilde{C}_i \\
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 A &\triangleq a(x).x.A + \tilde{a}.\mathbf{0} \\
 B &\triangleq b.\mathbf{0} \\
 \mathbf{P} &\triangleq c_A \cdot \mathbf{A} || c_B \cdot \mathbf{B} || c_C \cdot \mathbf{C}_0
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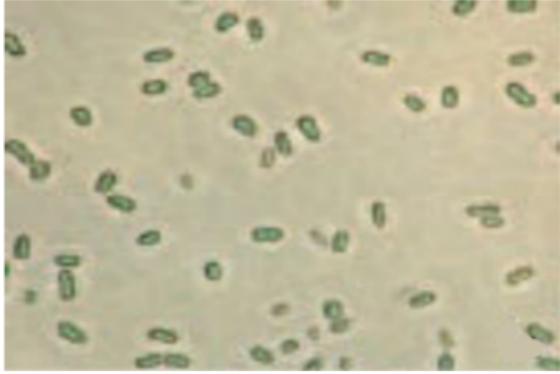
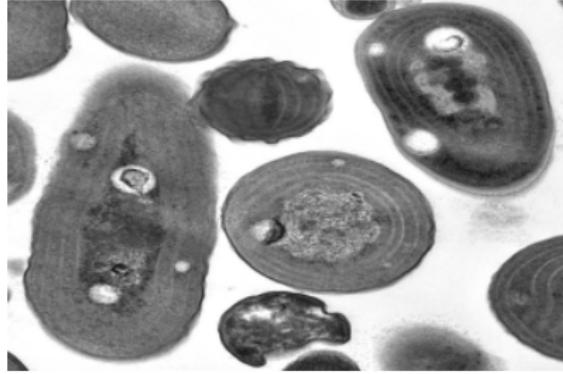
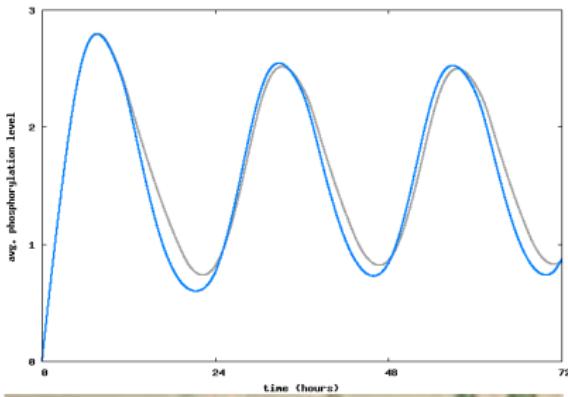
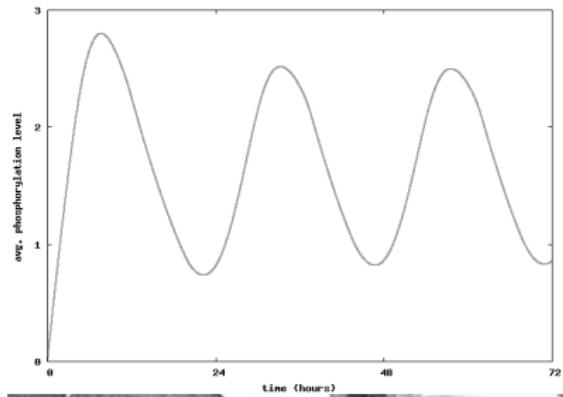


The model: no autonomous phosphorylation

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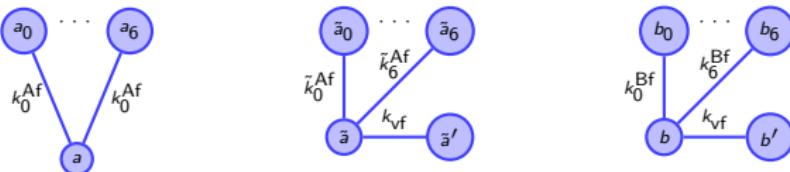


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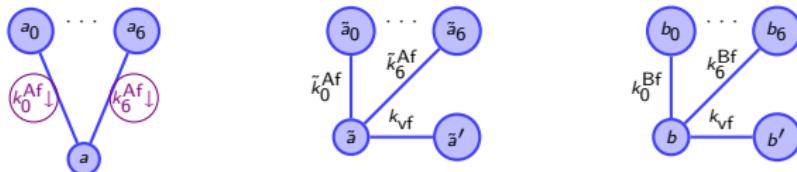
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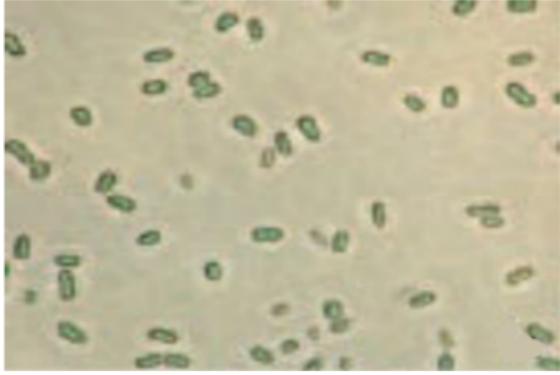
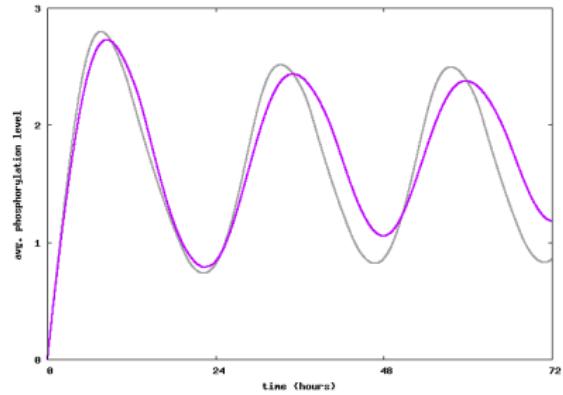
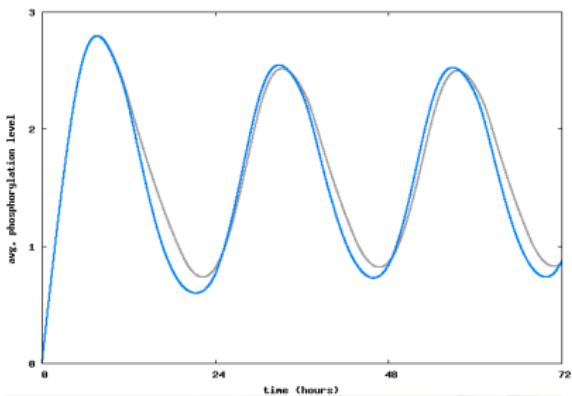
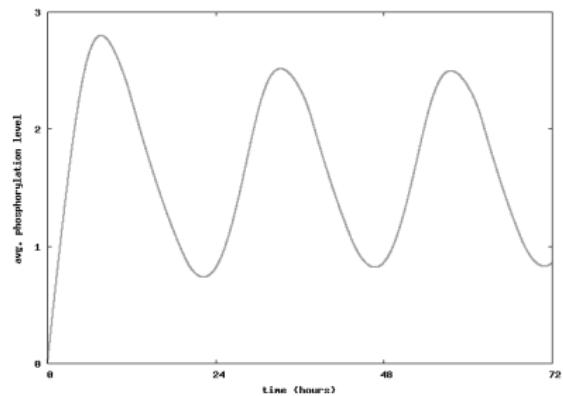


The model: weaker KaiA binding

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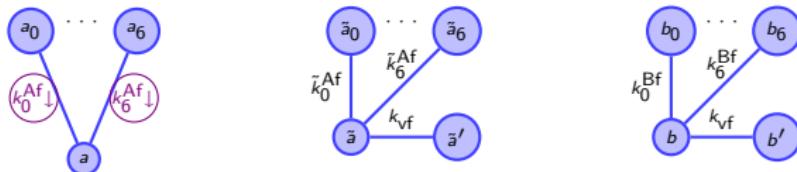


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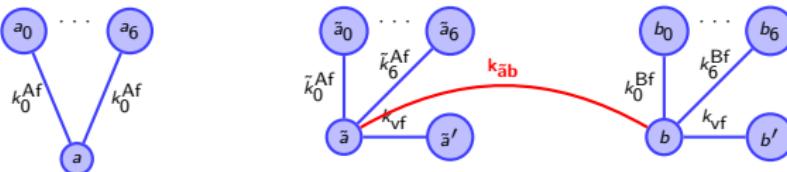
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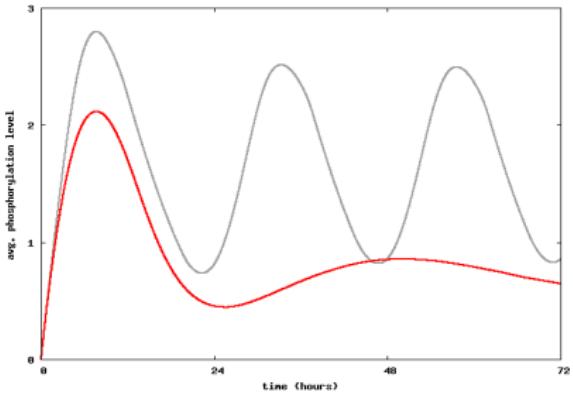
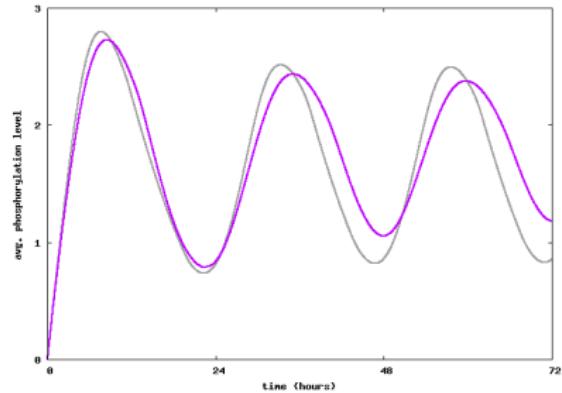
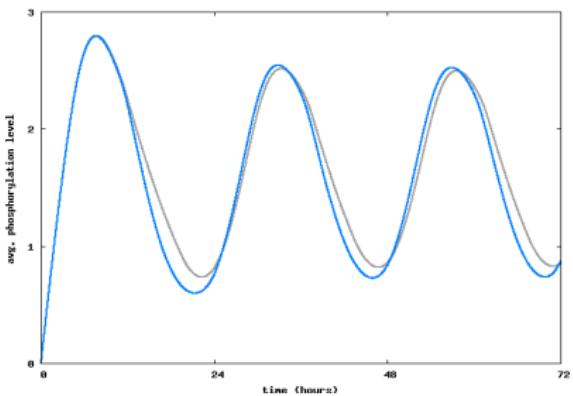
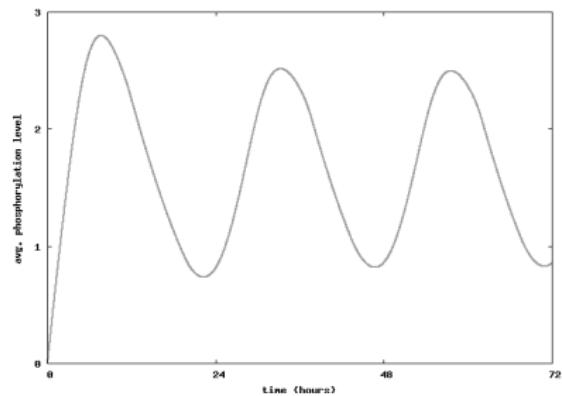


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- Robustness and evolvability (hard)
- The adaptive landscape (hard)

③ Hybrid Modelling

- Allows to model protein-DNA interactions

Conclusions

- ➊ ODEs and process algebras

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- ➌ Future work
 - Model Checking
 - Hybrid Modelling
 - Evolutionary Applications

Appendix

Key references:

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