

PACS Meeting

Parameters synthesis by using abstract interpretation in Parametric Stochastic Automata Networks

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Joint work with:

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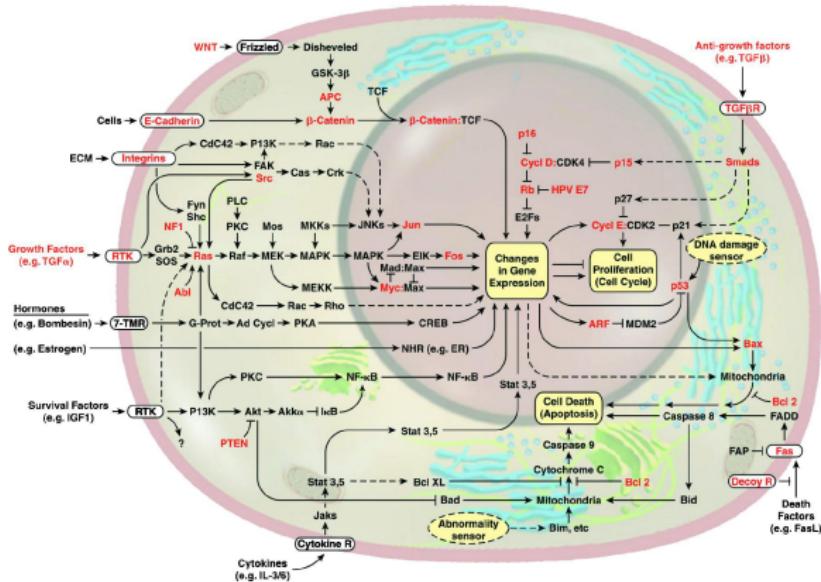
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- Context & Motivation

Context



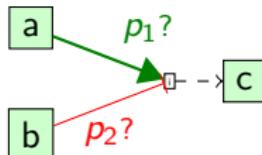
□

- Cellular processes \implies networks of biological interactions.
- Nodes (biological components), edges (interactions).

- Context & Motivation

Motivation

General knowledge
Literature
Hypotheses



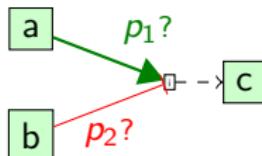
Times series data

Genes	1h	...	24h
Gene 1		...	
Gene 2		...	

- Context & Motivation

Motivation

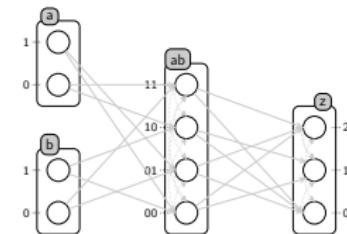
General knowledge
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Hypotheses



Times series data

Genes	1h	...	24h
Gene 1		...	
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Algebraic Modelling

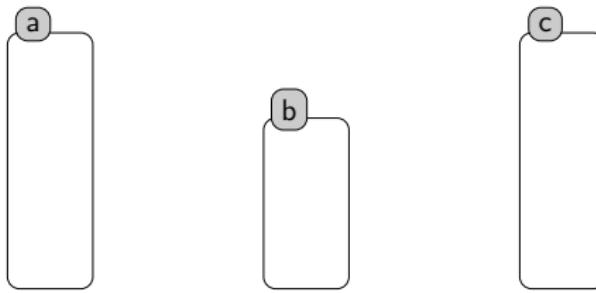


Formal inference of the parameters of Biological Networks:

- Avoid critical behaviors.

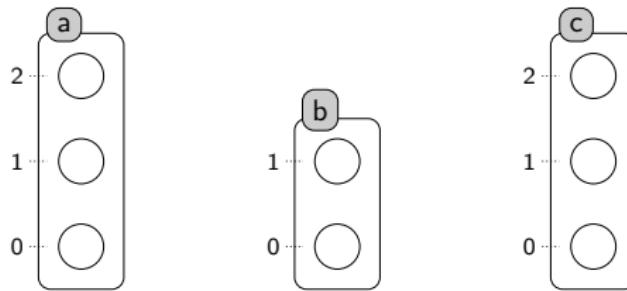
- Parametric Stochastic Automata Networks

Parametric Stochastic Automata Networks



Automata: components a, b, c

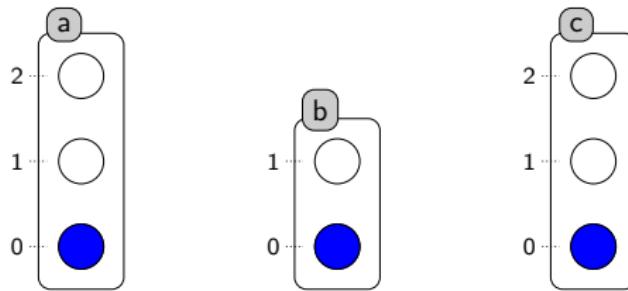
Parametric Stochastic Automata Networks



Automata: components *a, b, c*

local states: levels of expression c_0, c_1, c_2

Parametric Stochastic Automata Networks

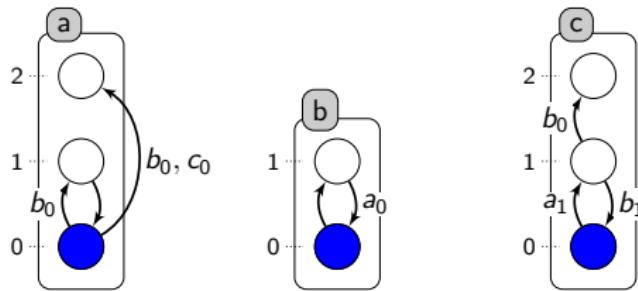


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States: sets of active local states a_0, b_0, c_0

Parametric Stochastic Automata Networks



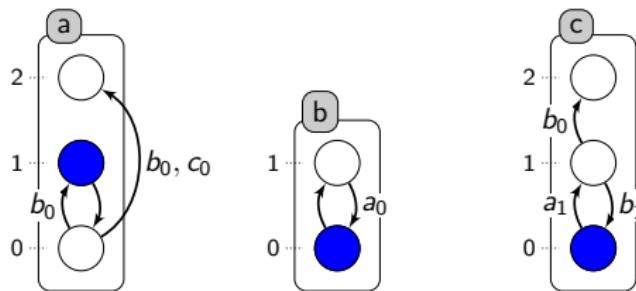
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States: sets of active local states a_0, b_0, c_0

Transitions: dynamics $t_1 = a_0 a_1 b_0, t_2 = a_1 a_0, t_3 = a_0 a_2 b_0, c_0, t_4 = b_0 b_1$

Parametric Stochastic Automata Networks



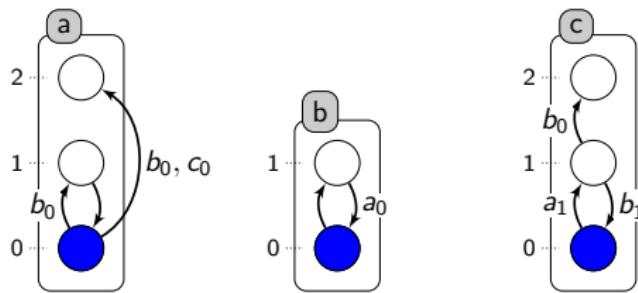
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Parametric Stochastic Automata Networks



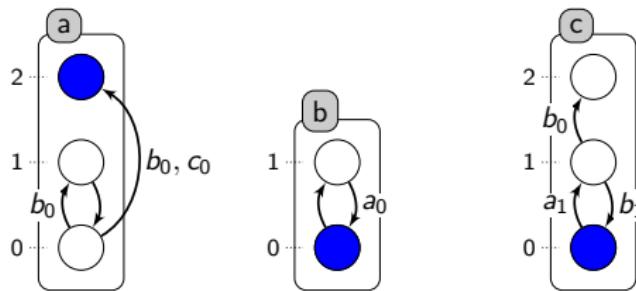
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Parametric Stochastic Automata Networks



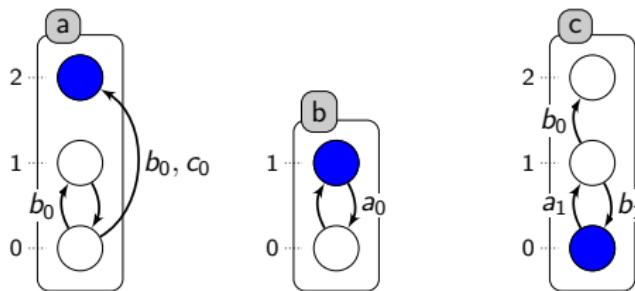
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Parametric Stochastic Automata Networks



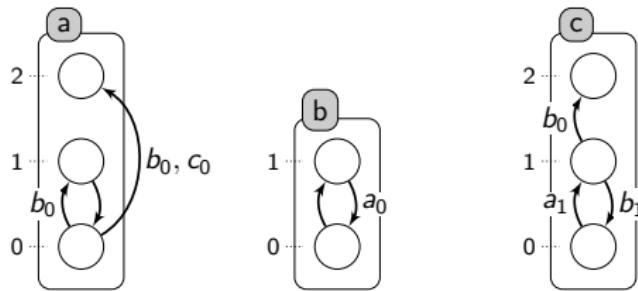
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Parametric Stochastic Automata Networks



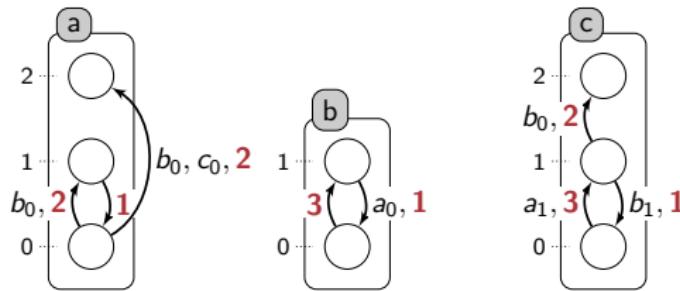
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Parametric Stochastic Automata Networks



Automata: components **a, b, c**

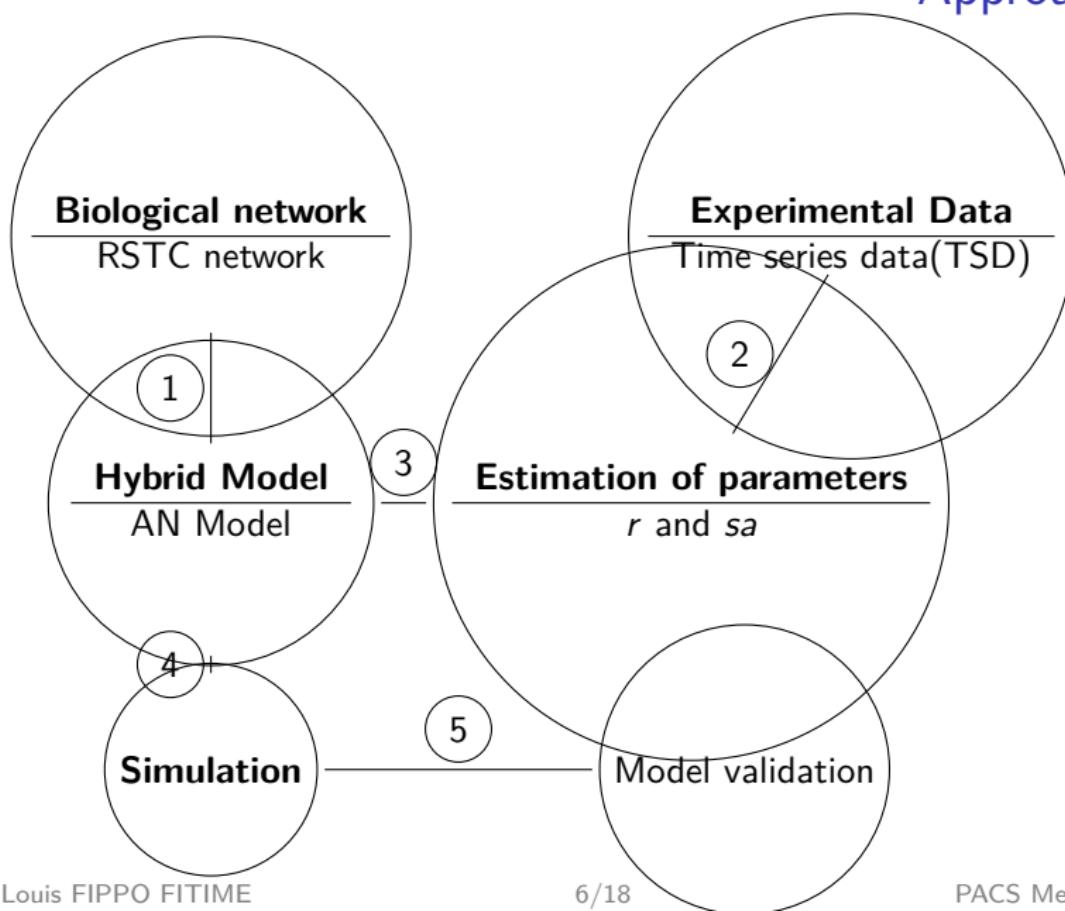
local states: levels of expression **c_0, c_1, c_2**

States: sets of active local states **a_2, b_1, c_0**

Transitions: dynamics **$t_1 = a_0 a_1 b_0, 2, t_2 = a_1 a_0 1, t_3 = a_0 a_2 b_0, c_0, 2, t_4 = b_0 b_1 3$**

- Parameters estimation from time-series data

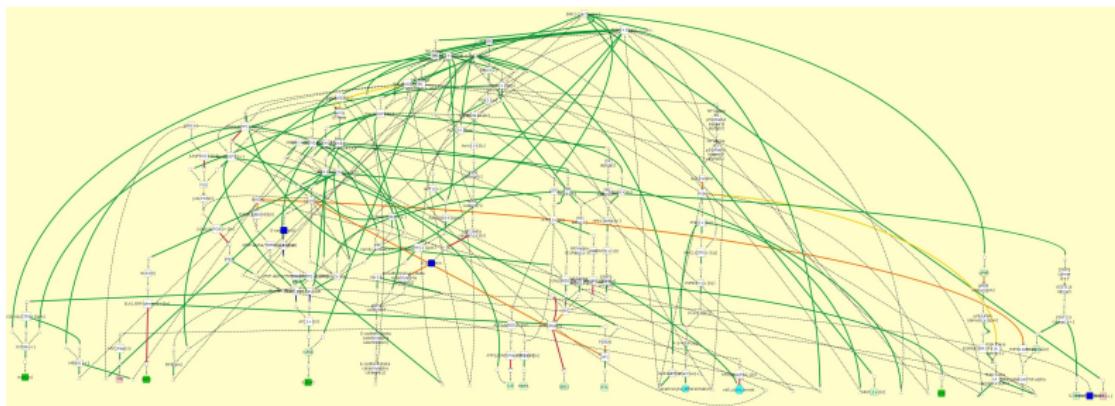
Approach



- Parameters estimation from time-series data

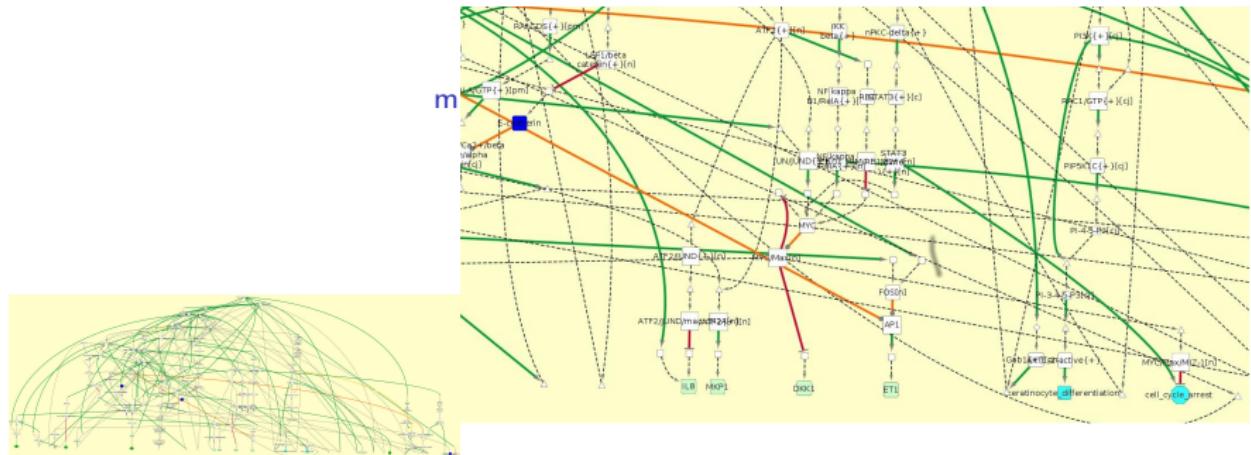
RSTC Network

multi-layer receptor-signaling-transcription-cell state

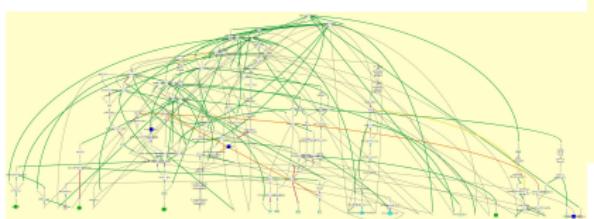


- Pathway Interaction Database
- 293 nodes: signaling proteins, transcription factors, mRNA expressions
- 375 interactions: activations, inhibitions, complexes dissociation

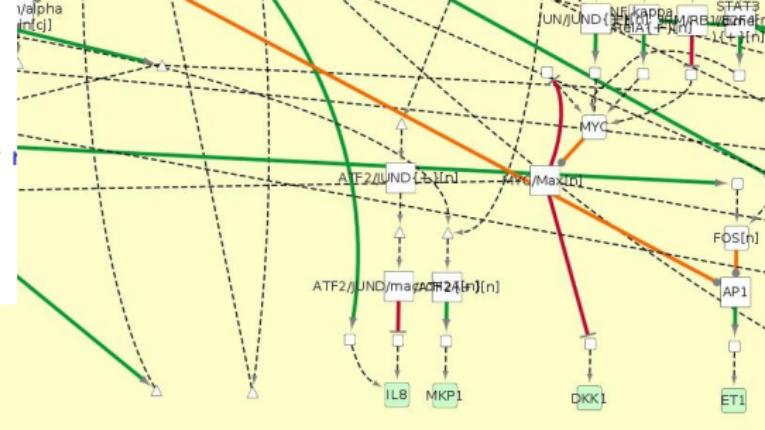
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- Parameters estimation from time-series data

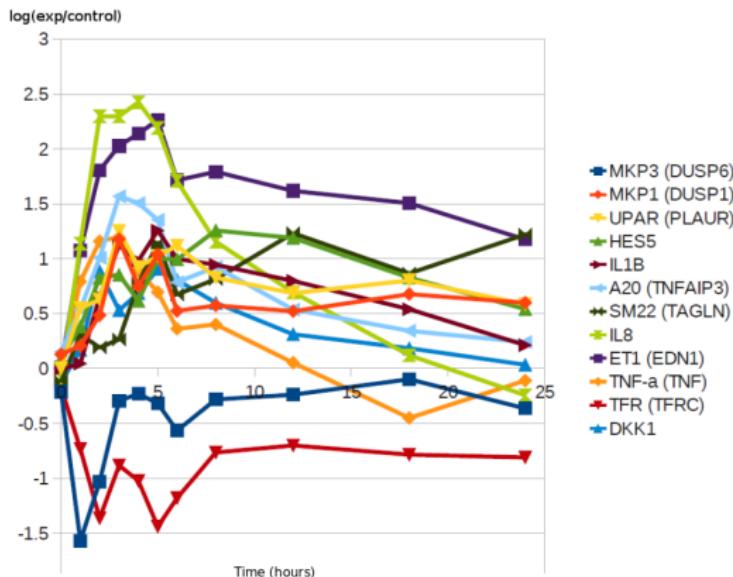


multi-layer



- Parameters estimation from time-series data

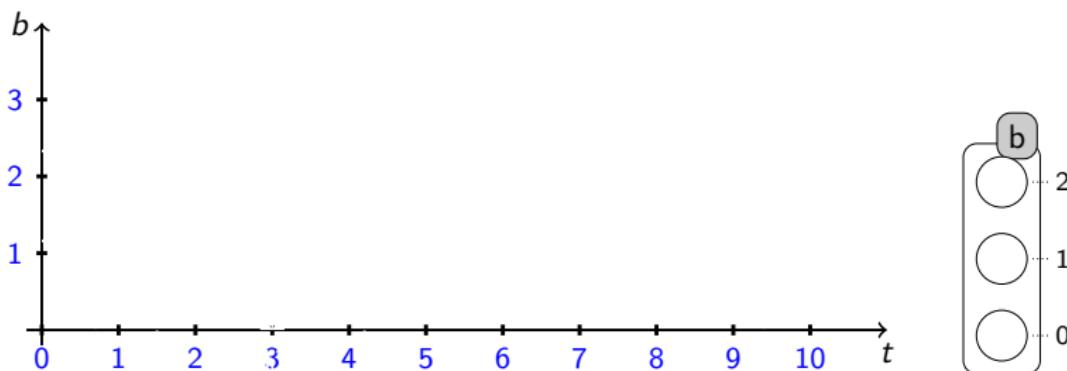
Time series data



- Experiment: calcium stimuli
- Measured at 10 time-points(0-24hrs)
- 200 transcripts selected (dynamic patterns)
- We included in our model a subset of 12 of them

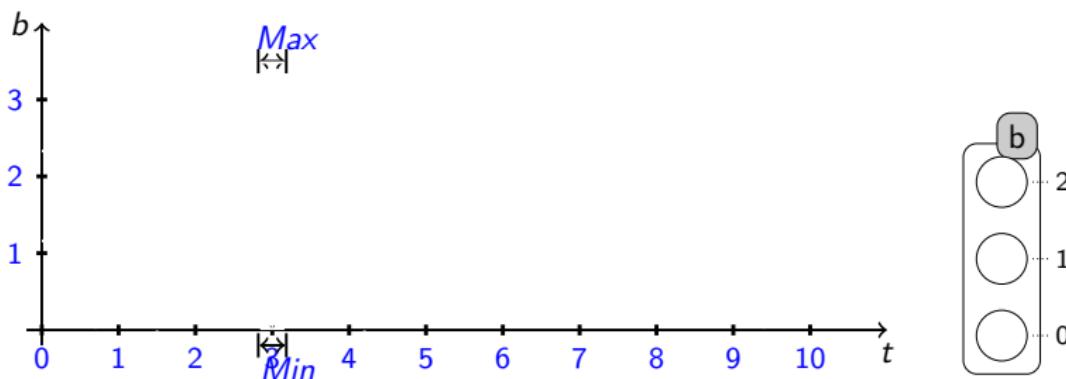
- Parameters estimation from time-series data

Data estimation from TSD



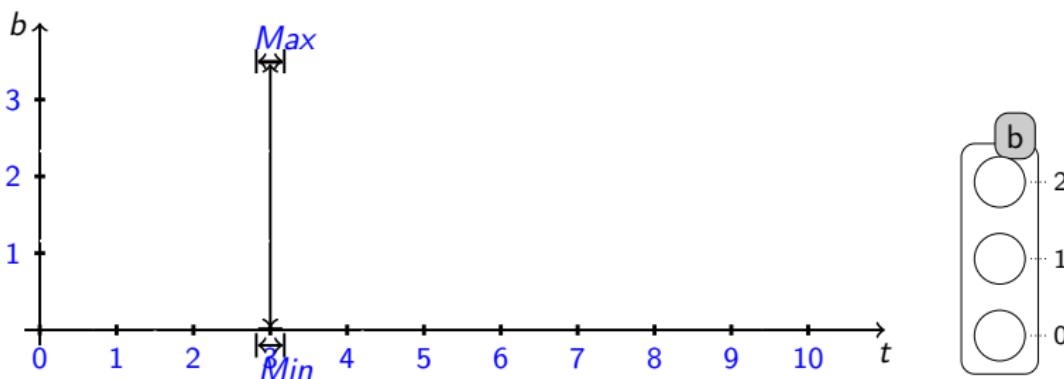
- Parameters estimation from time-series data

Data estimation from TSD



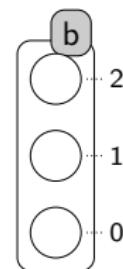
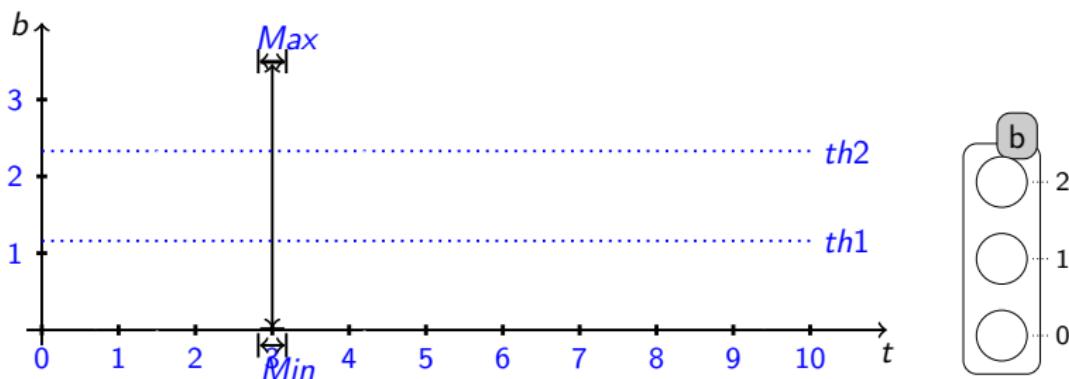
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Data estimation from TSD



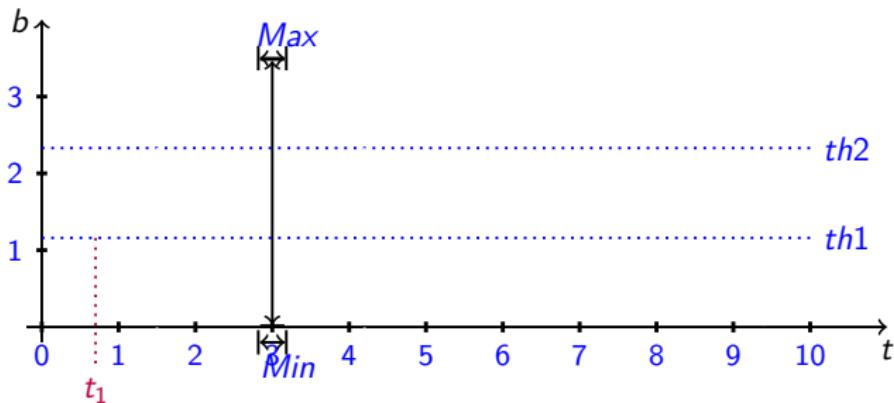
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Data estimation from TSD

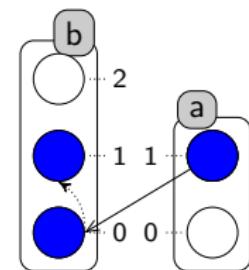


- Parameters estimation from time-series data

Data estimation from TSD

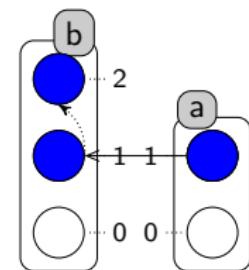
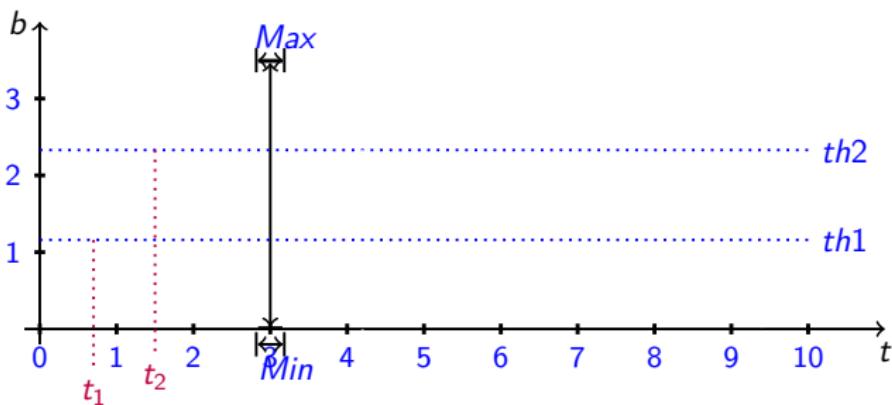


$$a_1 b_0 b_1 \text{ with } r_1 = \frac{1}{t_1 - t_0}$$



- Parameters estimation from time-series data

Data estimation from TSD

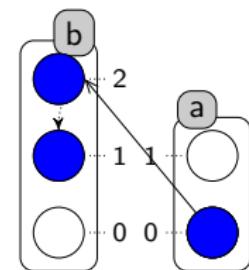
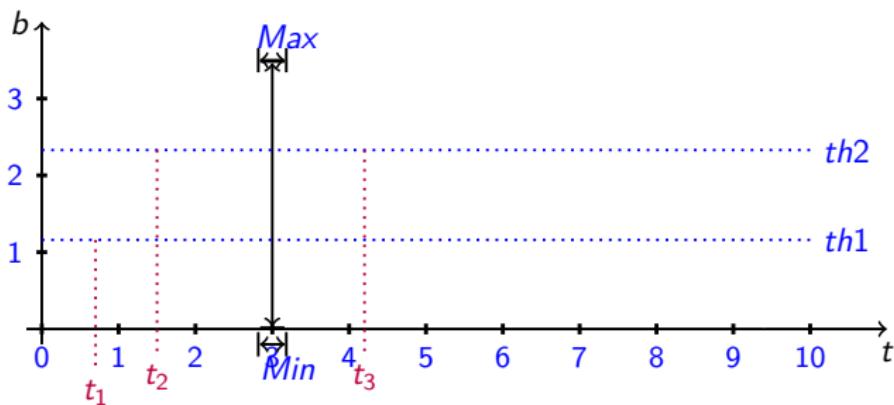


$$a_1 b_0 b_1 \text{ with } r_1 = \frac{1}{t_1 - t_0}$$

$$a_1 b_1 b_2 \text{ with } r_2 = \frac{1}{t_2 - t_1}$$

- Parameters estimation from time-series data

Data estimation from TSD



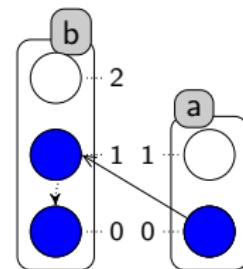
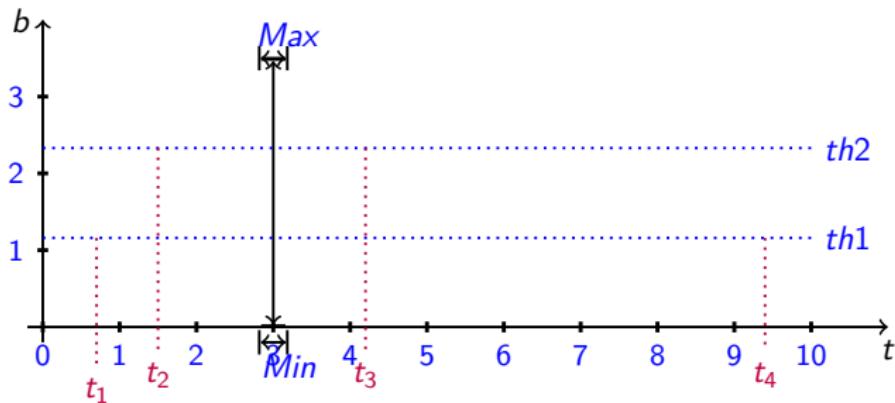
$$a_1 b_0 b_1 \text{ with } r_1 = \frac{1}{t_1 - t_0}$$

$$a_1 b_1 b_2 \text{ with } r_2 = \frac{1}{t_2 - t_1}$$

$$a_0 b_2 b_1 \text{ with } r_3 = \frac{1}{t_3 - t_2}$$

- Parameters estimation from time-series data

Data estimation from TSD



$$a_1 b_0 b_1 \text{ with } r_1 = \frac{1}{t_1 - t_0}$$

$$a_1 b_1 b_2 \text{ with } r_2 = \frac{1}{t_2 - t_1}$$

$$a_0 b_2 b_1 \text{ with } r_3 = \frac{1}{t_3 - t_2}$$

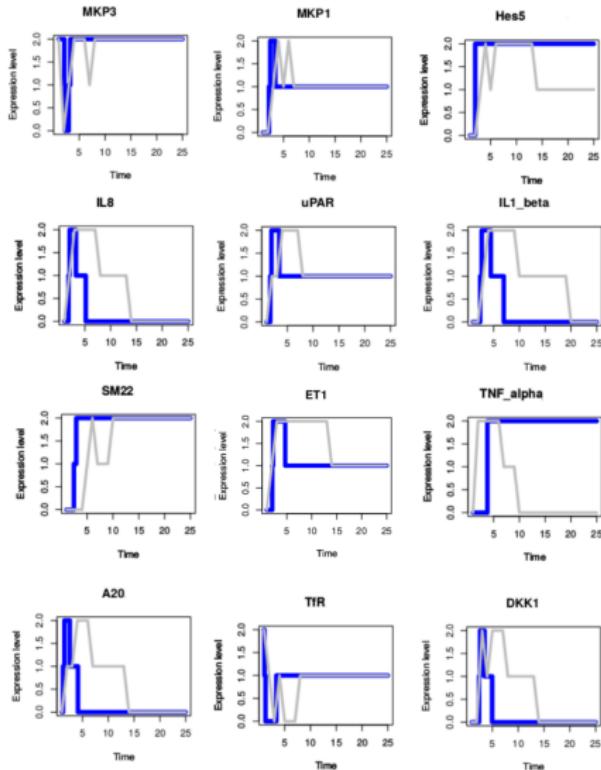
$$a_0 b_1 b_0 \text{ with } r_4 = \frac{1}{t_4 - t_3}$$

The formula to estimate the rate of the dynamics of a

component according to its TSD is $r_i = \frac{1}{t_i - t_{i-1}}$

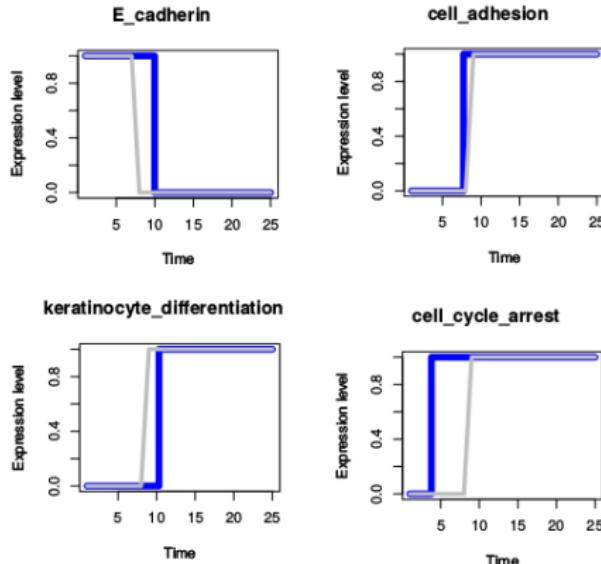
- Parameters estimation from time-series data

Simulations and analysis



- Parameters estimation from time-series data

Simulations and analysis

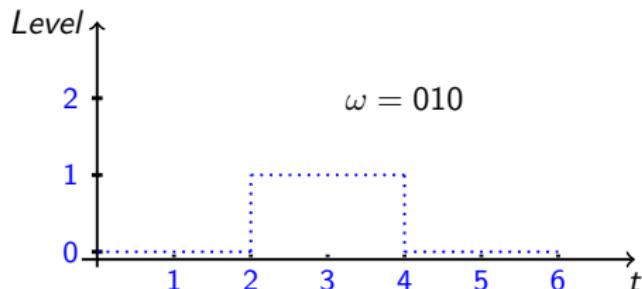


Simulations

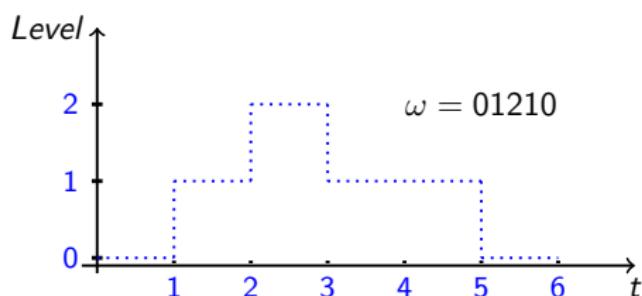
- Input node of the system ($E_cadherin$)
- For biological processes (Cell adhesion, Cell cycle arrest, Keratinocyte differentiation)

- Parameters estimation from time-series data

Simulation and Trace analysis



for each component C_i , $1 \leq i \leq P$, N simulations will generate $\omega_{i1}, \omega_{i2}, \dots, \omega_{iN}$ words.
 for $1 \leq j \leq N$



$\omega_{ij} \Rightarrow \boxed{\mathcal{A}_{C_i}} \Rightarrow \text{yes/no}$

$$\% \text{ofAcceptance} = \frac{\text{YES}}{\text{Simulations}}$$

- Parameters estimation from time-series data

Simulation and Trace analysis

Automate	components	% validation	% of acceptance T_1
$\mathcal{A}_2(01210)$	A20	91	100
$\mathcal{A}_2(01210)$	IL1_beta	81	100
$\mathcal{A}_2(01210)$	IL8	93	100
$\mathcal{A}_2(01210)$	TNF_alpha	0	0
$\mathcal{A}_3(01211)$	uPar	76	99
$\mathcal{A}_3(01211)$	ET1	8	19
$\mathcal{A}_4(0121210)$	DKK1	13	43
$\mathcal{A}_5(0121211)$	Hes5	0	17
$\mathcal{A}_5(0121211)$	MKP1	9	97
$\mathcal{A}_6(0212)$	SM22	11	100
$\mathcal{A}_7(02010)$	MKP3	11	98
$\mathcal{A}_8(02121)$	Tfr	0	94

- Formal inference of parameters

Formal inference of parameters

- Discussion

Discussion

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Thank you for your attention!!!