

Model Checking Liveness Properties of Genetic Regulatory Networks

Grégory Batt¹ Calin Belta¹ Ron Weiss²

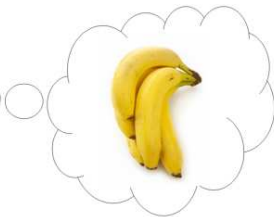
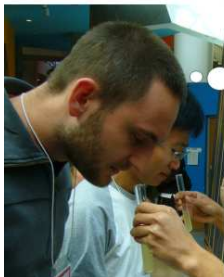
¹Center for Information and Systems Engineering and Center for Biodynamics,
Boston University

²Department of Electrical Engineering and Department of Molecular Biology,
Princeton University

Tools and Algorithms for Construction and Analysis of Systems
2007

Synthetic biology

- ✦ Synthetic biology: application of engineering approaches to produce novel artificial devices using biological building blocks

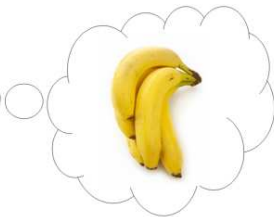


banana-smelling
bacteria

eau d'e coli | mit igem 2006

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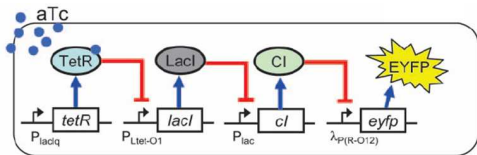
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- ✦ Numerous potential engineering and medical applications
 - biofuel production, environment depollution, ...
 - biochemical synthesis, tumor destruction, ...

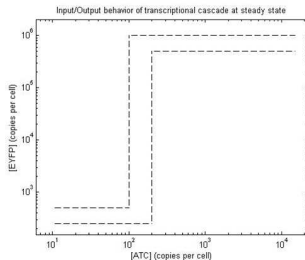
Need for rational design

- ✦ Gene networks are networks of genes, proteins, small molecules and their regulatory interactions



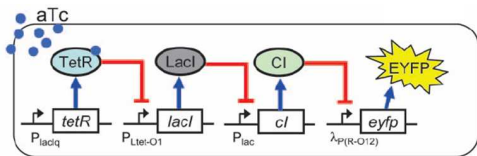
transcriptional cascade [Hooshangi *et al.*, PNAS 05]

ultrasensitive IO response



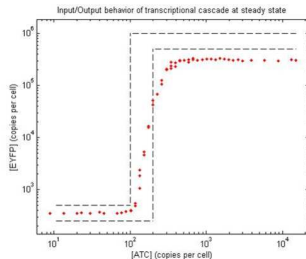
Need for rational design

- ✦ Gene networks are networks of genes, proteins, small molecules and their regulatory interactions



transcriptional cascade [Hooshangi *et al.*, PNAS 05]

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- ✦ Network design is difficult

Most newly-created networks are non-functioning and need tuning

Analysis of piecewise multi-affine (PMA) models

- ✦ Constraints: non-linear dynamical systems with uncertain parameters
 - genetic regulations described by sigmoidal functions
 - parameter uncertainties due to environmental fluctuations

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[Batt *et al.*, HSCC'07]

Analysis of piecewise multi-affine (PMA) models

- ✦ Constraints: non-linear dynamical systems with uncertain parameters
 - genetic regulations described by sigmoidal functions
 - parameter uncertainties due to environmental fluctuations
- ✦ Approach: combination of discrete abstraction and model checking tailored to efficient analysis of uncertain PMA models
[Batt *et al.*, HSCC'07]
- ✦ But: verification of liveness properties generally fails
 - liveness properties state that something will eventually happen
 - fails because quantitative aspects of time abstracted away:
need to enforce progress of time in discrete abstraction

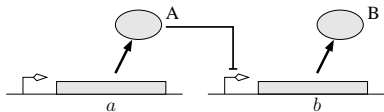
Outline

- 1 Introduction
- 2 Model checking uncertain PMA systems by discrete abstraction
- 3 Liveness checking using transient regions
- 4 Transient region computation for uncertain PMA systems
- 5 Analysis of a transcriptional cascade
- 6 Discussion

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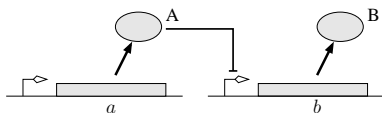
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Gene network models



inhibition network

Gene network models

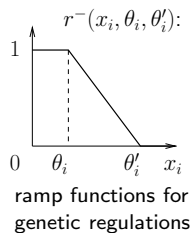


$$\dot{x}_a = \kappa_a - \gamma_a x_a$$

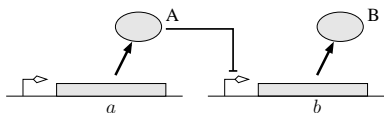
$$\dot{x}_b = \kappa_b r^-(x_a, \theta_a^1, \theta_a^2) - \gamma_b x_b$$

x : protein concentration,
 θ : threshold concentration,
 κ, γ : rate parameters,

inhibition network



Gene network models

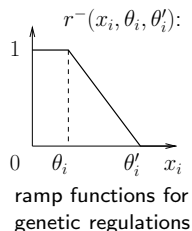


inhibition network

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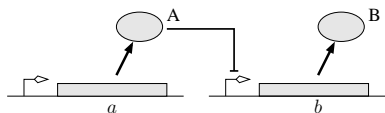
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✦ Check property: "At steady state, protein A concentration is high ($> \theta_a^2$) and protein B concentration is low ($< \theta_b$)"

Gene network models

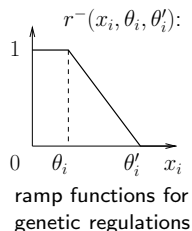


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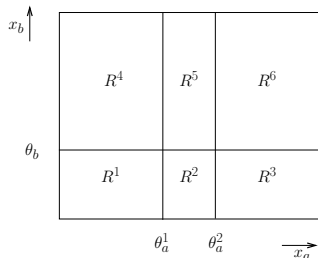
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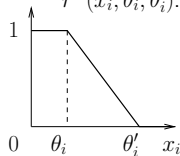
- ✦ Check property: "At steady state, protein A concentration is high ($> \theta_a^2$) and protein B concentration is low ($< \theta_b$)" for every parameter $p = (\kappa_a, \kappa_b) \in P = [14, 18] \times [10, 15]$

PMA systems

✦ Partition of the state space: rectangles $R \in \mathcal{R}$

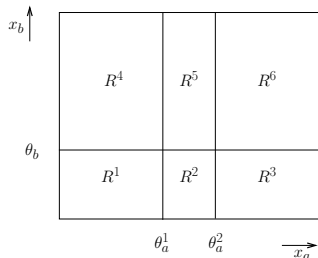


$$\begin{aligned}\dot{x}_a &= \kappa_a - \gamma_a x_a \\ \dot{x}_b &= \kappa_b r^-(x_a, \theta_a^1, \theta_a^2) - \gamma_b x_b \\ &\quad r^-(x_i, \theta_i, \theta'_i):\end{aligned}$$

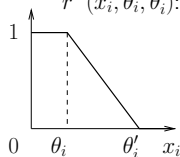


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✦ Differential equation models $\dot{x} = f(x, p)$, where

f is piecewise multiaffine function of state vector $x \in \mathcal{X}$

f is affine function of parameter vector $p \in \mathcal{P}$ (κ 's and γ 's)

(multiaffine: products of different variables allowed)

LTL specifications of dynamical properties

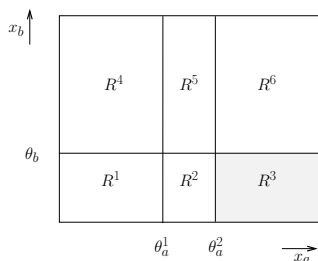
✚ Dynamical properties expressed in temporal logic LTL

- set of atomic proposition Π : $x_i < \lambda_i$, $x_i > \lambda_i$
- usual logical operators: $\neg\phi$, $\phi_1 \wedge \phi_2$, $\phi_1 \vee \phi_2$, $\phi_1 \rightarrow \phi_2$
- temporal operators: $X\phi$, $F\phi$, $G\phi$, $\phi_1 U \phi_2$

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"At steady state, protein A concentration is high ($> \theta_a^2$) and protein B concentration is low ($< \theta_b$)"

$$\forall p \in P, FG(x_a > \theta_a^2 \wedge x_b < \theta_b)$$

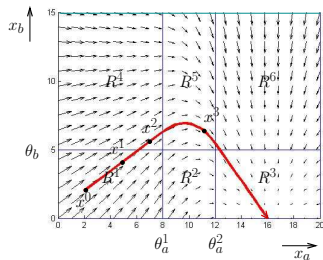
Discrete abstraction

- ✦ PMA system Σ and parameter set P associated with discrete abstraction $T_{\mathcal{R}}^{\exists}(P) = (\mathcal{R}, \rightarrow_{\mathcal{R}, P}^{\exists}, \models_{\mathcal{R}})$, where
- \mathcal{R} finite set of rectangles

Discrete abstraction

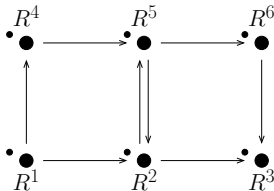
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- \mathcal{R} finite set of rectangles
- $\rightarrow_{\mathcal{R}, P}^{\exists}$ transition relation



$$p = (16, 12), x^0 = (2, 2)$$

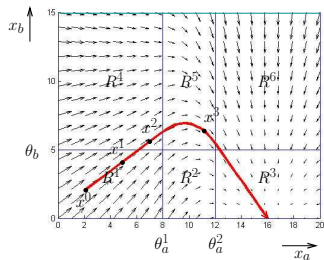
transition between same or adjacent rectangles R and R' iff for some $p \in P$ there exists a solution going from R to R'



Discrete abstraction

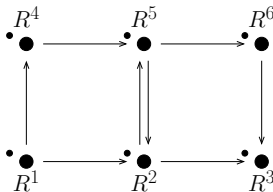
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$$R^1 \not\models_{\mathcal{R}} 'x_a > \theta_a^{2}'$$

$$R^1 \models_{\mathcal{R}} 'x_b < \theta_b'$$

Model checking using discrete abstraction

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✦ $T_{\mathcal{R}}^{\exists}(P)$ can be used for proving universal properties of original system Σ for sets of parameters

if $T_{\mathcal{R}}^{\exists}(P) \models \phi$, then $\forall p \in P, T_{\mathcal{X}}(p) \models \phi$

[Batt *et al.*, HSCC'07]

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✦ But: verification may fail because of spurious executions

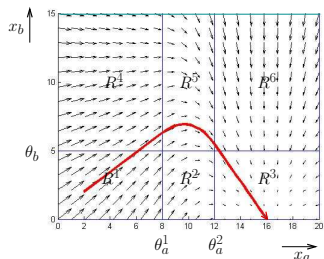
if $T_{\mathcal{R}}^{\exists}(P) \not\models \phi$, then no conclusion !

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Liveness checking

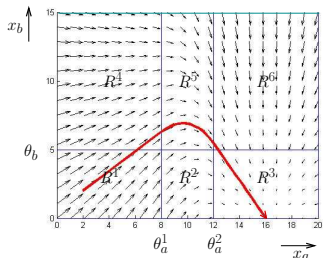
✦ Model checking liveness properties generally fails



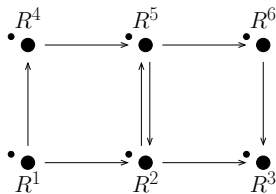
"Eventually, the system will remain in R^3 "

Liveness checking

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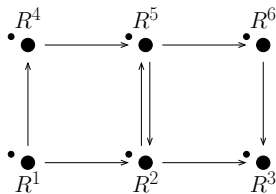
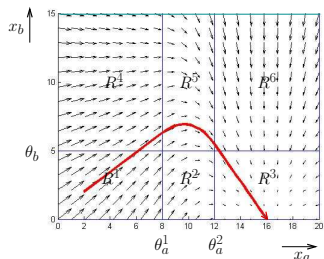
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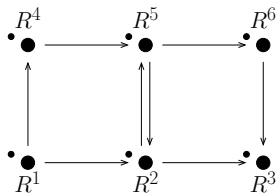
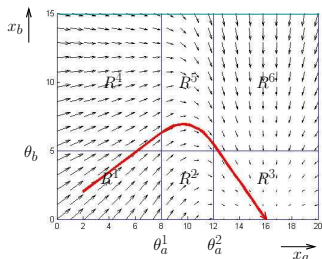
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False! counter-examples: $e_{R1} = (R^1, R^1, R^1, \dots)$
 $e_{R2} = (R^2, R^5, R^2, R^5, \dots)$

Liveness checking

✦ Model checking liveness properties generally fails



"Eventually, the system will remain in R^3 "

$$F G (x_a > \theta_a^2 \wedge x_b < \theta_b)$$

False! counter-examples: $e_{\mathcal{R}1} = (R^1, R^1, R^1, \dots)$
 $e_{\mathcal{R}2} = (R^2, R^5, R^2, R^5, \dots)$

✦ These counter-examples are spurious!

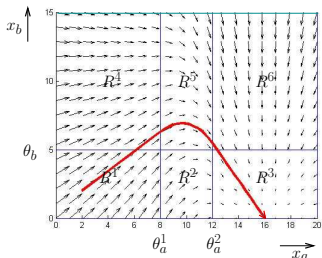
Definition

Let $p \in \mathcal{P}$ and $U \subseteq \mathcal{X}$. U is transient for parameter p if for every solution ξ such that $\xi(0) \in U$, there exists $\tau > 0$ such that $\xi(\tau) \notin \overline{U}$.

Transient regions

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all the regions not containing R^3 are transient

Time-diverging executions

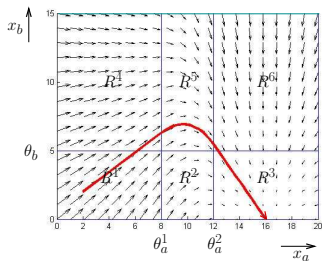
Definition

Let $P \subseteq \mathcal{P}$. An execution $e_{\mathcal{R}} = (R_0, R_1, \dots)$ of $T_{\mathcal{R}}^{\exists}(P)$ is time-diverging iff for some $p \in P$, there exist a solution ξ and a sequence of time instants $\tau = (\tau_0, \tau_1, \dots)$ such that $\lim_{i \rightarrow \infty} \tau_i = \infty$ and $\xi(\tau_i) \in R_i$, for all $i \geq 0$.

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$e_{\mathcal{R}1} = (R^1, R^1, R^1, \dots)$ and
 $e_{\mathcal{R}2} = (R^2, R^5, R^2, R^5, \dots)$
are time-converging executions

Transient regions and time-converging executions

- ✦ An execution $e_{\mathcal{R}}$ remains eventually always in a strongly connected component (SCC) of $T_{\mathcal{R}}^{\exists}(P)$, $SCC(e_{\mathcal{R}}) \subseteq \mathcal{X}$

Transient regions and time-converging executions

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- ✦ $SCC(e_{\mathcal{R}})$ cannot be transient if $e_{\mathcal{R}}$ is time-diverging!

Proposition

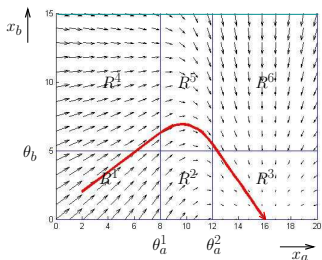
Let $P \subseteq \mathcal{P}$ and $e_{\mathcal{R}}$ be an execution of $T_{\mathcal{R}}^{\exists}(P)$. If $SCC(e_{\mathcal{R}})$ is transient for all $p \in P$, then $e_{\mathcal{R}}$ is time-converging.

Transient regions and time-converging executions

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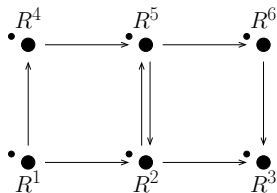


$SCC(e_{\mathcal{R}_1}) = \{R^1\}$ and
 $SCC(e_{\mathcal{R}_2}) = \{R^2, R^5\}$ are transient regions
So $e_{\mathcal{R}_1}$ and $e_{\mathcal{R}_2}$ are time-converging

Ruling-out time-converging executions

✦ Approach (assuming that transient regions can be computed)

① compute discrete abstraction $T_{\mathcal{R}}^{\exists}(P)$ and its SCCs

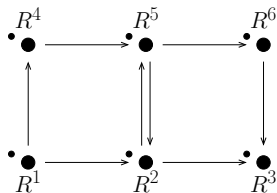


SCCs: $\{R^1\}$ $\{R^2, R^5\}$ $\{R^3\}$ $\{R^4\}$ $\{R^6\}$

Ruling-out time-converging executions

✦ Approach (assuming that transient regions can be computed)

- 1 compute discrete abstraction $T_{\mathcal{R}}^{\exists}(P)$ and its SCCs
- 2 test whether SCCs are transient or not

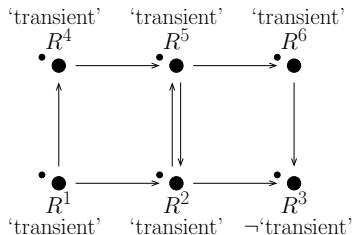


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transient? Y Y N Y Y

Ruling-out time-converging executions

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- 1 compute discrete abstraction $T_{\mathcal{R}}^{\exists}(P)$ and its SCCs
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- 3 label every rectangle in a transient SCC by 'transient', and test whether $T_{\mathcal{R}}^{\exists}(P) \models \phi'$, where $\phi' = (\neg F G \text{'transient'}) \rightarrow \phi$

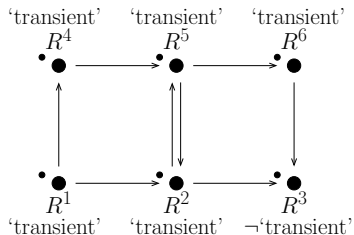


$T_{\mathcal{R}}^{\exists}(P) \models \phi'$? with $\phi' =$
 $(\neg F G \text{'transient'}) \rightarrow F G (x_a > \theta_a^2 \wedge x_b < \theta_b)$

Ruling-out time-converging executions

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True!

Outline

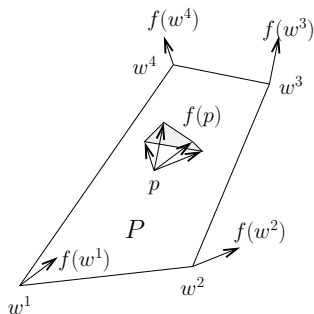
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Transient region computation for PMA systems

Convexity properties of affine and multiaffine functions

- Let f be an affine function and P be a polytope. Then, $\forall p \in P$, $f(p) \in \text{hull}(\{f(w) \mid w \in \mathcal{V}_P\})$.

[Habets et al., Trans Aut Contr, 06]



Transient region computation for PMA systems

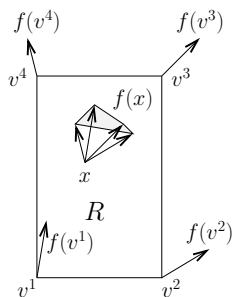
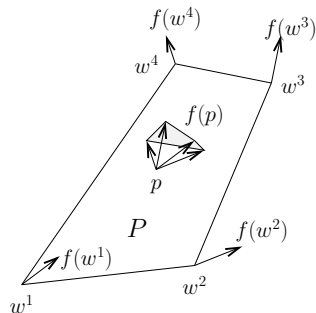
Convexity properties of affine and multiaffine functions

- Let f be an affine function and P be a polytope. Then, $\forall p \in P$, $f(p) \in \text{hull}(\{f(w) \mid w \in \mathcal{V}_P\})$.

[Habets et al., Trans Aut Contr, 06]

- Let f be a multiaffine function and R be a hyperrectangle. Then, $\forall x \in R$, $f(x) \in \text{hull}(\{f(v) \mid v \in \mathcal{V}_R\})$.

[Belta and Habets, Trans Aut Contr, 06]

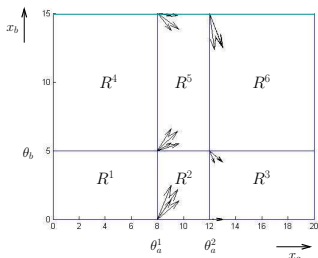


Transient region computation for PMA systems

Proposition

Let $P \subseteq \mathcal{P}$ be a polytope and U a union of rectangles.

If $0 \notin \text{hull}(\{f(v, w) \mid v \in \mathcal{V}_R, R \subseteq U, w \in \mathcal{V}_P\})$, then U is transient for all parameters $p \in P$.



$$x \in R^2 \cup R^5,$$

$$p \in P = [14, 18] \times [8, 14]$$

$$R^2 \cup R^5 \text{ is transient for all } p \in P$$

✦ Decidable by solving linear optimization problem

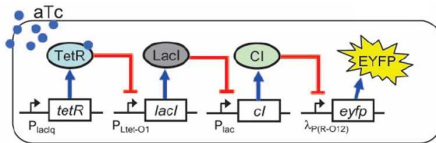
✦ Implemented in RoVerGeNe (Robust Verification of Gene Networks)

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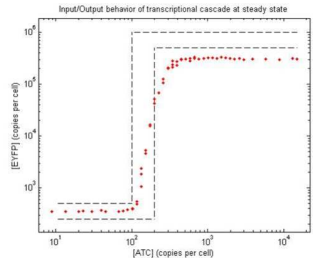
Robustness analysis of transcriptional cascade

- ✦ Previous analysis of synthetic transcriptional cascade suggested parameter modifications for network tuning



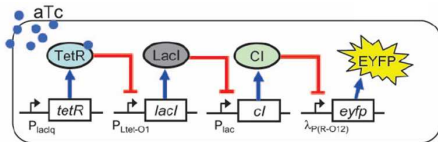
transcriptional cascade

ultrasensitive IO response



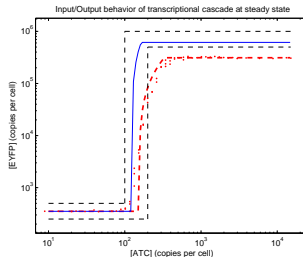
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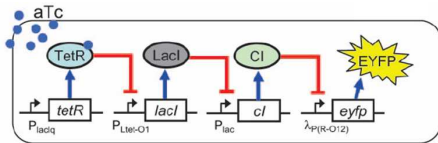


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 \dot{x}_{tetR} &= \kappa_{tetR} - \gamma_{tetR} x_{tetR}, \\
 \dot{x}_{lacI} &= \kappa_{lacI}^0 + \kappa_{lacI} (1 - r^+(x_{tetR}, \theta_{tetR}^1, \theta_{tetR}^2)) r^-(u_{aTc}, \theta_{aTc}^1, \theta_{aTc}^2) - \gamma_{lacI} x_{lacI} \\
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PMA model

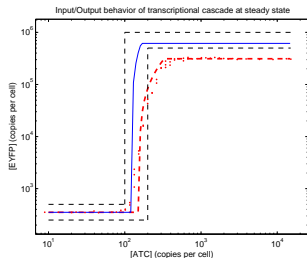
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PMA model

- Does modified network behave robustly?

Robustness analysis of transcriptional cascade

- ✦ Test whether expected property holds for parameter variations up to $\pm 10\%$ (or $\pm 20\%$) (11 uncertain parameters)

Robustness analysis of transcriptional cascade

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1 specify expected (liveness) property

$$\begin{aligned}\phi_1 = & \quad u_{aTc} < 100 \rightarrow \text{F G } (2.5 \cdot 10^2 < x_{eyfp} < 5 \cdot 10^2) \\ & \wedge 100 < u_{aTc} < 200 \rightarrow \text{F G } (2.5 \cdot 10^2 < x_{eyfp} < 10^6) \\ & \wedge \quad u_{aTc} > 200 \rightarrow \text{F G } (5 \cdot 10^5 < x_{eyfp} < 10^6).\end{aligned}$$

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- ✦ Approach can prove non-trivial liveness property of a 5-dimensional state space and 11-dimensional parameter space system in < 4 hrs

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- ✦ Approach implemented in RoVerGeNe and applied to analysis of synthetic gene network
 - Approach can answer efficiently non-trivial questions on networks of biological interest

✚ Related work:

- spurious behaviors introduced by abstraction process ruled out using fairness constraints
[Bouajjani *et al.*, SAS'01], [Dams *et al.*, WAVE'00]
- verification of liveness properties limited to systems having simple continuous dynamics (timed automata)
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✦ Future research directions:

- application to other classes of hybrid systems
- use abstraction that preserves quantitative aspects of time: timed abstraction

Thank you for your attention!

see also Model checking genetic regulatory networks with parameter uncertainty, HSCC'07
G. Batt, C. Belta and R. Weiss