## An automata-based formalism for analysing stochastic models of biological networks

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#### Context

- discrete-state stochastic models (applied to biology)
  - continuous-time Markov chains (CTMCs)
  - more generally discrete-event stochastic processes (DESPs)
- Performance analysis (desiderata):
  - Ianguages for definition of key performance indicators (KPIs)
  - tools for (automatically) assessing KPIs of a given model
  - in this talk: hybrid automata as a means to express KPIs
- What kind of performance indicators ?:
  - temporal logic reasoning: allow for sophisticated indicators, e.g.:
    - what is the population of nucleic β-catenin at time T if LRP5 receptor gets inhibited at least N times within T?
    - ► how many mRNA are transcribed within T if gene X stay repressed at most T' < T? ...</p>

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Hybrid Automata Specification Language

**Biological case studies** 

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#### Discrete event stochastic process (DESP)

- a countable set of states  $S = \{s_0, s_1, ...\}$
- a fine set of events  $E = \{e_1, e_2, \dots, e_n\}$ 
  - events occurr with a continuous delay given by a distribution of probability



## What kind of analysis for a DESP model ?

- computing state-probability distributions: probability to be in a given state s
  - at-time-t (transient-state distribution)
  - in-the-long-run,  $t \rightarrow \infty$  (steady-state distribution)

- computing average values: e.g. the average population of X at time t
  - boils down to computing state-probability distributions

- computing probability of a path event
  - path event: set of trajectories fulfilling given temporal conditions

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## Classification of path events

time-bounded state-reachability: reaching a state-region within given delay [Continuous Stochastic Logic, *Aziz* 2000]



"within time  $t \in [\alpha, \beta]$  population  $y_1$  reaches  $[0, n_a]$  without leaving  $[n_a, n_b]$ "

## Classification of path events

event-conditioned state-reachability: reaching a state by observing only specific events [asCSL, *Baier et al.*, 2003]



"within time  $t \in [\alpha, \beta]$  population  $y_1$  reaches  $[0, n_a]$  by traversing first  $[n_a, n_b]$ , where only events of  $E_1 \subset E$  are observed, then  $[n_b, n_c]$ , where only events of  $E_2 \subset E$  are observed"

## Classification of path events

multiple-bounded state-reachability: several time bounds on a single reachability condition [1-clock time-automaton, CSL<sup>TA</sup>, Haddad et al. 2007]



"within time  $t \in [\alpha', \beta']$   $y_1$  reaches  $[n_b, n_c]$  by traversing  $[n_a, n_b]$ , then within time  $t \in [\alpha'', \beta'']$  it reaches  $[0, n_a]$  while staying within  $[n_b, n_c]$ 

## Temporal logic for performance evaluation

allow for reasoning (to different extent) about behaviour of a DESP through a combination of:

- state-condition: CSL, pLTL,
- state/event-condition: asCSL, CSL<sup>TA</sup>
- reward-based-condition: CSRL (to some extent)

**Hybrid Automata Specification Language**: using of Hybrid Automata to specify path events.

- very powerful specification language
- allow for combining state+event+reward-based conditions for selecting relevant paths

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## HASL-based performance evaluation



#### input:

- model: a DESP D
- formula: a pair (A, Z)

output:

► 100(1-ε)% confidence interval of E[Z]

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## Synchronizying a DESP with a Hybrid Automata



 $\mathcal{A}$ :  $\Rightarrow$  selects specific paths of  $\mathcal{D}$ 

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HASL model-checking scheme (intuitively):

- a timed-path  $\sigma$  of  $\mathcal{D}$  is generated through stochastic simulation
- A decides whether σ is accepted or not, meanwhile collecting data about σ
- collected data is used for estimating relevant measures (wrt accepted paths)

#### example: selecting paths of gene-exp. toy model



DESP toy-model of gene-expression in Stochastic Petri Net form

#### Linear Hybrid Automata for selecting paths of DESP $\ensuremath{\mathcal{D}}$



## specifying the quantity to estimate w.r.t. the selected paths



 $\phi_1 \equiv (\mathcal{A}_1, E[last(n_1)]) : avg. number of completed transcriptions within T$ 

•  $\phi'_1 \equiv (A_2, E[max(r) - min(r)])$ : max. deviation of RBS population within completing *N* transcriptions

•  $\phi_2 \equiv (A_2, PDF(last(t), step, start, end))$ : PDF of delay for completing *N* transcriptions calculated by histogram over support [start, end] discretised into step-wide sub-intervals

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#### Gene-expr. with stochastic delayed dynamics

gene expression: the process through which proteins are synthesized from a sequence of DNA.

$$\begin{array}{l} R_{1} : Pro + *RNAp \xrightarrow{k_{1}} Prox \\ R_{2} : Prox \xrightarrow{\lambda_{1}} Pro + RBS + R(\Gamma(G_{len}, 0.09)) \\ R_{3} : *Rib + RBS \xrightarrow{k_{lr}} RBS(\delta(\tau_{1})) + Rib(\Gamma(G_{len}, 0.06)) + \\ & + P(\Gamma(\tau_{5_{sh}}, \tau_{5_{sc}})) \end{array}$$

$$\begin{array}{l} R_{4} : RBS \xrightarrow{rbsd} \emptyset \\ \\ R_{5} : Pro + Rep \xrightarrow{k_{r}} ProRep \\ \\ R_{6} : ProRep \xrightarrow{k_{unr}} Pro + Rep \end{array}$$

a single-gene model ([Ribeiro et al. 2006, Journal Comp. Biology]):



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## 1- measuring PDF of completed transcriptions

#### Model settings:

- unrep: no repressor
- rep(1): one mol. of repressor
- rep(2): two mol. of repressor
  LHA settings:
  - N: completed transcriptions



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#### 2- measuring sustainment of translation

**sustainment of translation** : "how long does it take for an on-going translation to halt since repression kicks in (given that translation halts)"



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## an LHA for measuring sustainment of translation





## measuring the sustainment of gene translation

experiment settings:

- constant repression duration i.e. unrepress  $\sim \delta(10)$
- varying RBS decay rate



cross point (~0.01): RBS decays so slowly that translations never stops for the majority of repression-intervals

## 3- Probability of inter-transcription translations

"with what probability N translations will complete in between two consecutive transcription events?"



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### measuring PDF of inter-transcription translations

experiment settings:

repressed vs unrepressed model



PDF num. of translations within transcription interval

- unrepressed model: probability density with maximum around N ~ 1.2
- repressed model: PDFs asymptotically decreasing (independent of the level of repression)

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## the problem: formal analysis of oscillations

Q1: can we find a temporal logic characterisation of oscillations for a stochastic model? Yes, through automata specifications

Q2: can we use it to decide whether a stochastic model oscillates ? Yes for CTMC [Spieler 2014]

Q3: can we use it to measure the characteristics (i.e. period, amplitude) of an oscillator ? to different extend with either timed or hybrid automata

 oscillation: the repetitive variation (in time), of some measure about a central value



#### measuring the period: noisy periodicity [Spieler 2009,2014]

given two thresholds L < H, a function σ<sub>A</sub> is noisy periodic iff it (perpetually) crosses the intervals *low*[0, L), *mid*[L, H), *low*[H, +∞).



noisy period realisation: delay between two consecutive mid-low crossing points interleaved by a visit to the high region

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#### Formal characterisation of noisy period (1)



- ▶  $\tau_{j\downarrow}$  (resp.  $\tau_{j\uparrow}$ ): the *j*<sup>th</sup> mid-to-low (resp. mid-to-high) crossing point
- ►  $T_{\downarrow} = \cup_j \tau_{j\downarrow}$  (resp.  $T_{\uparrow} = \cup_j \tau_{j\uparrow}$ ) set of all *low-crossing points*
- *T<sub>k↓</sub>* ⊆ *T<sub>↓</sub>*: *k*-th sequence of contiguous *low-crossing points* not interleaved by any *high-crossing point*

$$T_{1\downarrow} = \{\tau_{1\downarrow}, \tau_{2\downarrow}\}, T_{2\downarrow} = \{\tau_{3\downarrow}\}, \ldots$$

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#### Formal characterisation of noisy period (2)



For  $\sigma_A$  a noisy periodic trajectory we define:

- ►  $t_{\rho_k} = min(T_{(k+1)\downarrow}) min(T_{k\downarrow})$  ( $k^{th}$ noisy period realisation)
- ►  $\bar{t}_p(n) = \frac{1}{n} \sum_{k=1}^n t_{p_k}$  (average period estimator)

• 
$$s_{t_p}^2(n) = \frac{1}{n} \sum_{k=1}^n (t_{p_k} - \overline{t}_p(n))^2$$
 (period variance estimator)

## Hybrid automata for noisy period detection



- detect noisy-periodic traces of observed species A (stops at N<sup>th</sup> period)
- variables: t (total duration of periods) n (counter of periods) top (boolean flag) tp (duration of last detected period); µtp (avg. period until last detected); s<sup>2</sup><sub>tp</sub> (period variance until last detected)
- output measures:
  - $Z_1 \equiv E[last(\bar{t}_p)]$
  - $Z_2 \equiv PDF(\overline{t}_p, s, l, h)$
  - $Z_3 \equiv E[last(s_{t_p}^2)]$
- (average period duration)(PDF of the average period duration)(variance of period duration)

## Circadian-clock oscillator

[Vilar *et al.* 2002]



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# mean/variance of oscillation period measured with $\mathcal{A}_{\textit{period}}$



- ► HASL specifications:  $\phi_1 : (A_{period}, E[last(\bar{t}_p)]) \qquad \phi_2 : (A_{period}, E[last(s_{t_p}^2)])$
- experiment setting: num. of observed periods (per trace) N=100, L=1, H=1000 partition

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 outcome: slowing repressor degradation increases the period duration, but makes oscillations more "stochastic" (larger variance of period duration)

### Measuring the amplitude: noisy alternance

given a noise value  $\delta > 0$ , a function  $\sigma_A$  is  $\delta$  alternating if it contains infinitely many  $\delta$ -separated local minima (and equivalently  $\delta$ -separated local maxima).

- goal: to locate the peaks of oscillation
- local max : the maximum value distanced at least δ from previous local min



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remark: we don't impose any specific L < H thresholds</p>

## Hybrid automata for detecting peaks of $\delta$ alternating traces



- detect local maxima and minima for observed species A (stops at N<sup>th</sup> maxima)
- ▶ requires: *i*) partitioning event set  $(E = E_{A_{-}} \cup E_{A_{+}})$ ; *ii*) setting  $\delta$  par.
- variables: Lmax (detected local max); Lmin (detected local min)
- output measures:
  - $Z_{max} \equiv E[last(Smax)/n_M]$
  - $Z_{min} \equiv E[last(Smin)/n_m]$

(average height of  $\delta$ -separated maxima) (average height of  $\delta$ -separated minima)

## Circ. clock max/min peaks measured with $A_{peaks}$



- HASL measures: (A<sub>peaks</sub>, E[last(Smax)/n<sub>M</sub>])), (A<sub>peaks</sub>, E[last(Smin)/n<sub>m</sub>]))
- degradation of R reduces maximal peaks of R but has no effects on A's
- num. of observed local Max N=100 per trace
- ► δ=10% of absolute max of observed species

### Message to bring home ...

- hybrid automata are powerful means for expressing performance indicators of biological models
  - ► Example: need to measure oscillations ⇒ you can !

tool support: COSMOS statistical model-checker (https://www.lacl.fr/~barbot/cosmos/)

#### perspectives:

- HASL driven parameter estimation: devise the parameters of a DESP model so to maximise an HASL measure
- improving HASL runtime: resorting to approximated stochastic simulation techniques

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