Groupe de travail Dyliss

Analysis of Biological Networks: A Summary of my Works

Analyse des réseaux biologiques: un résumé de mes travaux

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Overview of This Presentation

Frameworks: modeling biological processes

- Thomas modeling (historically widespread)
- Asynchronous Automata Networks (generalization)
- Hybrid Thomas modeling (generalization)

Model completion: inferring missing information on the model

- Hybrid Hoare logic (parameters/logical gates on Hybrid Thomas modeling)
- Continuous transitions (logical thresholds from expression profiles)

Dynamic analyses: explore the dynamics of a model

- µ-calculus & Answer Set Programming (exhaustive)
- Abstract interpretation (approximations)

 $TGF-\beta$ pathways project: my work here as a postdoc

- Extract and build a big graph from databases
- Search for inconsistencies in cancerous types

Analysis of Biological Networks o Frameworks

Frameworks

Abstractions of the Representation



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[Kauffman, Journal of Theoretical Biology, 1969] [Thomas, Journal of Theoretical Biology, 1973]

• A set of components $N = \{a, b, z\}$



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- A set of discrete expression levels for each component $a \in \mathbb{F}^a = [0; 2]$
- The set of global states $\mathbb{F} = \mathbb{F}^a \times \mathbb{F}^b \times \mathbb{F}^z$



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- The set of global states $\mathbb{F} = \mathbb{F}^a imes \mathbb{F}^b imes \mathbb{F}^z$
- An evolution function for each component $f^z : \mathbb{F} \to \mathbb{F}^z$



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- Signs on the edges $a \xrightarrow{+} z$ or signs & thresholds $a \xrightarrow{2,+} z$



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- Signs on the edges $a \xrightarrow{+} z$ or signs & thresholds $a \xrightarrow{2,+} z$
- Discrete parameters / evolution functions $f^a: \mathbb{F} \to \mathbb{F}^a$



The state-graph depicts the whole dynamics Computation: **exponential** in the size of the model





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• Stable state = state with no successors

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- **Stable state** = state with no successors
- Complex attractor = minimal loop or composition of loops from which the dynamics cannot escape
- Reachability = from 000, can I reach 201?

Analysis of Biological Networks o Frameworks o Asynchronous Automata Networks

Asynchronous Automata Networks (AAN) Enriched Process Hitting (PH)







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Model from [François et al., Molecular Systems Biology, 2007]



Translations Between AAN and Thomas Modeling

[Folschette et al., Theoretical Computer Science, 2015a] [Folschette et al., CS2Bio'13, 2013]



- Asynchronous Automata Networks encompass Thomas modeling
- Mutual translations developed
- Results are also mutually applicable

Analysis of Biological Networks o Model Completion

Model Completion

A Simplified Circadian Cycle Model



- $m_1 = PER/CRY$ complex inhibits *per* and *cry* genes
- $m_2 = \text{transcription}$ and complexation
- $m_3 =$ light makes BMAL1/CLOCK complex activate *per* and *cry* genes
- $m_4 \& m_5 = 12h \text{ day/night oscillation}$

Analysis of Biological Networks o Model Completion o Hybrid Thomas Modeling & Hoare Logic



Analysis of Biological Networks o Model Completion o Hybrid Thomas Modeling & Hoare Logic



Hybrid Hoare Logic to Infer Parameters

$$\begin{cases} ???\\ ???\\ B+ \end{cases}; \begin{pmatrix} T_{3}\\ \text{slide}^{+}(B)\\ A- \end{pmatrix}; \begin{pmatrix} T_{2}\\ \top\\ B- \end{pmatrix}; \begin{pmatrix} T_{1}\\ \top\\ A+ \end{pmatrix} \begin{cases} D_{0} \equiv (\eta_{A} = 2 \land \eta_{B} = 0)\\ H_{0} \equiv (\pi_{\text{initial}} = \pi_{\text{final}}) \end{cases}$$



Maxime FOLSCHETTE

$$\begin{array}{l} ((((((((\pi_{p'}^{0'} = 0.12) \land ((\pi_{pc}^{0'} = 0.12) \land (\pi_{p}^{0'} = 0))) \land ((((\pi_{1}^{1} = 1) \land (((C_{1, \{m5\}, 0} > 0) \land (\pi_{1}^{1'} = (\pi_{1}^{1} - (C_{L, \{m5\}, 0} \times 6.6))))) \land ((((C_{pc, g, 1} < 0) \land (\pi_{pc}^{1'} < (\pi_{1}^{1} - (C_{pc, g, 1} \times 6.6)))) \land ((((C_{p, g, 0} > 0) \land (\pi_{1}^{1'} > (\pi_{1}^{1} - (C_{x, g, 0} \times 6.6))))) \land (((\pi_{1}^{1} = (1 - \pi_{1}^{0'})) \land (((\pi_{1}^{1} = \pi_{1}^{0'}) \land (((\pi_{1}^{1} = \pi_{1}^{0'}) \land ((\pi_{1}^{1} = \pi_{1}^{0'}) \land ((\pi_{1}^{1} = \pi_{1}^{0'}) \land (((\pi_{1}^{1} = \pi_{1}^{1'}) \land (((\pi_{1}^{2} = \pi_{1}^{1'}) \land (((\pi_{1}^{2} = \pi_{1}^{1'}) \land (((\pi_{1}^{2} = \pi_{1}^{1'}) \land (((\pi_{1}^{2} = \pi_{1}^{1'})))))) \land ((((\pi_{1}^{3} = 0) \land ((C_{2, g, 0} \land ((\pi_{1}^{3} \cap ((((\pi_{1}^{1} = \pi_{1}^{2'}) \land ((\pi_{1}^{2} = \pi_{1}^{1'}) \land ((\pi_{2}^{2} = \pi_{2}^{1'}) \land (((\pi_{2}^{2} = \pi_{2}^{2'}) \land (((\pi_{2}^{3} = ((\pi_{1}^{2} - (C_{2, g, 1} \times ((\pi_{1}^{3} = \pi_{1}^{2'}) \land ((\pi_{2}^{3} = \pi_{2}^{2'}) \land ((\pi_{2$$

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Results

- Simplifications of the constraints
- Let's use a solver! :-)
- Results checked with a simulation:



Simulation with compatible values

Experiments

Modeling Gene Interactions

Goal: understand biological dynamics, i.e. gene interactions.

Data: time series

- discrete/regular time steps
- continuous value

Model: Boolean network

- discrete/regular time steps
- discrete values





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Continuum Logic Program



INPUT: time series data

OUTPUT: A continuum logic program

$$\begin{array}{l} \rho([0,0.5],t) \leftarrow q([0,0.5],t-1).\\ \rho([0.5,1],t) \leftarrow q([0.5,1],t-1).\\ q([0,0.5],t) \leftarrow \rho([0,0.5],t-1) \wedge r([0.5,1],t-1).\\ q([0.5,1],t) \leftarrow \rho([0.5,1],t-1) \wedge r([0.5,1],t-1).\\ r([0,0.5],t) \leftarrow \rho([0.5,1],t-1).\\ r([0.5,1],t) \leftarrow \rho([0,0.5],t-1). \end{array}$$

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Analysis of Biological Networks o Exhaustive Dynamic Analyses

Dynamic Analysis


- Enumeration of attractors & disruptions
- Bisimulation between two models (regarding some observables)
- Searching Zeno behaviors



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Answer Set Programming (ASP): Declarative & logic programming

Rule: $head \leftarrow body$.

"If body is true, then head must be true (usual logical consequence)"

```
act: head.
"head is always tru
```

```
Constraint: \bot \leftarrow body.
"If body is true, it invalidates the whole answer set"
```

```
Example:

node(a). node(b). node(c).

edge(a, b). edge(b, c). edge(a, c).

edge(X, Y) \leftarrow edge(Y, X).
```



```
Solving: Finding the minimal set of atoms satisfying the problem
node(a) node(c) node(b)
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Cardinalities: $min \{ atom : enum \} max \leftarrow body.$

- Enumerates all atoms of the form *atom* according to the variables of *enum*
- Keep between *min* and *max* possibilities
- Creates as many answer sets as there are combinations

```
General method:
```

Answer set 3: attrib(b,blue) attrib(c,green) attrib(a,red

: (6 answer sets)

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General method:

```
1) Enumerate of all candidate combinations using cardinalities
  color(red). color(green). color(blue).
  1 { attrib(X, C) : color(C) } 1 \leftarrow node(X).
Answer set 1: attrib(b,red) attrib(c,red) attrib(a,red)
Answer set 2: attrib(b,red) attrib(c,red) attrib(a,blue)
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  :
  : (27 answer sets)
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2) Filter out the undesired candidates using constraints

```
\perp \leftarrow attrib(X, C), attrib(Y, C), edge(X, Y).
Answer set 1: attrib(b,green) attrib(c,blue) attrib(a,red)
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```

```
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```

Conclusion on ASP for Model-checking

[Ben Abdallah, Folschette, Roux, Magnin, BIBM'15, 2015] [Ben Abdallah, Folschette, Roux, Magnin, AMB, 2017]

• General approach applied to dynamical analysis:

- 1) Describe the model with facts and rules (automata, actions, dynamics)
- 2) Enumerate all states/all dynamics with cardinalities
- 3) Filter out unwanted results
- Applications: Stable states, Reachability analysis, Attractors enumeration
- Pros: Very flexible (programming language) & Complexity handled by the solver
- Cons: Iterative approach (requires to cap the search) & Still computational

Models		Stable states	Reachability analysis		
Name	States	ASP	libddd ¹	GINsim ²	ASP
egfr20	2 ⁶⁴	0.017s	1min 55s	2min 32s	12s
tcrsig40	2 ⁷³	0.021s	∞	∞	4min 28s

¹ LIP6/Move [Couvreur et al., Lecture Notes in Computer Science, 2002]

² TAGC/IGC [Chaouiya, Naldi, Thieffry, Methods in Molecular Biology, 2012]

egfr20 : Epithelial Growth Factor Receptor (20 components) [Sahin et al., 2009]

tcrsig40 : T-Cell Receptor (40 components) [Klamt et al., 2006]

Analysis of Biological Networks o Static Analyses o Classical Results of Static Analysis on Thomas Modeling

Static Analysis of Thomas Modeling

[Thomas, Numerical Methods in the Study of Critical Phenomena, 1981]

Conjectures of René Thomas:



Analysis of Biological Networks o Static Analyses o Classical Results of Static Analysis on Thomas Modeling

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Conjectures of René Thomas:

• Multiple stable states \Rightarrow positive cycle in the graph



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Proofs: [Remy, Ruet & Thieffry, Advances in Applied Mathematics, 2008] [Richard, Advances in Applied Mathematics, 2010] [Richard & Comet, Discrete Applied Mathematics, 2007]

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Conjectures of René Thomas:

- Multiple stable states ⇒ positive cycle in the graph
 No positive cycle in the graph ⇒ The stable state (if any) is unique
- Sustained oscillations (complex attractor) ⇒ negative cycle in the graph



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Conjectures of René Thomas:

- Multiple stable states ⇒ positive cycle in the graph
 No positive cycle in the graph ⇒ The stable state (if any) is unique
- Sustained oscillations (complex attractor) ⇒ negative cycle in the graph No negative cycle in the graph ⇒ No complex attractor (only stable states)



Proofs: [Remy, Ruet & Thieffry, Advances in Applied Mathematics, 2008] [Richard, Advances in Applied Mathematics, 2010] [Richard & Comet, Discrete Applied Mathematics, 2007]

- \rightarrow Directly checking *R* is hard (exponential)
- \rightarrow Rather check **approximations** *P* and *Q* so that: $P \Rightarrow R \Rightarrow Q$ Computing *P* or *Q* is much simpler (roughly **polynomial**)



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GT Dyliss - 2017/11/15









OK! :-) scenario = $\{c_0, f_1\} \rightarrow a_0
ightharpoonup a_1$






Analysis of Biological Networks o Static Analyses o Static Analysis by Abstract Interpretation



Analysis of Biological Networks o Static Analyses o Static Analysis by Abstract Interpretation



 $\mathsf{OK!:-)} \quad \{a_0\} \rightarrow c_1 \mathrel{\upharpoonright} c_0 \; :: \; \{c_0,f_1\} \rightarrow a_0 \mathrel{\upharpoonright} a_1$

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Implementation of the Abstract Interpretation

Complexity:

- Computation of the local causality graph:
 - · Polynomial in the number of automata
 - Exponential in the number of local states of each automata (usually very low, max. 4)
- Analysis of the graph (sufficient condition):
 - Polynomial in the size of the abstract graph
- Enumeration of the subsets of solutions (if needed):
 - Exponential in the size of the abstract graph

ightarrow Very efficient on biological networks: many components with few local states

Model					
egfr20					
tcrsig40	54			∞	
tcrsig94	133	1124	$[>1$ min – ∞]		
egfr104			$[>1 min - \infty]$		

¹ LIP6/Move [Couvreur et al., Lecture Notes in Computer Science, 2002]

² TAGC/IGC [Chaouiya, Naldi, Thieffry, Methods in Molecular Biology, 2012]

³ Loïc Paulevé [http://loicpauleve.name/pint/]

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Model	Automata	Actions	States	libddd ¹	GINsim ²	PINT ³
egfr20	35	670	2 ⁶⁴		< 1s	0.02s
tcrsig40	54	301	2 ⁷³		∞	0.02s
tcrsig94	133	1124	2 ¹⁹⁴	$[>1min - \infty]$		0.03s
egfr104	193	2356	2 ³²⁰	$[>1min - \infty]$		0.16s

¹ LIP6/Move [Couvreur et al., Lecture Notes in Computer Science, 2002]

² TAGC/IGC [Chaouiya, Naldi, Thieffry, Methods in Molecular Biology, 2012]

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Analysis of Biological Networks o Ongoing work in IRISA

Ongoing Work









TGF-β Pathways Project



TGF-β Pathways Project





Inconsistency Search With Coloring

- Some observations from experiments give an initial coloring
- Propagate the coloring to neighbor nodes
- Minimize inconsistencies
- Minimize the repairs to fix the inconsistencies



Summary

Frameworks: modeling biological processes

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- µ-calculus & Answer Set Programming (exhaustive)
- Abstract interpretation (approximations)

TGF-β pathways project: my work here as a postdoc

- Extract and build a big graph from databases
- Search for inconsistencies in cancerous types

Collaborations



Olivier ROUX



Morgan MAGNIN



Emna BEN ABDALLAH



Tony RIBEIRO



Katsumi INOUE



Martin LANGE



Loïc PAULEVÉ



Jean-Paul COMET



Jonathan BEHAEGEL

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[Paulevé et al., Mathematical Structures in Computer Science, 2012]



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 $\begin{array}{c} \rightarrow \text{ Concretization of the objective} = \text{scenario} \\ \underline{a_0 \rightarrow c_0 \mathrel{\upharpoonright} c_1} :: b_0 \rightarrow d_0 \mathrel{\upharpoonright} d_1 :: c_1 \rightarrow b_0 \mathrel{\upharpoonright} b_1 :: b_1 \rightarrow d_1 \mathrel{\upharpoonright} d_2 \end{array}$

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 $\label{eq:alpha} \begin{array}{c} \rightarrow \text{ Concretization of the objective} = \text{scenario} \\ a_0 \rightarrow c_0 \mathrel{\Bar{\upharpoonright}} c_1 :: \underline{b_0} \rightarrow d_0 \mathrel{\Bar{\upharpoonright}} d_1 :: c_1 \rightarrow b_0 \mathrel{\Bar{\upharpoonright}} b_1 :: b_1 \rightarrow d_1 \mathrel{\Bar{\upharpoonright}} d_2 \end{array} \end{array}$

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- \rightarrow Directly checking *R* is hard (exponential)
- \rightarrow Rather check **approximations** *P* and *Q* so that: $P \Rightarrow R \Rightarrow Q$ Computing *P* or *Q* is much simpler (roughly **polynomial**)



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 $\{a_0\} \rightarrow c_1 \stackrel{\scriptstyle{\uparrow}}{} c_0 \ :: \ \{c_0, f_1\} \rightarrow a_0 \stackrel{\scriptstyle{\uparrow}}{} a_1$



 $\{a_0\} \rightarrow c_1 \stackrel{\scriptscriptstyle}{\sqcap} c_0 \ :: \ \{c_0, f_1\} \rightarrow a_0 \stackrel{\scriptscriptstyle}{\sqcap} a_1$

Implementation of the Abstract Interpretation

Complexity:

- Computation of the local causality graph:
 - · Polynomial in the number of automata
 - Exponential in the number of local states of each automata (usually very low, max. 4)
- Analysis of the graph (sufficient condition):
 - Polynomial in the size of the abstract graph
- Enumeration of the subsets of solutions (if needed):
 - Exponential in the size of the abstract graph

ightarrow Very efficient on biological networks: many components with few local states

Model					
egfr20					
tcrsig40	54			∞	
tcrsig94	133	1124	$[>1$ min – ∞]		
egfr104			$[>1 min - \infty]$		

¹ LIP6/Move [Couvreur et al., Lecture Notes in Computer Science, 2002]

² TAGC/IGC [Chaouiya, Naldi, Thieffry, Methods in Molecular Biology, 2012]

³ Loïc Paulevé [http://loicpauleve.name/pint/]

egfr20 : Epithelial Growth Factor Receptor (20 components) [Sahin et al., 2009]

egfr104 : Epithelial Growth Factor Receptor (104 components) [Samaga et al., 2009]

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 \rightarrow Very efficient on biological networks: many components with few local states

Model	Automata	Actions	States	libddd ¹	GINsim ²	PINT ³
egfr20	35	670	2 ⁶⁴		< 1s	0.02s
tcrsig40	54	301	2 ⁷³		∞	0.02s
tcrsig94	133	1124	2 ¹⁹⁴	$[>1min - \infty]$		0.03s
egfr104	193	2356	2 ³²⁰	$[>1min - \infty]$		0.16s

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Under-approximation





Under-approximation

Sufficient condition:

- no cycle
- · each objective has a solution





Under-approximation

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P is **true** \Rightarrow *R* is **true**









Necessary condition:





Necessary condition:

- objective \rightarrow follow **one** solution
- solution \rightarrow follow **all** processes
- process \rightarrow follow **all** objectives





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Necessary condition:

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- process \rightarrow follow **all** objectives

Q is **false** \Rightarrow *R* is **false**





Necessary condition:

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- solution \rightarrow follow **all** processes
- process → follow all objectives





Necessary condition:

There exists a traversal with no cycle

- objective \rightarrow follow **one** solution
- solution \rightarrow follow **all** processes
- process \rightarrow follow **all** objectives

R is true \Rightarrow Inconclusive



Analysis of Biological Networks o Static Analysis on the Process Hitting o Exhaustive Analysis with µ-calculus

The Polyadic µ-caculus



Analysis of Biological Networks o Static Analysis on the Process Hitting o Exhaustive Analysis with µ-calculus

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The Polyadic μ -caculus



Modal and Polyadic µ-calculus [Andersen, Technical report, 1994]

LTL: Implicit fixed point of the "Until" operator $p \ U \ q \equiv$ "Either q, or p and the next state also verifies $p \ U \ q$ "

(Modal) µ-calculus makes such fixed points explicit

 $\varphi = p \mid \neg \varphi \mid \varphi \land \varphi \mid \varphi \lor \varphi \mid \Diamond \varphi \mid \Box \varphi \mid \mu X.\varphi \mid \nu X.\varphi \mid X$

- Basic property: *p* ("*p* is verified in this node"
- Modal operators: □ ("for all successors"), ◊ ("there exists a successor")
- Fixed points: μ (least fixed point), ν (greatest fixed point)

Polyadic (modal) µ-calculus allows to manipulate several tokens in parallel

 $\varphi = p_i \mid i \leftarrow j \mid i = j \mid \neg \varphi \mid \varphi \land \varphi \mid \varphi \lor \varphi \mid \Diamond_i \varphi \mid \Box_i \varphi \mid \mu X.\varphi \mid \nu X.\varphi \mid X$

Token manipulations:

i = *j* ("make tokens *i* and *j* point to the same node") *i* ← *j* ("move token *i* to the position of token *j*")

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No tokens: only one evolution is studied **Atomic property (**p, q, r**)** $\llbracket p \rrbracket = \{p\}$ $\llbracket q \lor r \rrbracket = \{q; r\}$ **Possible future ("may")** $\llbracket \diamond q \rrbracket = \{p\}$ **Necessary future ("must")** $\llbracket \Box q \rrbracket = \varnothing$ $\llbracket \Box p \rrbracket = \{q; r\}$



No tokens: only one evolution is studied

Atomic property (p, q, r) $\begin{bmatrix} p \end{bmatrix} = \{p\}$ $\begin{bmatrix} q \lor r \end{bmatrix} = \{q; r\}$

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Examples with Polyadic μ -calculus



Atomic property (p, q, r) $[\![p_1 \wedge r_2]\!] = \{(p, r)\}$

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Atomic property (p, q, r) $[\![p_1 \wedge r_2]\!] = \{(p, r)\}\$ $[p_1] = \{(p, p); (p, q); (p, r)\}$


Atomic property (p, q, r) $[p_1 \land r_2] = \{(p, r)\}$ $[p_1] = \{(p, p); (p, q); (p, r)\}$ Token affectation $(i \leftarrow j)$ $[\{2 \leftarrow 1\} p_1 \land p_2] = \{(p, p); (p, q); (p, r)\}$ Token comparison (i = j) $[1 = 2] = \{(p, p); (q, q); (r, r)\}$ Possible future ("may") $[[\Diamond_1 q]] = \{(p, p); (p, q); (p, r)\}$

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Least fixed point (
$$\mu$$
)
 $\phi = \mu X.(\Box_1 \bot \land \Box_2 \bot) \lor \Diamond_1 \Diamond_2 X$

terations: $\begin{bmatrix} \phi \end{bmatrix}_0 = \emptyset \\ \begin{bmatrix} \phi \end{bmatrix}_1 = \{(a_1, b_1)\} \\ \begin{bmatrix} \phi \end{bmatrix}_2 = \{(a_1, b_1); (a_2, b_2)\} \\ \begin{bmatrix} \phi \end{bmatrix}_3 = \{(a_1, b_1); (a_2, b_2); (a_3, b_3)\} \\ \vdots$

Generalization: $\llbracket \phi \rrbracket = \{(a_i, b_i) \mid i \in [1; \min(m, n)]\}$



Least fixed point (μ) $\phi = \mu X.(\Box_1 \bot \land \Box_2 \bot) \lor \Diamond_1 \Diamond_2 X$

Iterations:

$$\begin{split} \llbracket \phi \rrbracket_0 &= \varnothing \\ \llbracket \phi \rrbracket_1 &= \{(a_1, b_1)\} \\ \llbracket \phi \rrbracket_2 &= \{(a_1, b_1); (a_2, b_2)\} \\ \llbracket \phi \rrbracket_3 &= \{(a_1, b_1); (a_2, b_2); (a_3, b_3)\} \end{split}$$

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Generalization: $\llbracket \phi \rrbracket = \{(a_i, b_i) \mid i \in [1; \min(m, n)]\}$

Applications of the Polyadic μ -calculus



Objective: Unify formulas for many dynamical problems

Not always possible with classical temporal logics (LTL, CTL, CTL*):

1) From the initial state (a, b, z) = (0, 0, 0), is it possible to reach z = 2? $(a = 0 \land b = 0 \land z = 0) \Rightarrow EF(z = 2)$

2) Does (0,0,0) belong to an attractor? $(a = 0 \land b = 0 \land z = 0) \Rightarrow N \bot \lor AG(EF(a = 0 \land b = 0 \land z = 0))$

What is the set of attractors of the model?
 ??? — Requires a quantification on the set of all states

Idea: Use polyadic μ -calculus with one token per automata



= belongs to an attractor

$$\varphi_{\mathsf{att}} = \{ \mathbf{y} \leftarrow \mathbf{x} \} \nu W.\underbrace{(\mu Z. (\mathbf{x} = \mathbf{y}) \lor (\Diamond_{\mathbf{x}} Z))}_{\varphi_{\mathsf{reach}}} \land (\Box_{\mathbf{x}} W)$$

•
$$\llbracket \varphi_{\text{reach}} \rrbracket = \{(s; t) \mid s \to^* t\}$$

 $\varphi_{\text{reach}} \equiv \text{``There exists a path from } x \text{ to } y$ ''

- $\llbracket \varphi_{explore} \rrbracket = \{(s; t) \mid \forall s', s \to^* s' \Rightarrow s' \to^* t\}$ $\varphi_{explore} \equiv$ "All successors of x can reach y"
- $\llbracket \varphi_{\text{att}} \rrbracket = \{(s; s) \mid \forall s', s \to^* s' \Rightarrow s' \to^* s\}$ $\varphi_{\text{att}} \equiv "x \text{ belongs to an attractor"}$



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 $\varphi_{att} \equiv "x$ belongs to an attractor"



- $\llbracket \varphi_{noreach} \rrbracket = \{(s; t) \mid \neg(t \rightarrow^* a)\}$ $\varphi_{noreach} \equiv$ "There exists no path from y to a"
- $\llbracket \varphi_{\text{disr}} \rrbracket = \{(s; t) \mid s \to t \land s \to^* a \land \neg(t \to^* a)\}$ $\varphi_{\text{disr}} \equiv$ "There is a disruption between x and y"

 $\varphi_{\text{disr}} \equiv$ "There is a disruption between x and y"

Bisimulation with Polyadic μ -calculus

Generic bisimulation between two models:

$$\varphi_{\mathsf{bisim}} = \nu X . (\bigwedge_{p \in P} p_1 \Leftrightarrow p_2) \land (\Box_1 \Diamond_2 X \land \Box_2 \Diamond_1 X)$$

Bisimulation only on two sets of **observable components** O and O':

$$\varphi_{\mathsf{bisim-obs}} = \nu X. (\bigwedge_{p \in P} \bigwedge_{(i:j) \in C} p_i \Leftrightarrow p_j) \land (\Box_{\overline{O}}^* \Box_O \Diamond_{\overline{O'}}^* \Diamond_{O'} X)$$

where:

$$\Box_{S}\Psi = \bigwedge_{i \in S} \Box_{i}\Psi \qquad \qquad \Diamond_{S}\Psi = \bigvee_{i \in S} \Diamond_{i}\Psi$$
$$\Box_{S}^{*}\Psi = \nu Y.\Psi \land \Box_{S}Y \qquad \qquad \Diamond_{S}^{*}\Psi = \mu Y.\Psi \lor \Diamond_{S}\Psi$$

Conclusion on Polyadic μ -calculus

Properties expressed so far:

- Enumeration of attractors
- Enumeration of disruptions
- Bisimulation between two models (regarding a set of observables)
- Highlighting Zeno behaviors

Aim: Unification of properties without quantifiers

Complexity: Exponential (equivalent to building the state graph)

Outlooks:

- New formulas
- Implementation
- Generate µ-calculus formulas? (More readable interface)

Hybrid Thomas Modeling

[Cornillon et al., Modelling Complex Biological Systems in the Context of Genomics, 2016]

lacI repressor regulation of the lactose operon in E. Coli

$$A = NRI$$
 protein + glnG gene + glnA promoter

 $\mathrm{B}=\mathrm{lacI}$ gene repressor $+~\mathrm{glnK}$ promoter

 $m_1 = \text{glnA}$ promoter is regulated by phosphorylated NRI

 $m_2 = \text{glnA}$ promoter is also regulated by lacI

 $m_3 = {
m lacI}$ gene repressor is regulated by ${
m NRIp}$

Hybrid Thomas Modeling

Hybrid Thomas Modeling

Hybrid Hoare Logic to Infer Parameters

$$\begin{cases} D_4 \\ H_4 \end{cases} \begin{pmatrix} T_4 \\ \top \\ B+ \end{pmatrix}; \begin{pmatrix} T_3 \\ \text{slide}^+(B) \\ A- \end{pmatrix}; \begin{pmatrix} T_2 \\ \top \\ B- \end{pmatrix}; \begin{pmatrix} T_1 \\ \top \\ A+ \end{pmatrix} \begin{cases} D_0 \equiv (\eta_A = 2 \land \eta_B = 0) \\ H_0 \equiv \top \end{cases}$$

Maxime FOLSCHETTE

$$\begin{split} H_F &\equiv \left(\neg (C_{B,\varnothing,0} > 0) \lor \neg (1 > \pi_B^{0\,'} - C_{B,\varnothing,0} \cdot T_1)\right) \\ &\wedge (C_{A,\{m_1,m_3\},1} > 0) \land (\pi_A^{1\,'} = 1 - C_{A,\{m_1,m_3\},1} \cdot T_1) \\ &\wedge \left(\neg (C_{A,\{m_1\},1} > 0) \lor \neg (1 > \pi_A^{1\,'} - C_{A,\{m_1\},1} \cdot T_2)\right) \\ &\wedge \left((C_{A,\varnothing,0} > 0) \lor \neg (C_{A,\{m_1\},1} < 0) \lor \neg (1 < \pi_A^{1\,'} - C_{A,\{m_1\},1} \cdot T_2)\right) \\ &\wedge (C_{B,\varnothing,1} < 0) \land (1 = 0 - C_{B,\varnothing,1} \cdot T_2) \\ &\wedge \left(\neg (C_{B,\{m_2\},1} < 0) \lor \neg (0 < 1 - C_{B,\{m_2\},1} \cdot T_3)\right) \\ &\wedge \left((C_{A,\{m_1\},2} < 0 \land (\pi_A^{3\,'} = 0 - C_{A,\{m_1\},2} \cdot T_3)\right) \\ &\wedge \left(\neg (C_{B,\{m_2\},1} > 0) \lor (0 > 1 - C_{B,\{m_2\},1} \cdot T_3)\right) \\ &\wedge \left(\neg (C_{A,\{m_1,m_3\},2} < 0) \lor \neg (0 < \pi_A^{3\,'} - C_{A,\{m_1,m_3\},2} \cdot T_4)\right) \\ &\wedge (C_{B,\{m_2\},0} > 0) \land (\pi_B^{0\,'} = 1 - C_{B,\{m_2\},0} \cdot T_4) \ . \end{split}$$

A Simplified Circadian Cycle Model

$$\begin{array}{l} ((((((((\pi_{p}^{0'} = 0.12) \land ((\pi_{p}^{0'} = 0.12) \land (\pi_{p}^{0'} = 0))) \land ((((\pi_{1}^{1} = 1) \land (((L_{{}_{1}} \{m_{5}^{1}, 0 > 0) \land (\pi_{1}^{1'} = (\pi_{1}^{1} - (L_{{}_{1}} \{m_{5}^{1}, 0 > 0) \land (\pi_{2}^{1'} > (\pi_{3}^{1} - (L_{{}_{2}} (m_{0} > 0 > 0) \land (\pi_{1}^{1'} > (\pi_{3}^{1} - (L_{{}_{2}} (m_{0} > 0 > 0) \land (\pi_{1}^{1'} = (1 - \pi_{0}^{1'})) \land (((\pi_{1}^{1} = \pi_{0}^{0'}) \land (((\pi_{1}^{1} = \pi_{0}^{0'}) \land ((\pi_{1}^{1} = \pi_{0}^{0'}) \land (\pi_{1}^{1} = \pi_{0}^{0'}) \land (((L_{{}_{2}} (m_{0} > 0) \land (\pi_{1}^{1'} > (\pi_{1}^{1} - (L_{{}_{2}} (m_{0} > 0 < 0)))) \land ((((L_{{}_{2}} (m_{0} > 0) \land ((\pi_{2}^{1'} = \pi_{0}^{1'}) \land ((((L_{{}_{2}} (m_{0} > 0) \land (((L_{{}_{2}} (m_{0} < 0) \land ((\pi_{2}^{2'} = (\pi_{2}^{2} - (L_{{}_{2}} (m_{0} < 0 < 0))))) \land ((((L_{{}_{2}} (m_{0} < 0) \land (((m_{1}^{2} = \pi_{0}) \land (((L_{{}_{2}} (m_{0} < 0) \land ((\pi_{2}^{2'} = (\pi_{2}^{2} - (L_{{}_{2}} (m_{0} < 0 < 0))))) \land ((((\pi_{1}^{2} = \pi_{0}) \land (((L_{{}_{2}} (m_{0} < 0) \land ((\pi_{2}^{2'} = (\pi_{2}^{2} - (L_{{}_{2}} (m_{0} < 0 < 0))))) \land ((((\pi_{2}^{2} = \pi_{1}^{2'}) \land (((\pi_{2}^{2} = \pi_{1}^{2'}) \land ((\pi_{1}^{2} = \pi_{1}^{1'})))))) \land ((((\pi_{2}^{2} = \pi_{1}^{2'}))))) \land ((((\pi_{2}^{2} = \pi_{1}^{2'}) \land ((\pi_{2}^{2} = \pi_{1}^{2'} (m_{1}^{2} - (L_{{}_{2}} (m_{1} < 0) \land (\pi_{2}^{3'} < (\pi_{2}^{2} - (L_{{}_{2}} (m_{1} < 0) \land (\pi_{3}^{3'} < (\pi_{2}^{2} - (L_{{}_{2}} (m_{2} < (m_{1} < 0) \land (\pi_{3}^{3'} < ((\pi_{2}^{2} - (L_{{}_{2}} (m_{1} < 0) \land (\pi_{3}^{3'} < (\pi_{2}^{2} - (L_{{}_{2}} (m_{2} < (m_{2} < (m_{1} < 0) \land (\pi_{3}^{3'} < (\pi_{2}^{2} - (L_{{}_{2}} (m_{2} < (m_{2} <$$

Manually simplified constraints

Célérités sur g et pc		Célérités sur L et X	
$C_{g,\varnothing,0} < 0$ $C_{g,\varnothing,1} < 0$ $C_{g,\{L\},0} < 0$ $C_{g,\{L\},1} < 0$ $C_{g,\{pc\},0} > 0$ $C_{g,\{pc\},0} > 0$ $C_{g,\{pc\},1} > 0$	$C_{g,\{pc,L\}_{0}} > 0$ $0 < C_{g,\{pc,L\}_{1}} < \frac{1}{5.53}$ $C_{pc,\varnothing,0} < 0$ $C_{pc,\emptyset,1} = -\frac{0.12}{0.9}$ $0 < C_{pc,\{g\},0} < \frac{1}{6.13}$ $0 < C_{pc,\{g\},1} < \frac{1}{4}$		$C_{X,\emptyset,0} < 0 -\frac{1}{6} \leq C_{X,\emptyset,1} < 0 0 < C_{X,\{L\},0} < \frac{1}{5.1} C_{X,\{L\},1} > 0$

Results with compatible constraints from another work

