Journée MDSC

Analysing Biological Networks with Exhaustive and Abstract Methods

Analyse des réseaux biologiques par des méthodes exhaustives et d'approximation

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Overview of This Presentation

Frameworks: the models we will talk about

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

Exhaustive analyses: classical model-checking approaches with a high complexity

- Modal logic with an explicit fixed point: **µ-calculus**
- Logic programming: Answer Set Programming

Static analyses: approximations of the dynamics for lower complexity

- Classical results of static analysis
- Abstract interpretation: a finer approach

Abstractions of the Representation



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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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- 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 $a \xrightarrow{2,+} z$
- Discrete parameters / evolution functions $f^a : \mathbb{F} \to \mathbb{F}^a$



Analysing Biological Networks with Exhaustive and Abstract Methods o Frameworks o Asynchronous Automata Networks







Analysing Biological Networks with Exhaustive and Abstract Methods \circ Frameworks \circ Asynchronous Automata Networks



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

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



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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Attractor = minimal set of states from which the dynamics cannot escape

- Stable state (state with no successors)
- Complex attractor (loop or composition of loops)

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













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



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









Analysing Biological Networks with Exhaustive and Abstract Methods o Exhaustive Dynamic Analyses o Analysis with µ-calculus

The Polyadic μ -caculus



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Analysing Biological Networks with Exhaustive and Abstract Methods \circ Exhaustive Dynamic Analyses \circ Analysis with μ -calculus

The Polyadic µ-caculus



The Modal μ -calculus

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")

• $i \leftarrow j$ ("move token *i* to the position of token *j*")

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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



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

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

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



= belongs to an attractor

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

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Conclusion on Polyadic μ -calculus

Properties expressed so far:

- Enumeration of attractors
- Enumeration of switches
- 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)

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
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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:
```

nswer 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)
Answer set 3: attrib(b,red) attrib(c,green) attrib(a,blue)
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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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Analysing Biological Networks with Exhaustive and Abstract Methods o Exhaustive Dynamic Analyses o Analysis with Logic Programming

ASP for Model-checking

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

Usage: Describe the problem instead of its resolution

Stable states enumeration

- 1) Describe the model with facts (automata, actions)
- 2) Describe what a playable action is with rules
- 3) Enumerate all states with cardinalities
- 4) Filter out states with a playable action

Reachability analysis (reaching a given state)

- 1) Describe the model with facts (automata, actions, initial & target states)
- 2) Create the dynamics:
 - describe playability with rules
 - enumerate potential futures with cardinalities and constraints
- 3) Filter out paths that don't end in the target state

Conclusion on ASP for Model-checking

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

Complexity: Exponential (exhaustive computation of the dynamics) But strong heuristics that give good results

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]

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

Pros: Very flexible (programming language),

The complexity taken care of by the solver

Outlooks:

- New properties to check (reverse reachability, Eden gardens)
- Optimizations (exclude cycles)

Static Analysis of Thomas Modeling

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

Conjectures of René Thomas:



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Conjectures of René Thomas:

- Multiple stable states \Rightarrow positive cycle in the graph
- Sustained oscillations (complex attractor) ⇒ negative cycle in the graph



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

Static Analysis of Thomas Modeling

[Thomas, Numerical Methods in the Study of Critical Phenomena, 1981] [Paulevé & Richard, Electronic Notes in Theoretical Computer Science, 2012]

Contrapositives:

- No positive cycle in the graph \Rightarrow The stable state (if any) is unique
- No negative cycle in the graph \Rightarrow No complex attractor (only stable states)

Other results:

- Lower & upper bounds of the number of attractors
- Functionality of the cycles
- Sufficient condition for no stable state
- Topological stable states

Complexity: Usually very low (searching for all cycles)

Limitations: Very broad results on the dynamics (cannot predict the evolution of one particular component)

 \rightarrow Need for more precise methods

Over- and Under-approximations

- \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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 $\{c_0, f_1\} \rightarrow a_0
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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/]

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

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

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

tcrsig94 : T-Cell Receptor (94 components) [Saez-Rodriguez et al., 2007]

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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]

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]

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

tcrsig94 : T-Cell Receptor (94 components) [Saez-Rodriguez et al., 2007]

• Discrete modeling = coherent abstraction of real biochemical phenomena

- \rightarrow Discrete Networks / Thomas modeling
- \rightarrow Asynchronous Automata Networks
- \rightarrow ...And other extensions related to Asynchronous Automata Networks
- Polyadic μ-calculus
 - ightarrow More generic than CTL*
 - \rightarrow Examples: enumeration of attractors, switches, bisimulation...
 - \rightarrow Ongoing implementation
- Answer Set Programming
 - → Logic programming works!
 - ightarrow Powerful heuristics giving good performances
- Static analysis by abstract interpretation
 - \rightarrow (Only) reachability properties (CTL operator EF)
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Under-approximation





Under-approximation

Sufficient condition:

- no cycle
- each objective has a solution





Under-approximation

Sufficient condition:

- no cycle
- each objective has a solution

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









Over-approximation

Necessary condition:





Necessary condition:

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





Necessary condition:

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





Necessary condition:

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

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





Necessary condition:

- objective \rightarrow follow one solution
- 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 → follow all objectives

R is true \Rightarrow Inconclusive



Examples with Modal μ -calculus



No tokens: only one evolution is studied

Atomic property (p, q, r) $\llbracket p \rrbracket = \{p\}$

Examples with Modal μ -calculus



No tokens: only one evolution is studied

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

Examples with Modal $\mu\text{-calculus}$



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Necessary future ("must") $\llbracket \Box \ q \rrbracket = \varnothing$

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No tokens: only one evolution is studied

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

Possible future ("may") $[\Diamond q] = \{ p \}$

Necessary future ("must") $\begin{bmatrix} \Box & q \end{bmatrix} = \emptyset$ $\begin{bmatrix} \Box & p \end{bmatrix} = \{q; r\}$



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



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***)** $[[{2 \leftarrow 1} p_1 \land p_2]] = \{(p, p); (p, q); (p, r)\}$



Atomic property (p, q, r) $\begin{bmatrix} p_1 \land r_2 \end{bmatrix} = \{(p, r)\} \\
 \begin{bmatrix} p_1 \end{bmatrix} = \{(p, p); (p, q); (p, r)\}$ Token affectation (i \leftarrow j) $\begin{bmatrix} \{2 \leftarrow 1\} \ p_1 \land p_2 \end{bmatrix} = \{(p, p); (p, q); (p, r)\}$ Token comparison (i = j) $\begin{bmatrix} 1 = 2 \end{bmatrix} = \{(p, p); (q, q); (r, r)\}$



Atomic property (p, q, r) $\begin{bmatrix} p_1 \land r_2 \end{bmatrix} = \{(p, r)\} \\
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Examples with Polyadic μ -calculus



Atomic property (p, q, r) $[p_1 \wedge r_2] = \{(p, r)\}$ $[p_1] = \{(p, p); (p, q); (p, r)\}$ 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") $[[\diamond_1 q]] = \{(p, p); (p, q); (p, r)\}$ Necessary future ("must") $\llbracket \Box_1 \ q \rrbracket = \varnothing$

Examples with Polyadic $\mu\text{-calculus}$





Examples with Polyadic $\mu\text{-calculus}$



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

Iterations:

÷

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

Examples with Polyadic $\mu\text{-calculus}$



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

Iterations:

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

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

Examples with Polyadic μ -calculus



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

Iterations: $\llbracket \phi \rrbracket_{a} = \emptyset$

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

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

Idea: use one (or *n*) token per automata