Constraint-based abstraction of reaction networks to Boolean networks

Athénaïs Vaginay

@Caen, 5th December 2023

Systems Biology

Formal modelling and reasoning about biological systems

A set of species of interest genes, proteins, cells, animals...



How does the system evolve?

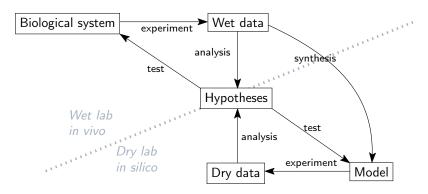
Is the population of some cell type stable over time?

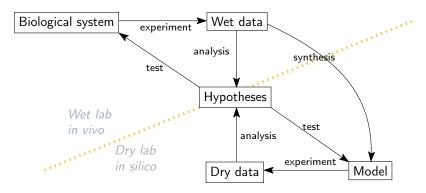


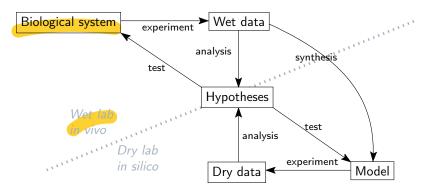
How to control the system?

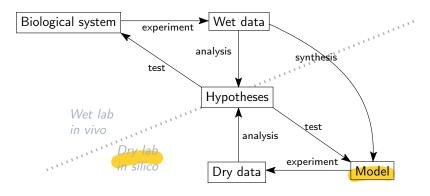
Cure a pathological system
Produce more of some species of
interest





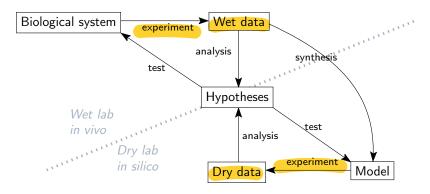






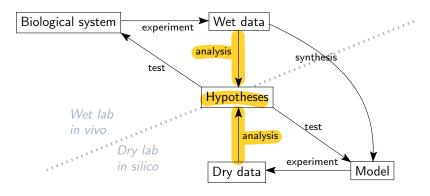
Definition (Model)

Abstract representation (abbreviated and convenient) of the reality (more complex and detailed).



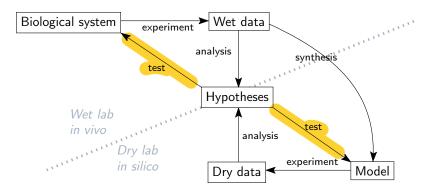
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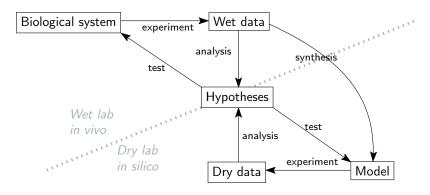
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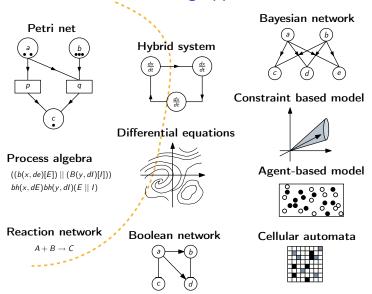
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A dichotomic zoo of modelling approaches



Synthesis

- from available knowledge and data about the structure and the dynamics
- parameter fitting task find models that optimise some criteria

Usage

- encodes our knowledge, cannot be exact
- various analyses simulation, control

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Use the simplest model that contains enough information to answer the question at hand [Bornholdt, 2005].

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Use the simplest model that contains enough information to answer the question at hand [Bornholdt, 2005]. Boolean networks are simpler than reaction networks.

Synthesis

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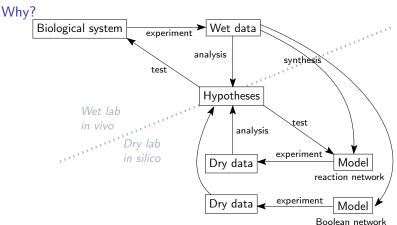
Usage

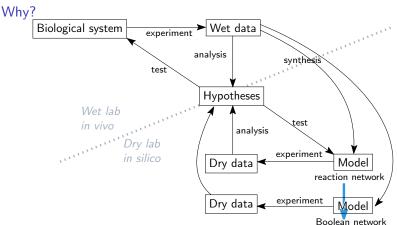
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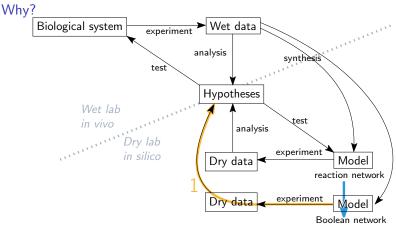
Use the simplest model that contains enough information to answer the question at hand [Bornholdt, 2005]. Boolean networks are simpler than reaction networks.

- Problem statement

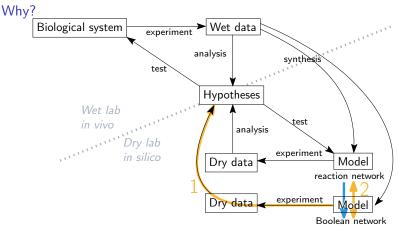
Automatic transformation (abstraction) of reaction networks to Boolean networks





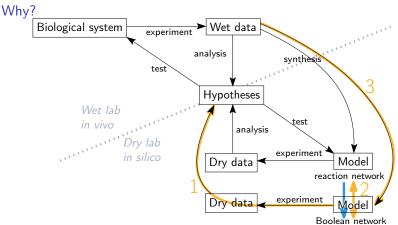


1. Use BNs to facilitate some analyses



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- 2. Explore the formal relationship between RN and BN

Introduction _______ 5 / 34



- 1. Use BNs to facilitate some analyses
- 2. Explore the formal relationship between RN and BN
- 3. Improve the BN synthesis methods

Outline

- 1. Preliminaries on reaction networks and Boolean networks
- 2. My method and its guarantees (where constraints pop in)
- 3. Evaluation of the approach
- 4. Conclusion and perspectives

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Preliminaries

 $\mathcal{R} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$ reaction, reactants, products, kinetics

$$\mathcal{S} = \{\mathsf{A},\mathsf{B},\mathsf{C}\}$$

$$\mathcal{R}_1:\mathsf{A}+\mathsf{B}\xrightarrow{e_1}2\times\mathsf{C}$$

$$\mathcal{R}_2:\mathsf{A}+\mathsf{C} \xrightarrow{e_2} \mathsf{A}+\mathsf{B}$$

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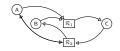
Reaction graph $(S \cup \mathcal{R}, E \subseteq (S \times \mathcal{R}) \cup (\mathcal{R} \times S))$

Example

$$\mathcal{S} = \{\mathsf{A},\mathsf{B},\mathsf{C}\}$$

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Reaction graph $(S \cup \mathcal{R}, E \subseteq (S \times \mathcal{R}) \cup (\mathcal{R} \times S))$

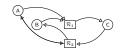
Differential semantics ordinary differential equation (ODE) $\left\{\dot{X} = \sum_{i \in 1...m} e_i \times (P_i(X) - R_i(X))\right\}_{X \in \mathcal{S}}$

Example

$$S = \{A, B, C\}$$

$$\mathcal{R}_1:\mathsf{A}+\mathsf{B}\xrightarrow{e_1}2\times\mathsf{C}$$

$$\mathcal{R}_2:\mathsf{A}+\mathsf{C} \xrightarrow{e_2} \mathsf{A}+\mathsf{B}$$



$$\begin{cases} \dot{A} &= -1 \times e_1 \\ \dot{B} &= -1 \times e_1 + 1 \times e_2 \\ \dot{C} &= 2 \times e_1 + (-1) \times e_2 \end{cases}$$



Preliminaries

Boolean network, structure and dynamics

One transition function per species in \mathcal{S} : $\left\{f_{\mathsf{X}}:\mathbb{B}^{|\mathcal{S}|} \to \mathbb{B}\right\}_{\mathsf{X} \in \mathcal{S}} \qquad \mathbb{B} = \{0,1\}$

$$\mathcal{S} = \{\mathsf{A}, \mathsf{B}, \mathsf{C}\}$$

$$f_A := 0$$

$$f_{\mathsf{B}} := \! (\mathsf{B} \wedge \neg \mathsf{C}) \vee (\neg \mathsf{B} \wedge \mathsf{C})$$

$$f_{\mathsf{C}} := \neg \mathsf{C}$$

Boolean network, structure and dynamics

One transition function per species in S:

$$\left\{ \mathit{f}_{X} : \mathbb{B}^{|\mathcal{S}|} \to \mathbb{B} \right\}_{X \in \mathcal{S}} \qquad \qquad \mathbb{B} = \left\{ 0, 1 \right\}$$

Influence graph

$$\textit{IG} = (\mathcal{S}, \textit{E} \subseteq \mathcal{S} \times \mathcal{S}, \sigma : \textit{E} \rightarrow \{+, -, \underset{-}{+}\})$$

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Influence graph

$$\textit{IG} = (\mathcal{S}, E \subseteq \mathcal{S} \times \mathcal{S}, \sigma : E \to \{+, -, \underline{+}\})$$

Transition graph (TG) $(\mathbb{B}^{|\mathcal{S}|}, E \subseteq \mathbb{B}^{|\mathcal{S}|} \times \mathbb{B}^{|\mathcal{S}|})$ general asynchronous update scheme:

$$\mathcal{P}(\mathcal{S})\setminus\emptyset$$

Example

$$\mathcal{S} = \{\mathsf{A},\mathsf{B},\mathsf{C}\}$$

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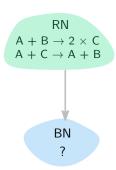
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My method and its guarantees

(where constraints pop in)

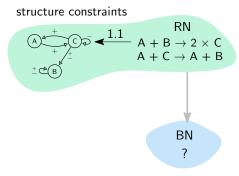
From RN to BN: which constraints



structure constraints $\begin{array}{c} RN \\ A+B\to 2\times C \\ A+C\to A+B \end{array}$ $\begin{array}{c} BN \\ ? \end{array}$

dynamics constraints

STEP 1: Retrieve constraints from the input RN

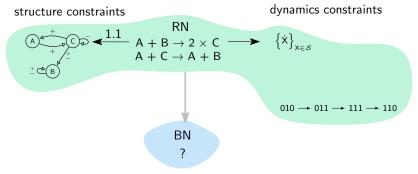


dynamics constraints

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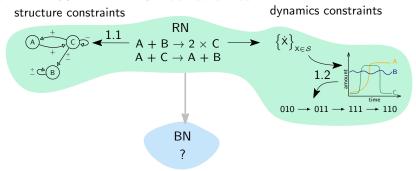
Structure: influence graph

1.1: syntactic parsing of the RN



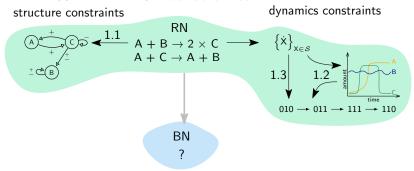
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STEP 1: Retrieve constraints from the input RN

1.1: syntactic parsing of the RN 1.2: ODEs simulation + binarisation



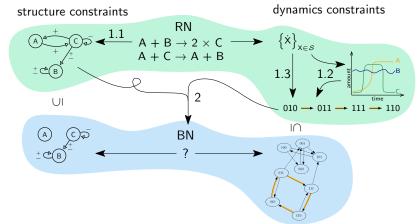
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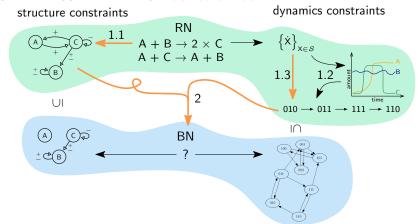
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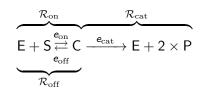
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STEP 2: BN synthesis

Running example $\mathcal{R}_{\mathsf{enz}}$



Its ODEs (reconstructed)

$$egin{cases} \dot{\mathsf{S}} &= -\mathit{e}_{\mathrm{on}} + \mathit{e}_{\mathrm{off}} \ \dot{\mathsf{E}} &= -\mathit{e}_{\mathrm{on}} + \mathit{e}_{\mathrm{off}} + \mathit{e}_{\mathrm{cat}} \ \dot{\mathsf{C}} &= \mathit{e}_{\mathrm{on}} - \mathit{e}_{\mathrm{off}} + \mathit{e}_{\mathrm{cat}} \ \dot{\mathsf{P}} &= 2 \times \mathit{e}_{\mathrm{cat}} \end{cases}$$

Its parameters (given)

$$e_{
m on} = 10^6 imes extsf{E} imes extsf{S}$$
 $e_{
m off} = 0.2 imes extsf{C}$ $e_{
m cat} = 0.1 imes extsf{C}$

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STEP 1: Retrieve constraints from the input reaction network

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▶ 1.3: abstract simulation of the ODEs [Niehren et al., 2022]

STEP 2: BN synthesis with ASK&D-BN [Vaginay et al., 2021]

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Retrieve an influence graph and

Boolean transitions

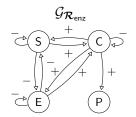


Which contraints to build the influence graph $\mathcal{G}_{\mathcal{R}}$?

Constraints inspired from [Fages, Soliman, 2008b]

$$Y \xrightarrow{-} X \in \mathcal{G}_{\mathcal{R}}$$
 if $\exists \mathcal{R} = (R, e, P) : Y \in R$ and $R(X) > P(X)$

$$Y \stackrel{+}{\Rightarrow} X \in \mathcal{G}_{\mathcal{R}}$$
 if $\exists \mathcal{R} = (R, e, P) : Y \in R$ and $R(X) < P(X)$



Guaranty: Overapproximates the possible signs of $\frac{\partial X}{\partial Y}$ \rightarrow capture all the direct influences between the species

Abstract simulation — Intuition

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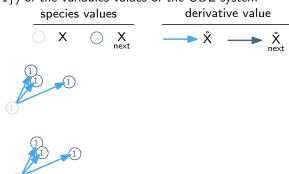


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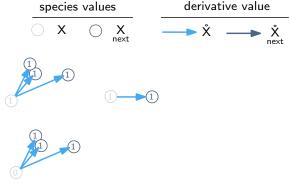




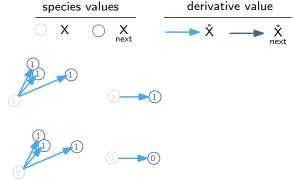
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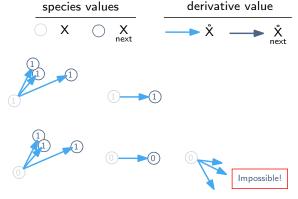
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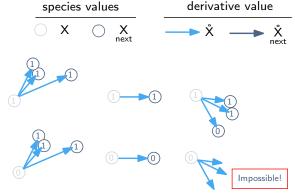


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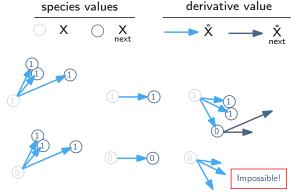
Joint work with Joachim Niehren and Cristian Versari [Niehren et al., 2022] Use the rule of signs to reason on the causal relationship between the signs ($\mathbb{S}=\{-1,0,1\}$) of the variables values of the ODE system



X was above 0 and its derivative was negative $plus - plus = unknown \sim$ nondeterminism

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Abstract simulation — In practice

Contribution

$$\mathcal{V} = \bigcup_{X \in \mathcal{S}} \left\{ X, \mathring{X}, \underset{\mathrm{next}}{X}, \mathring{\underset{\mathrm{next}}{X}} \right\}$$

- ightharpoonup Causal relationships encoded by a first-order logic formula ϕ
- Solve ϕ on $\mathbb{S} = \{-1, 0, 1\}$ $\Rightarrow \text{ relation } \mathbb{B}^{\left| \mathcal{S} \cup \hat{\mathcal{S}} \right|} \times \mathbb{B}^{\left| \substack{\mathcal{S} \cup \mathcal{S} \\ \text{next}} \right| \cdot \text{next}}$
- $lackbox{\sf Restrict}$ the solutions on $\mathcal{S} \cup \underset{\mathrm{nex}}{\mathcal{S}}$

$$ightsquigar$$
 relation $\mathbb{B}^{|\mathcal{S}|} imes \mathbb{B}^{\left| \substack{\mathcal{S} \\ \text{next}} \right|}$

- Keep the causalities of changes
- Proof of correctness: overapproximation of an ideal Euler simulation (perfectly adjusted time step and no computation error)

FOBNN: First-Order Boolean networks with nondeterministic updates

Abstract simulation — Example on $\mathcal{R}_{\mathsf{enz}}$

$$\overset{\circ}{S} = - \quad e_{on} + \quad e_{off} \qquad \qquad \wedge \quad \overset{\circ}{S}_{\substack{next}} = - \quad \underbrace{e_{on} + e_{off}}_{next}$$

$$\wedge \quad \overset{\circ}{E} = - \quad e_{on} + \quad e_{off} + \quad e_{cat} \qquad \wedge \quad \overset{\circ}{E}_{\substack{next}} = - \quad \underbrace{e_{on} + e_{off}}_{next} + \quad \underbrace{e_{cat}}_{next}$$

$$\wedge \quad \overset{\circ}{C} = \quad e_{on} - \quad e_{off} - \quad e_{cat} \qquad \wedge \quad \overset{\circ}{C}_{\substack{next}} = \quad \underbrace{e_{on} - e_{off}}_{next} - \quad \underbrace{e_{cat}}_{next}$$

$$\wedge \quad \overset{\circ}{P} = \qquad \qquad e_{cat} \qquad \wedge \quad \overset{\circ}{P}_{\substack{next}} = \qquad \qquad \underbrace{e_{cat}}_{next}$$

$$\wedge \quad \overset{\circ}{S} = \quad S + \overset{\circ}{S} \quad \wedge \quad S \leq \underset{next}{S}_{next}$$

$$\wedge \quad \overset{\circ}{S} = \quad E + \overset{\circ}{E} \quad \wedge \quad E \leq \underset{next}{E}_{next}$$

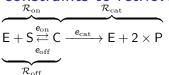
$$\wedge \quad \overset{\circ}{C} = \quad C + \overset{\circ}{C} \quad \wedge \quad C \leq \underset{next}{C}_{next}$$

$$\wedge \quad \overset{\circ}{P} = \quad P + \overset{\circ}{P} \quad \wedge \quad P \leq \underset{next}{P}_{next}$$

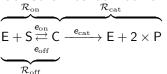
$$\overset{\circ}{P} = \quad \overset{\circ}{P} = \stackrel{\circ}{P} + \overset{\circ}{P} \quad \wedge \quad P \leq \underset{next}{P}_{next}$$

$$\overset{\circ}{P} = \quad \overset{\circ}{P} = \stackrel{\circ}{P} + \overset{\circ}{P} \quad \wedge \quad P \leq \underset{next}{P} = 0.2 \times \overset{\circ}{C} \quad e_{cat} = 0.1 \times \overset{\circ}{C}_{next}$$

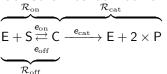
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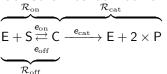
Expected transitions [SECP]:
$$1100 \rightarrow **10 \rightarrow ***1$$



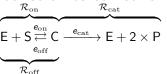
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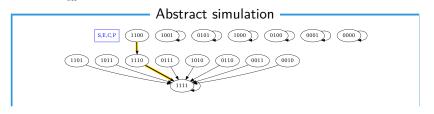


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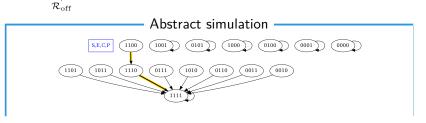


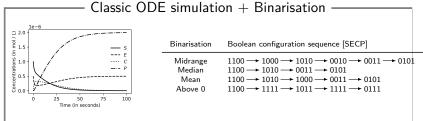
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Structure: influence graph

▶ 1.1: syntactic parsing of the reactions

Dynamics: Boolean transitions

▶ 1.2: ODEs simulation + binarisation

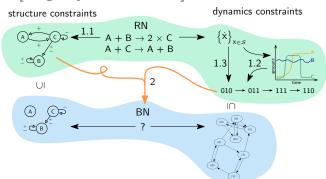
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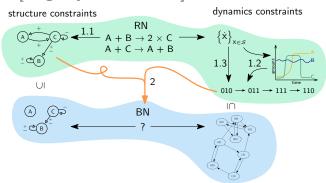
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ASK&D-BN

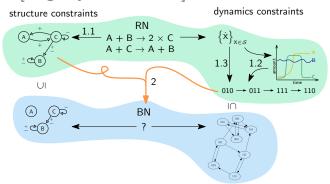
STEP 2: Boolean network synthesis with





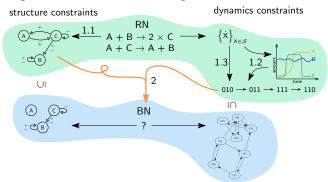
1. **Local search** species-wise synthesis of *all* the transition functions compatible with the given influence graph and time series

 $\mbox{Generate candidates} \rightarrow \mbox{Structure constraint} \rightarrow \mbox{Dynamic constraint} \rightarrow \mbox{Minimality constraint}$



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 $\begin{tabular}{lll} Generate candidates \rightarrow Structure constraint \rightarrow Dynamic constraint \rightarrow Minimality constraint \\ & Answer-Set Programming \\ \end{tabular}$



1. **Local search** species-wise synthesis of *all* the transition functions compatible with the given influence graph and time series

 $\begin{tabular}{lll} Generate \ candidates & \to \ Structure \ constraint & \to \ Dynamic \\ constraint & \to \ Minimality \ constraint \\ & & Answer-Set \ Programming \\ \end{tabular}$

2. Global assembly produce all the possible BNs

ASK&D-BN— Local search

 ${\sf Generate\ candidates} \to {\sf Structure\ constraint} \to {\sf Dynamic\ constraint} \to {\sf Minimality\ constraint}$

Search space: 2^{3^k} non-redundant DNF = non-redundant disjunction of non-redundant conjunctions ideally: the set of minimal DNF with k inputs.

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Pick a subset of non-redundant conjunctions without subsomption and not locally-adjacent

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Examples

valid candidate.

$$(A) \lor (A \land B)$$

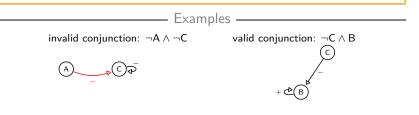
 $(A \land B) \lor (A \land \neg B)$

Generate candidates → Structure constraint → Dynamic constraint → Minimality constraint

influence graph of the Boolean network \subseteq influence graph of the reaction network



Do not select a conjunction that uses a forbidden literal



 $\mathsf{Generate} \ \mathsf{candidates} \to \mathsf{Structure} \ \mathsf{constraint} \to \mathsf{Dynamic} \ \mathsf{constraint} \to \mathsf{Minimality} \ \mathsf{constraint}$

 $m{--}$ (1) input: Boolean transitions $m{--}$

Build partial truth tables for each species X: what were the values of its putative inputs when its value changed? \leadsto Do not assume the underlying update scheme Compare the truth table of a candidate function to the reconstructed truth table

putative output input

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	putative input	output	_
	С	Α	
input influence graph (unsigned) $(A)^{\Delta} \longrightarrow (C)_{\mathbb{R}^2}$			
œB Ď	BC	В	
	AC	С	_

 $\mathsf{Generate} \ \mathsf{candidates} \to \mathsf{Structure} \ \mathsf{constraint} \to \mathsf{Dynamic} \ \mathsf{constraint} \to \mathsf{Minimality} \ \mathsf{constraint}$

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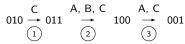
						putative input	output
						С	А
010 → 011 ①	2	100	→ ③	001		BC	В
						AC	С

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input	output	
С	Α	
ВС	В	





nutative

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	putative input	output	
	С	А	
	1	1	2
$010 \xrightarrow{C} 011 \xrightarrow{A, B, C} 100 \xrightarrow{A, C} 001$	ВС	В	
	AC	С	

 $\mathsf{Generate} \ \mathsf{candidates} \to \mathsf{Structure} \ \mathsf{constraint} \to \mathsf{Dynamic} \ \mathsf{constraint} \to \mathsf{Minimality} \ \mathsf{constraint}$

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	putative input	output	
	C 0	A 0	(3)
	1	1	2
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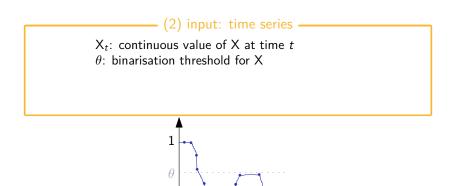
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	putative input	output	:
	С	Α	
	0	0	(3)
	1	1	2
C A, B, C A, C			
$010 \rightarrow 011 \rightarrow 100 \rightarrow 001$	BC	В	
(1)	11	0	2
	AC	С	
	00	1	1
	01	0	2
	10	1	3

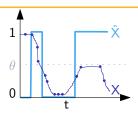
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Generate candidates → Structure constraint → Dynamic constraint → Minimality constraint



 X_t : continuous value of X at time t θ : binarisation threshold for X



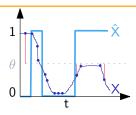
Generate candidates → Structure constraint → Dynamic constraint → Minimality constraint



 X_t : continuous value of X at time t

 θ : binarisation threshold for X

 \mathcal{U} : set of unexplained time steps



 $\mathsf{Generate} \ \mathsf{candidates} \to \mathsf{Structure} \ \mathsf{constraint} \to \mathsf{Dynamic} \ \mathsf{constraint} \to \mathsf{Minimality} \ \mathsf{constraint}$

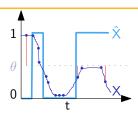
(2) input: time series

 X_t : continuous value of X at time t

 θ : binarisation threshold for X

 \mathcal{U} : set of unexplained time steps

 $E = \sum_{t \in \mathcal{U}} |\theta - X_t|$ To minimise (ideally 0)



 $\mathsf{Generate} \ \mathsf{candidates} \ \to \ \mathsf{Structure} \ \mathsf{constraint} \ \to \ \mathsf{Dynamic} \ \mathsf{constraint} \ \to \ \mathsf{\underline{Minimality}} \ \mathsf{\underline{constraint}}$

Select candidates with the smallest expressions (subset and/or cardinal minimal) \leadsto most general conditions

putative input	observed output
AB	X
00	
01	0
10	1
11	

Generate candidates → Structure constraint → Dynamic constraint → Minimality constraint

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putative input AB	observed output X	pos	sible o	comple	etions
00		0	1	0	1
01	0	0	0	0	0
10	1	1	1	1	1
11		0	0	1	1

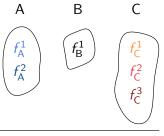
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putative input AB	observed output X	possible completions			
00		0	1	0	1
01	0	0	0	0	0
10	1	1	1	1	1
11		0	0	1	1
subset m	ninimal candidates	$A \wedge \neg B$	¬В	Α	$A \vee \neg B$
	size	2	1	1	2
			/		
card. min.					
			candida	tes	

ASK&D-BN— Global assembly

Cartesian product of the set of transition functions synthesised for each species



$$\mathcal{B}_{1} = \{f_{A}^{1}, f_{B}^{1}, f_{C}^{1}\}$$

$$\mathcal{B}_{2} = \{f_{A}^{1}, f_{B}^{1}, f_{C}^{2}\}$$

$$\mathcal{B}_{3} = \{f_{A}^{1}, f_{B}^{1}, f_{C}^{2}\}$$

$$\mathcal{B}_{4} = \{f_{A}^{2}, f_{B}^{1}, f_{C}^{1}\}$$

$$\mathcal{B}_{5} = \{f_{A}^{2}, f_{B}^{1}, f_{C}^{2}\}$$

$$\mathcal{B}_{6} = \{f_{A}^{2}, f_{B}^{1}, f_{C}^{2}\}$$

Outline

- 1. Preliminaries on reaction networks and Boolean networks
- 2. My method and its guarantees (where constraints pop in)
- 3. Evaluation of the approach
- 4. Conclusion and perspectives

Evaluation of the approach

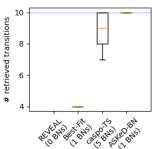
Evaluation of the approach

- The BN synthesis itself [Vaginay et al., 2021] ASK&D-BN versus REVEAL¹, Best-Fit² and Caspo-TS³
- 2. One specific variant of the complete approach on real-world reaction networks [Vaginay et al., 2021, Vaginay et al., 2022] influence graph + time series and midrange binarisation
- 3. Several variants of the complete approach on \mathcal{R}_{enz} compare concrete and abstract simulation

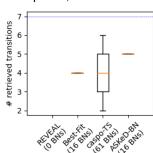
¹[Liang et al., 1998] ²[Lähdesmäki et al., 2003] ³[Ostrowski et al., 2016]

Evaluation of the approach

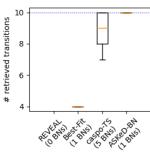
A. thaliana5 species, 10 transitions



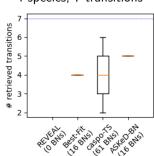
yeast4 species, 7 transitions



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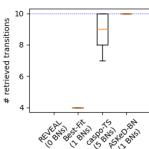


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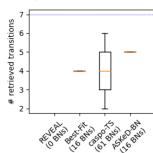
REVEAL fails

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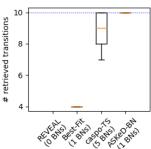
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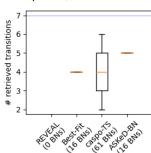
► Best-Fit lacks consistency

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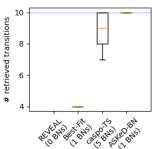
- REVEAT, fails
- Caspo-TS returns more BNs, some of them with poor coverage because of reachability constraint

yeast
4 species, 7 transitions



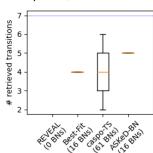
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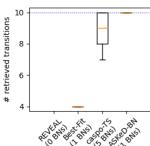
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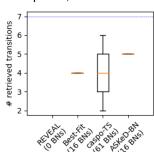
- ► Best-Fit lacks consistency
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- REVEAT, fails
- Caspo-TS returns more BNs, some of them with poor coverage because of reachability constraint
- \sim Confirmed on > 300 datasets generated from existing BNs from the repository of PyBoolNet

yeast4 species, 7 transitions



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- ASK&D-BN returns a small number of BN, with good coverage and low variance √

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Conclusion and perspectives

Automatic synthesis of Boolean networks from a given reaction network, with guarantees. \checkmark

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Methodology: Boolean networks synthesis from constraints
 Structure: Influence graph from syntactic parsing of the reactions

captures all the direct influences among species

Dynamics: Boolean transitions

from numerical simulation of the ODEs + binarisation

- good approximation or the analytical solution
- but we lose causality

from abstract simulation of the ODEs

 correct overapproximation of perfect Euler that captures causality

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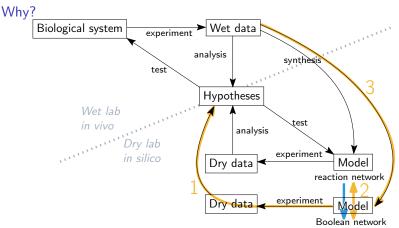
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- ▶ Evaluation

From reactions to Boolean influences with guarantees



- 1. Use BNs to facilitate some analyses
- 2. Explore the formal relationship between RN and BN
- 3. Improve the BN synthesis methods

Perspectives

1. To facilitate some analyses

Make SBML2BNET easy to use, use more evaluation criteria, include more knowledge in the synthesis, analyse FO-BNN themselves (process more RN, compute attractors(*))

Explore the formal relationship between RN and BN Two conjectures to investigate, reverse process(*)

3. Improve the BN synthesis methods

Investigate, in a controled environnement

- ▶ when we can't fullfill the constraints(*)
- overfitting to the sequence of configuration?
- impact of the choice of the binarisation procedure and error measure

Perspectives

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Publications

J. Niehren, C. Lhoussaine and AV. Core SBML and its Formal Semantics CMSB: International Conference on Computational Methods in Systems Biology 2023

Abstract simu. J. Niehren, AV, and C. Versari. Abstract Simulation of Reaction Networks via Boolean Networks CMSB: International Conference on Computational Methods in Systems Biology 2022

SBML2BNET AV, T. Boukhobza, and M. Smaïl-Tabbone. From Quantitative SBML Models to Boolean Networks CNA: Complex Networks & Their Applications X 2022

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ASK&D-BN AV, T. Boukhobza, and M. Smaïl-Tabbone. Automatic Synthesis of Boolean Networks from Biological Knowledge and Data OLA: Optimization and Learning 2021

> A. Hirtz, N. Lebourdais, F. Rech, Y. Bailly, AV, M. Smaïl-Tabbone, H. Dubois-Pot-Schneider, and H. Dumond. GPER Agonist G-1 Disrupts Tubulin Dynamics and Potentiates Temozolomide to Impair Glioblastoma Cell Proliferation Cells 2021

Thank you for your attention.



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 ► [Vaginay et al., 2021]
- A. Vaginay, et al.
 - Automatic Synthesis of Boolean Networks from Biological Knowledge and Data
 - Communications in Computer and Information Science pp. 156-170, 2021

References IV

- ► [Vaginay et al., 2021]
 A. Vaginay, et al.
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 Complex Networks & Their Applications X 2021
- ► [Vaginay et al., 2022]
 A. Vaginay, et al.
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 Applied Network Science vol. 7-1 pp. 1–23, 2022

Our abstraction versus other abstractions Reaction-thinking Reaction network

Boolean network Influence thinking

Our abstraction versus other abstractions Reaction-thinking Reaction network

differential Boolean network Influence thinking

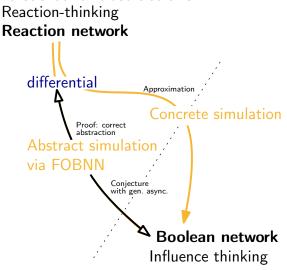
Our abstraction versus other abstractions Reaction-thinking Reaction network differential Approximatio Boolean network

Influence thinking

Our abstraction versus other abstractions

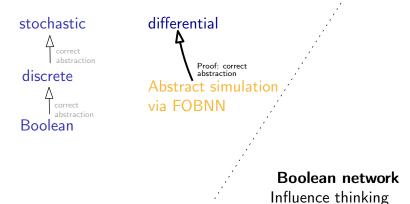
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Our abstraction versus other abstractions



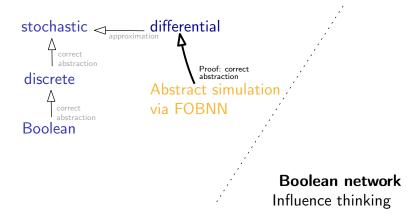
Our abstraction versus other abstractions

Reaction-thinking Reaction network



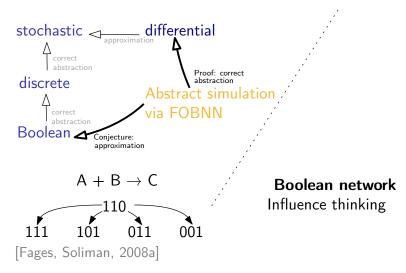
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Candidate transition function

Search space: $2^{3^{|\mathcal{S}|}}$ non-redundant DNF = non-redundant disjunction of non-redundant conjunctions

Candidate transition function

Search space: $2^{3^{|S|}}$ non-redundant DNF = non-redundant disjunction of non-redundant conjunctions

Pick a subset of non-redundant conjunctions –

```
% GIVEN: conj(ID, Component, Sign}
% conj(ID, Species, Sign}
conj(1, a, 1). conj(1, b,-1). conj(1, c, 0). % A ∧ ¬B
conj(2, a, -1). conj(2, b, 0). conj(2, c, -1). % ¬A ∧ ¬C
conj(3, a, -1). conj(3, b,-1). conj(3, c, -1). % ¬A ∧ ¬B ∧ ¬C
...
1{conjTakenID(0..maxNbPossibleConj)}. % choice rule
```

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```

Example ————

 $\texttt{conjTakenID(1). conjTakenID(2).} \Rightarrow \texttt{candidate} = (A \land \neg B) \lor (\neg A \land \neg C)$

Structure constraints

influence graph of the Boolean network \subseteq influence graph of the reaction network



Do not select a conjunction that uses a forbidden literal

ig(ParentID, x, V) :- conjTaken(ConjID, ParentID, V); V!=0.
:- ig(ParentID, x, V); not pig(ParentID, x, V).

Example -

invalid conjunction: $\neg A \land \neg C$



valid conjunction: $\neg C \land B$



Dynamics constraints

— (1) input: Boolean transitions

Build partial truth tables for each species X: what were the values of its putative inputs when its value changed? \leadsto Do not assume the underlying update scheme Compare the truth table of a candidate function to the reconstructed truth table

putative output input

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putative input	output
С	Α

input influence graph (unsigned)



BC	В	
	_	
AC	С	

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	putative input output	
	C A	
$010 \xrightarrow{C} 011 \xrightarrow{A,B,C} 100 \xrightarrow{A,C} 001$	1 1 (2
	BC B	
		_

Dynamics constraints

— (1) input: Boolean transitions

Build partial truth tables for each species X: what were the values of its putative inputs when its value changed? \leadsto Do not assume the underlying update scheme Compare the truth table of a candidate function to the reconstructed truth table

$010 \xrightarrow{C} 011$	A,B,C, 104	A,C, 001
$010 \longrightarrow 011$	\longrightarrow 100	$1 \longrightarrow 001$
(1)	(2)	(3)

putative input	output	
С	Α	
0	0	(3)
1	1	2
BC	В	
AC	C	

Dynamics constraints

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$$010 \xrightarrow{C} 011 \xrightarrow{A,B,C} 100 \xrightarrow{A,C} 001$$

putative input	output	
С	Α	
0	0	(3)
1	1	2
BC	В	
11	0	2
AC	C	
00	1	(1)
01	0	(2)
10	1	3

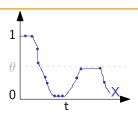
Dynamics constraints

(2) input: time series

#minimize{E02 : error(E)}. %

 X_t : continuous value of X at time t

 θ : binarisation threshold for X



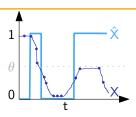
Dynamics constraints

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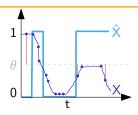
Dynamics constraints

(2) input: time series

#minimize{E@2 : error(E)}. %

 X_t : continuous value of X at time t θ : binarisation threshold for X

 \mathcal{U} : set of unexplained time steps



Dynamics constraints

(2) input: time series

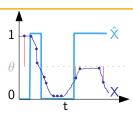
#minimize{E@2 : error(E)}. %

 X_t : continuous value of X at time t

 θ : binarisation threshold for X

 $\mathcal{U}\colon$ set of unexplained time steps

 $E = \sum_{t \in \mathcal{U}} |\theta - X_t|$ To minimise (ideally 0)



Minimality constraint

```
Select candidates with the smallest expressions (subset and/or cardinal minimal)
```

 \leadsto most general conditions

```
sizeconj(C, S):-conjTakenID(C);S=#sum{|V|,N:conj(C, N, V)} .
sizeDNF(S):- S=#sum{N,C: sizeconj(C, N), conjTakenID(C)} .
#minimize{S@1 : sizeDNF(S)}. % Find mincard expressions
% + generate all combinations to find all the subset min expressions
```

putative input	observed output
AB	X
00	
01	0
10	1
11	

Minimality constraint

Select candidates with the smallest expressions (subset and/or cardinal minimal)

 $\rightsquigarrow \mathsf{most} \mathsf{\ general} \mathsf{\ conditions}$

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putative input	observed output	pos	sible o	omple	etions
AB	X				
00		0	1	0	1
01	0	0	0	0	0
10	1	1	1	1	1
11		0	0	1	1

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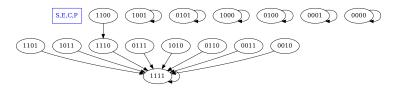
% + generate all combinations to find all the subset min expressions
```

putative input AB	observed output	possible completions			
00		0	1	0	1
01	0	0	0	0	0
10	1	1	1	1	1
11		0	0	1	1
subset m	ninimal candidates	$A \wedge \neg B$	¬В	Α	$A \lor \neg B$
	size	2	1	1	2
card. min. candidates					

FOBNN fix-points with SAT

Given an FOBNN ϕ with variables $\mathcal{V} = \bigcup_{X \in \mathcal{S}} \{X, \mathring{X}, \underset{next}{\mathring{X}}, \underset{next}{\mathring{X}} \}$, find the signed assignments α of ϕ such that:

$$\forall X \in \mathcal{S} : \alpha(X) = \alpha(\underset{next}{X}) \text{ (and no others!)}$$



Hans-Jörg Schurr (Univ. of Iowa).

Functional dependency for detecting dynamics conflicts

Set of attributes V (relation scheme)

A set r of tuples that maps each attributes to a value of its domain $(t[X] \in dom(X))$

A functional dependency (FD) F is an expression of the form $X \to Y$, where $X, Y \subseteq \mathcal{V}$ F holds in a relation r $(r \models f)$ if:

$$\forall t_1, t_2 \in r, t_1[X] = t_2[X] \implies t_1[Y] = t_2[Y]$$

Find counterexamples when it does not hold (work on the conflict-graph). Find the maximum (biggest) independent sets.

g3-error: minimal proportion of tuples to remove from r to satisfy $F \sim$ coverage measure

Simon Vilmin (AMU) and Pierre Faure–Giovagnoli (LIRIS): relax the equality by using a predicate p instead, study how the complexity of the problems depends on the properties of p (reflexivity, symetry, transitivity, antisymetry)

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Functional dependency for detecting dynamics conflicts

Set of variables $\mathcal{V} = \mathcal{S} \cup \mathcal{S}_{\text{next}}$ (relation scheme)

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t_1	0	0	0	0	0	0	•
t ₂	0	1	1	1	0	0	
t_3	0	0	0	0	0	1	•

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t ₂ t ₃	0	0	0	0 1 0	0	1	•

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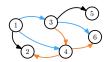
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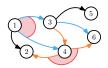
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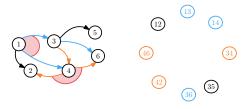
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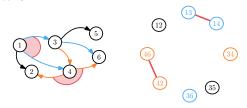
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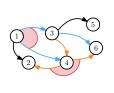
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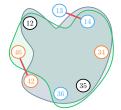
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Learn reaction networks from Boolean transitions

Implication base with variables in \mathcal{S} : $\mathcal{R} = \{R_i \to P_i\}_{i=1...m}$ Closed-set: "element of $\mathcal{P}(\mathcal{S})$ such that we cannot derive anything new using \mathcal{R} " Closure system = the set \mathcal{C} of closed-sets of \mathcal{R} \mathcal{C} ordered by $C \to A$ a lattice

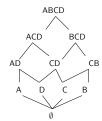
$$\mathcal{R} = \{$$

$$\mathcal{R}_1 : A + B \rightarrow C + D$$

$$\mathcal{R}_2 : A + C \rightarrow D$$

$$\mathcal{R}_3 : B + D \rightarrow C$$

$$\}$$



Simon Vilmin (AMU), Loïc Paulevé? (LABRI)

Learn reaction networks from Boolean transitions

Reaction network with species in $S: \mathcal{R} = \{R_i \rightarrow P_i\}_{i=1...m}$

Closed-set: "element of $\mathcal{P}(\mathcal{S})$ such that we cannot derive anything new using \mathcal{R} "

Closure system = the set C of closed-sets of R

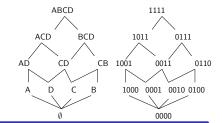
 ${\mathcal C}$ ordered by $\subseteq\, \leadsto$ a lattice

$$\mathcal{R} = \{$$

$$\mathcal{R}_1 : A + B \rightarrow C + D$$

$$\mathcal{R}_2 : A + C \rightarrow D$$

$$\mathcal{R}_3 : B + D \rightarrow C$$

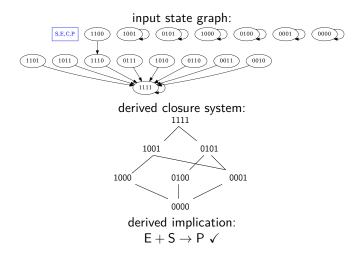


given a closure system, find the implication base(s) $% \left(s\right) =\left(s\right) \left(s\right)$

given Boolean fixed-points, find the reaction network(s)

Simon Vilmin (AMU), Loïc Paulevé? (LABRI)

Learn reaction networks from Boolean transitions

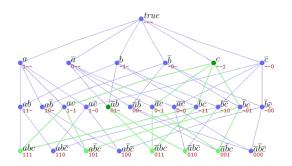


Minimal DNF

Given a set S of inputs for which a function f eval. to 1, each minimal-by-inclusion set of nodes that covers exactly S forms a (subset-)minimal DNF of f.

f might have several (subset-)minimal DNFs.

Example: $S = \{abc, \overline{abc}, \overline{abc}, \overline{abc}, \overline{abc}\}$ (light green) $\sim \{\overline{ab}, c\}$ (dark green)



Not well-formed reaction networks

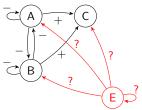
$$X \xrightarrow{k \times Y}$$

 $\frac{\partial X}{\partial Y} \neq 0$ NOT captured by the syntactic influence graph.

Impact of SBML inconsistencies on structure extraction

Ex. BIOMD n°44: 1 BN generated; coverage=0.55 some kinetics use components not listed in the reactants nor modifiers \rightarrow incomplete SIG (missing parents)

$$A + B \xrightarrow{f(A,B,E)} C$$

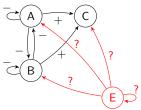


⁴[Fages et al. 2012]

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> 60% of SBML models from Biomodels are not "well-formed"⁴, but some can be fixed \rightarrow add a step in the pipeline

⁴[Fages et al. 2012]

Results to real-world reaction networks (from BioModels⁵)

Input: an extended reaction network rules and events
Output: a set of compatible Boolean networks, according to ASK&D-BN

Setting:

- hard structure constraint (extended influence graph)
- soft dynamics constraints (time series and midrange binarisation)
- mincard DNF

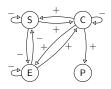
Result:

- on 155 reaction networks processed in less than 30 hours
- ▶ we synthesise perfect Boolean networks for \sim 90% of them \checkmark 139/155 sets of BNs have a coverage proportion median = 1

⁵[Malik-Sheriff et al., 2020]

Comparison of two settings on $\mathcal{R}_{\mathsf{enz}}$

$$\underbrace{ \underbrace{ \begin{array}{c} \mathcal{R}_{\mathrm{on}} \\ E + S \stackrel{e_{\mathrm{on}}}{\rightleftarrows} C \\ \stackrel{e_{\mathrm{cat}}}{\longrightarrow} \end{array}}_{\mathcal{R}_{\mathrm{off}}} \mathsf{E} + 2 \times \mathsf{P}$$



- influence graph
- time series
- binarised time series

midrange (0.8) and median (0.6):

$$f_{S} := \neg E$$

 $f_{E} := \neg S$
 $f_{C} := S$
 $f_{P} := C$

ightarrow Coverage depends on the binarisation procedure, BNs miss some influences

full graph from abstract simulation

$$f_{S} := C \lor S$$

$$f_{E} := E \lor C$$

$$f_{C} := (E \land S) \lor C$$

$$f_{P} := C \lor P$$

→ Perfect coverage, but does not comply with the influence graph