# Simulation and synthesis of formal models of biological systems

Athénaïs Vaginay Post-doc in MTV (dep. M2F), with Loïc Paulevé

Sémidoc @ LaBRI, Bdx — 2024 July 19

#### Outline

- 1. My curriculum :)))
- 2. A light intro to systems biology and formal models in general
- 3. Formal methods for the simulation of reaction networks
- 4. Formal methods for the simulation of Boolean networks
- 5. Formal methods for the synthesis of Boolean networks
- 6. Conclusion

# Curriculum

#### Me and my background

Currently (for two more weeks): post-doc in MTV, under the supervision of Loïc Paulevé.

- Medical studies, 1 year
- Biology, licence
- Bio-info, master + "ingénieure d'études" a few months
- Theoretical systems biology (~ computer science), PhD, postdoc, ...

Reach out: room B353, athenais.vaginay@labri.fr

My first time in this amphi: in 2021 (CMSB conference).

# Introduction

# Systems biology

Formal modelling and reasoning about biological systems

A model = an abstract representation (abbreviated and convenient) of the reality (more complex and detailed)

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

#### Questions

#### 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





The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



The workflow of system biology [Kohl et al., 2010]



#### Synthesis:

from available knowledge and data about the structure and the dynamics

parameter fitting task find models that optimise some criteria Experiment: e.g. simulation = execution of the model

# A zoo of modelling approaches

Reaction network

continuous time Markov chain

ODEs

statistical models

Petri net

Boolean transition system

informal diagrams

Boolean automata network



# A zoo of modelling approaches

#### Reaction network

continuous time Markov chain

ODEs

statistical models

Petri net

Boolean transition system

informal diagrams

#### Boolean automata network



# Formal methods for the simulation of reaction networks

#### Static analysis of a reaction network



Static analysis = derive correct conclusions about the dynamics without having to actually simulate the model.

FM for RN simulation

## Static analysis of a reaction network



Static analysis = derive correct conclusions about the dynamics without having to actually simulate the model.

## Static analysis of a reaction network



Static analysis = derive correct conclusions about the dynamics without having to actually simulate the model.

6 / 13

**Reaction network** 

 $\boldsymbol{\mathcal{R}} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$ 

# **Reaction network** $\mathcal{R} = \{\mathcal{R}_i : \mathcal{R}_i \xrightarrow{e_i} \mathcal{P}_i\}_{i=1...m}$ $A + B \xrightarrow{e} 2C$

**Reaction network**  $\mathcal{R} = \{\mathcal{R}_i : \mathcal{R}_i \xrightarrow{e_i} \mathcal{P}_i\}_{i=1...m}$  $A + B \xrightarrow{e} 2C$ 

Continuous Time Markov chain

**Ordinary Differential Equations** 

Petri net

**Boolean transition system** 

**Reaction network**  $\mathcal{R} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$  $A + B \xrightarrow{e} 2C$ 

**Continuous Time Markov chain** 

Ordinary Differential Equations continuous time, continuous values

 $\dot{A} = \dot{B} = -e; \dot{C} = 2e$ 

Petri net

Boolean transition system

**Reaction network**  $\mathcal{R} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$  $A + B \xrightarrow{e} 2C$ 

Continuous Time Markov chain

continuous time, discrete values p(e) : A - -; B - -; C += 2 Ordinary Differential Equations continuous time, continuous values

 $\dot{A} = \dot{B} = -e; \dot{C} = 2e$ 

Petri net

**Boolean transition system** 

**Reaction network**  $\mathcal{R} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$  $A + B \xrightarrow{e} 2C$ 

**Continuous Time Markov chain** continuous time, discrete values p(e) : A - -; B - -; C += 2 Ordinary Differential Equations continuous time, continuous values

 $\dot{A} = \dot{B} = -e; \dot{C} = 2e$ 

**Petri net** discrete time, discrete values *A*--; *B*--; *C*+=2

**Boolean transition system** 

7 / 13

**Reaction network**  $\mathcal{R} = \{\mathcal{R}_i : R_i \xrightarrow{e_i} P_i\}_{i=1...m}$  $A + B \xrightarrow{e} 2C$ 

**Continuous Time Markov chain** continuous time, discrete values p(e) : A - -; B - -; C += 2

Ordinary Differential Equations continuous time, continuous values

 $\dot{A} = \dot{B} = -e; \dot{C} = 2e$ 

**Petri net** discrete time, discrete values *A*--; *B*--; *C*+=2

Boolean transition system discrete time, boolean values

$$\begin{array}{c} A,B \text{ in } \{0,1\}; C \text{ in } \{1\} \\ 110 \\ 111 \\ 111 \\ 001 \end{array}$$



Abstract simulation = derive correct conclusions using a simpler simu. of the model [Cousot, Cousot, 1977], [Fages, Soliman, 2008a]

# Formal methods for the simulation of Boolean networks

A BN f is a function  $\mathbb{B}^n \to \mathbb{B}^n$  usually expressed in propositional logics.

#### The dynamics of a Boolean network using a SAT solveur A BN f is a function $\mathbb{B}^n \to \mathbb{B}^n$ usually expressed in propositional logics.

Example 
$$x'_1 = (x_1 \land x_2 \land x_3) \land x'_2 = (x_1 \lor x_3) \land x'_3 = ((x_2 \land x_3) \lor (x_1 \land x_2 \land x_3) \lor (x_1 \land x_2 \land x_3))$$

A BN *f* is a function  $\mathbb{B}^n \to \mathbb{B}^n$  usually expressed in propositional logics. **Transition graph**:  $G = (\mathbb{B}^n, E \subseteq \mathbb{B}^n \times \mathbb{B}^n)$ . Is  $(x, x') \in G$ ?



A BN *f* is a function  $\mathbb{B}^n \to \mathbb{B}^n$  usually expressed in propositional logics. **Transition graph**:  $G = (\mathbb{B}^n, E \subseteq \mathbb{B}^n \times \mathbb{B}^n)$ . Is  $(x, x') \in G$ ?



A BN *f* is a function  $\mathbb{B}^n \to \mathbb{B}^n$  usually expressed in propositional logics. **Transition graph**:  $G = (\mathbb{B}^n, E \subseteq \mathbb{B}^n \times \mathbb{B}^n)$ . Is  $(x, x') \in G$ ? **Fixpoint**: a configuration  $x \in \mathbb{B}^n$  such that f(x) = x.



A BN *f* is a function  $\mathbb{B}^n \to \mathbb{B}^n$  usually expressed in propositional logics. **Transition graph**:  $G = (\mathbb{B}^n, E \subseteq \mathbb{B}^n \times \mathbb{B}^n)$ . Is  $(x, x') \in G$ ? **Fixpoint**: a configuration  $x \in \mathbb{B}^n$  such that f(x) = x. **Trapspace**: a subcube *t* of  $\mathbb{B}^n$  such that  $\forall x \in t : f(x) \in t$ 



#### Boolean networks as concurent systems The impact of updates

A Boolean network is a function  $f : \mathbb{B}^n \to \mathbb{B}^n$ . Alternatively, f consists of n local functions  $\mathbb{B}^n \to \mathbb{B}$  (one per species in S).

#### Boolean networks as concurent systems The impact of updates

A Boolean network is a function  $f : \mathbb{B}^n \to \mathbb{B}^n$ . Alternatively, f consists of n local functions  $\mathbb{B}^n \to \mathbb{B}$  (one per species in S).

The update mode dictates which components can be updated at each time.

#### Boolean networks as concurent systems The impact of updates

A Boolean network is a function  $f : \mathbb{B}^n \to \mathbb{B}^n$ . Alternatively, f consists of n local functions  $\mathbb{B}^n \to \mathbb{B}$  (one per species in S).

The update mode dictates which components can be updated at each time.



Strongly impacts the dynamics  $\rightarrow$  adapt your SAT constraints accordingly

Formal methods for the synthesis of Boolean networks

$$\begin{cases} \textbf{Boolean network} \\ \left\{ f_X : \mathbb{B}^{|\mathcal{S}|} \to \mathbb{B} \mid X \in \mathcal{S} \right\} \\ \text{influence graph} \\ ? \end{cases}$$

10 / 13



100 is a fixpoint  $000 \longrightarrow 011 \longrightarrow 111 \longrightarrow 110$ 

dynamics specifications







**Tool:** ASP (Answer set programming) provides an expressive modeling language + fast solvers Check BoNesis from Loïc Paulevé and co.! https://bnediction.github.io/bonesis/

- A Boolean network *f* consists of *n* local functions B<sup>n</sup> → B (one per species in S).
- BN synthesis may be UNSAT because of conflicting dynamics specifications.



- A Boolean network *f* consists of *n* local functions B<sup>n</sup> → B (one per species in S).
- BN synthesis may be UNSAT because of conflicting dynamics specifications.



- A Boolean network *f* consists of *n* local functions B<sup>n</sup> → B (one per species in S).
- BN synthesis may be UNSAT because of conflicting dynamics specifications.
- To remove as few conflicting specifications as possible, find maximum independent sets in the conflict graph.



- A Boolean network *f* consists of *n* local functions B<sup>n</sup> → B (one per species in S).
- BN synthesis may be UNSAT because of conflicting dynamics specifications.
- To remove as few conflicting specifications as possible, find maximum independent sets in the conflict graph.



- A Boolean network *f* consists of *n* local functions B<sup>n</sup> → B (one per species in S).
- BN synthesis may be UNSAT because of conflicting dynamics specifications.
- To remove as few conflicting specifications as possible, find maximum independent sets in the conflict graph.



# Conclusion and perspectives

# To sum up



# To sum up



#### My research questions



# Thank you for your attention.



From RN to BN: the big picture



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

#### Perspectives

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

#### 2. Facilitate RN 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(\*))

#### 3. Improve the BN synthesis methods

Investigate, in a controled environnement

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

#### Perspectives

- Formalize the relationship between RN and BN Two conjectures to investigate(\*), reverse process(\*)
- 2. Facilitate RN 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(\*))

3. Improve the BN synthesis methods

Investigate, in a controled environnement

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

#### 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)



#### References I

#### [Cousot, Cousot, 1977]

P. Cousot, R. Cousot,

Abstract interpretation: A unified lattice model for static analysis of programs by construction or approximation of fixpoints, 1977

#### ▶ [Bornholdt, 2005]

S. Bornholdt Less Is More in Modeling Large Genetic Networks, 2005

#### [Fages, Soliman, 2008a] F. Fages, S. Soliman, Abstract Interpretation and Types for Systems Biology, *Theoretical Computer Science*, vol. 403, pp. 52–70, 2008

 [Fages, Soliman, 2008b]
 F. Fages, S. Soliman,
 From Reaction Models to Influence Graphs and Back: A Theorem, Lecture Notes in Computer Science, pp. 90–102 2008

#### References II

- [Hoops et al., 2006]
  S. Hoops et al.
  COPASI—a COmplex PAthway Simulator,
  - Bioinformatics, vol. 22, pp. 3067-3074 2006
- [Kohl et al., 2010]
  P. Kohl et al.
  Systems Biology: An Approach,
  *Clinical Pharmacology & Therapeutics* vol. 88-1 pp. 25–33 2010,

 [Lähdesmäki et al., 2003]
 H. Lähdesmäki et al.
 On Learning Gene Regulatory Networks under the Boolean Network Model, Machine Learning, vol. 52-1 pp. 147–167 2003,

[Liang et al., 1998]
 S. Liang et al.
 REVEAL, a General Reverse Engineering Algorithm for Inference of Genetic Network Architectures
 Pacific Symposium on Biocomputing. pp. 18–29, 1998,

## References III

# [Malik-Sheriff et al., 2020] R. Malik-Sheriff et al.

BioModels—15 Years of Sharing Computational Models in Life Science *Nucleic Acids Research* vol. 48-D1, pp. D407-D415, 2020

#### [Niehren et al., 2022]

J. Niehren et al.

Abstract Simulation of Reaction Networks via Boolean Networks CMSB: International Conference on Computational Methods in Systems Biology 2022,

#### [Ostrowski et al., 2016]

M. Ostrowski et al.

Boolean Network Identification from Perturbation Time Series Data Combining Dynamics Abstraction and Logic Programming *Biosystems* vol. = 149, pp. 139–153, 2016

#### References IV

#### ▶ [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

#### ▶ [Vaginay et al., 2021]

A. Vaginay, et al. From Quantitative SBML Models to Boolean Networks Complex Networks & Their Applications X 2021

#### ▶ [Vaginay et al., 2022]

A. Vaginay, et al.

From Quantitative SBML Models to Boolean Networks *Applied Network Science* vol. 7-1 pp. 1–23, 2022