

Modeling and Analysis of Large Biological Regulatory Networks thanks to the “Process Hitting” Framework

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Joint work with: Olivier ROUX¹, Morgan MAGNIN¹, Loïc PAULEVÉ²

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The MeForBio Team

MeForBio (team): formal methods for bioinformatics
IRCCyN (laboratory): domains related to computer science
École Centrale de Nantes (engineer school)



Olivier ROUX
Professor & team leader



Morgan MAGNIN
Associate professor



Philippe BORDRON
Post-doc



Julien GRAS
Research engineer



Maxime FOLSCHETTE
PhD student



Loïc PAULEVÉ
Post-doc at LIX
former member of MeForBio

The MeForBio Team

Team activities (computer science / bioinformatics):

- Using formal & algebraic models to study the dynamics of biological systems
- Projects: CirClock (CNRS), BioTempo (French agency ANR), BIL (region)
- Collaborations: several projects with German teams, Microsoft Research (Cambridge)

Loïc PAULEVÉ's PhD thesis: [Paulevé11]

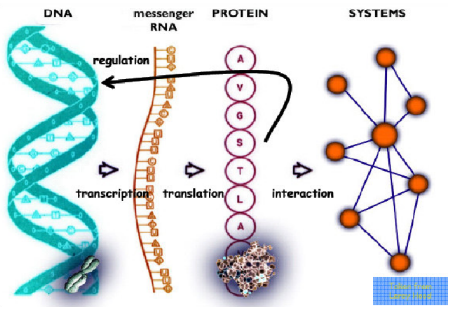
- Modeling, Simulation and Checking of Large Biological Regularoty Networks with Process Hitting
 - Discrete approach, chronological data

My PhD subject:

- Adding a temporal dimension to the Process Hitting by introducing chronometric data
 - Discrete approach, continuous data/constraints

Context and Aims

Algebraic modeling to study complex dynamical biological systems:



Context and Aims

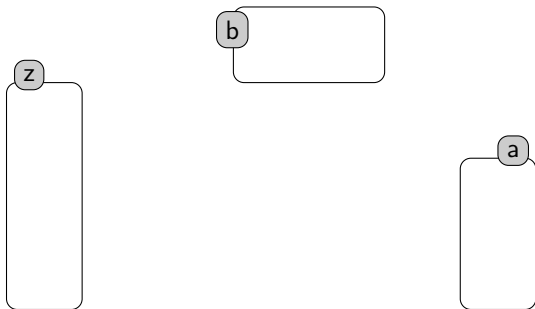
Algebraic modeling to study complex dynamical biological systems:

Some related works:

- Timed Petri Nets [Heiner, ...]
- Continuous-Time Markov Chains (PRISM) [Kwiatkowska, Parker, ...]
- Biocham [Fages]
- Kappa [Danos, Feret, Fontana, Harmer, Krivine]
- Timed Automata [Siebert, Bockmayr, ...]
- Linear Hybrid Automata [Ahmad, Roux]
- Hoare logic [Bernot, Comet, Roux]
- ...

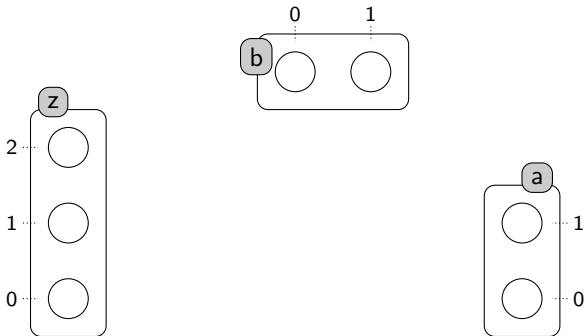
→ How to cope with **very large systems** & combinatorial explosion?

The Process Hitting Framework



Sorts: components *a, b, z*

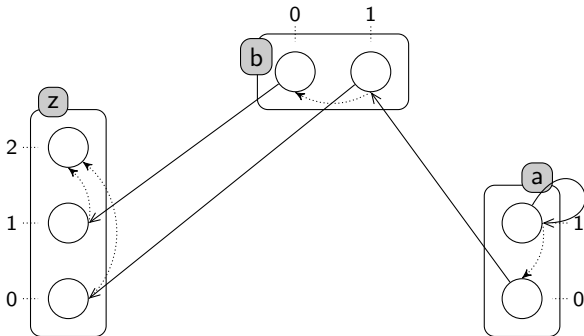
The Process Hitting Framework



Sorts: components a, b, z

Processes: local states / levels of expression $0, 1, 2$

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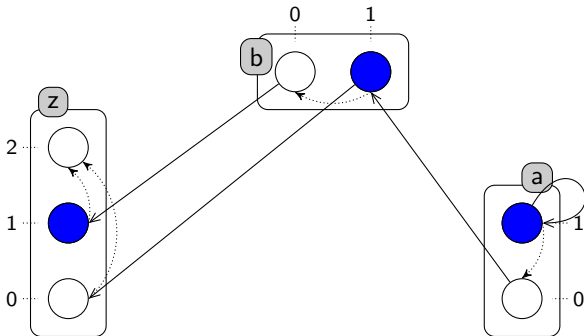


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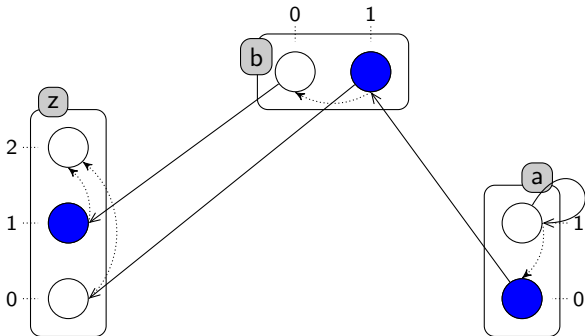
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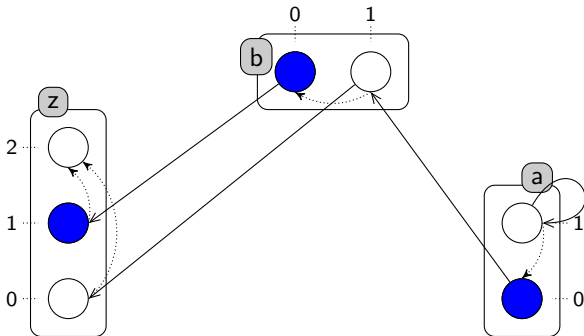
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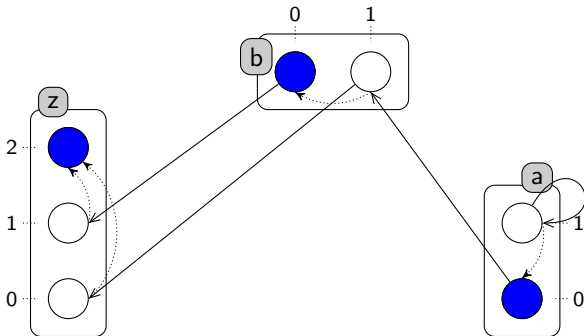
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Stochastic Features

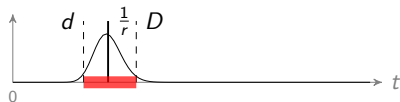
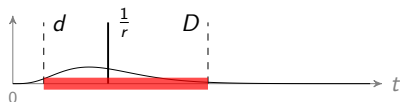
[PMR10-TSE]


- Introduces time features
- Parameters: either (r, sa) , or the **firing interval** $[d; D]$.
 - Tests by simulation

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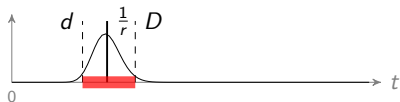
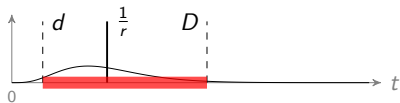



 action duration

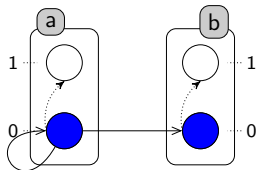
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$$a_0 \rightarrow b_0 \overset{r}{\rightarrow} b_1$$


A horizontal timeline with time t on the right. A red bar is shown between two vertical tick marks, representing the duration of the transition from a_0 to b_0 to b_1 .

$$a_0 \rightarrow a_0 \overset{r}{\rightarrow} a_1$$


A horizontal timeline with time t on the right. An orange bar is shown between two vertical tick marks, representing the duration of the transition from a_0 to a_0 to a_1 .

→ b_1 reached with a **very low probability**.

Static Analysis

Problem: the simulation still faces combinatorial explosion

Idea: study the model **without running it**

- avoiding combinatorial explosion
- focusing on the interesting parts of the model

Two main results:

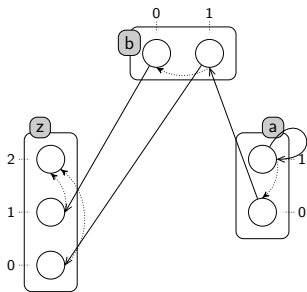
- **Fixed points**
 - Deadlocks
- **Process reachability**
 - From a state where we have processes p_1, p_2, \dots
can we reach the process q_1 , then q_2 , then ... ?

Static Analysis: Fixed Points

[PRM10-TCSB]

Fixed point = state where no action can be fired

→ avoid couples of processes bounded by an action

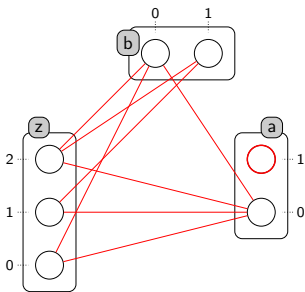
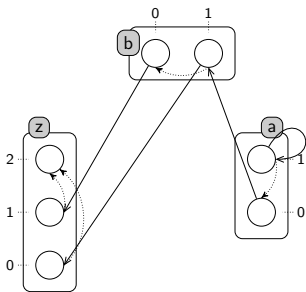


Static Analysis: Fixed Points

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- Hitless Graph



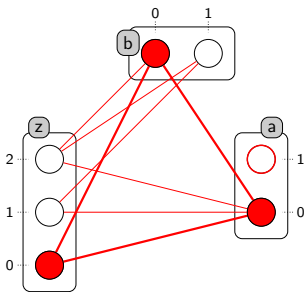
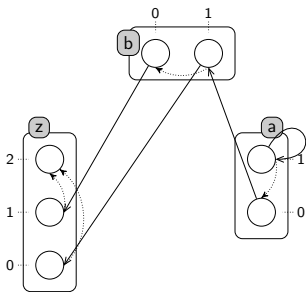
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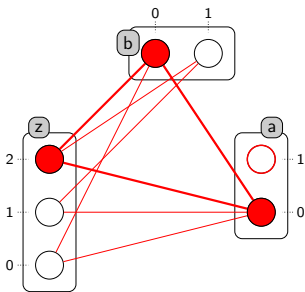
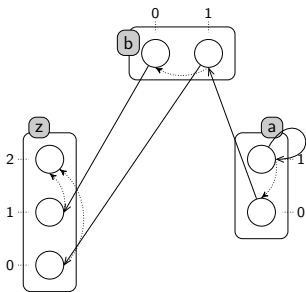


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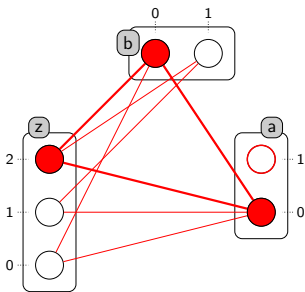
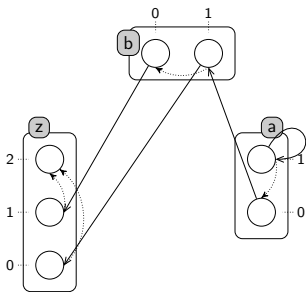


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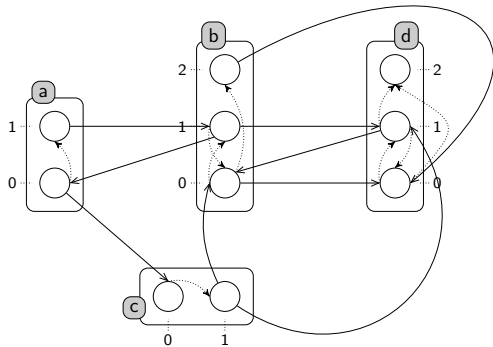


Exponential complexity w.r.t. the number of sorts

Static Analysis: Successive Reachability

[PMR12-MSCS]

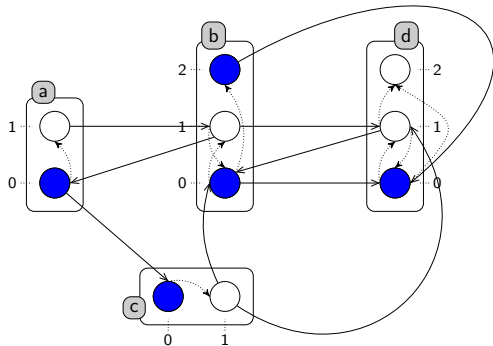
Successive reachability of processes:



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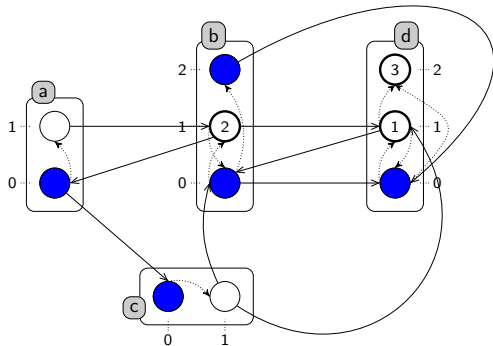
- Initial context

 $\langle a_1, \{b_0, b_1\}, c_0, z_0 \rangle$

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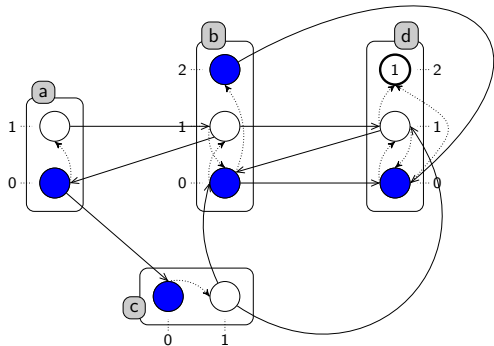
- Objectives

$$d_0 \uparrow^* d_1 :: b_0 \uparrow^* b_1 :: d_1 \uparrow^* d_2$$

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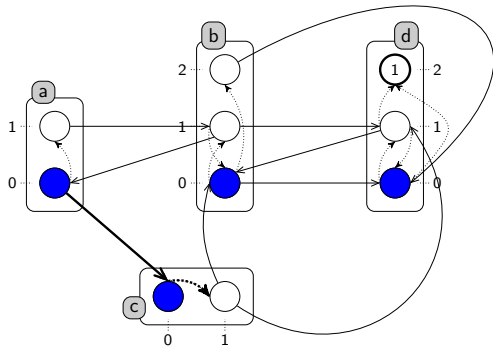
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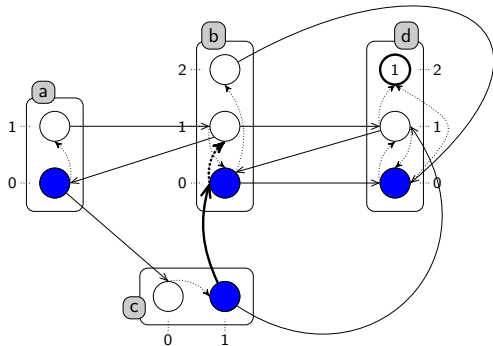
→ Concretization of the objective = scenario

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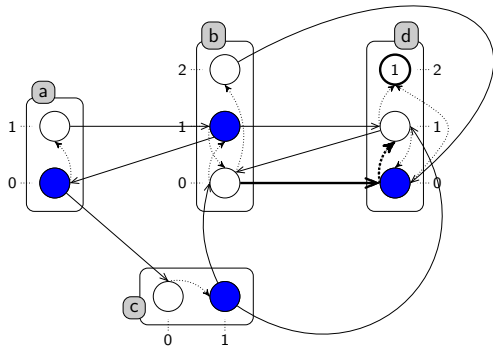
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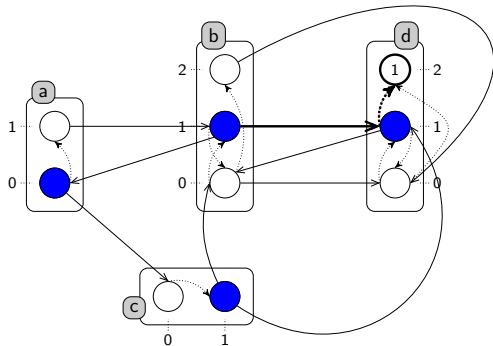
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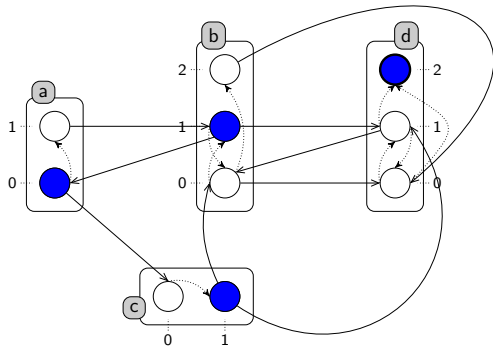
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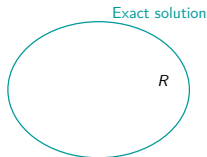
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Over- and Under-approximations

[PMR12-MSCS]

Static analysis by abstractions:

- Directly checking an objective sequence R is hard
- Rather check the approximations P and Q , where $P \Rightarrow R \Rightarrow Q$:

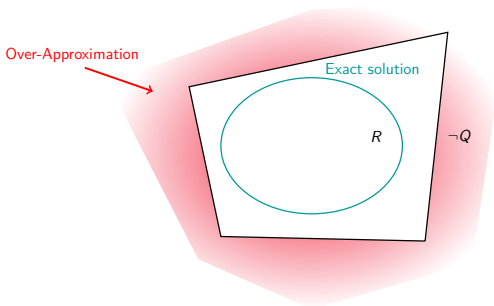


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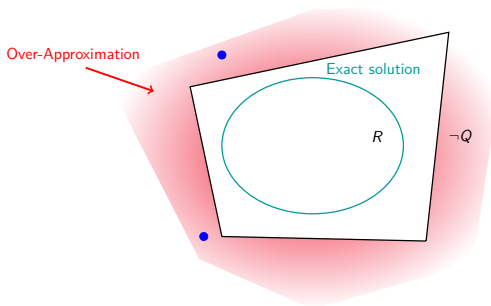


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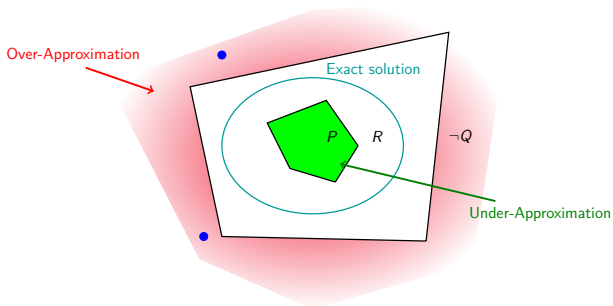


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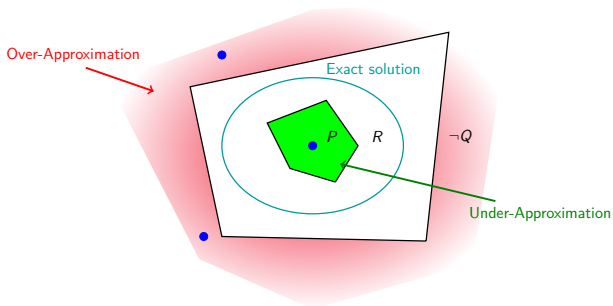


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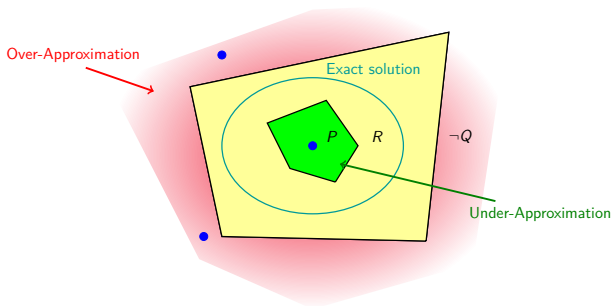


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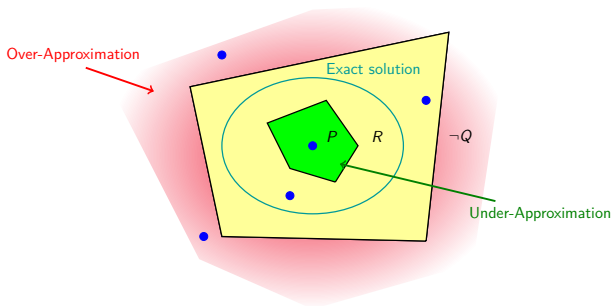


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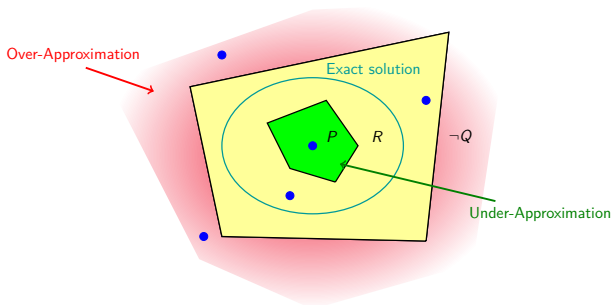


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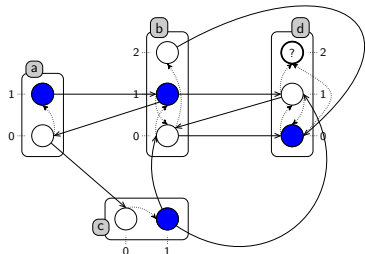
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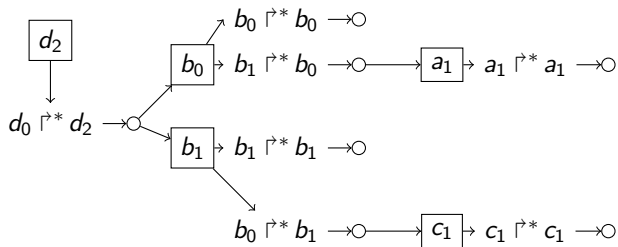
Linear w.r.t. the number of sorts and
 exponential w.r.t. the number of processes in each sort

- Efficient for big models with few levels of expression

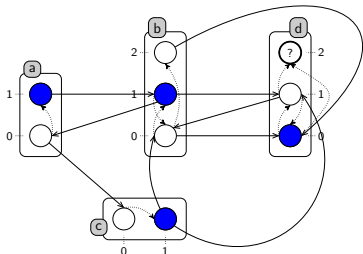
Under-approximation



→ New abstract structure
Sufficient condition:

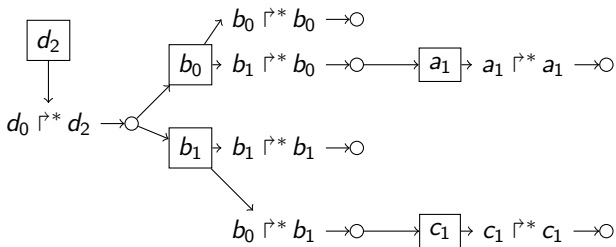


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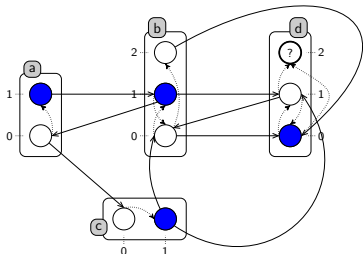


→ New abstract structure
Sufficient condition:

- no cycle
- each objective has a solution



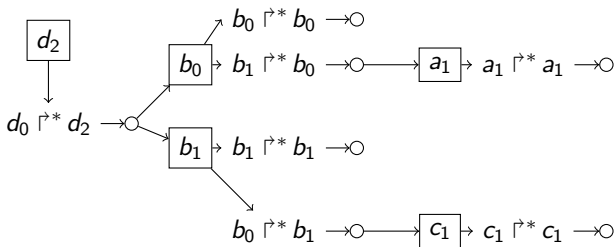
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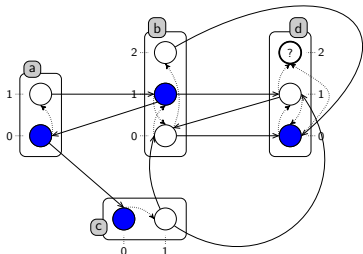
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***R* is true**

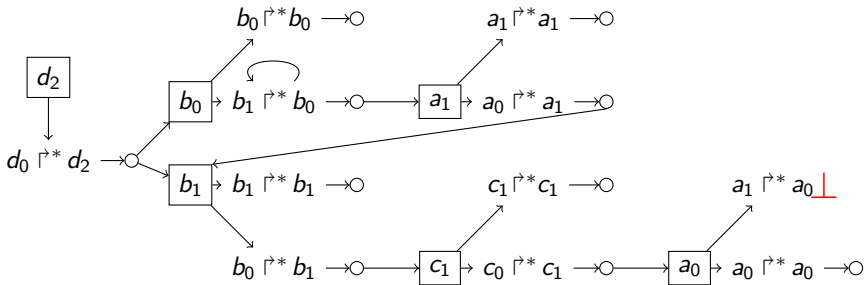


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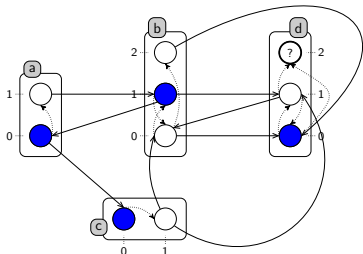


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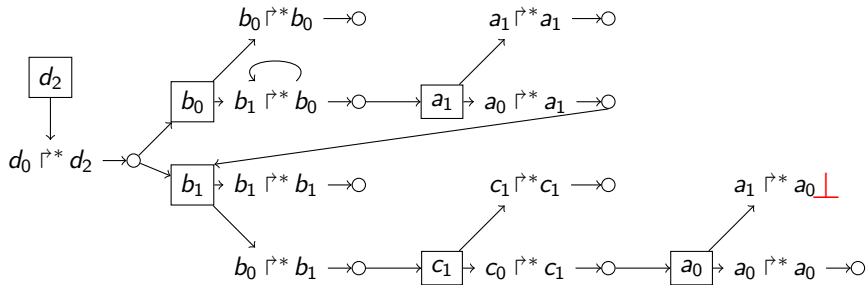
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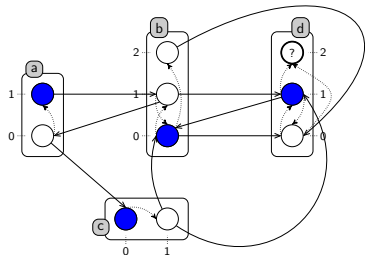
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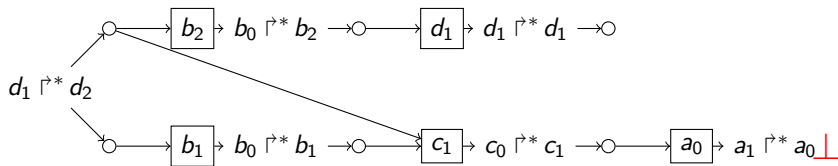
Inconclusive



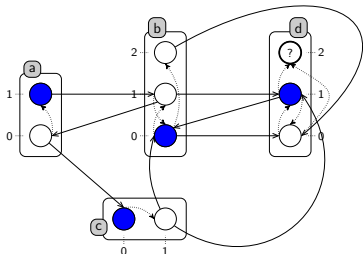
Over-approximation



Necessary condition:



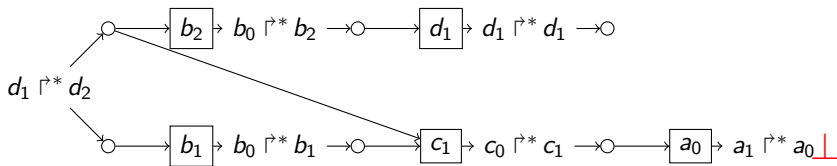
Over-approximation



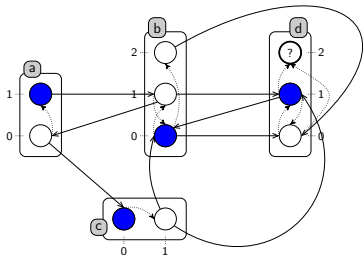
Necessary condition:

There exists a traversal with no cycle

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



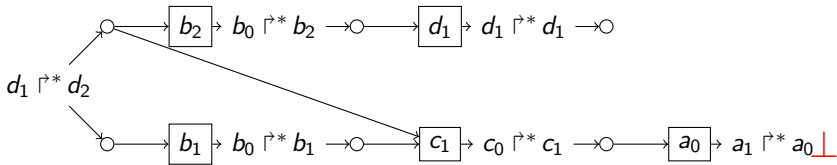
Over-approximation



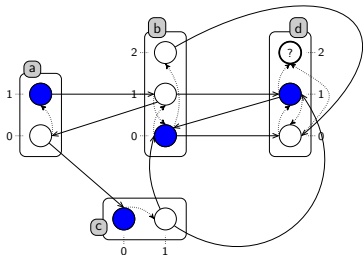
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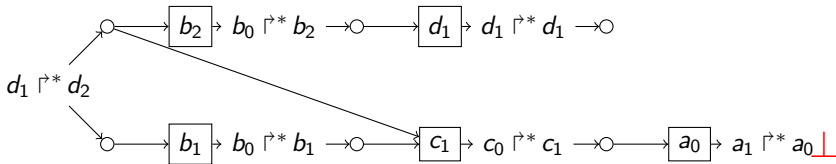


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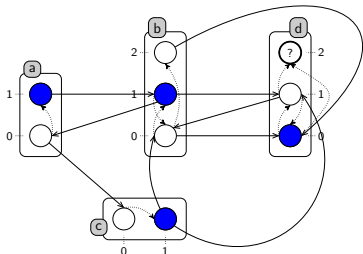
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R is false

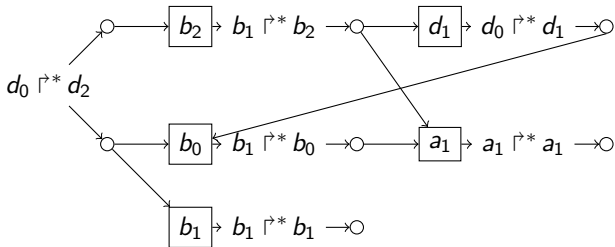


Over-approximation

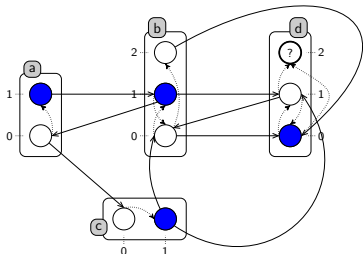
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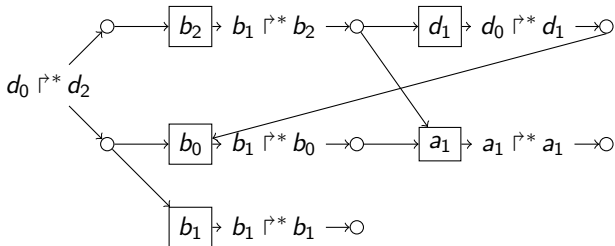


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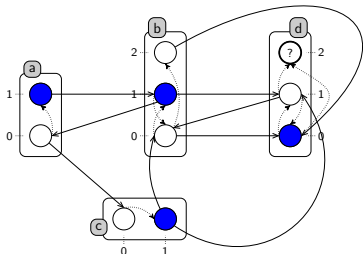
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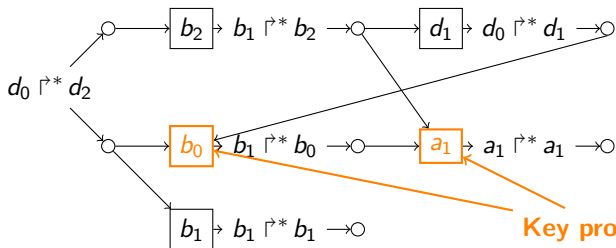


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The Pint Tool

[processhitting.wordpress.com]

Textual language to describe a Process Hitting

Tools implemented:

- fixed points research
- stochastic simulation
- reachability checker
- translations from and to various other models

→ Free API available for future developments

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Results and performance (reachability analysis):

Model	sorts	procs	actions	states	Biocham ¹	libddd ²	PINT
egfr20	35	196	670	2^{64}	[3s-KO]	[1s-150s]	0.007s
tcrsig40	54	156	301	2^{73}	[1s-KO]	[0.6s-KO]	0.004s
tcrsig94	133	448	1124	2^{194}	KO	KO	0.030s
egfr104	193	748	2356	2^{320}	KO	KO	0.050s

¹ [Inria Paris-Rocquencourt/Contraintes]² [LIP6/Move]

Application to Biological Systems

The Process Hitting framework:

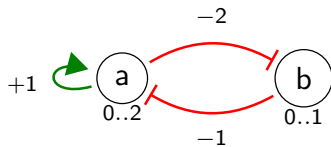
- new formalism with simple elements
- dynamic modeling
- efficient reachability checking
- general framework that could be applied to...

Biological systems:

- gene/protein couples
- Thomas' Modeling: Interaction Graphs
- hard to study → use Process Hitting

Interaction Graphs

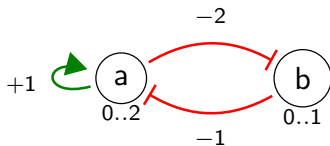
- Nodes = Genes
- Directed edges = Interactions



+ Parametrization

Interaction Graphs

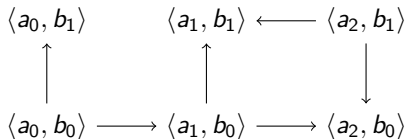
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+ Parametrization

State Graphs

- One level at a time
- Asynchronous



Exponential number of states w.r.t. the number of genes

Tools for Interaction Graphs Study

Interaction Graphs [RCB08]:

- No positive circuit \Rightarrow only 1 attractor
- No negative circuit \Rightarrow no cyclic attractor
- Positive circuits \Rightarrow criterion for max. number of attractors
- Temporal logics \Rightarrow check properties (needs State Graph)
 \rightarrow SM-BIONET

Boolean Networks [PR10-CRAS]:

- Results on topological fixed points

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Boolean Networks [PR10-CRAS]:

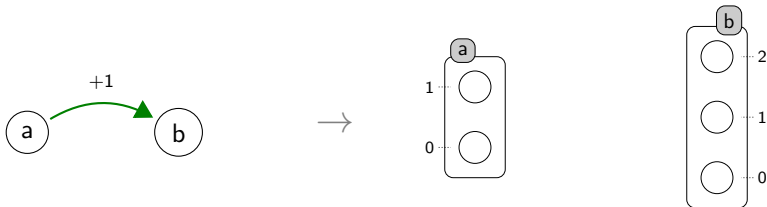
- Results on topological fixed points

Problem: combinatorial explosion when computing the State Graph

\rightarrow Need for static analysis \rightarrow Use the Process Hitting

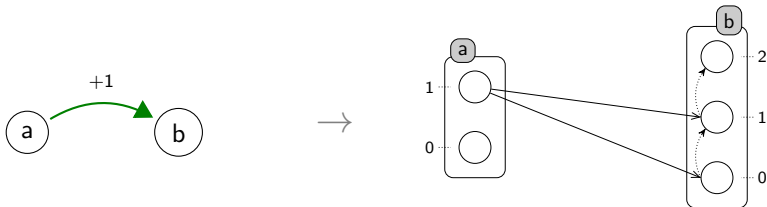
Translation of the Generalized Dynamics

Positive interaction:



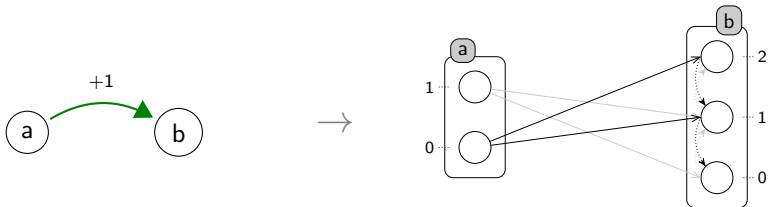
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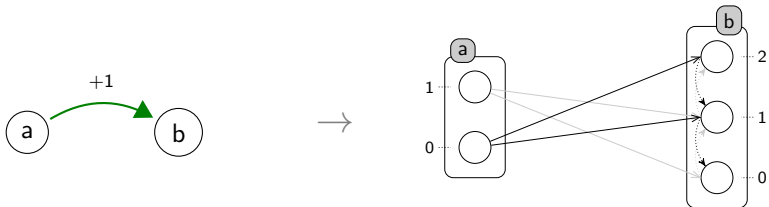
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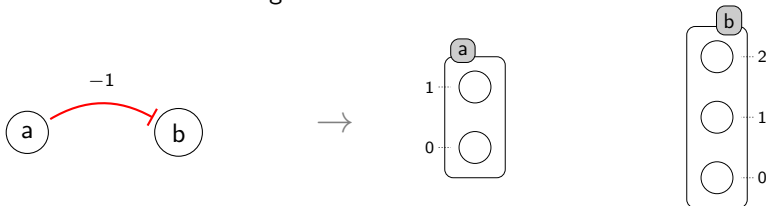


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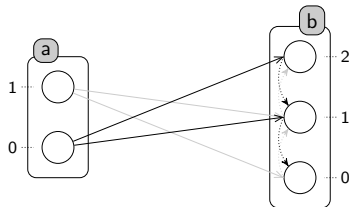
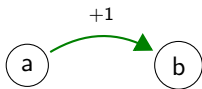


Negative interaction:

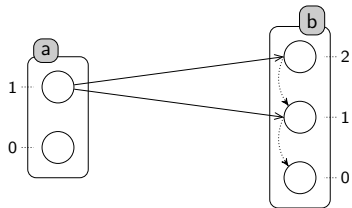
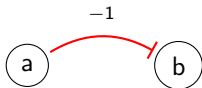


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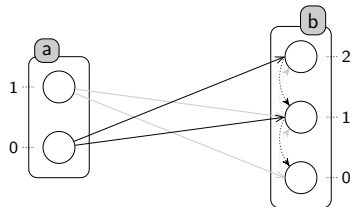
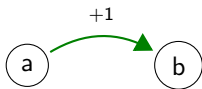


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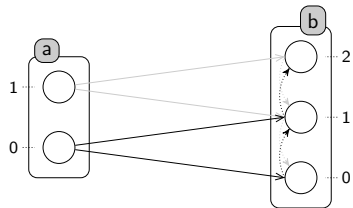
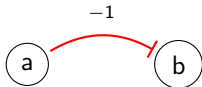


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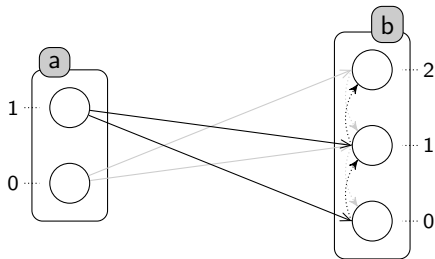


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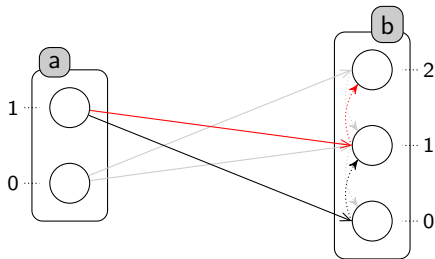
Refining with Actions Removal

Prevent behaviors by deleting **unrealistic actions**



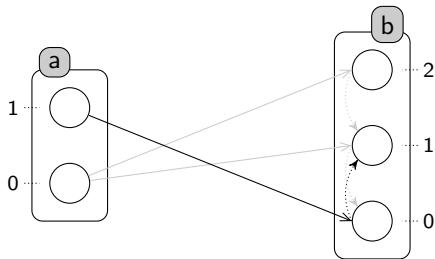
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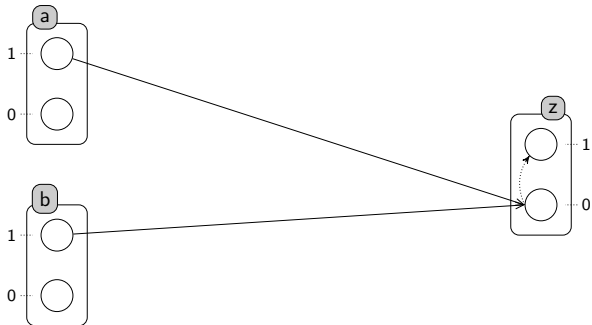


Refining with Cooperation

Allow **cooperation** between two genes

- How to express $(a_1 \wedge b_1) \rightarrow z_0 \uparrow z_1$?

→ Add a “**cooperative sort**” reflecting the state of a and b

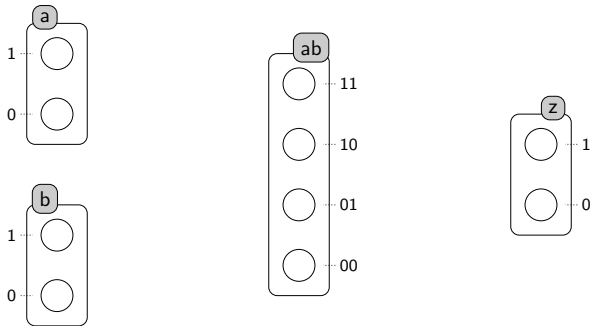


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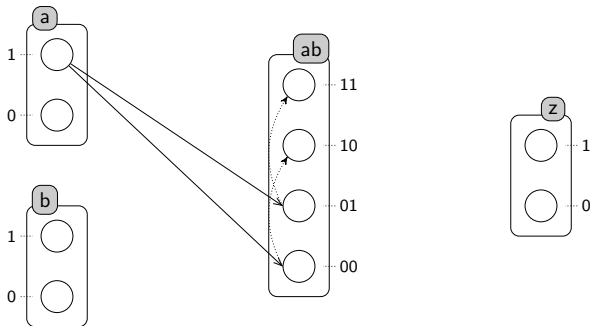


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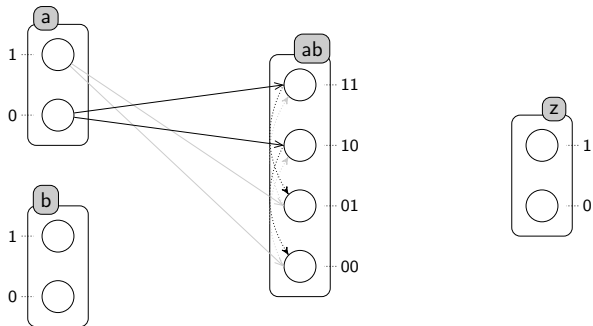


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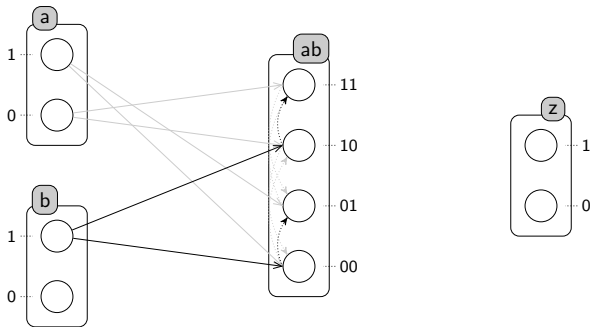


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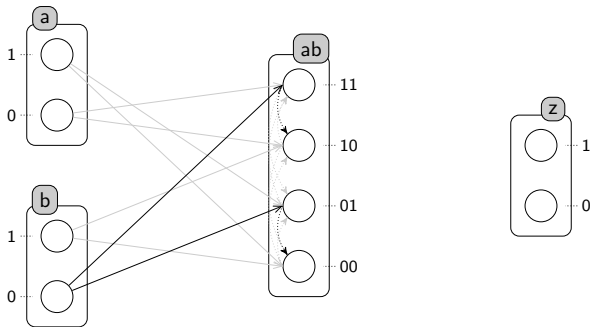


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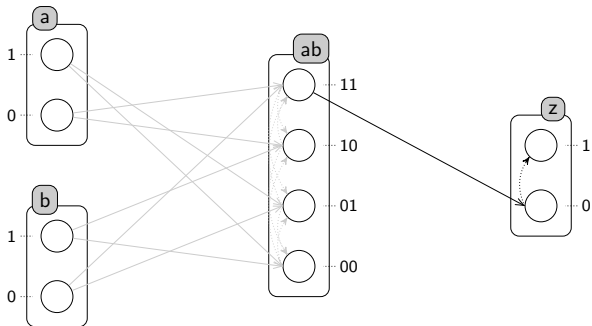


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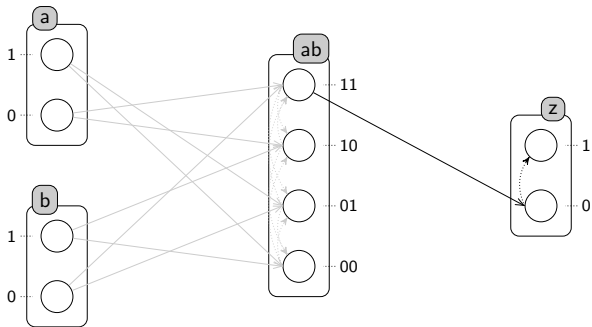


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→ Introduces a temporal shift (over-approximation)

Using Process Hitting for Interaction Graphs Study

The Interaction Graph is the historical discrete model
Adapted to and widespread in biological studies

Several tools to study Interaction Graphs
But for some results, the State Graph is needed

→ **Combinatorial explosion**

Process Hitting to study large Biological Regulatory Networks

→ Translation from Interaction Graphs + Refining

→ **Efficient static analysis**

Ongoing Work

Several student projects:

- Optimization of fixed points research
 - OOP-oriented research (Java)
 - CSP solver-oriented research (Choco) [choco.emn.fr]
- Study of the circadian clock
 - use of the Process Hitting
- Graphical interface for the Process Hitting
 - generalize its use by biologists
 - show/use the static analysis results

Ongoing Work

Some developments:

- Framework evolutions
 - Priorities between actions
 - Neutralizing Edges (weak bisimulation)
- Working with Interaction Graphs
 - Translation to Process Hitting
 - Joint Actions (weak bisimulation)

Suggested personal subject:

- Using solvers to gain knowledge on Interaction Graphs
- Translation, then refining and constraints
 - Information on the parametrization

Conclusion

Study of systems

- **Combinatorial explosion**

Process Hitting

- Simple modeling for **large systems**
- Applications to Biological Regulatory Networks
- Efficient static analysis
- Further development (priorities, temporal data)

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Thank you

Bibliography

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