

KUBIC-NII Joint Seminar on Bioinformatics 2014

# Perturbations and Recovery Costs in Biological Regulatory Networks with Process Hitting

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Ongoing work with: **Morgan MAGNIN** and **Katsumi INOUE**

2014/11/17

## Studying the Perturbations of a Biological Model

Biological models are well-known for being resilient

- Alternative pathways
- Restoration of oscillations

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- Running the models → slow and inefficient
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- Resilience times → requires timing data
- Observation of specific characteristics → **impact degree**

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Refine this analysis with new model checking methods:

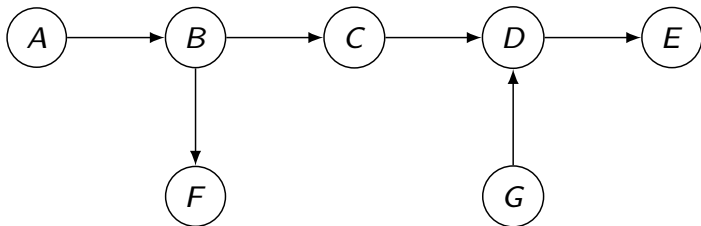
- The Process Hitting framework
- Efficient **reachability analysis**
- Finer study of the perturbations

## Impact Degree

[Jiang, Tamura, Ching, Akutsu in *Communications and Computer Sciences*, 2013]

**Reaction networks** = set of species consumed and produced by reactions

- Reaches an equilibrium state

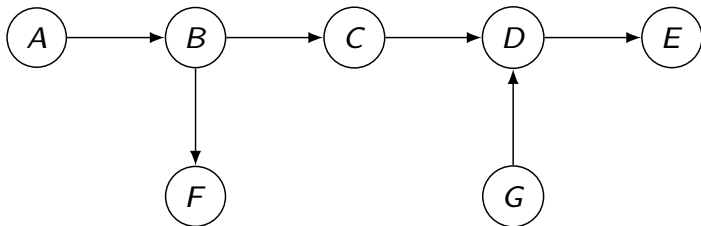


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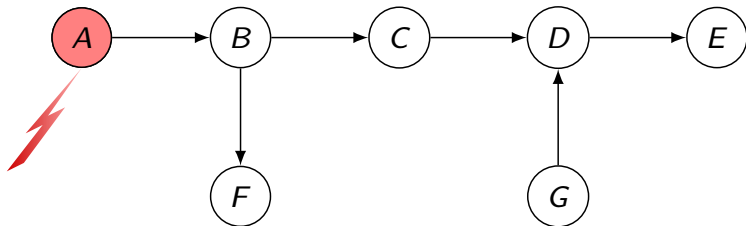
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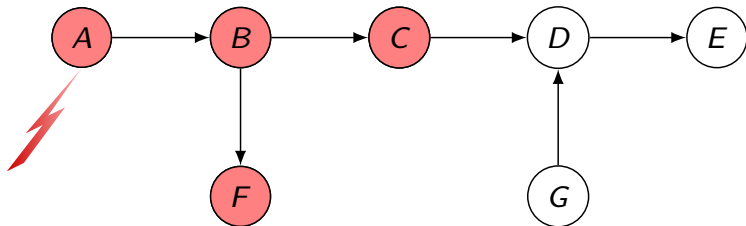
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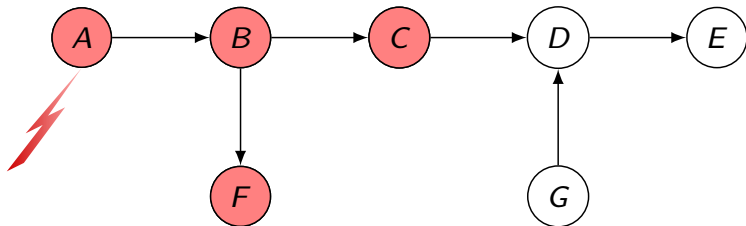


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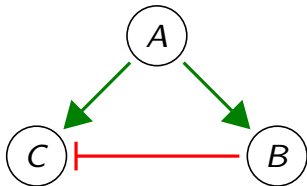
- Notion of importance/criticality of a node
- Highlights the resilience of biological systems (alternative paths)

## Application to regulation networks

Model from [Comet, Bernot in *Nice Spring school on Modelling and simulation of biological processes in the context of genomics*, 2010]

**Regulation networks** = set of species regulated by other species

- The regulating species are not consumed
- Negative regulations → Not always a steady state

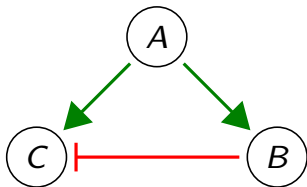


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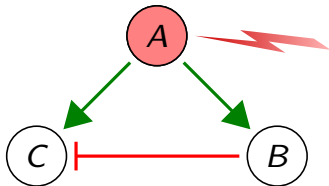
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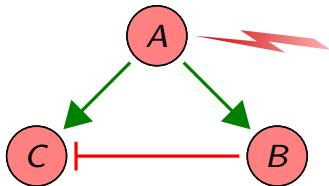
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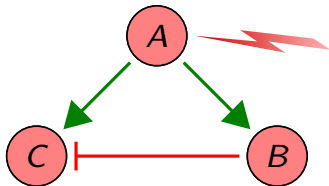
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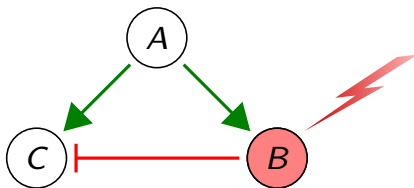
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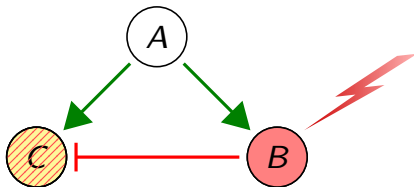
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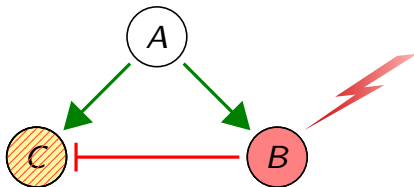


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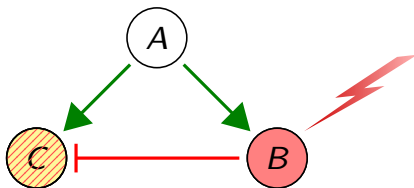
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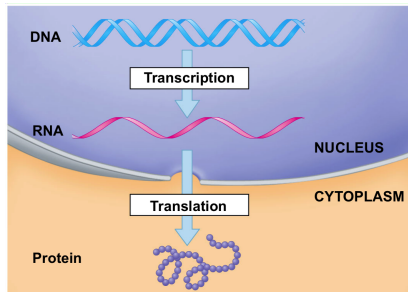
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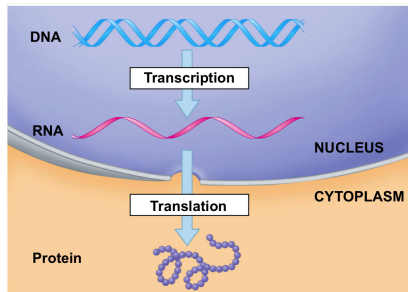
- Number of species that are completely turned off → For A: 3
  - Number of species whose behavior is modified → For B: 1 + 1 = 2
- Requires a more precise study of the behavior

## Abstractions of the Representation

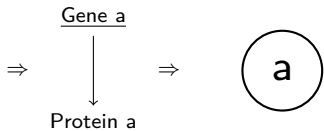


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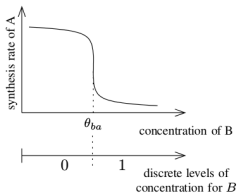


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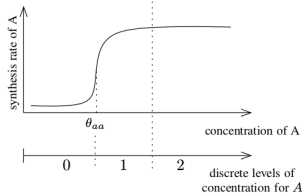
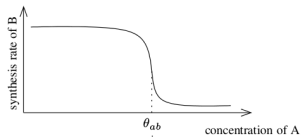
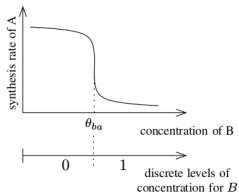
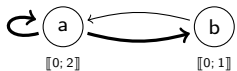
## Discretization and Asynchronism

[Richard, Comet, Bernot (tutorial), 2008]



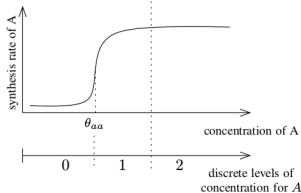
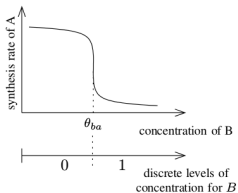
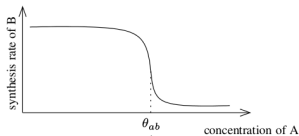
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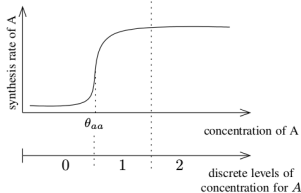
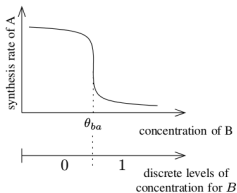
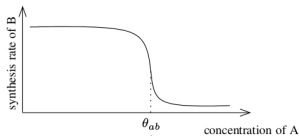
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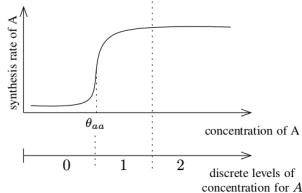
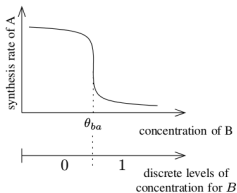
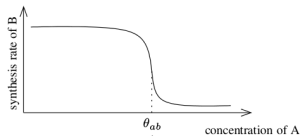
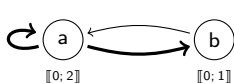


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- Continuous variations of the real values  
→ **Unitary** dynamics



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- Continuous variations of the real values  
→ **Unitary** dynamics
- Simultaneous crossings of two thresholds never occurs  
→ **Asynchronous** dynamics

## Discrete Networks / Thomas Modeling

[Kauffman in *Journal of Theoretical Biology*, 1969]

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



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

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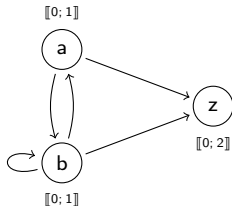
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- An evolution function for each component  $f^z : \mathbb{F} \rightarrow \mathbb{F}^z$

$b$	$f^a(b)$
0	1
1	0

$a$	$b$	$f^b(a, b)$
0	0	1
0	1	1
1	0	0
1	1	1

$a$	$b$	$f^z(a, b)$
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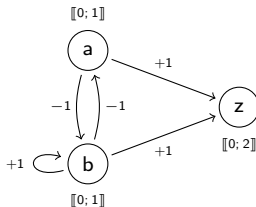
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- Signs and thresholds on the edges  $a \xrightarrow{+1} z$

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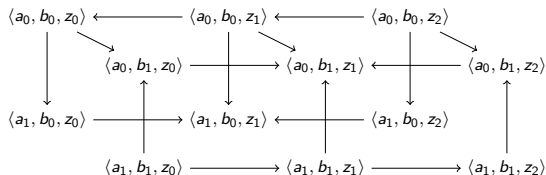
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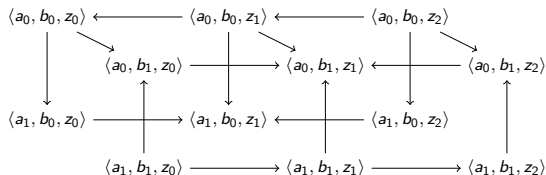
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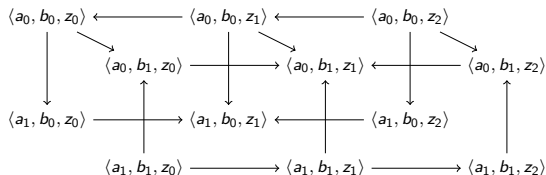
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- **Thomas' conjectures** (conditions for multi-stationarity or sustained oscillations)
  - Boolean case: [Remy, Ruet, Thiéffry in *Advances in Applied Mathematics*, 2008]
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But reachability properties require to compute the whole state graph:

Example: From the initial state  $(a, b, z) = (0, 0, 0)$ , is it possible to reach  $z = 2$ ?

- **Temporal logics**
  - CTL: [Bernot, Comet, Richard, Guespin in *Journal of Theoretical Biology*, 2004]
  - LTL: [Ito, Izumi, Hagihara, Yonezaki in *Bioinformatics and BioEngineering*, 2010]



## Process Hitting

[Paulevé *et al.* in *Transactions on Computational Systems Biology*, 2011]

The **Process Hitting** is:

- A recent formalism well-adapted to the modeling of BRNs
- An **atomistic, qualitative and asynchronous** modeling (explicit & discrete expression levels)
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Previously developed tools:

- **Reachability analysis** by abstract interpretation
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- The **reachability analysis** is very efficient (polynomial time)
- The Process Hitting is also well-adapted to study **large BRNs**

## Standard Process Hitting

[Paulevé *et al.* in *Transactions on Computational Systems Biology*, 2011]



**Sorts:** components  $a, b, z$

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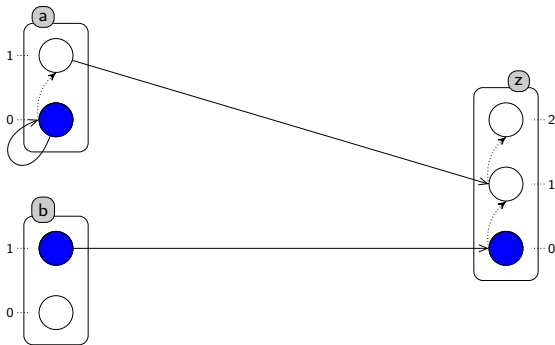
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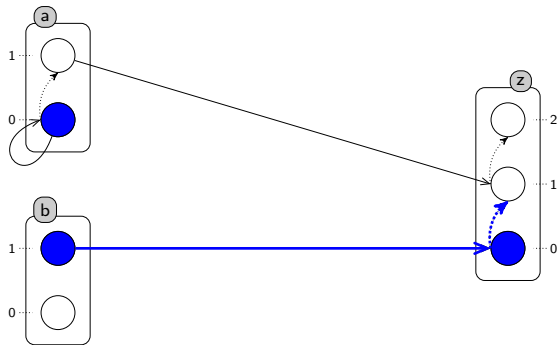
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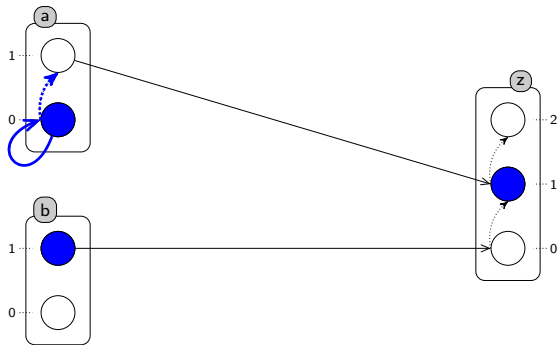
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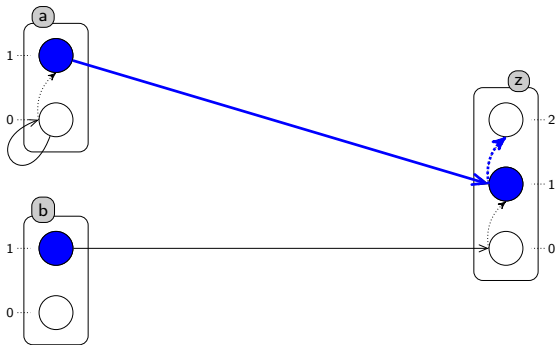
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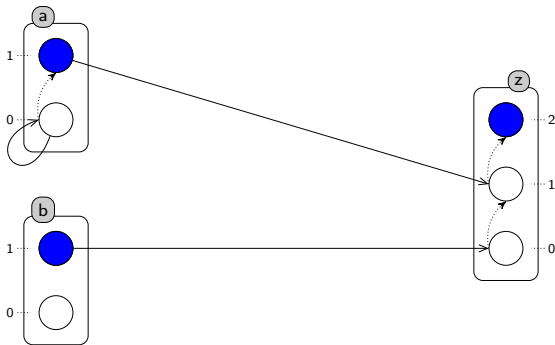
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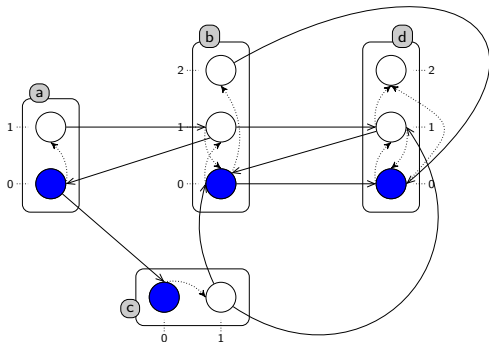
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**Actions:** dynamics  $b_1 \rightarrow z_0 \uparrow z_1, a_0 \rightarrow a_0 \uparrow a_1, a_1 \rightarrow z_1 \uparrow z_2$

## Static analysis: successive reachability

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

Successive reachability of processes:



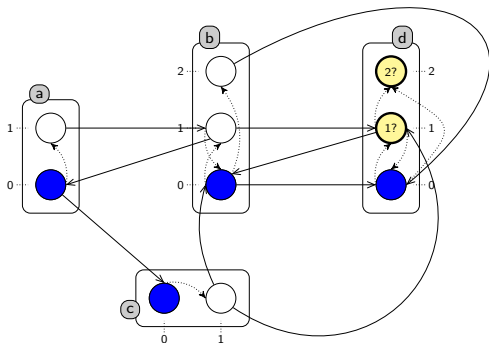
- Initial state

$\langle a_1, b_0, c_0, d_0 \rangle$

## Static analysis: successive reachability

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

Successive reachability of processes:



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- Objectives

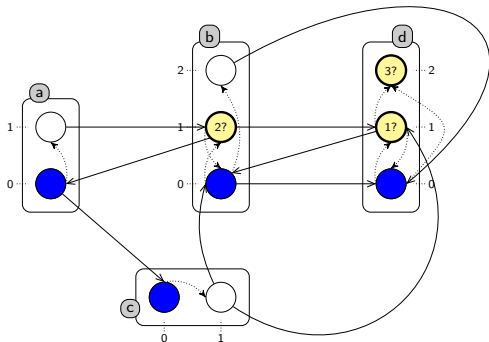
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$[\uparrow d_1 :: \uparrow d_2]$

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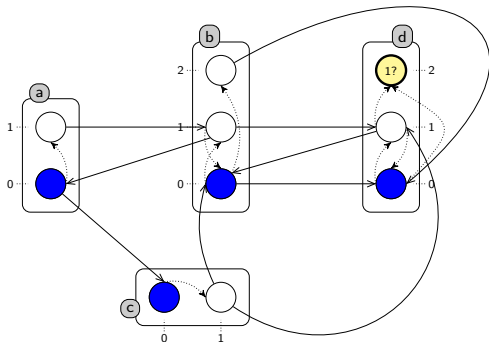
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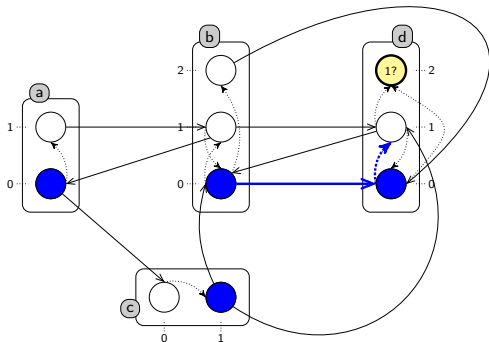




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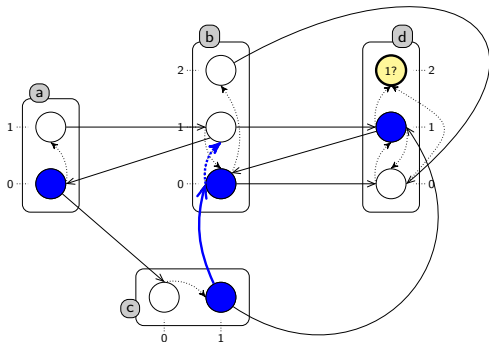
→ Concretization of the objective = scenario

$a_0 \rightarrow c_0 \uparrow c_1 :: \underline{b_0 \rightarrow d_0 \uparrow d_1} :: c_1 \rightarrow b_0 \uparrow b_1 :: b_1 \rightarrow d_1 \uparrow d_2$

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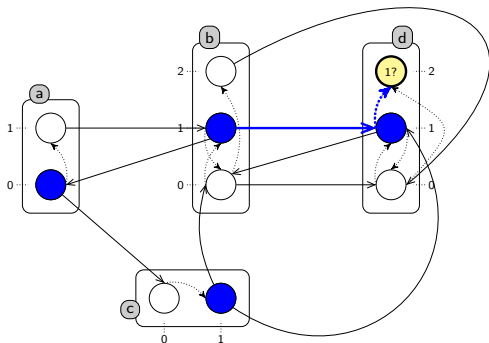
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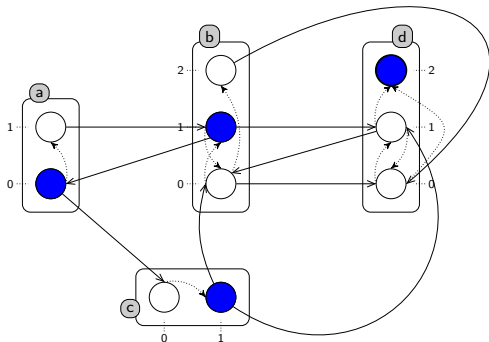
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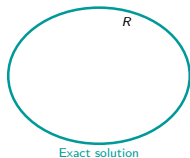
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[Paulevé *et al.* in *Mathematical Structures in Computer Science*, 2012]

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Approximations:  $P$  and  $Q$ , built so that  $P \Rightarrow R \Rightarrow Q$



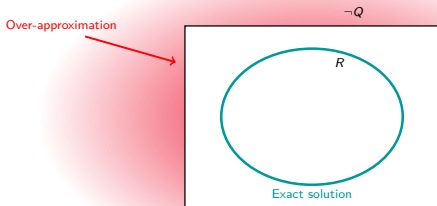
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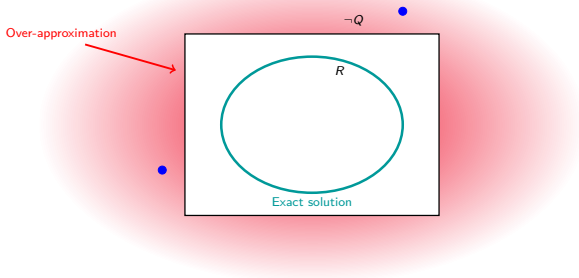
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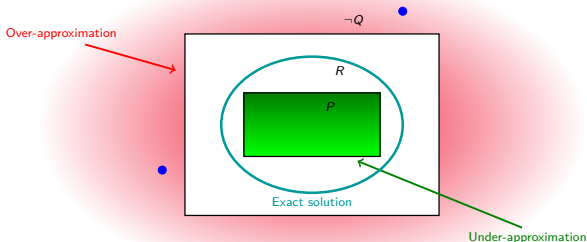
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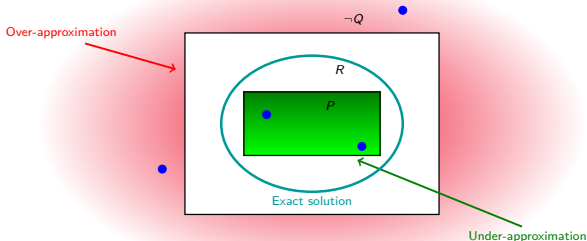
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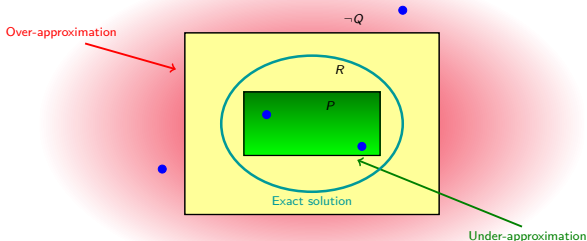
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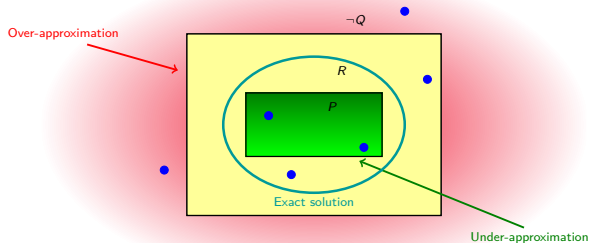
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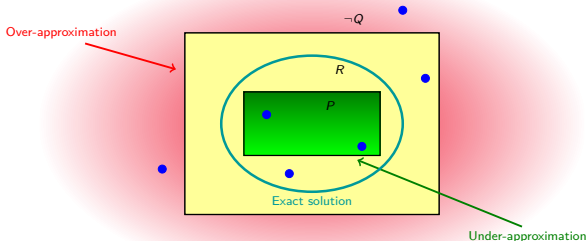
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Polynomial complexity in the number of sorts

Exponential complexity in the number of processes in each sort

→ Efficient for big models with few expression levels

## Implementation & Execution times

### **PINT: Existing free OCaml library**

- Compiler + tools for Process Hitting models
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## Computation time for various reachability analyses:

Model	Sorts	Procs	Actions	States	Biocham <sup>1</sup>	libddd <sup>2</sup>	PINT
<b>egfr20</b>	35	196	670	$2^{64}$	[3s-∞]	[1s-150s]	<b>0.007s</b>
<b>tcrsig40</b>	54	156	301	$2^{73}$	[1s-∞]	[0.6s-∞]	<b>0.004s</b>
<b>tcrsig94</b>	133	448	1124	$2^{194}$	∞	∞	<b>0.030s</b>
<b>egfr104</b>	193	748	2356	$2^{320}$	∞	∞	<b>0.050s</b>

<sup>1</sup> Inria Paris-Rocquencourt/Contraintes

<sup>2</sup> LIP6/Move

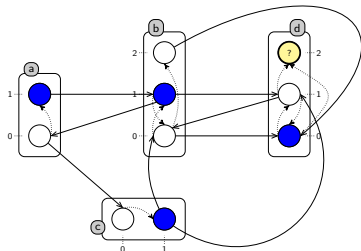
**egfr20** : Epithelial Growth Factor Receptor (20 components) [Sahin *et al.*, 2009]

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

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

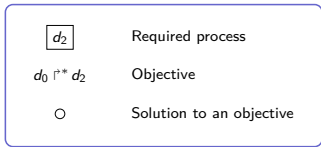
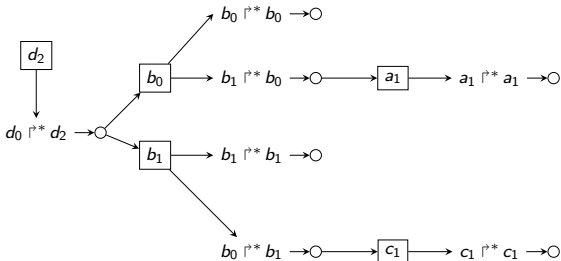
**tcrsig94** : T-Cell Receptor (94 components) [Saez-Rodriguez *et al.*, 2007]

## Under-approximation

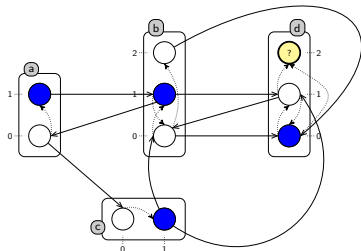


### Sufficient condition:

- no cycle
- each objective has a solution



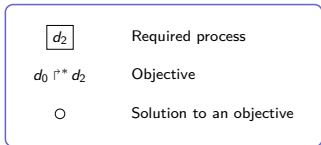
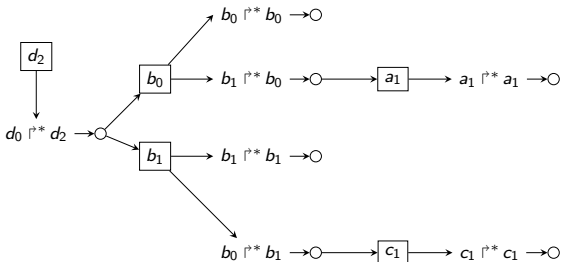
## Under-approximation



**Sufficient condition:**

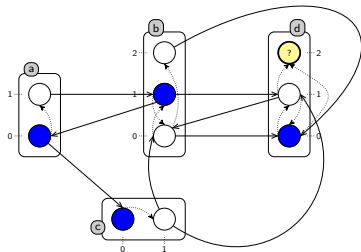
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*R* is true



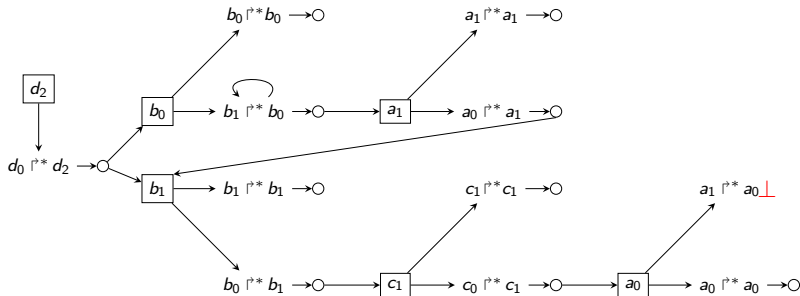


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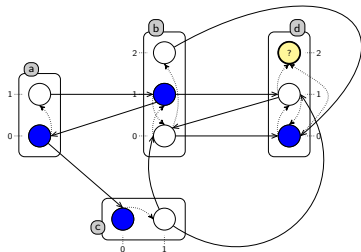


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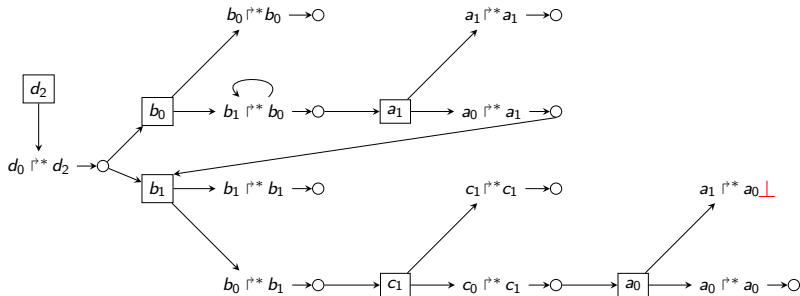
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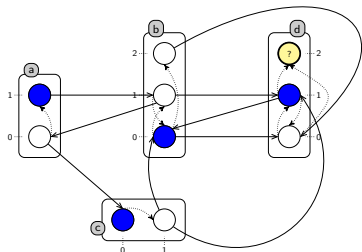
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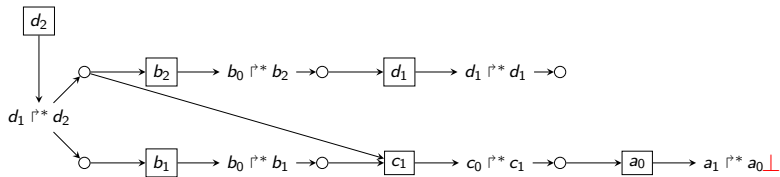
**Inconclusive**



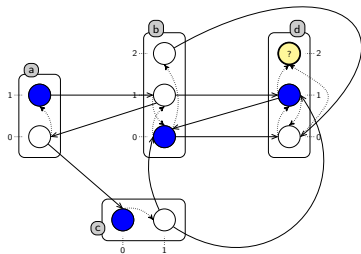
## Over-approximation



**Necessary condition:**



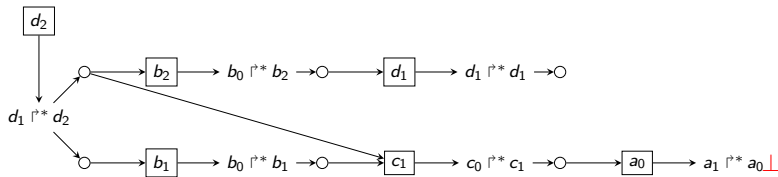
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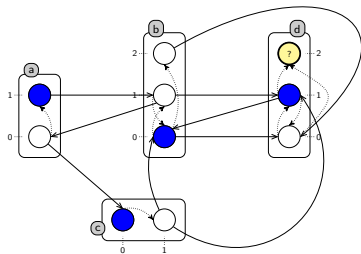
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There exists a traversal with no cycle

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



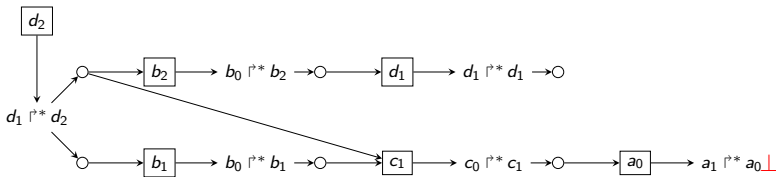
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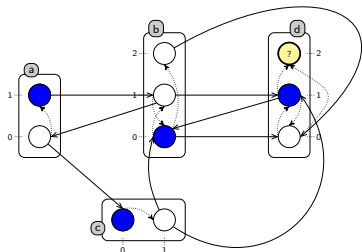
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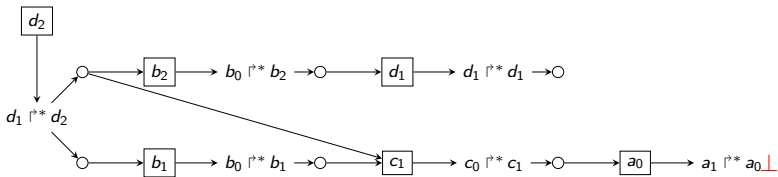


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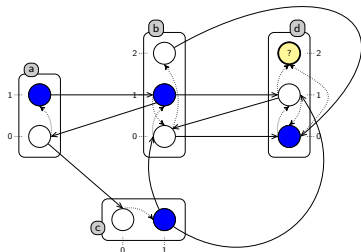
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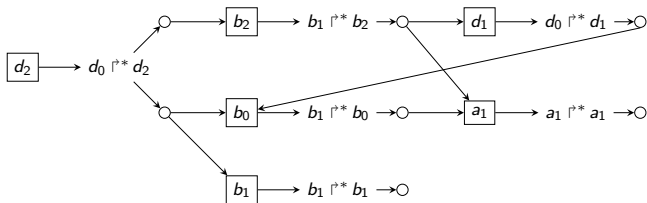
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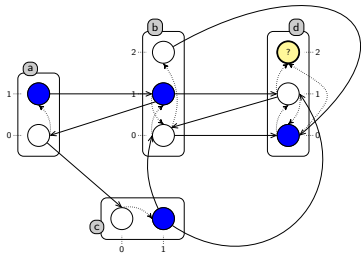
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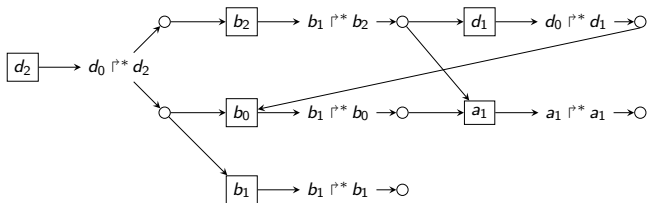


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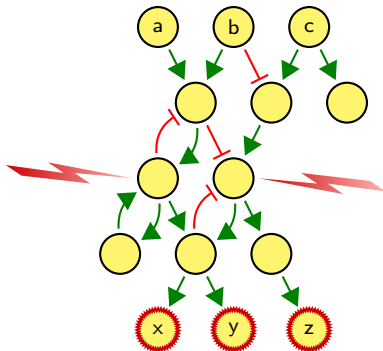




## Cut sets

[Paulevé, Andrieux, Koepl in *Computer Aided Verification*, 2013.]

**Cut set** = set of nodes whose knockout is sufficient to turn off some outputs

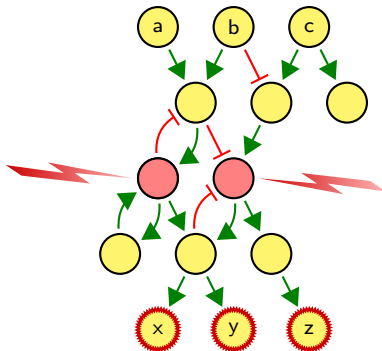


- “Absolute” vision of possible perturbations
- Need for an intermediate point of view → Finer analysis

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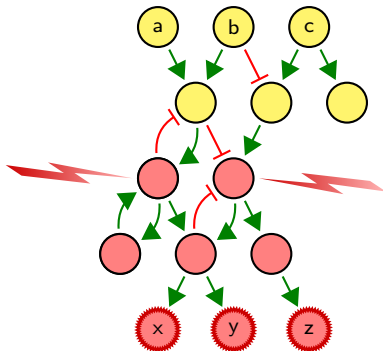


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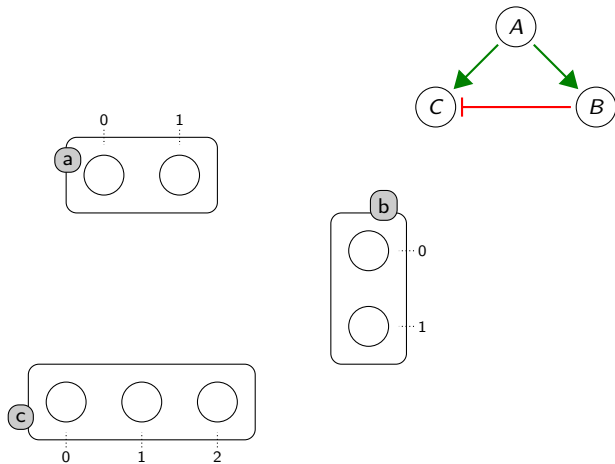
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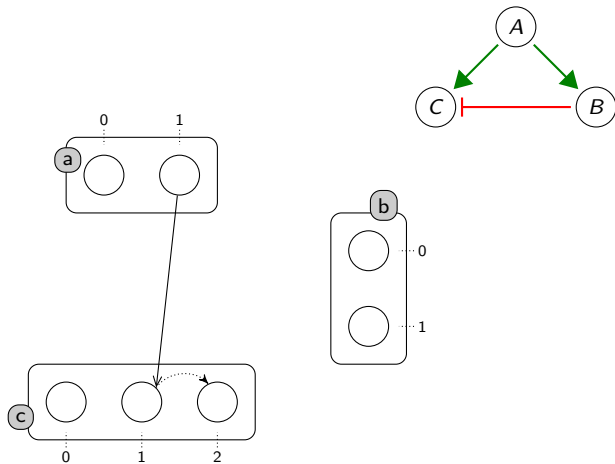


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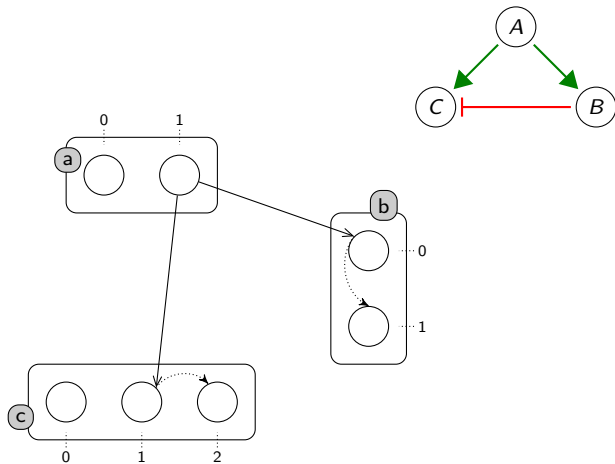
## Translation in Process Hitting



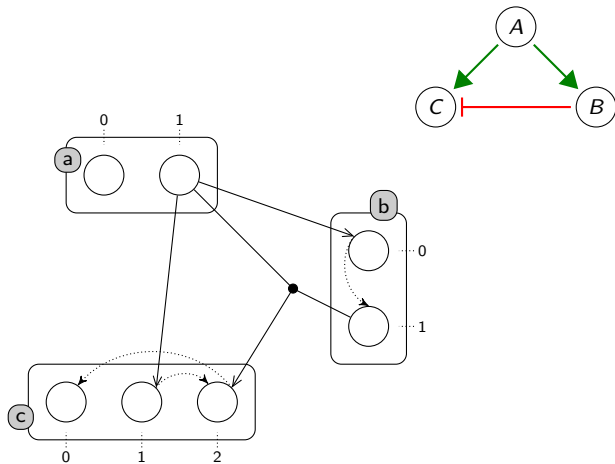
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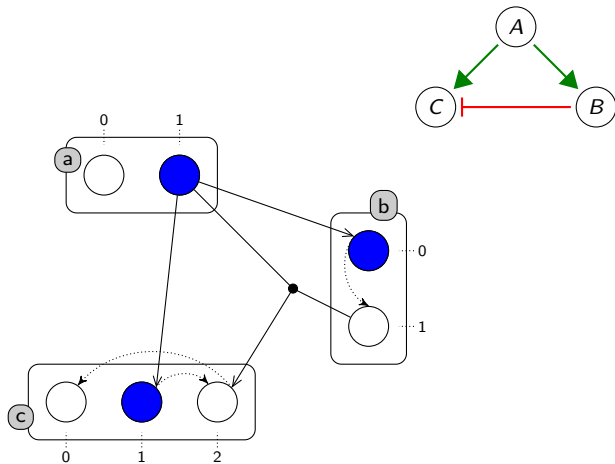
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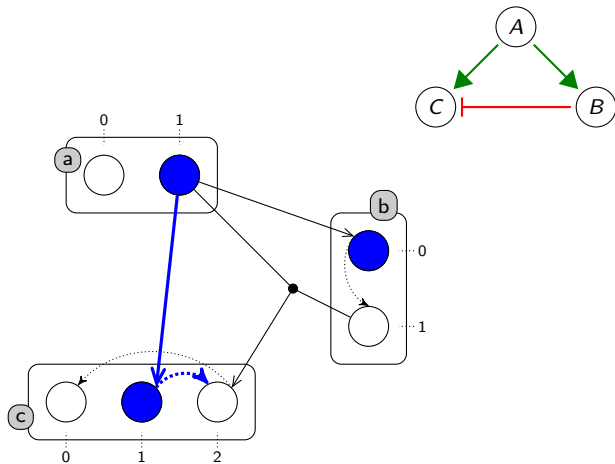


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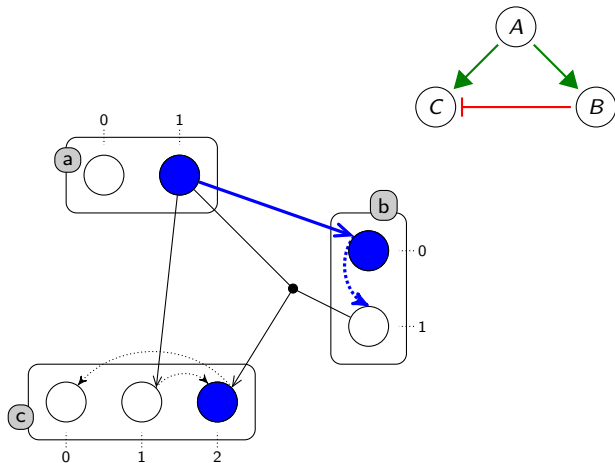




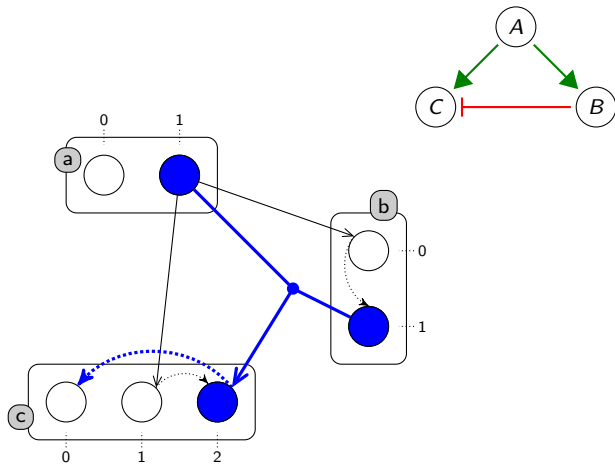
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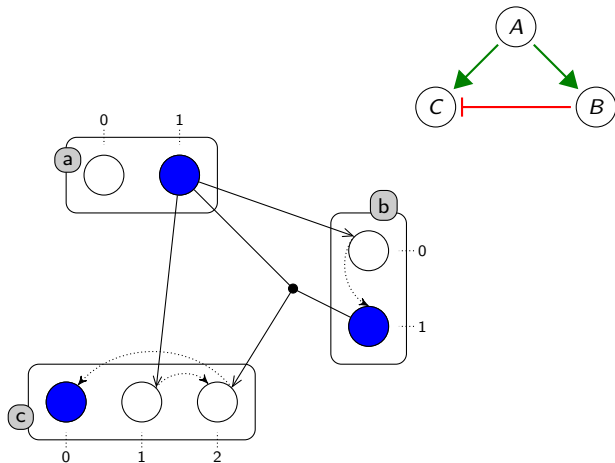
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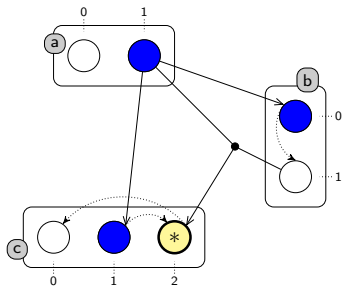
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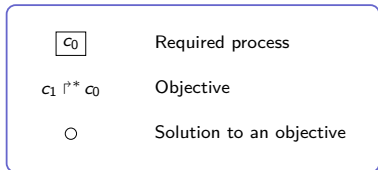
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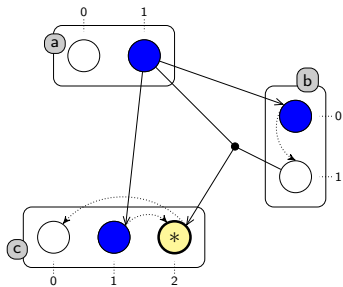
## Detailed application of the Static Analysis



**Graph of local causality:**

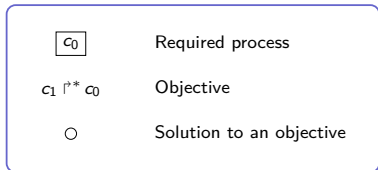


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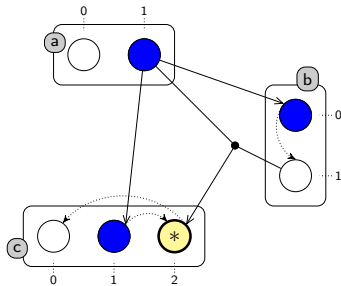


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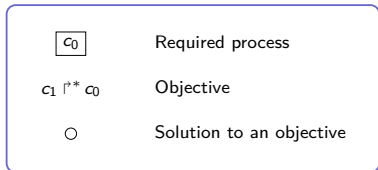
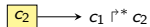
$c_2$



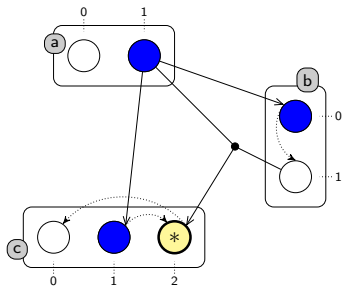
## Detailed application of the Static Analysis



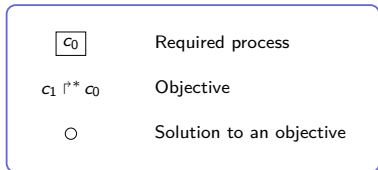
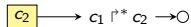
Graph of local causality:



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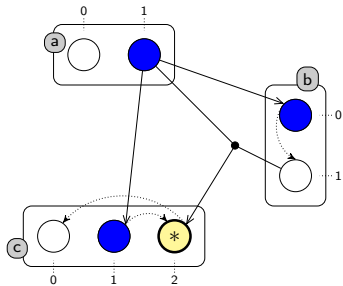


Graph of local causality:

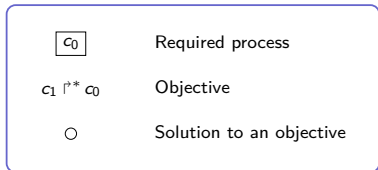
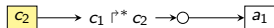




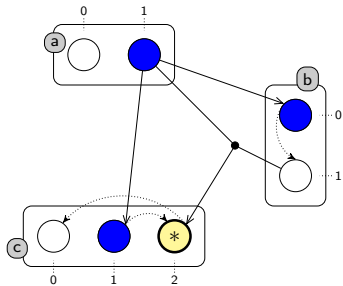
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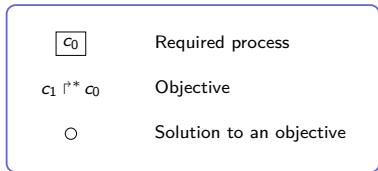
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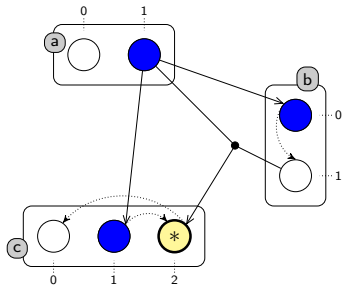
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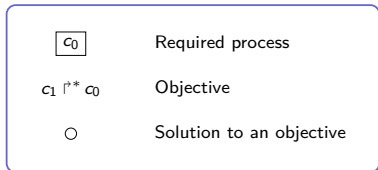
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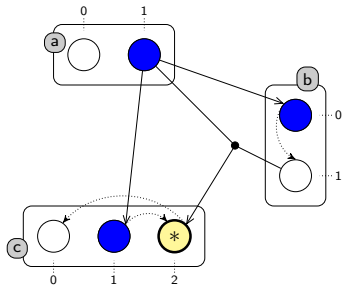
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OK



$c_0$

Required process

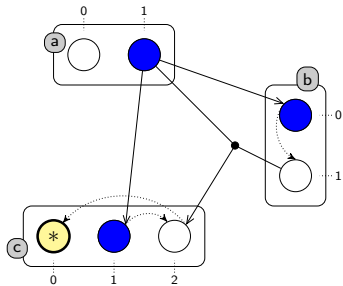
$c_1 \uparrow^* c_0$

Objective

○

Solution to an objective

## Detailed application of the Static Analysis

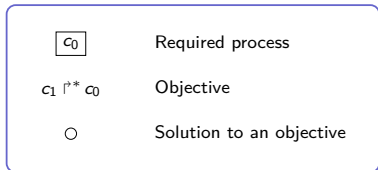


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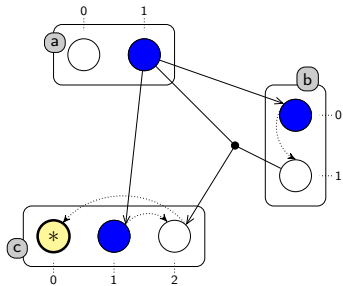
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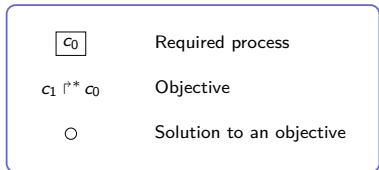
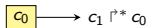


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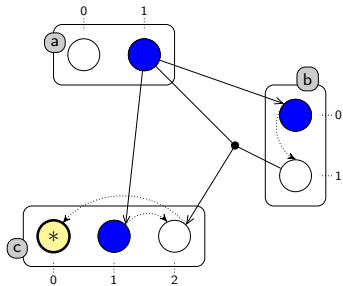
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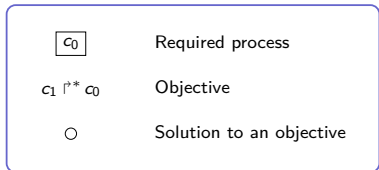
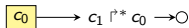


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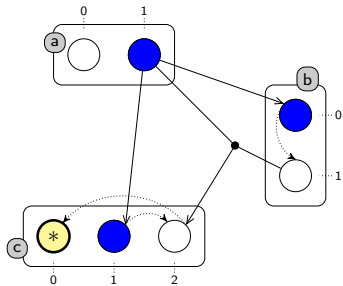
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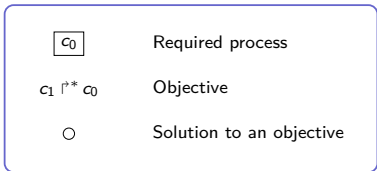
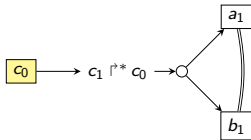


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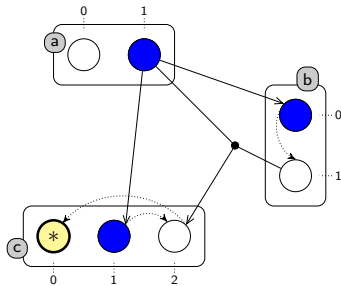
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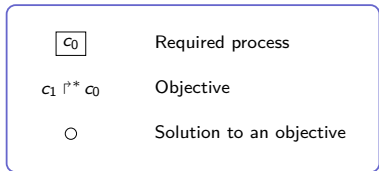
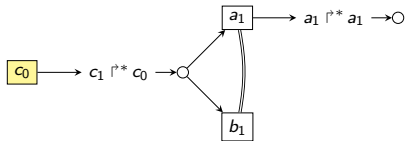


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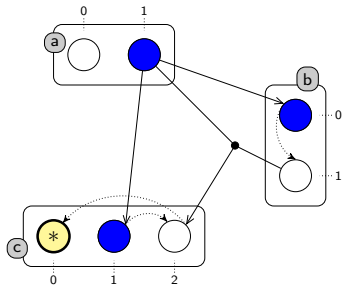
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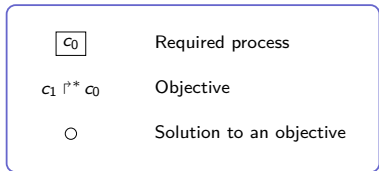
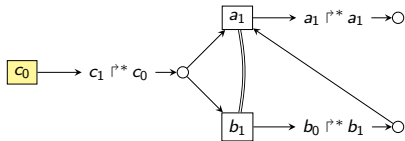


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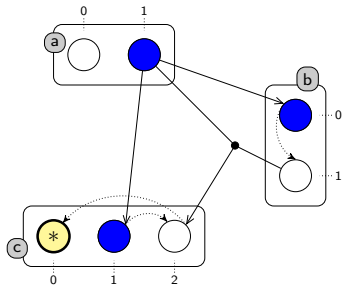
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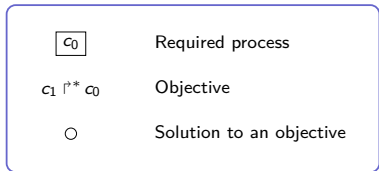
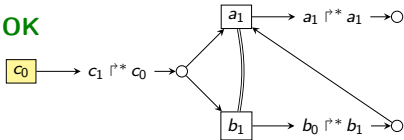
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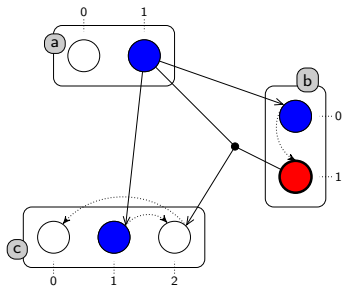
OK



OK



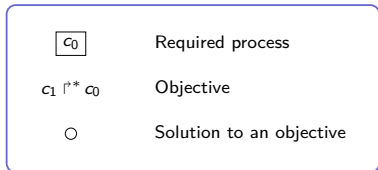
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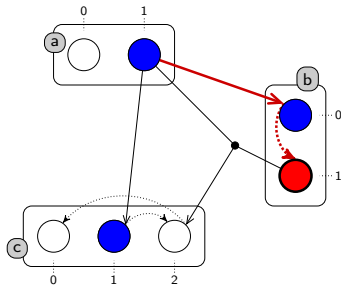
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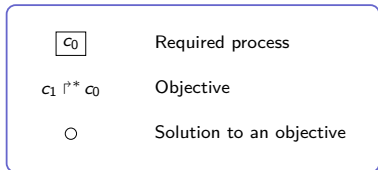
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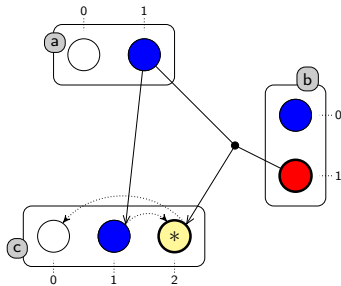
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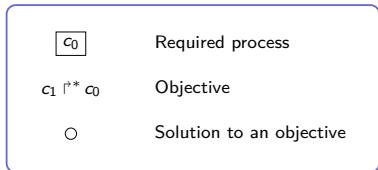


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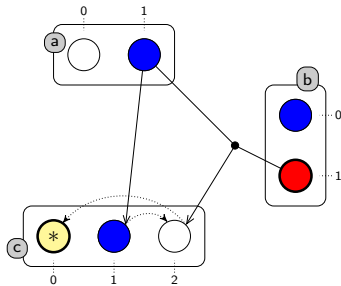
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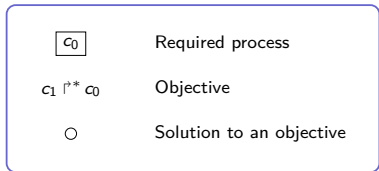
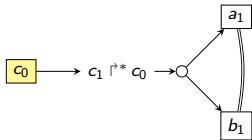


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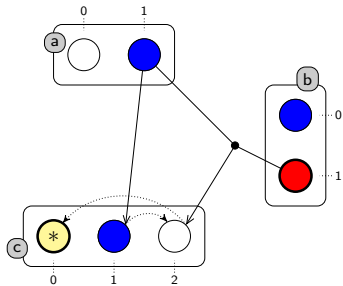
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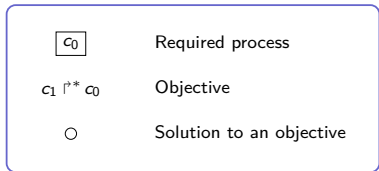
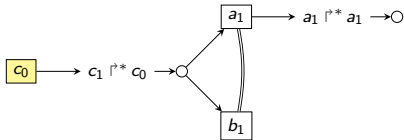


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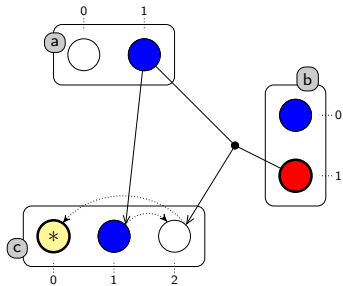
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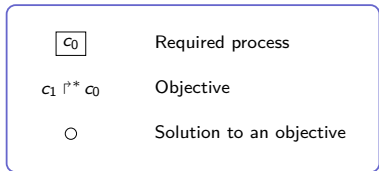
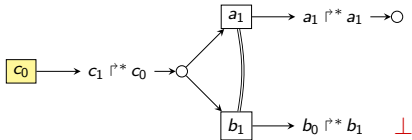


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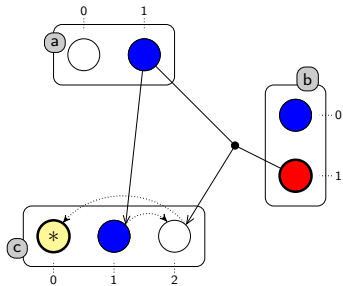
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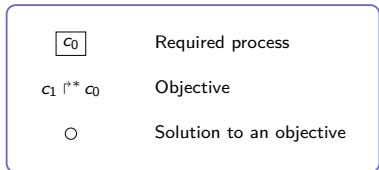
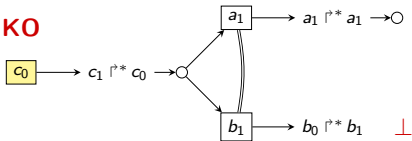
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KO



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- Knocking out a component in a path may reveal an alternative path
  - Resilience  $\Rightarrow$  existence of alternative paths (cf. cut sets)
  - New path  $\Rightarrow$  New costs or new delays

## Conclusion

The Process Hitting allows to represent biological regulatory networks:

- Qualitative and atomistic modeling
- Existing efficient **reachability analysis**
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Quantification of the perturbation using Process Hitting:

- Adapted notion of **impact degree** (multiple values)
- Thanks to the powerful **reachability analysis**
- Additional properties with the graph of local causality



**Thank you!**

**Do you have questions  
or suggestions?**

## Bibliography

- Hao Jiang, Takeyuki Tamura, Wai-Ki Ching and Tatsuya Akutsu. [On the Complexity of Inference and Completion of Boolean Networks from Given Singleton Attractors](#). In *IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences E96.A*, n. 11, pages 2265–74, 2013.
- Jean-Paul Comet and Gilles Bernot. [Introducing continuous time in discrete models of gene regulatory networks](#). In *Proceedings of the Nice Spring school on Modelling and simulation of biological processes in the context of genomics*, EDP Sciences, 2010.
- Loïc Paulevé, Geoffroy Andrieux and Heinz Koepl. [Under-approximating cut sets for reachability in large scale automata networks](#). In Natasha Sharygina and Helmut Veith, editors, *Computer Aided Verification*, volume 8044 of *Lecture Notes in Computer Science*, pages 69–84. Springer Berlin Heidelberg, 2013.

## Cooperations

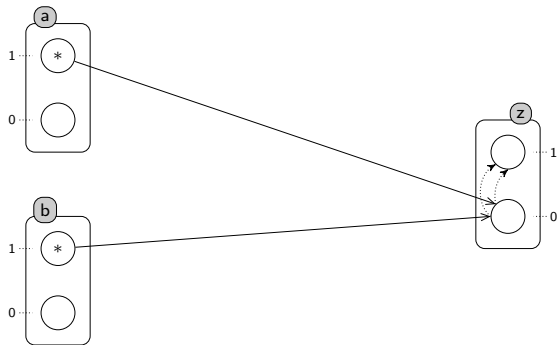
[Paulevé *et al.* in *Transactions on Computational Systems Biology*, 2011]



Cooperation between  $a_1$  and  $b_1$ :  $\underline{a_1 \wedge b_1} \rightarrow z_0 \uparrow z_1$

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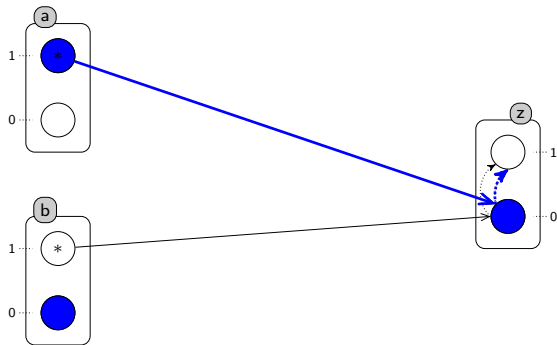
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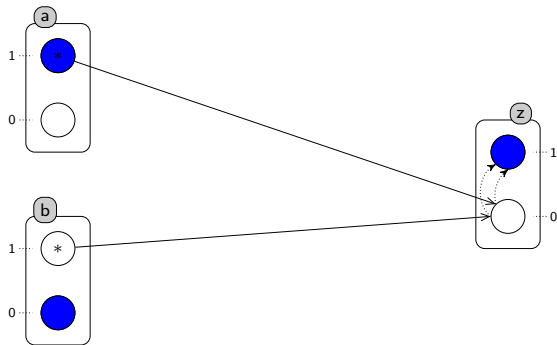
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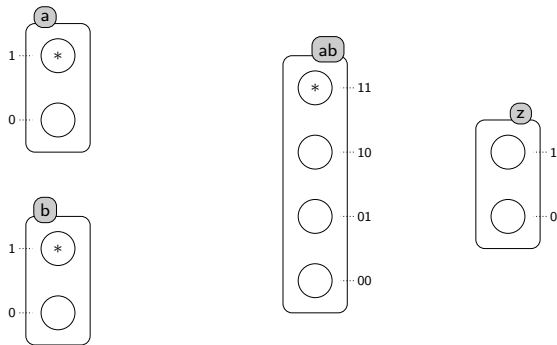
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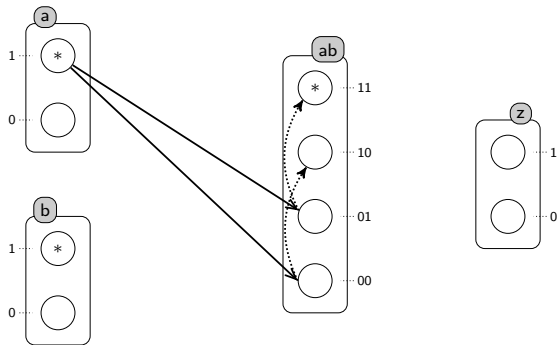


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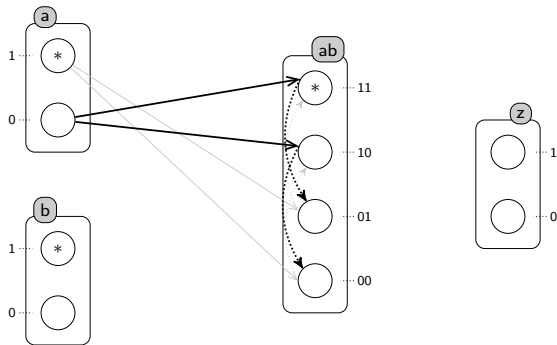
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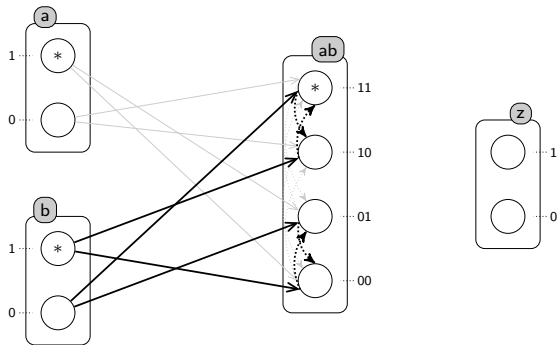


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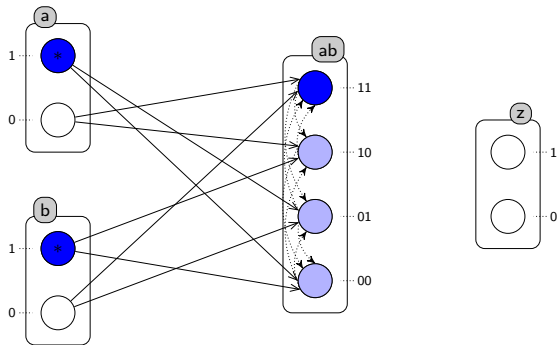


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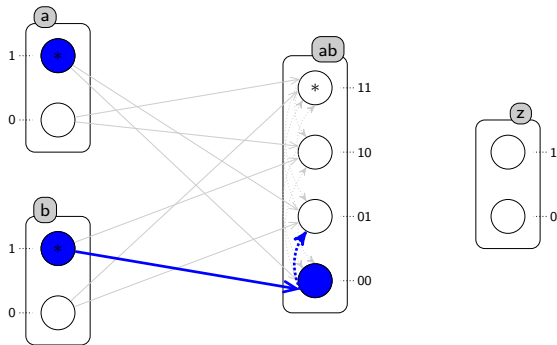
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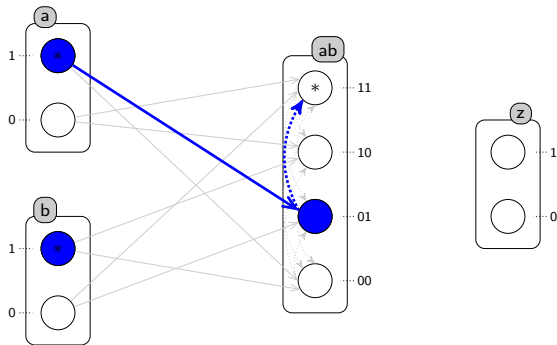
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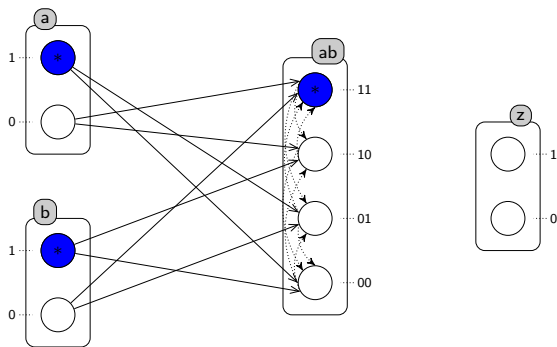
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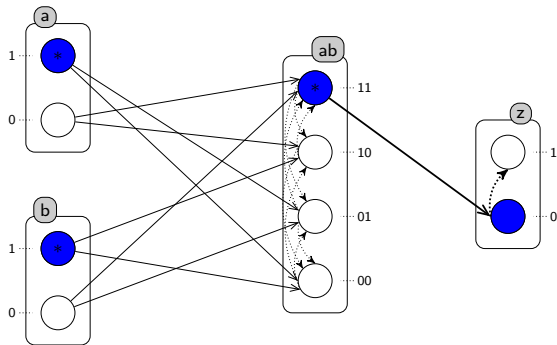
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Each configuration is represented by one process  $\underline{a_1 \wedge b_1} \Rightarrow ab_{11}$

## Cooperations

[Paulevé et al. in *Transactions on Computational Systems Biology*, 2011]



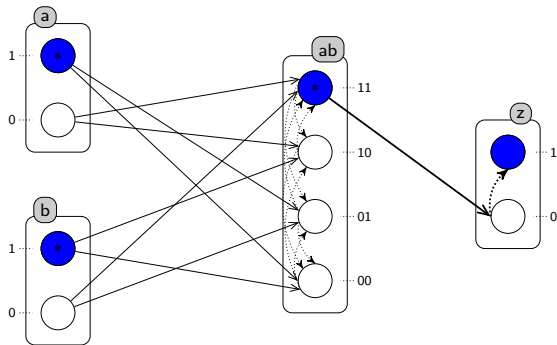
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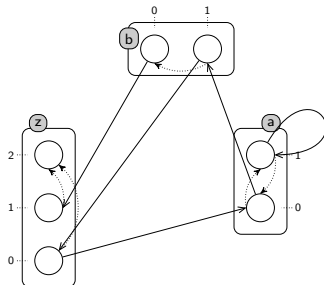


## Static Analysis: Fixed Points

[Paulevé *et al.* in *Transactions on Computational Systems Biology*, 2011]

**Fixed point** = state where no action can be fired

→ avoid couples of processes bounded by an action

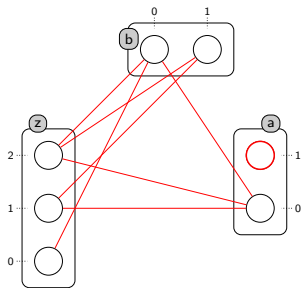
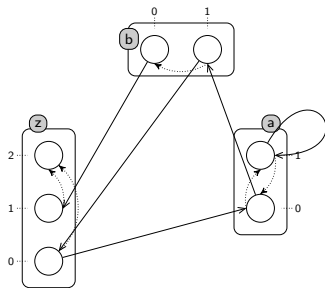


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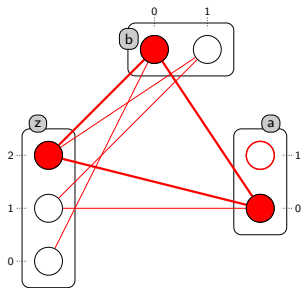
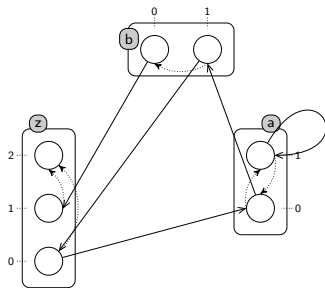


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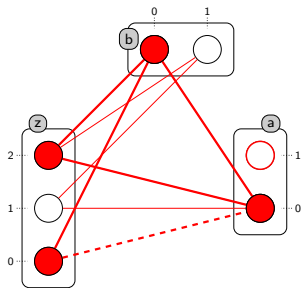
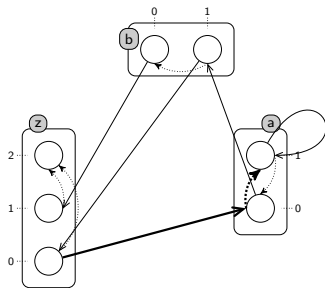


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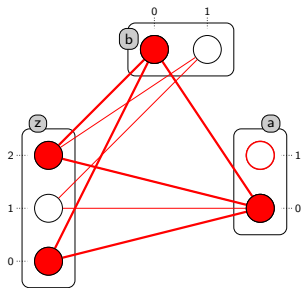
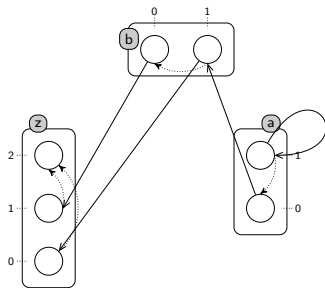


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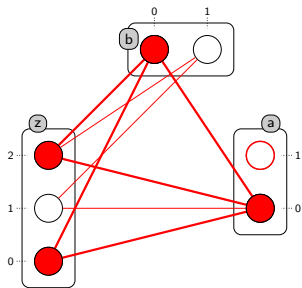
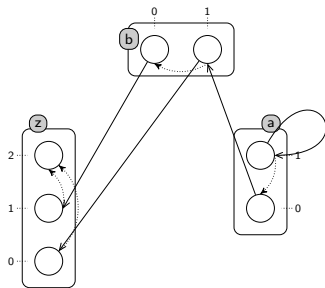


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Exponential complexity w.r.t. the number of sorts