

Public seminar of team Lifeware

Modeling and analysis of large regulatory networks with the Process Hitting framework

Maxime FOLSCHETTE

FMV team / Department of Electronics & Informatics / University of Kassel
maxime.folschette@uni-kassel.de
<http://maxime.folschette.name/>

2015/04/01

The Modeling/Analysis duality

Modeling a system is the first step towards its comprehension



Modeling

Analysis

The Modeling/Analysis duality

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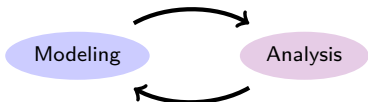


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- The modeling tools must be adapted to the observed properties

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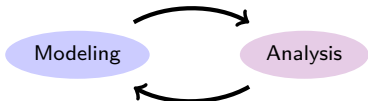
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Modeling choices have an impact on the results of the analysis

- The level of details changes the quantity of obtained info
- The size of the model increases the analysis duration

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The modeling and analysis steps of a system are strongly linked

Overview of This Presentation

State of the Art of the modeling of biological regulatory networks

- Discrete asynchronous representations and Thomas modeling
- Standard Process Hitting

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Enriching the Process Hitting

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- Synchronicity between actions
 - Adding of priorities, neutralizing edges or synchronous actions

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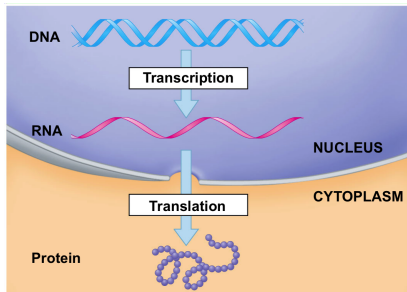
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Analysis of the Process Hitting

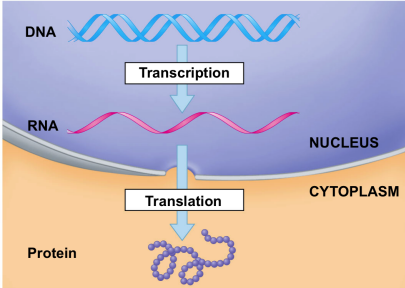
- Correction of the cooperative sorts
- Static analysis of reachability
- Equivalences and links with other formalisms

Abstractions of the Representation

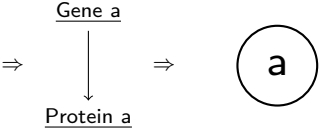


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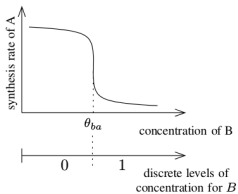


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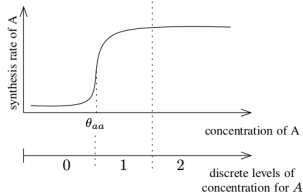
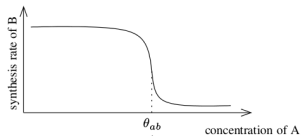
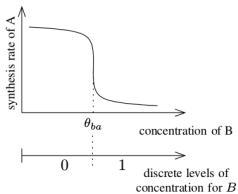
Discretization and Asynchronism

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



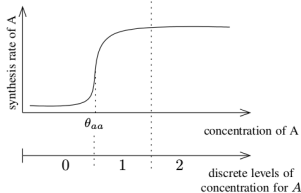
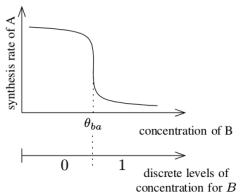
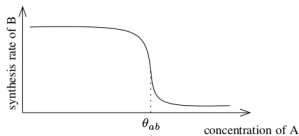
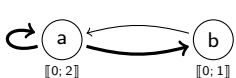
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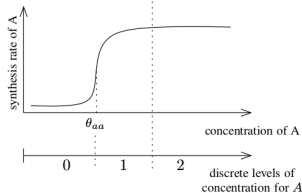
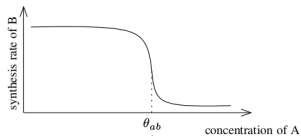
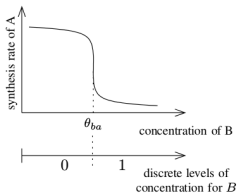
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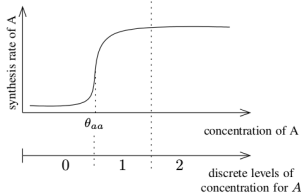
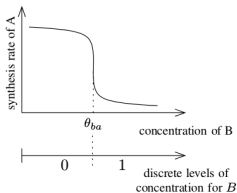
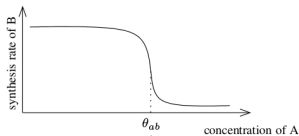
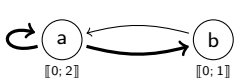
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→ **Unitary** dynamics

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→ Abstracted as thresholds or **discrete levels**
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→ **Unitary** dynamics
- Simultaneous crossings of two thresholds never occurs
→ **Asynchronous** dynamics

Discrete Networks / Thomas Modeling

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

[Thomas in *Journal of Theoretical Biology*, 1973]

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



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

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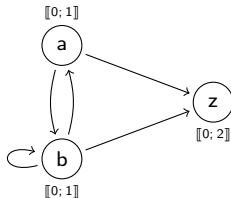
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b	$f^a(b)$
0	1
1	0

a	b	$f^b(a, b)$
0	0	1
0	1	1
1	0	0
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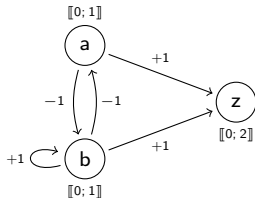
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- Signs and thresholds on the edges $a \xrightarrow{+1} z$

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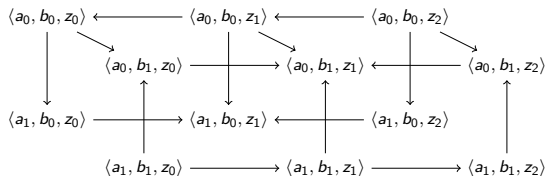
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Analysis of Thomas Modeling

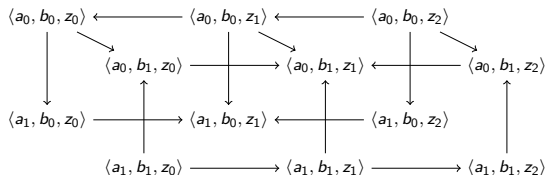
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→ **Exponential** size in the number of components

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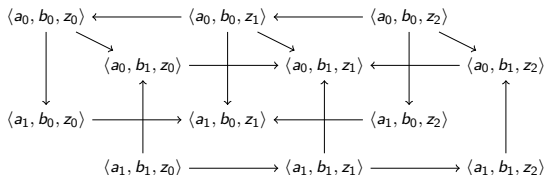
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Some works all to link the structure of the model and some dynamic properties:

- **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]

Standard Process Hitting

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

Standard Process Hitting is:

- Well-adapted to the modeling of BRNs
- An **atomistic and qualitative** modeling (explicit & discrete expression levels)
- **Simple but powerful** dynamics (constraints on the form of actions)

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Several missing features:

- Faulty representation **cooperations**
- **Possible enrichment** of the expressivity
 - Which requires to adapt the previous tools

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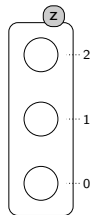
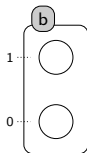
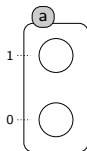
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Sorts: components *a, b, z*

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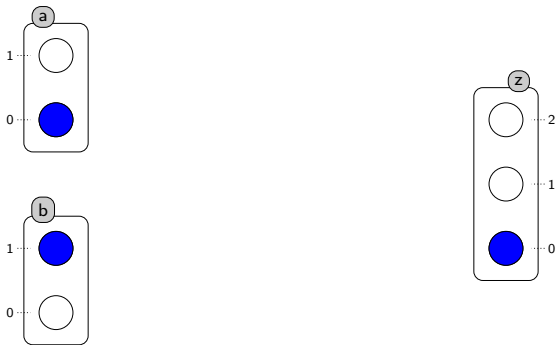
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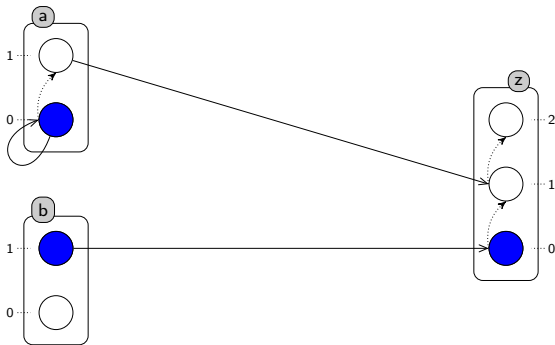
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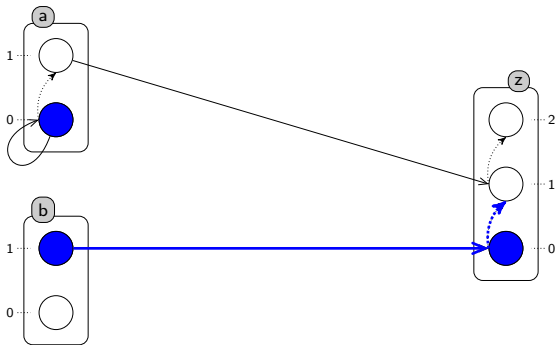
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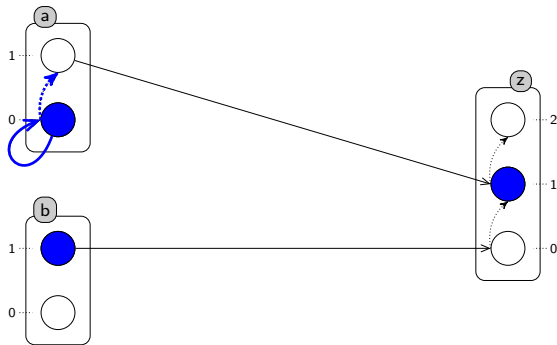
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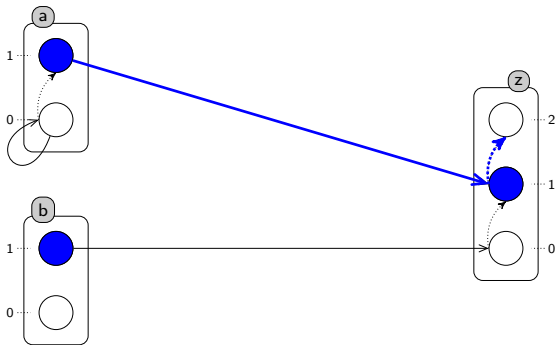
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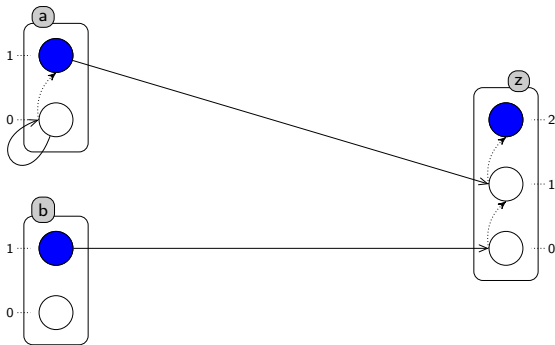
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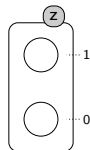
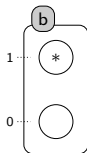
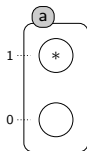
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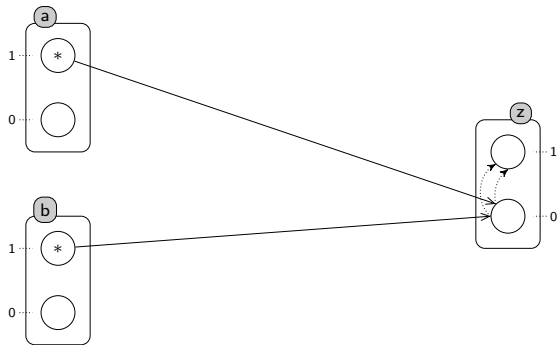
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Cooperations

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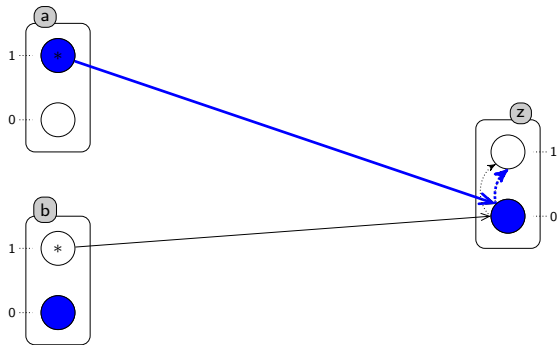
Cooperation between a_1 and b_1 : $\underline{a_1 \wedge b_1} \rightarrow z_0 \uparrow z_1$

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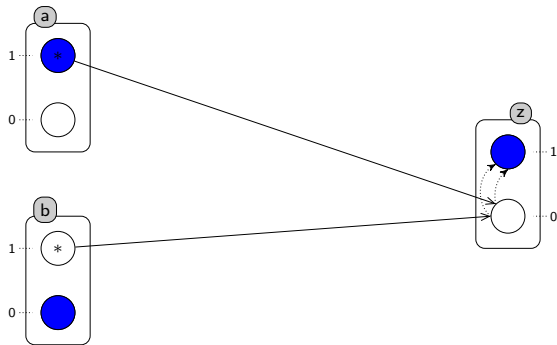
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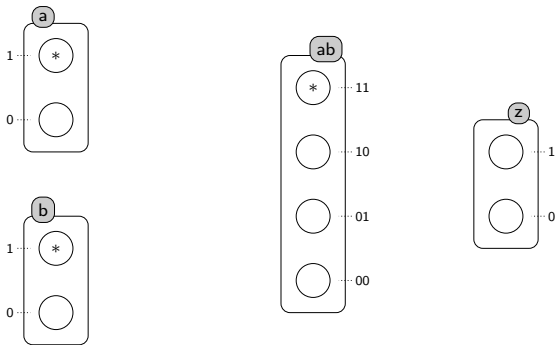
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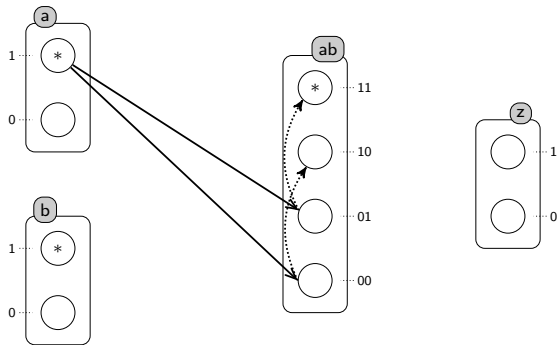
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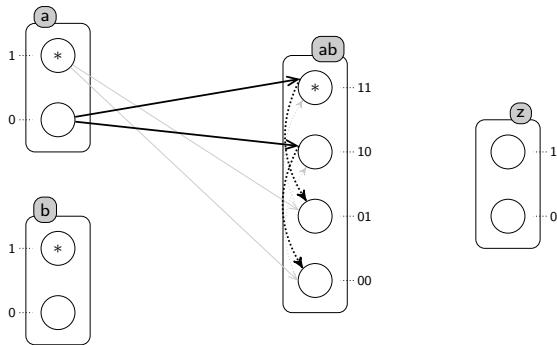
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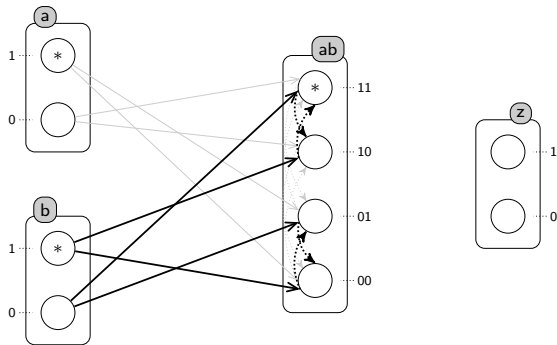
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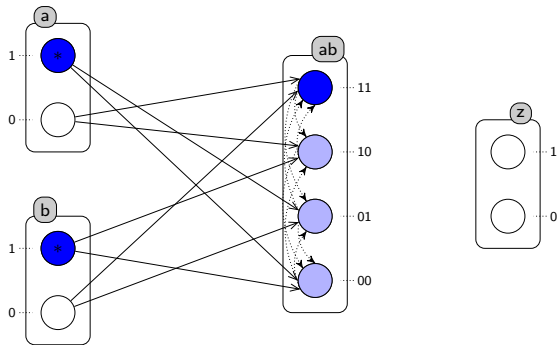
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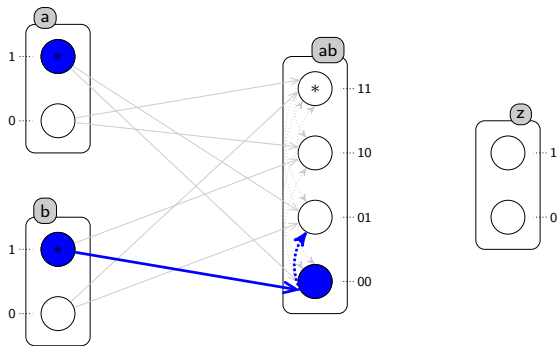
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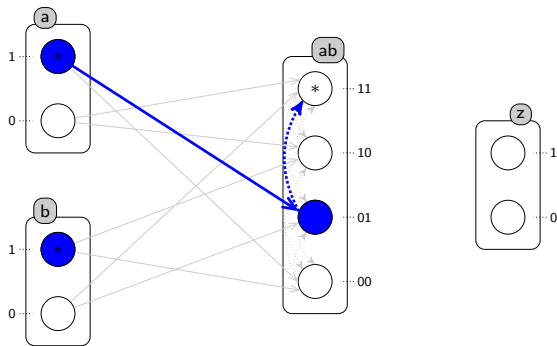
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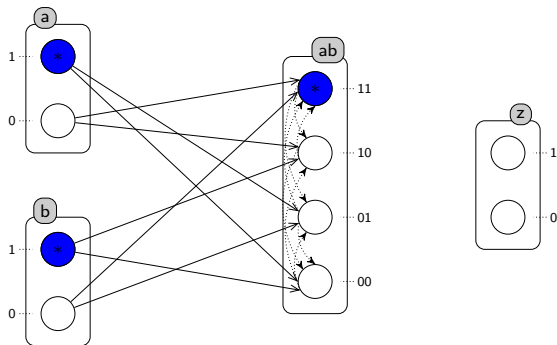
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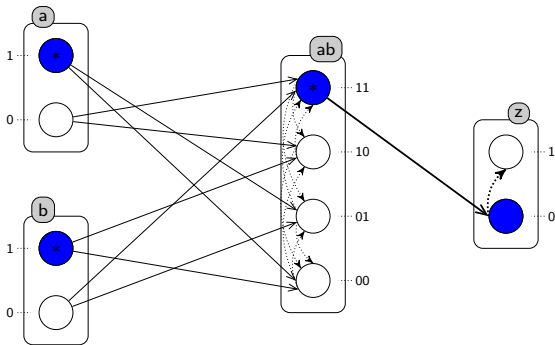
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Cooperation between a_1 and b_1 : $\underline{a_1 \wedge b_1} \rightarrow z_0 \uparrow z_1$

Solution: a **cooperative sort** ab to express $\underline{a_1 \wedge b_1}$

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

Cooperations

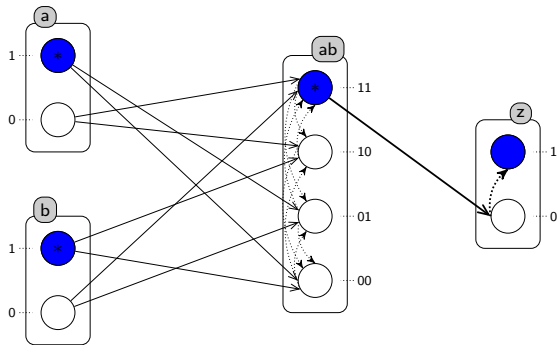
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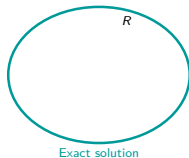
Approximations for the Reachability Analysis

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

Check reachability properties:

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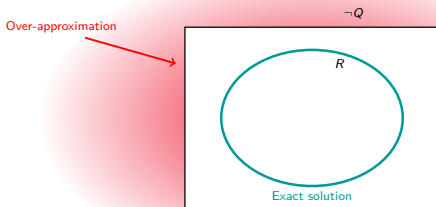
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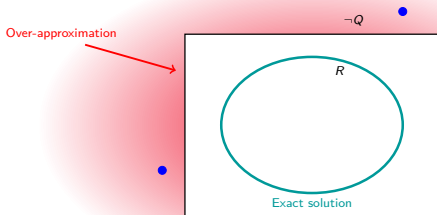
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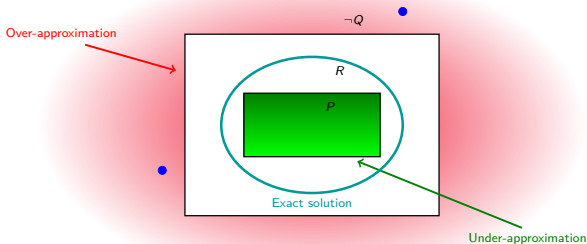
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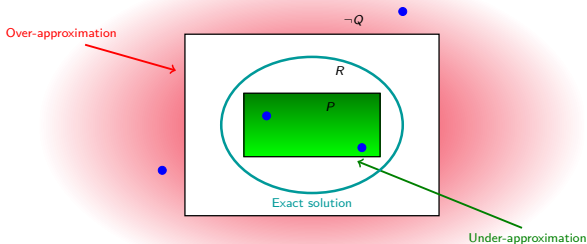
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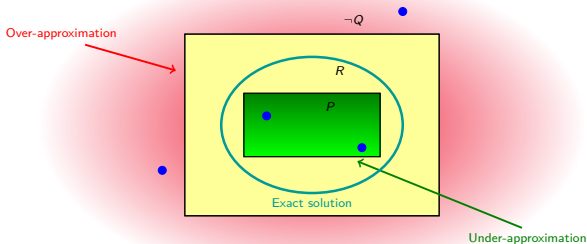
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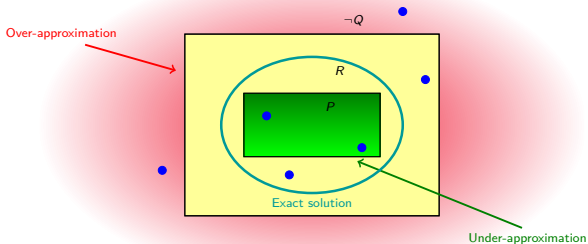
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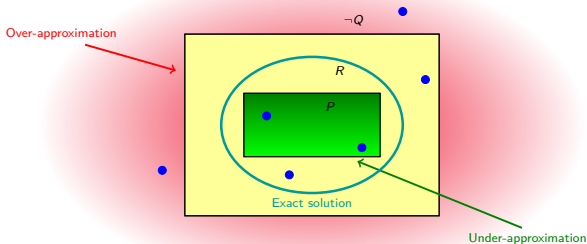
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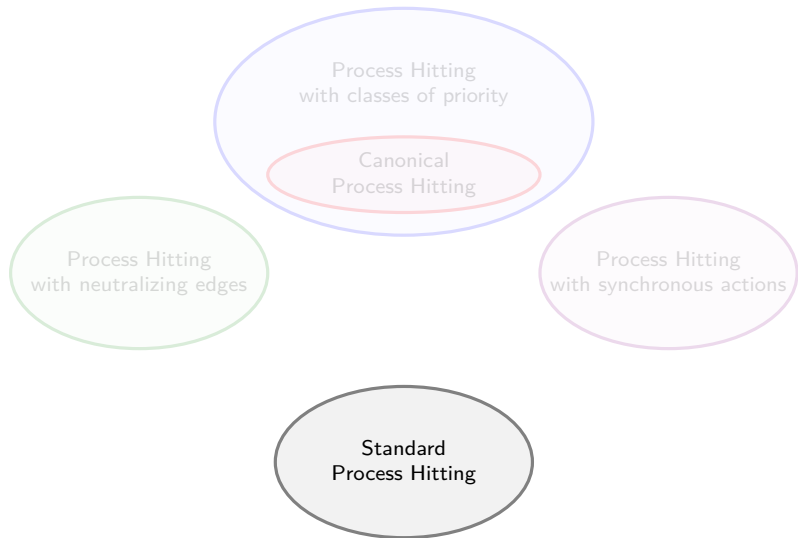


Polynomial complexity in the number of sorts

Exponential complexity in the number of processes in each sort

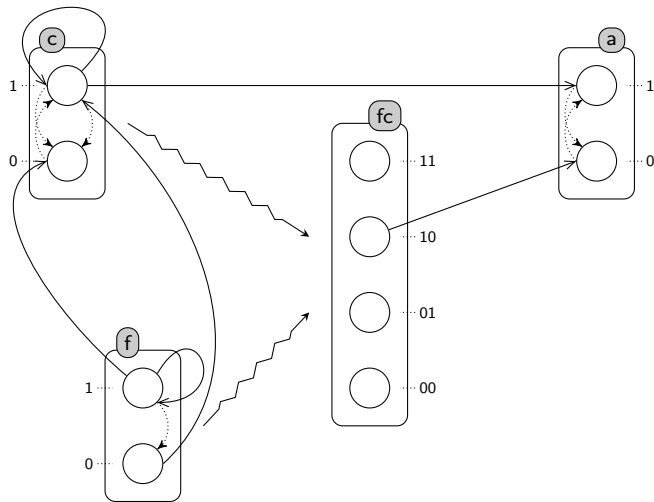
→ Efficient for big models with few expression levels

Standard Process Hitting



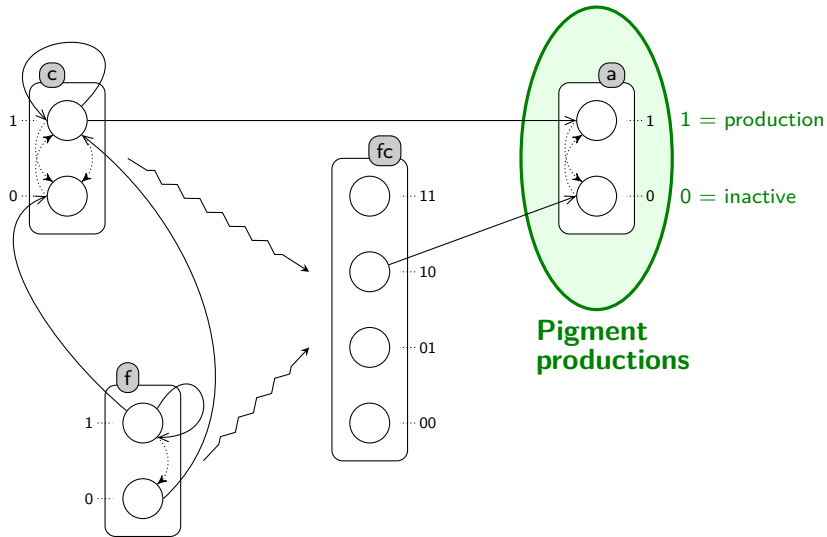
Permissiveness of the Standard Dynamics

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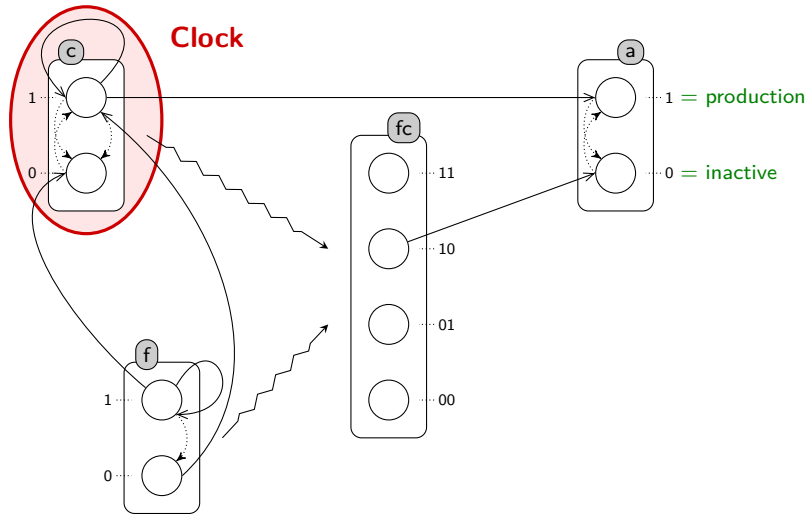
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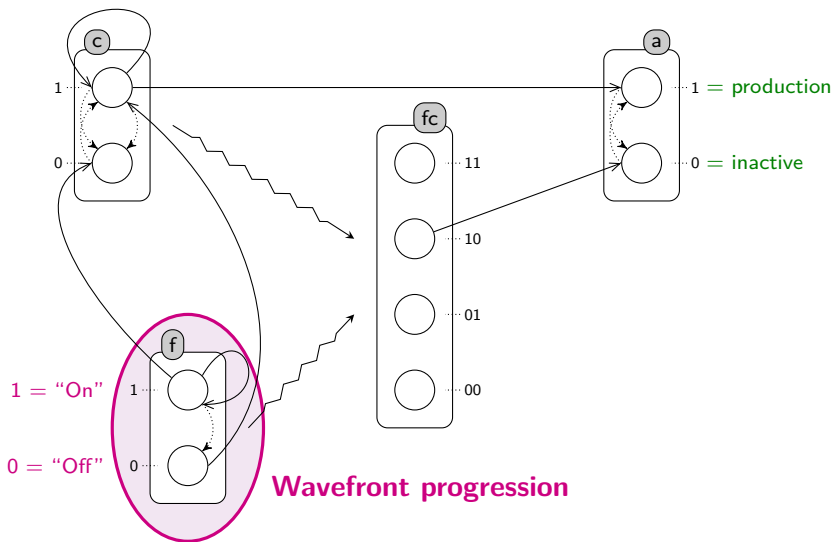
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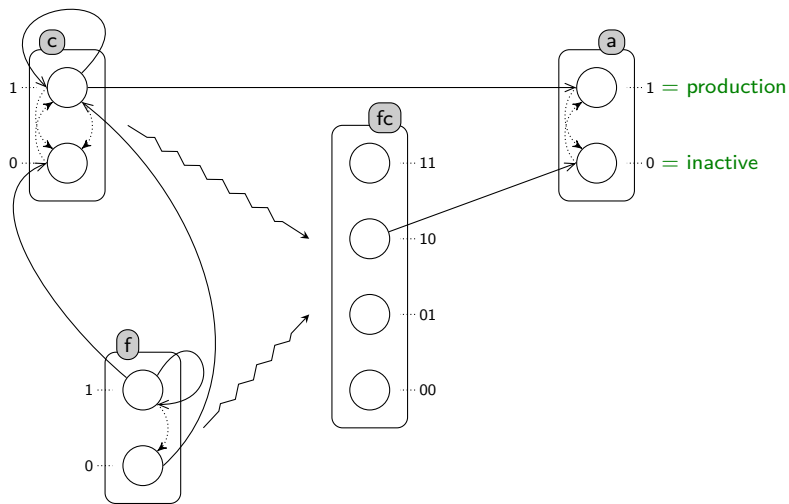
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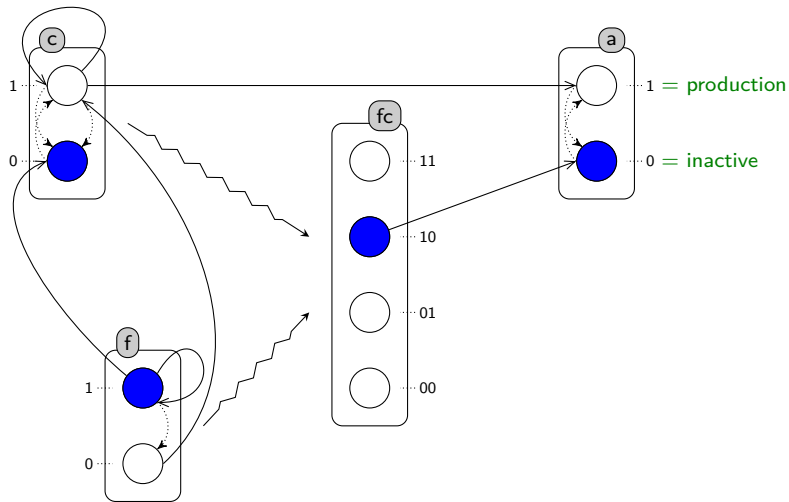
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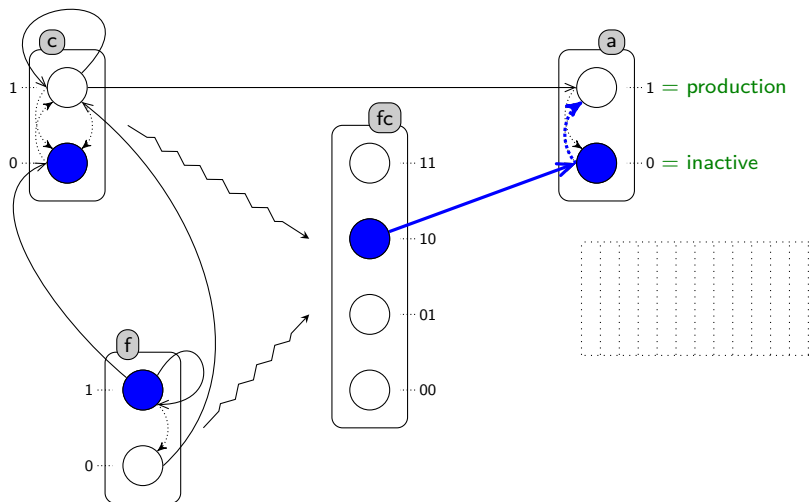
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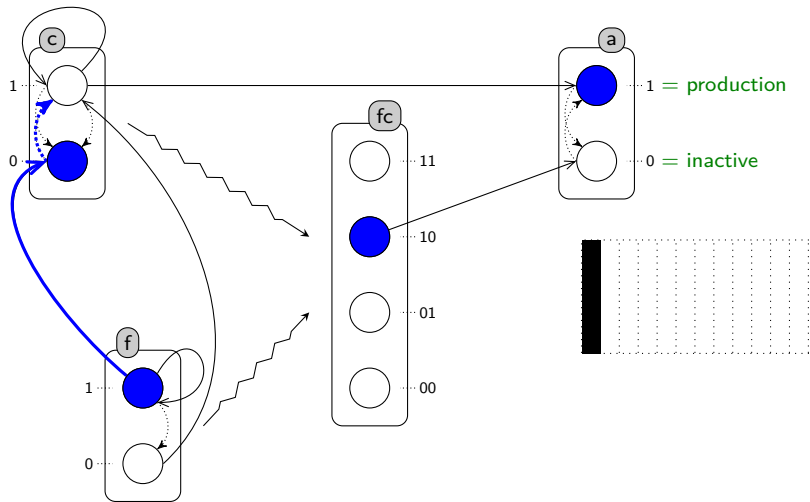
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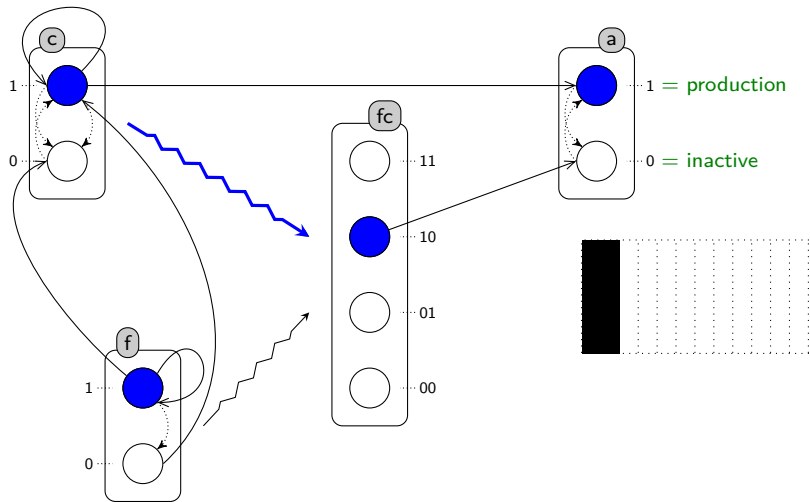
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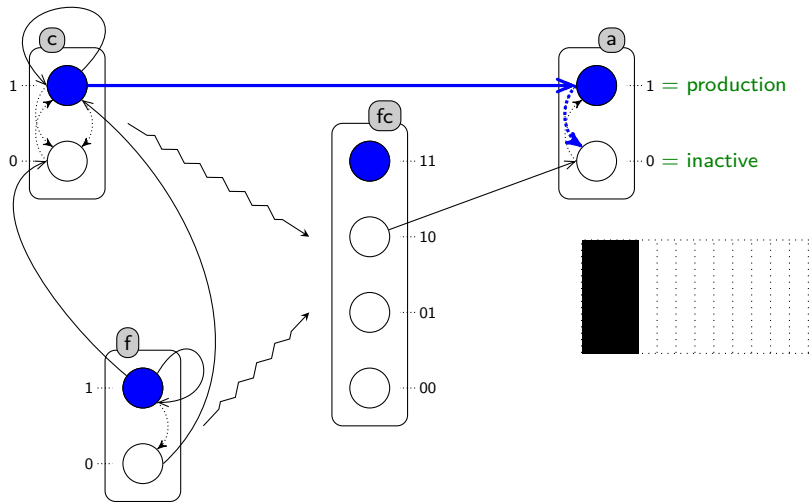
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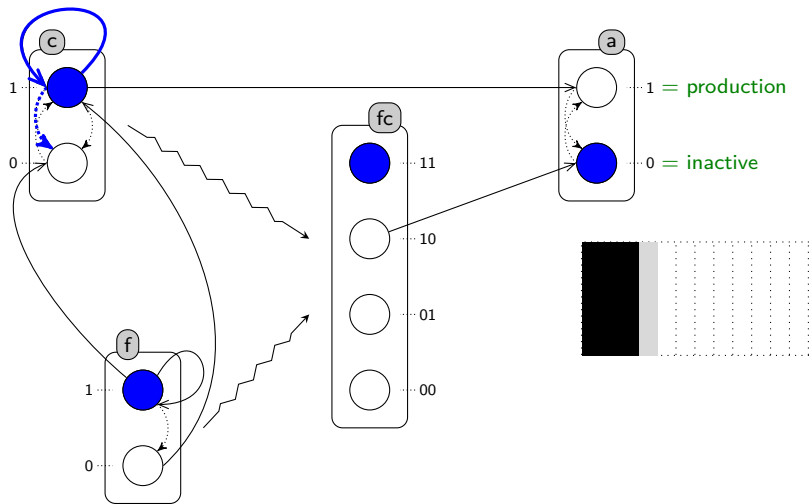
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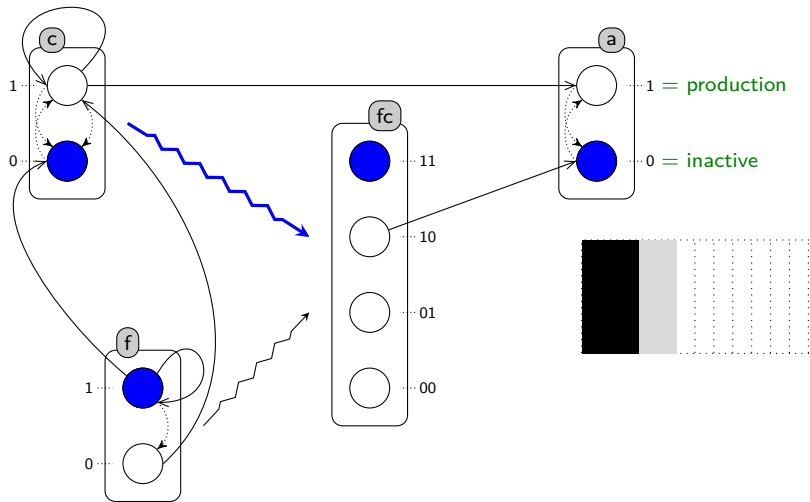
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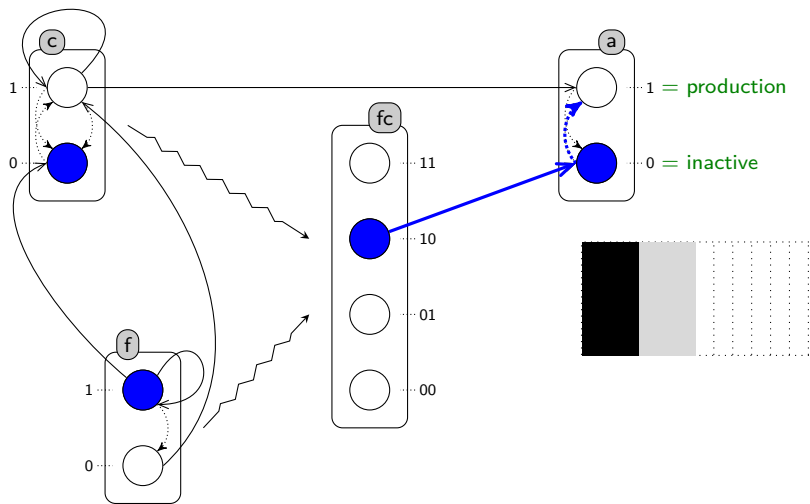
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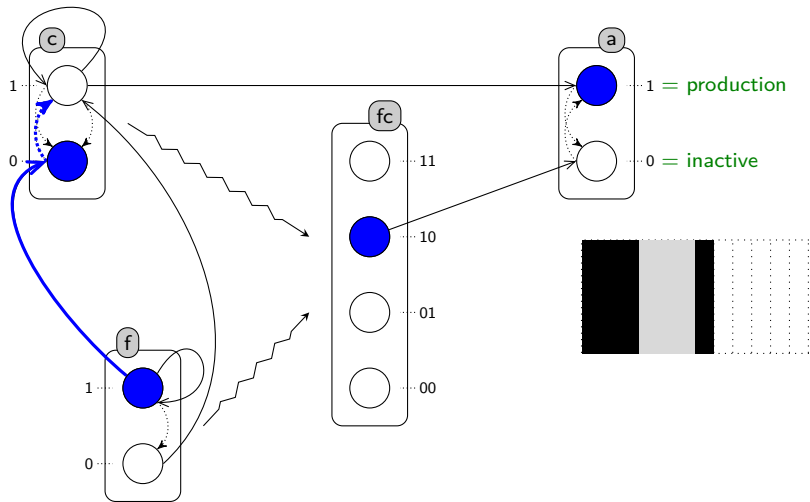
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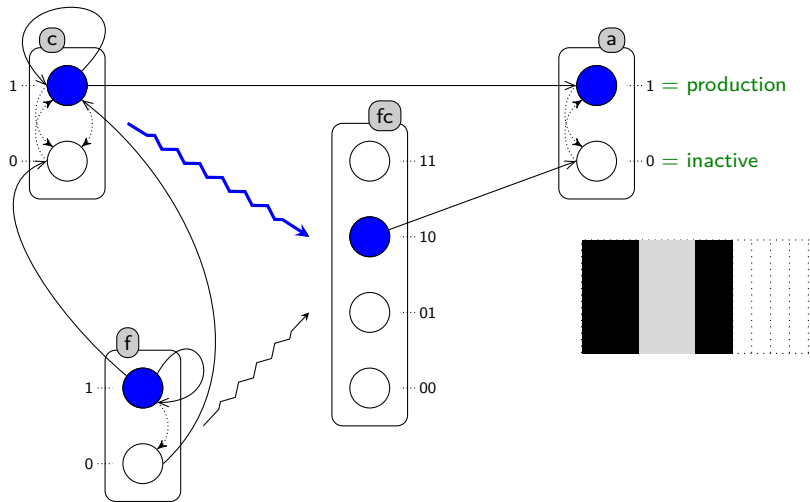
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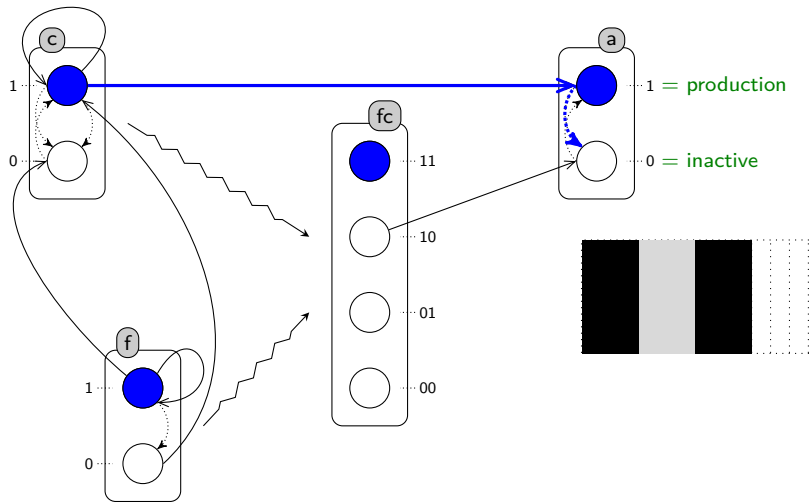
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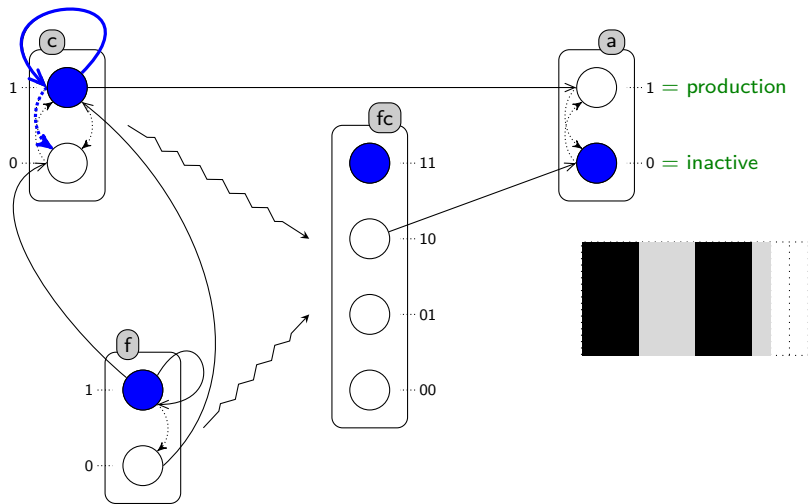
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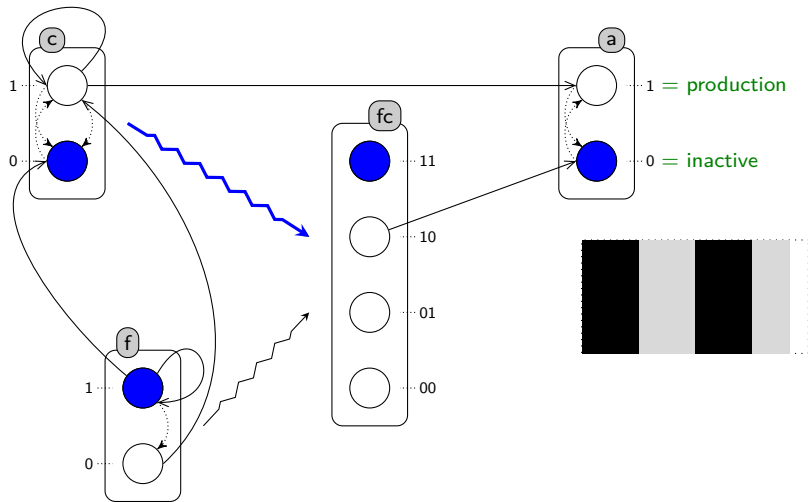
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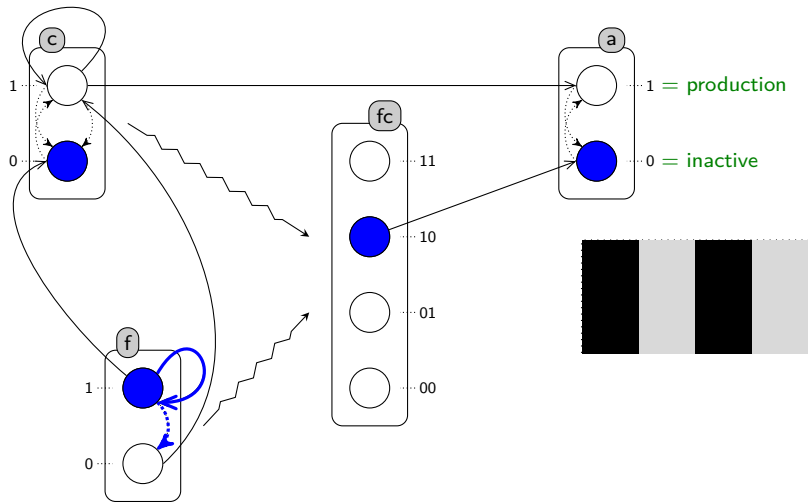
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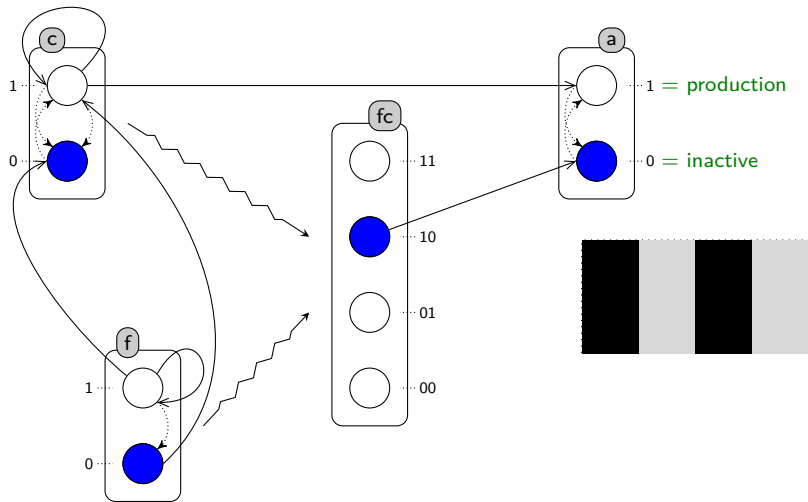
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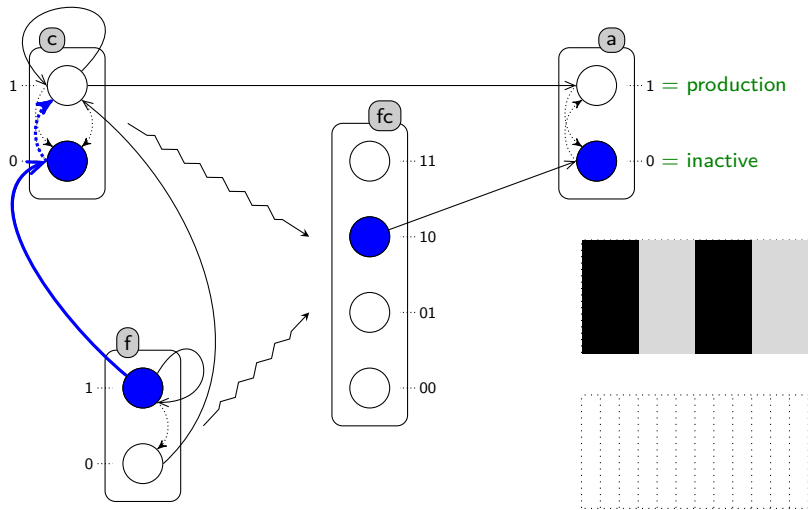
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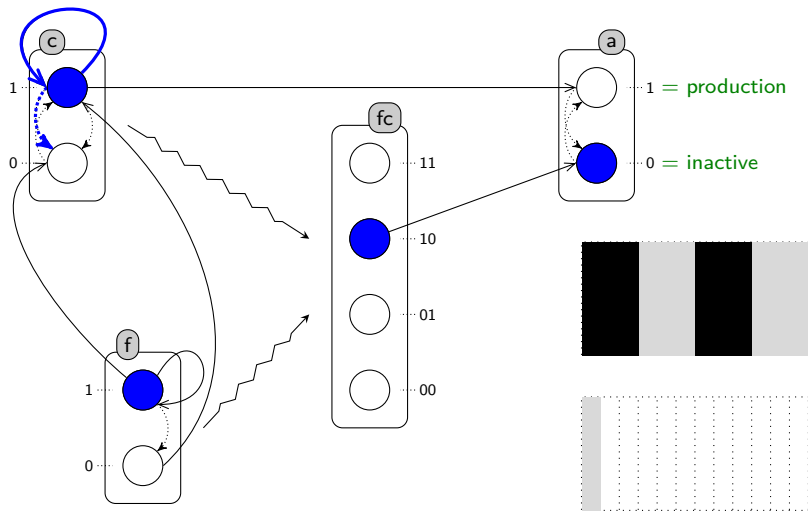
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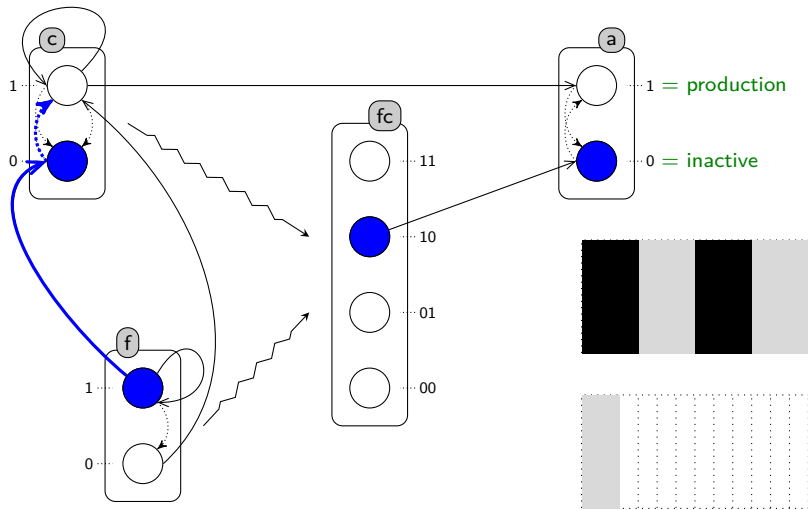
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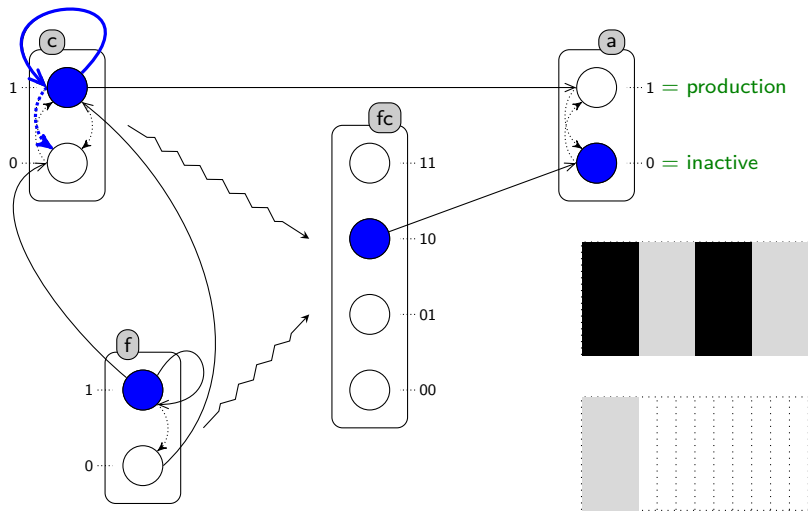
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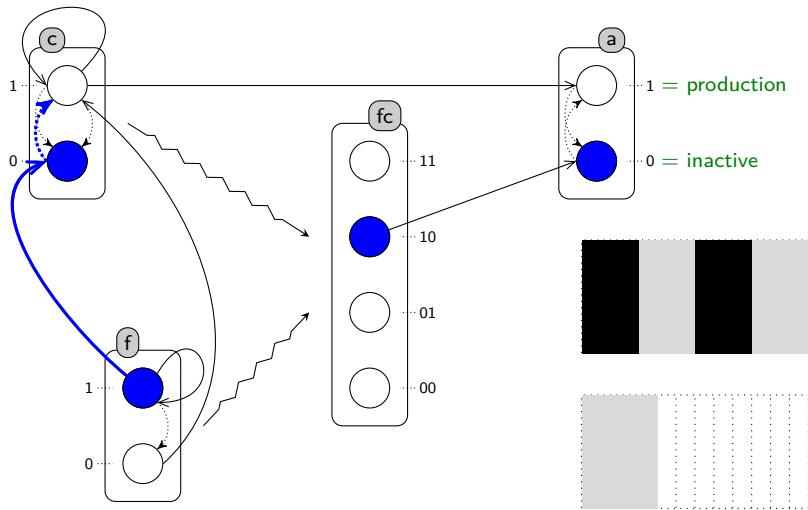
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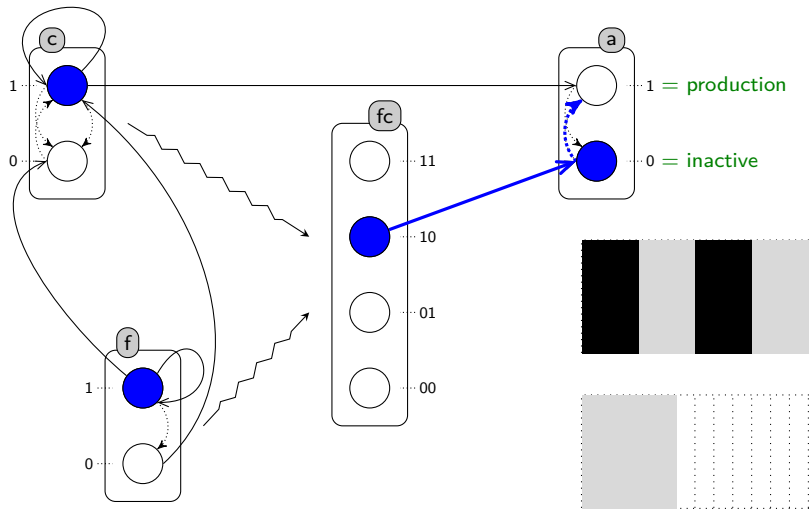
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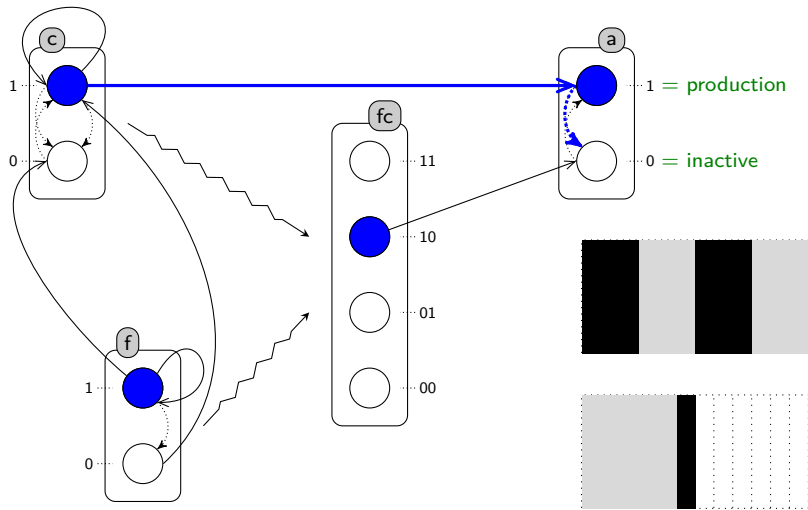
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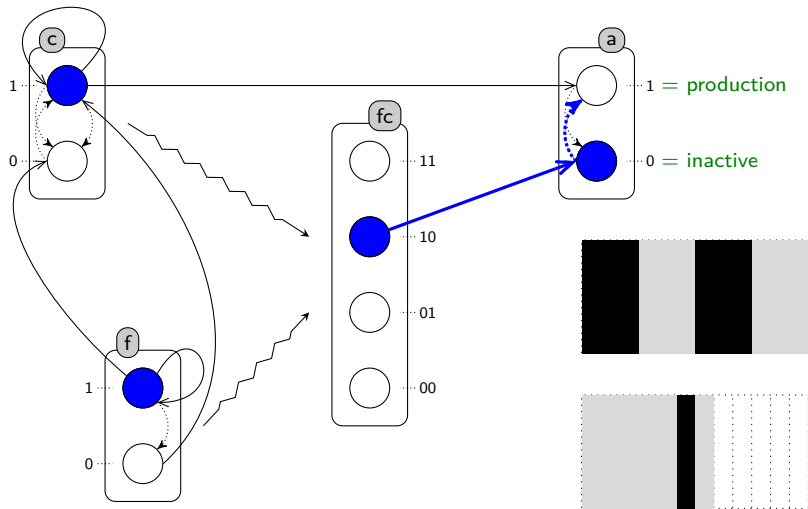
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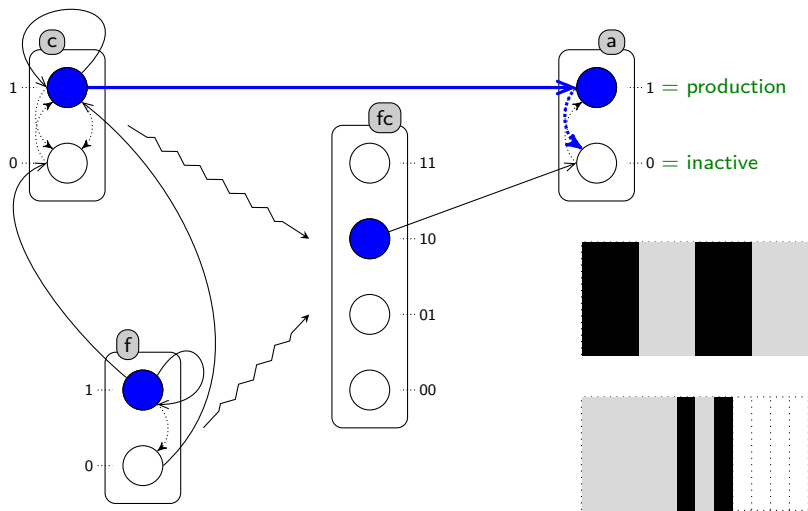
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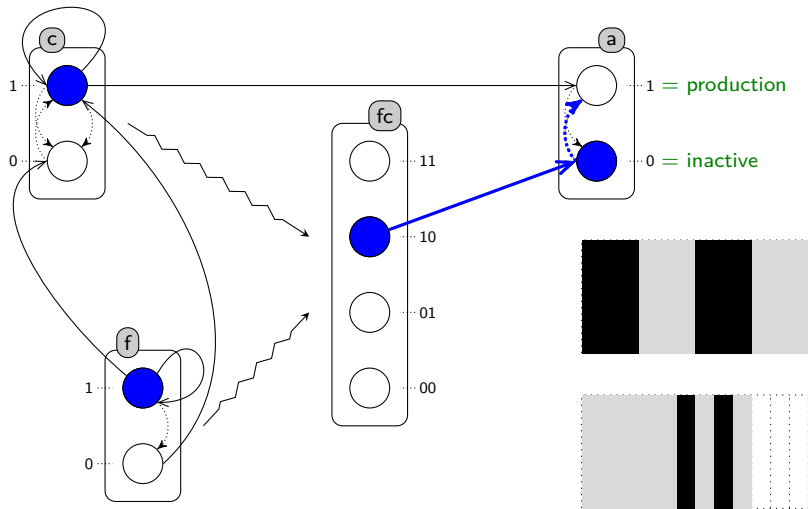
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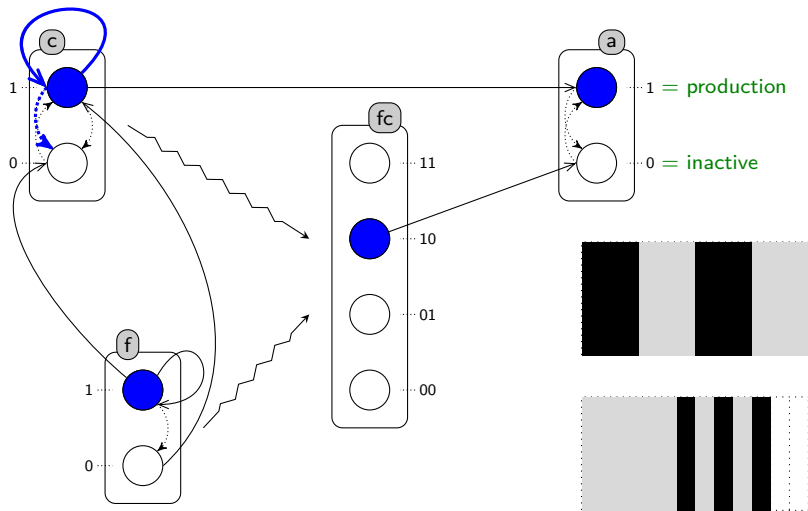
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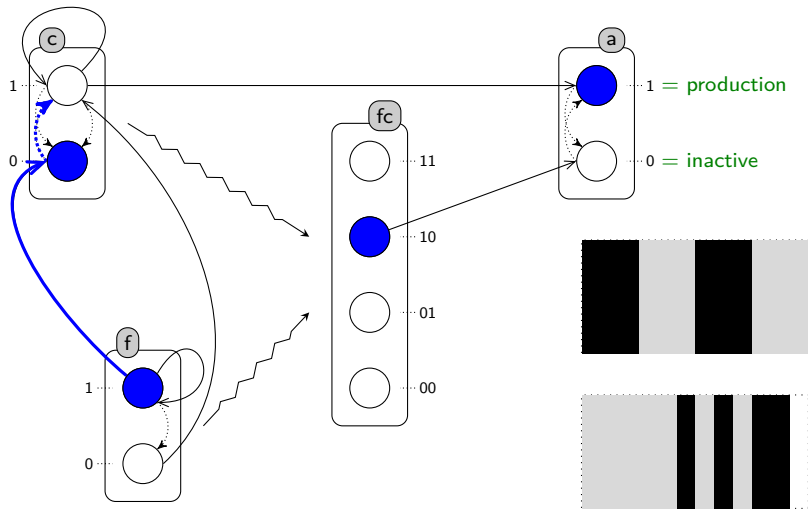
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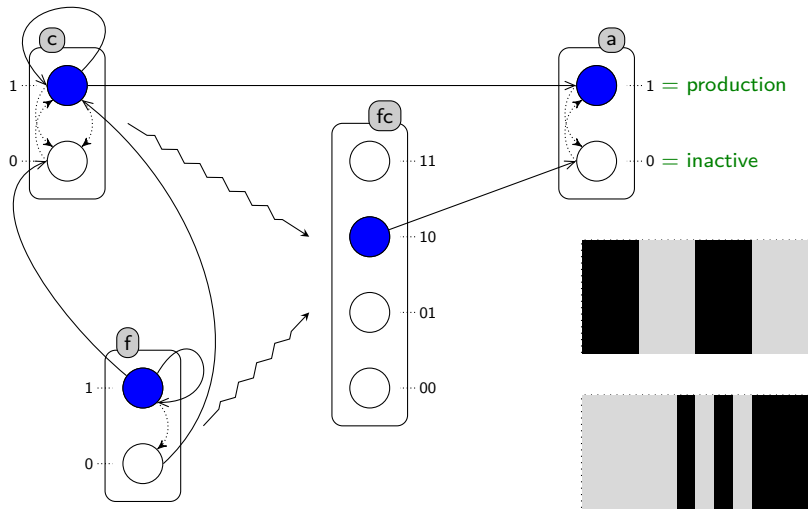
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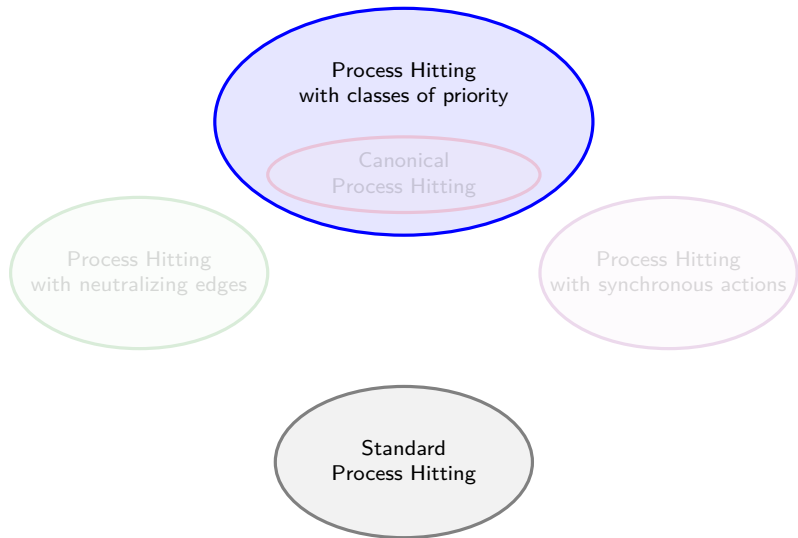


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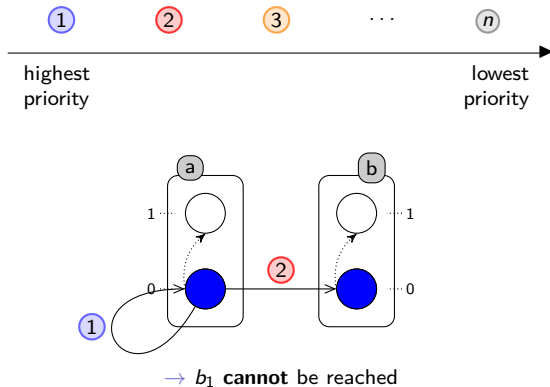
Process Hitting with Classes of Priorities



Addition of classes of priorities

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]

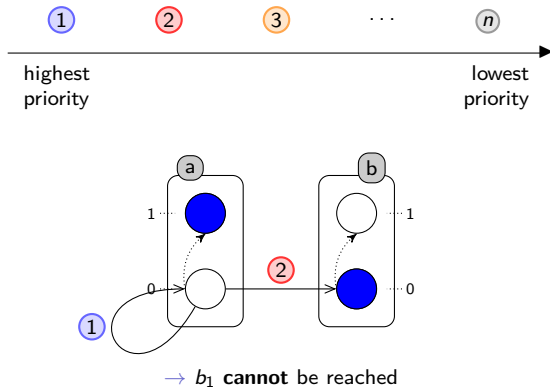
- Each action is associated to a discrete priority
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Addition of classes of priorities

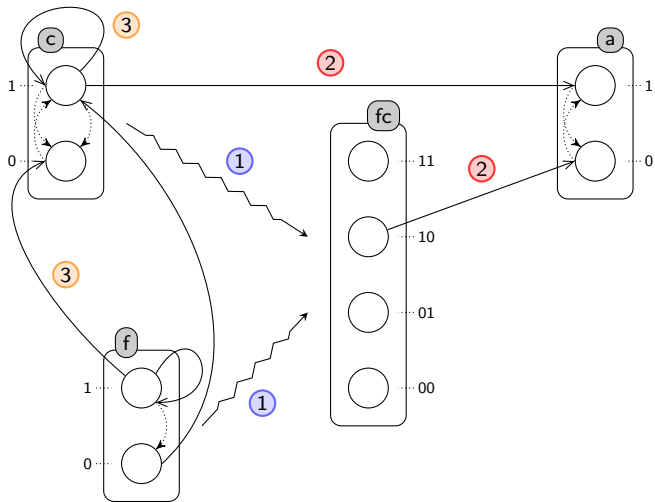
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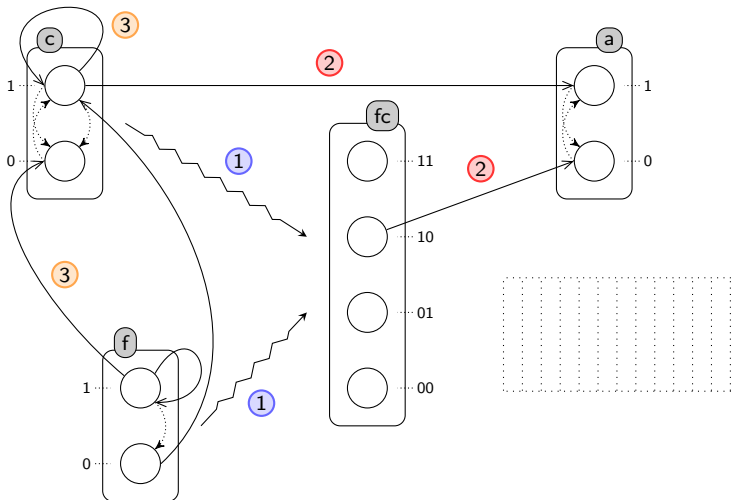
Use of the Classes of Priorities

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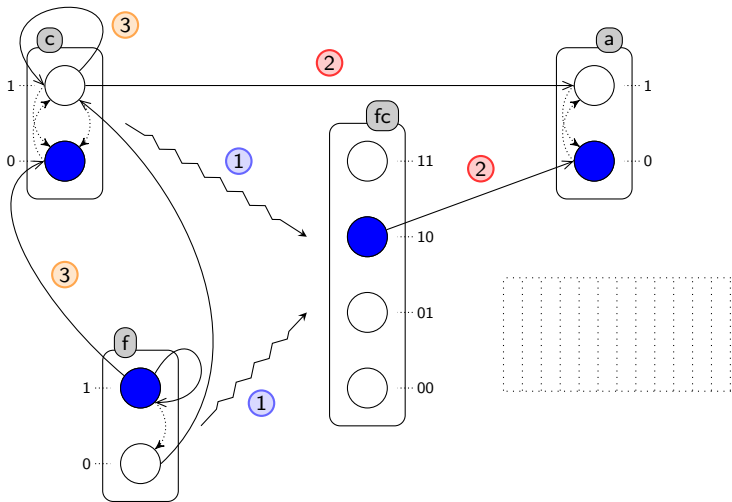
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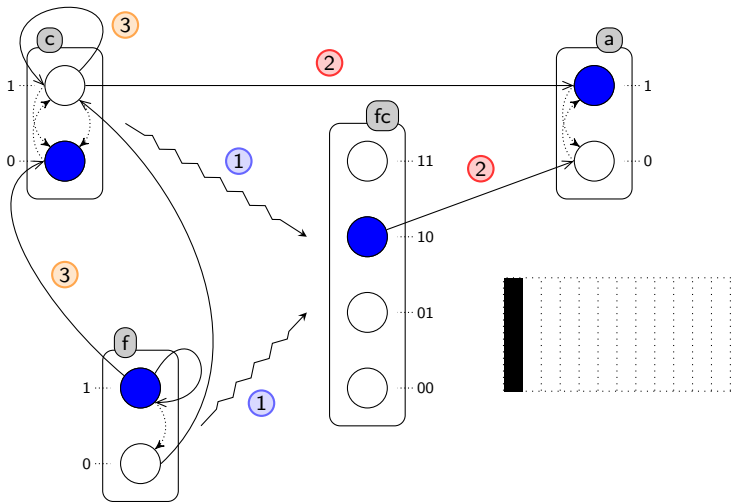
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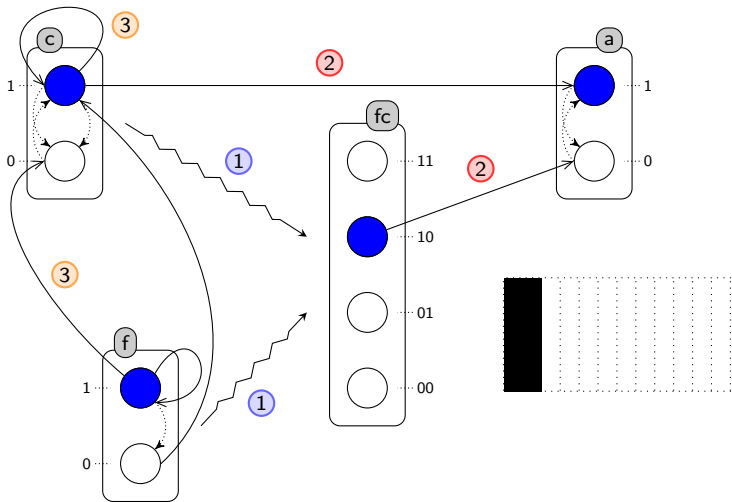
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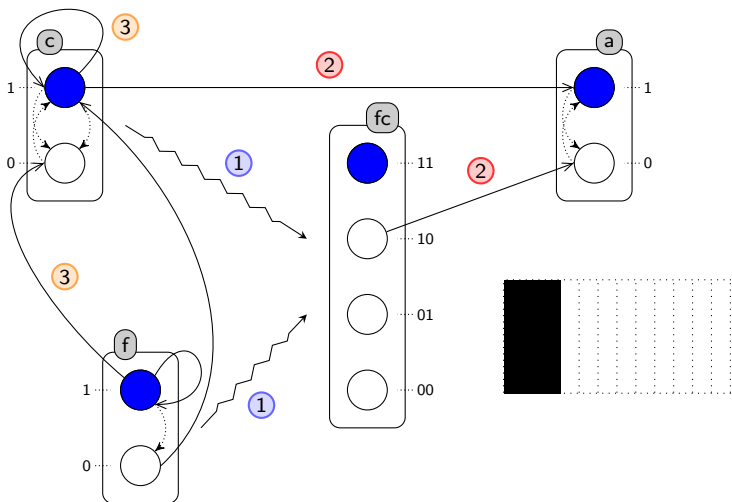
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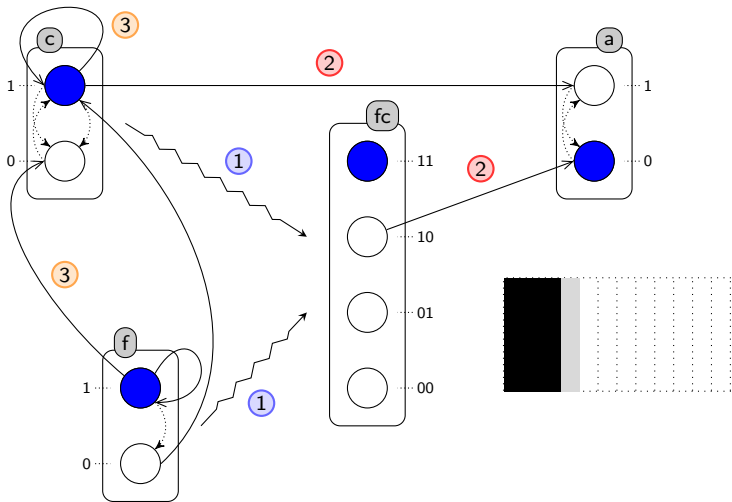
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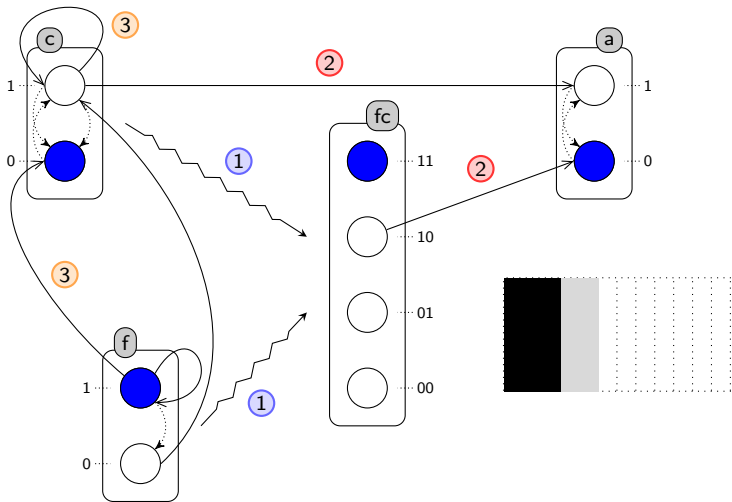
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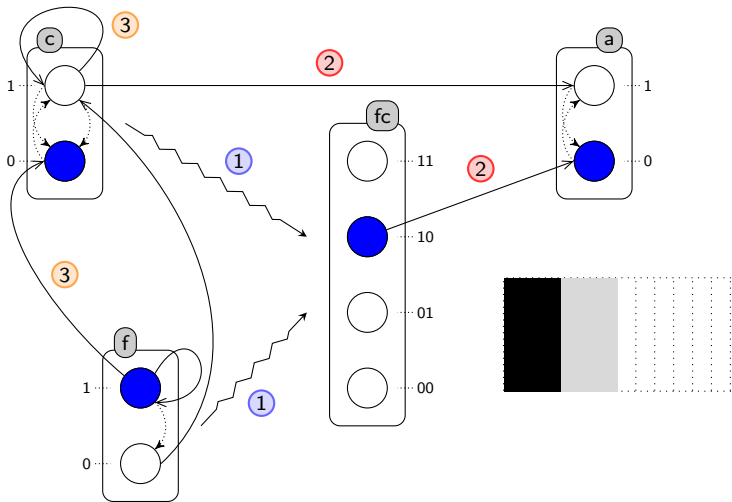
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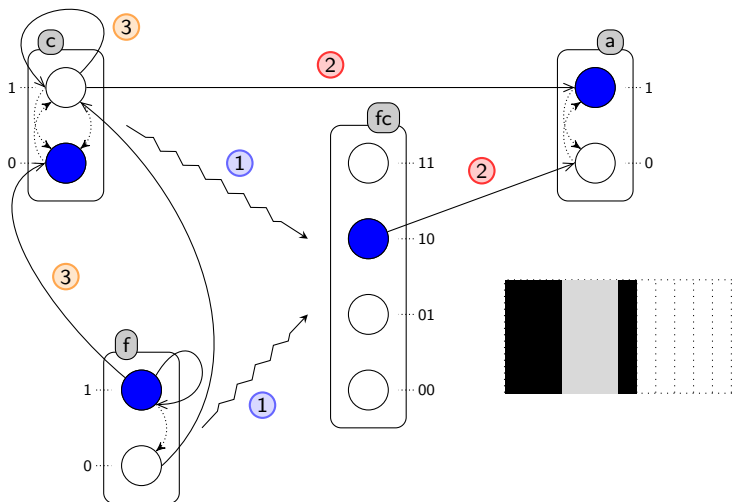
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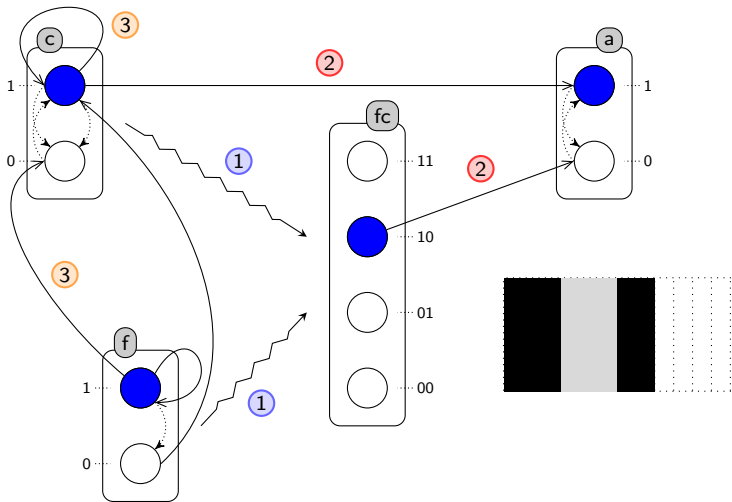
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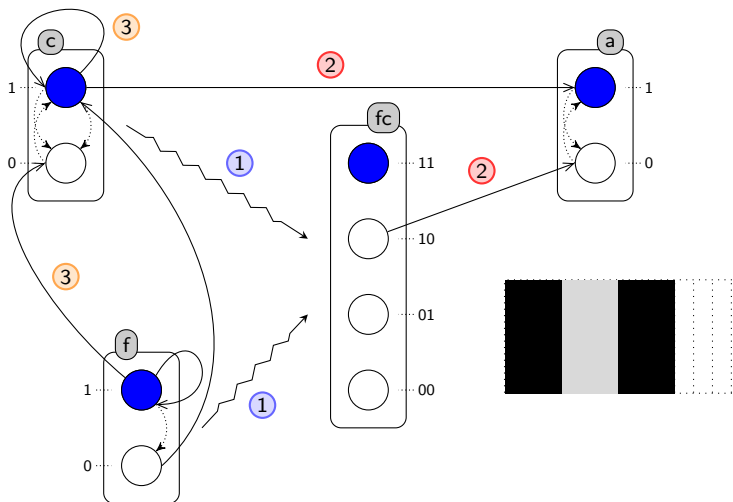
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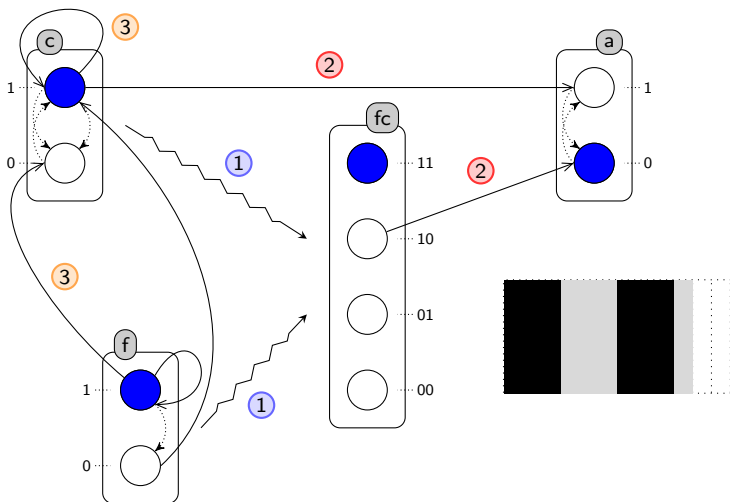
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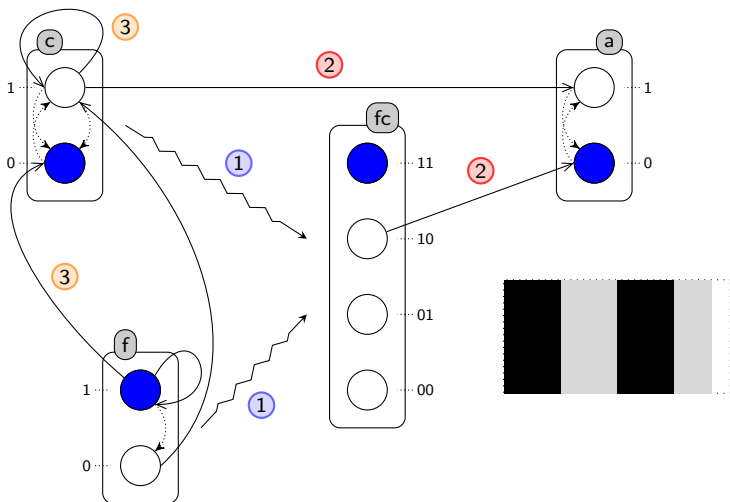
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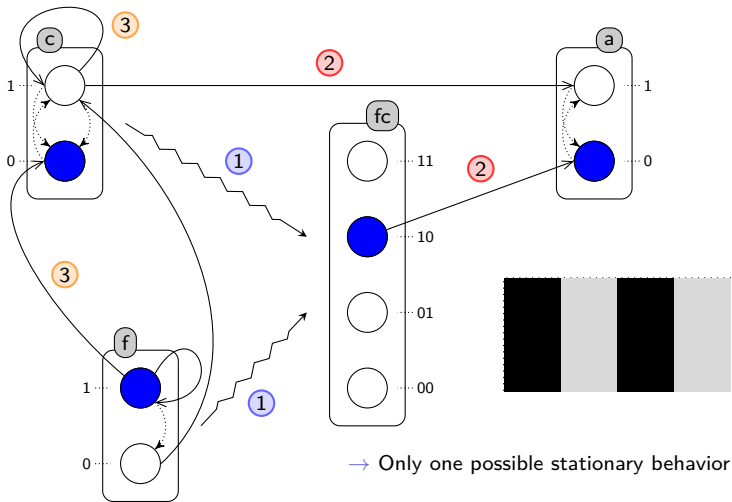
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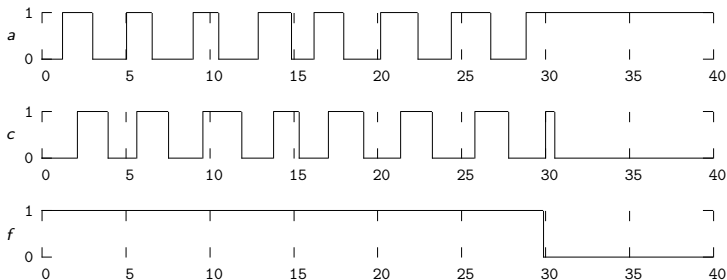
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Abstraction of Temporal Parameters

[Paulevé (PhD thesis), 2011]

- Simulation with stochastic parameters:

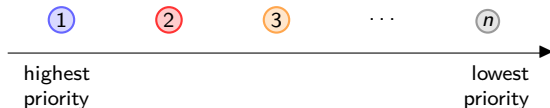


- Other possible analysis: stochastic model checkers (PRISM)
 - But combinatoric explosion: PRISM fails for more than 5 components

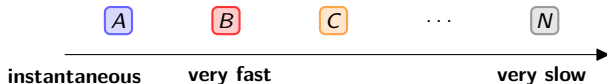
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- Each action is associated to a discrete priority
- An action is playable only if no other action with higher priority is playable

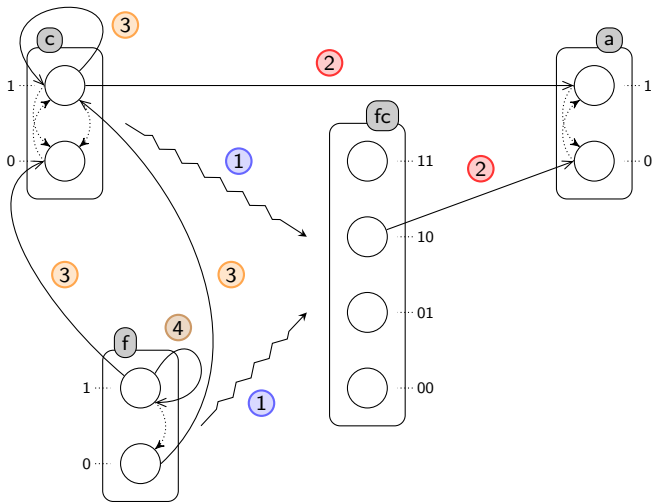


- Allow to model classes of actions with similar speeds or temporal parameters



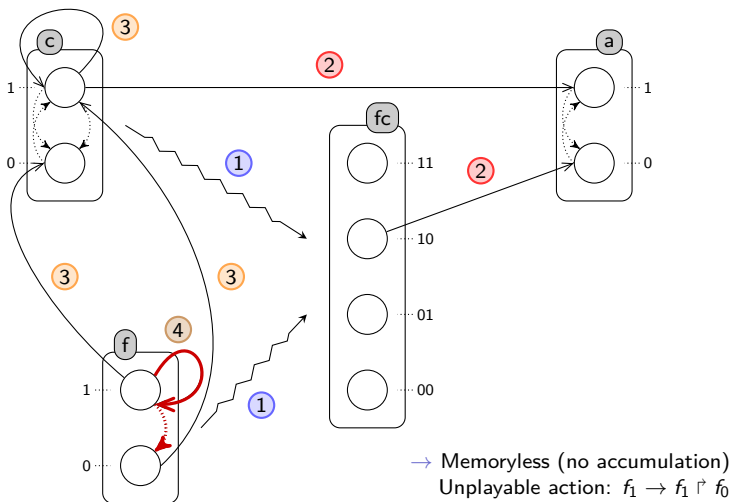
Limitation of the Classes of Priorities

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



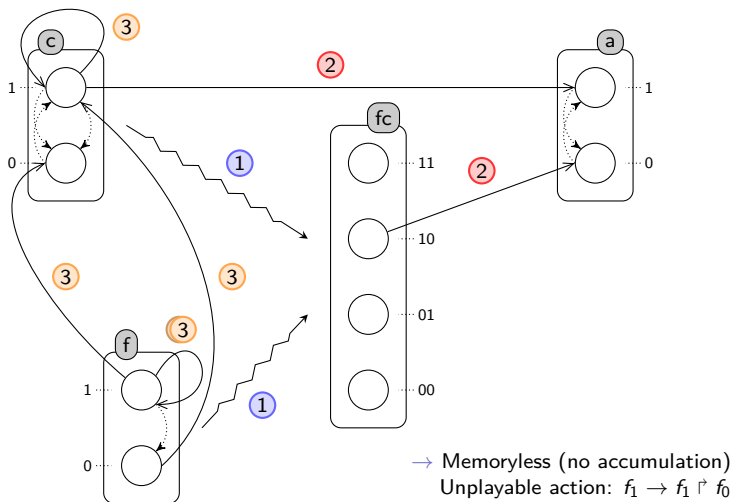
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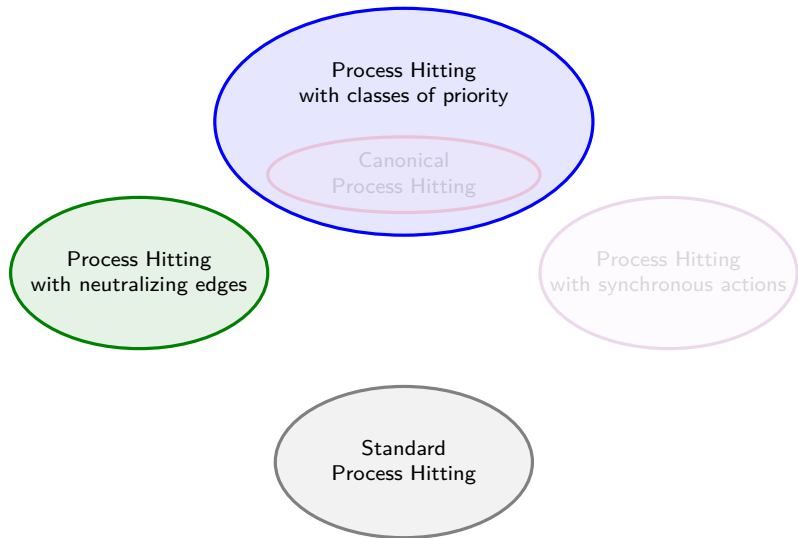


Limitation of the Classes of Priorities

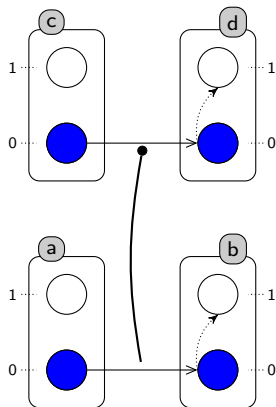
[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



Process Hitting with Neutralizing Edges



Addition of Neutralizing Edges



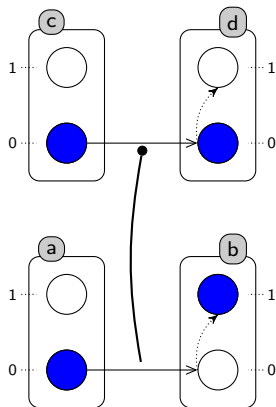
- Integration of temporal data about relative reaction speeds
- Atomistic preemptions between actions similar to “atomistic priorities”

$c_0 \rightarrow d_0 \uparrow d_1$ cannot be played **while**

$a_0 \rightarrow b_0 \uparrow b_1$ is playable

$\rightarrow d_1$ is **always** reached after b_1

Addition of Neutralizing Edges



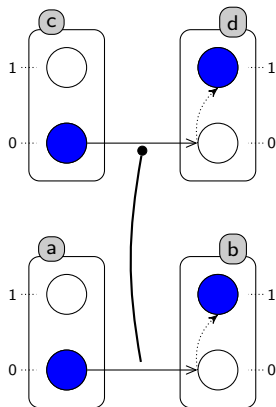
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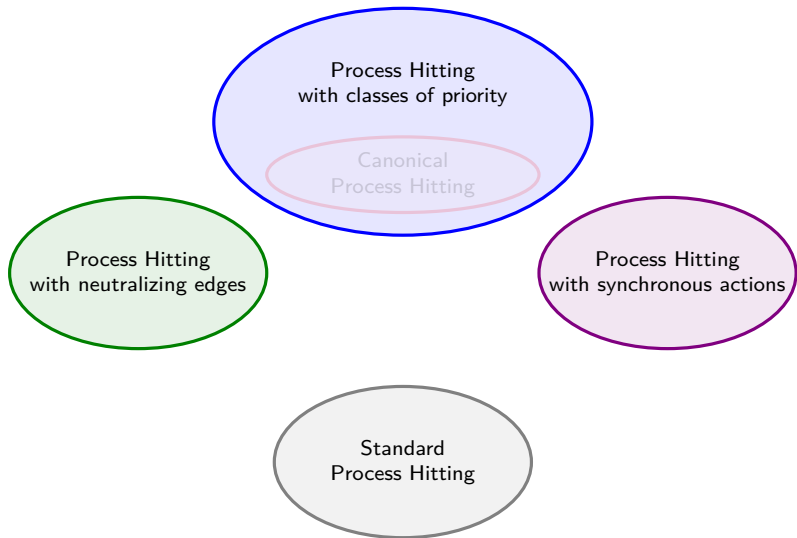
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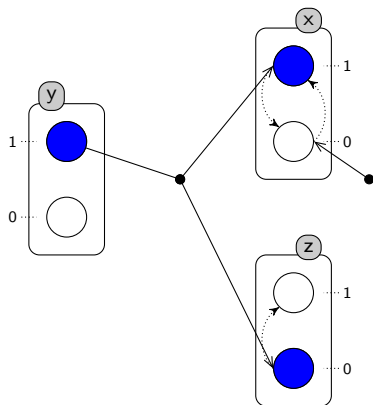
$a_0 \rightarrow b_0 \uparrow b_1$ is playable

$\rightarrow d_1$ is **always** reached after b_1

Process Hitting with Synchronous Actions



Addition of Synchronous Actions



- Synchronizations between actions:
 - All catalysts must be present
 - Reactants are consumed all together
 - Simultaneous creation of the products
- Representation of biochemical equations:



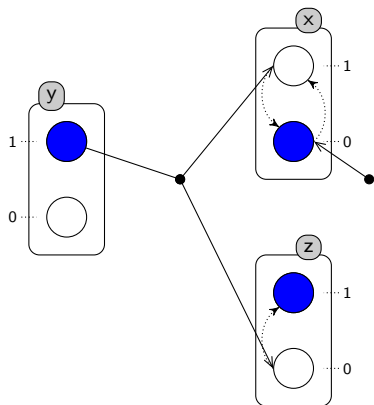
under the form:

$$h_2 = \{x_1, y_1, z_0\} \rightsquigarrow \{x_0, z_1\}$$

All processes of A
must be present to play $A \rightsquigarrow B$

After the play of $A \rightsquigarrow B$,
all processes of B are present

Addition of Synchronous Actions



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 - All catalysts must be present
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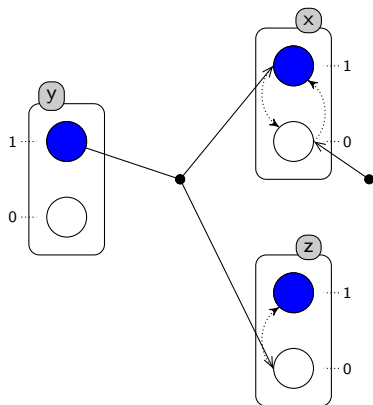
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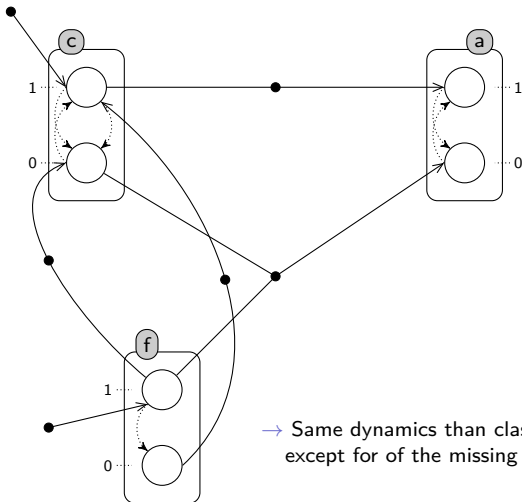
under the form:

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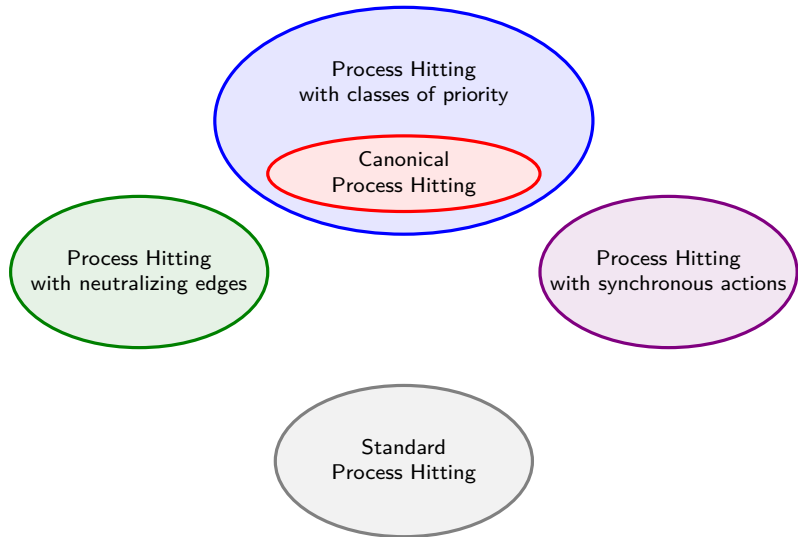
All processes of A
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After the play of $A \rightsquigarrow B$,
all processes of B are present

Use of Synchronous Actions

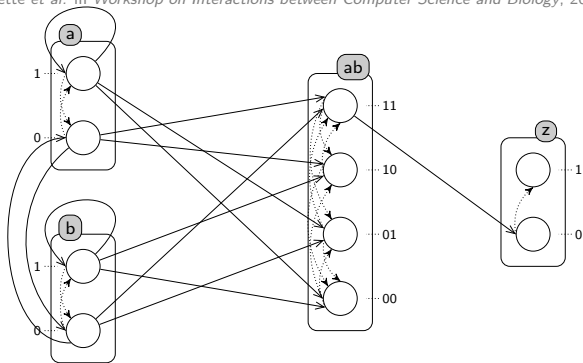


Canonical Process Hitting



Temporal Shift in Cooperative Sorts

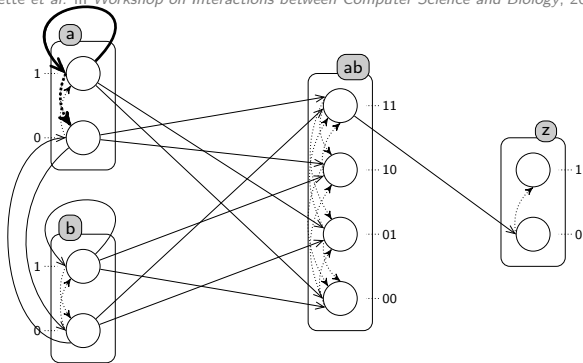
[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]



Drawback: the cooperative sorts are too “loose” (temporal shift)

Temporal Shift in Cooperative Sorts

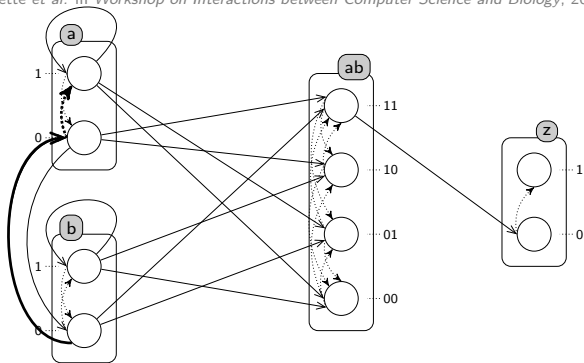
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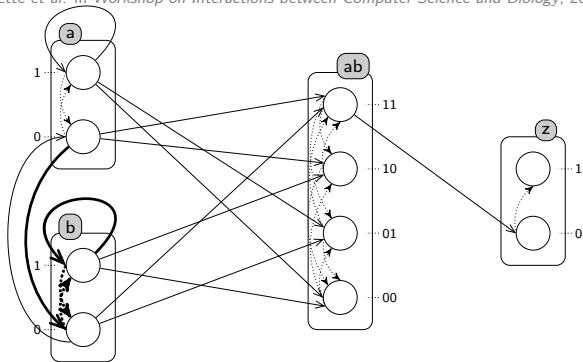
[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]



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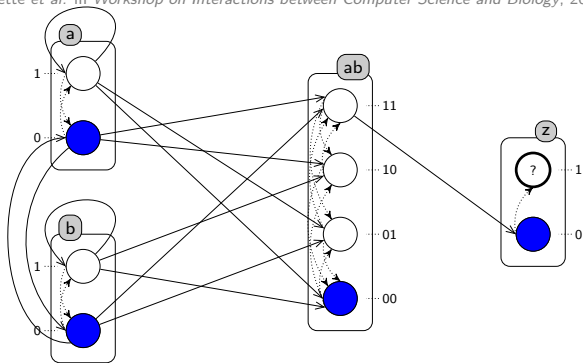
[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]



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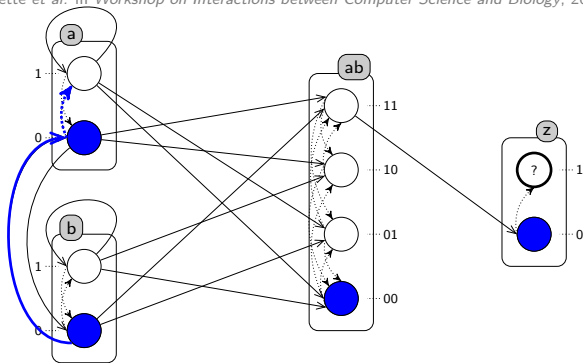


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$\langle a_0, b_0, ab_{00}, z_0 \rangle$

Temporal Shift in Cooperative Sorts

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]

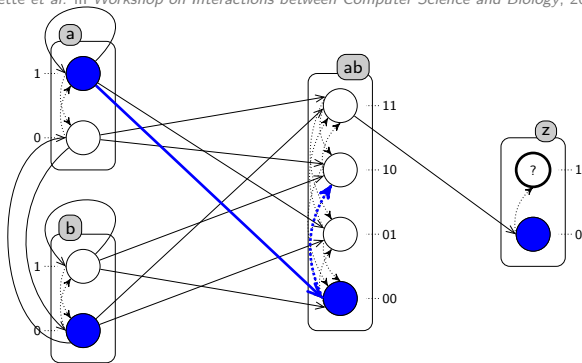


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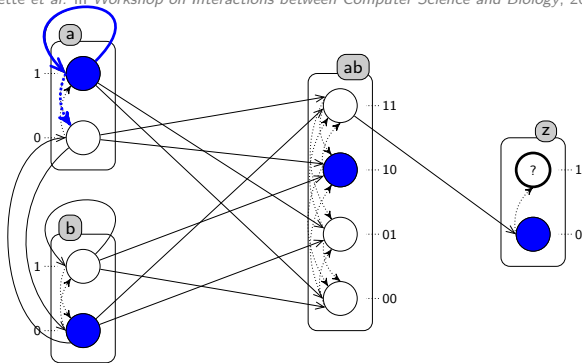


Drawback: the cooperative sorts are too “loose” (temporal shift)

$$\langle a_0, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{00}, z_0 \rangle$$

Temporal Shift in Cooperative Sorts

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]

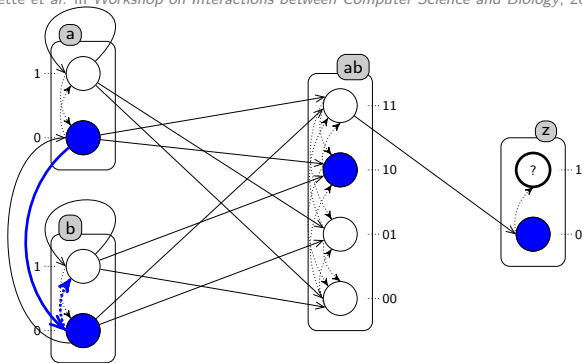


Drawback: the cooperative sorts are too “loose” (temporal shift)

$$\langle a_0, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{10}, z_0 \rangle$$

Temporal Shift in Cooperative Sorts

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]

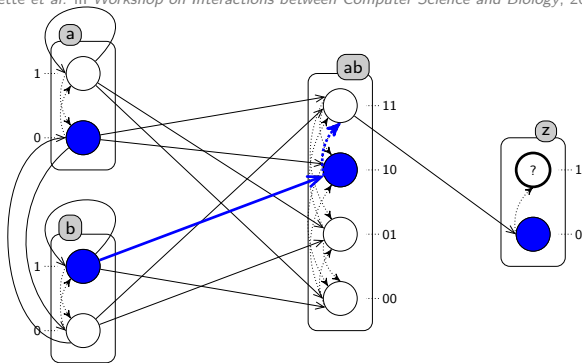


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Temporal Shift in Cooperative Sorts

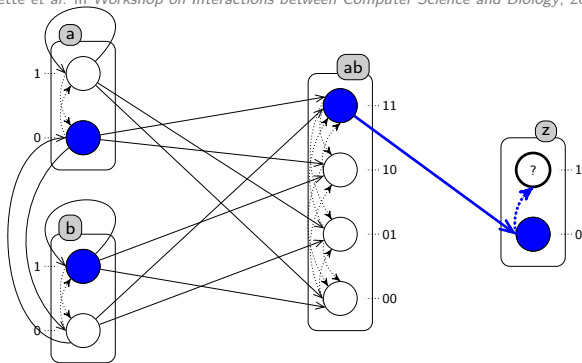
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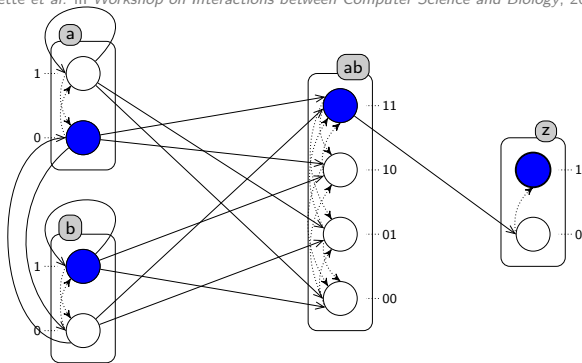
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Temporal Shift in Cooperative Sorts

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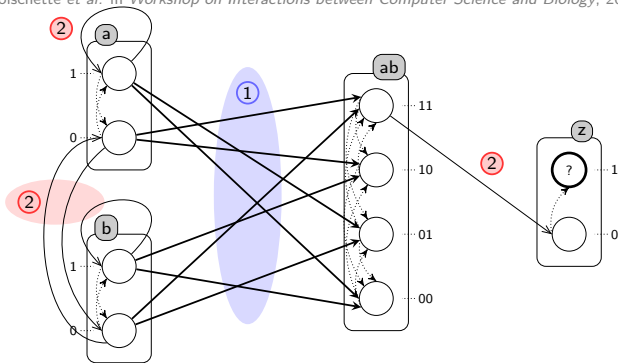
$$\langle a_0, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{10}, z_0 \rangle \rightarrow \langle a_0, b_0, ab_{10}, z_0 \rangle \\ \rightarrow \langle a_0, b_1, ab_{10}, z_0 \rangle \rightarrow \langle a_0, b_1, ab_{11}, z_0 \rangle \rightarrow \langle a_0, b_1, ab_{11}, z_1 \rangle$$

Expected behavior: $a_1 \wedge b_1$ **simultaneously** i.e. “in the same state”

Obtained behavior: $\mathbf{P}(a_1) \wedge \mathbf{P}(b_1)$ with \mathbf{P} = “previously”

Canonical Process Hitting

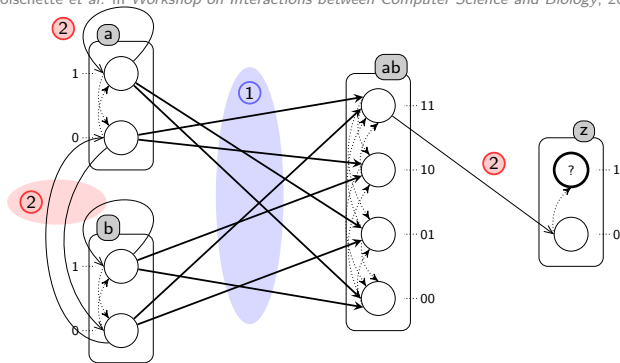
[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



- Primary actions (updating cooperative sorts) → ①
non-biological / non-controllable actions
- Secondary actions (all the other ones) → ②
biological / controllable actions / with delays

Canonical Process Hitting

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]

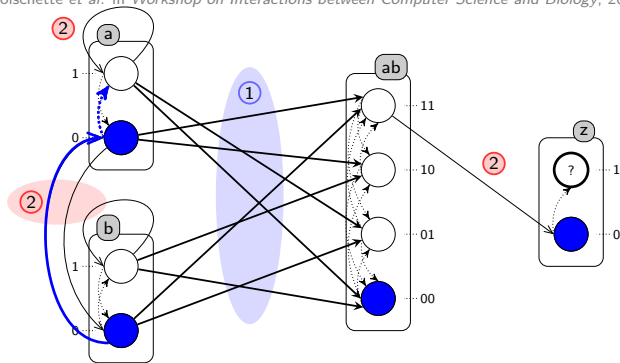


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⇒ Whenever a secondary action is played, all cooperative sorts are already updated

Canonical Process Hitting

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



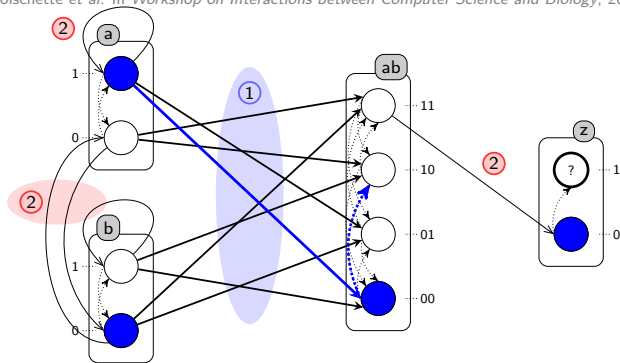
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Canonical Process Hitting

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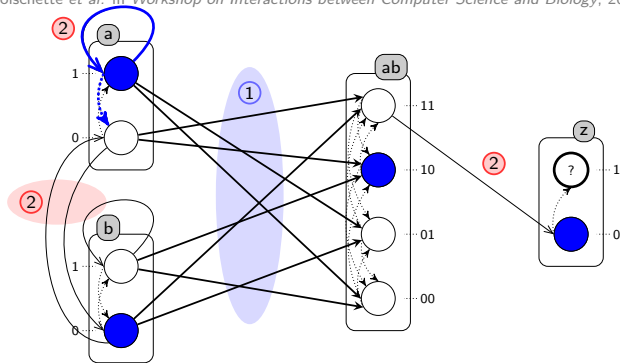
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Canonical Process Hitting

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



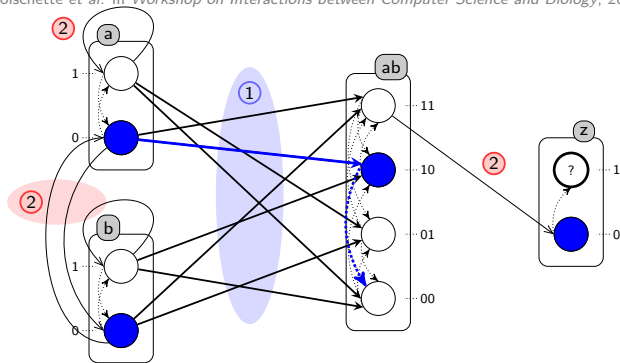
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Canonical Process Hitting

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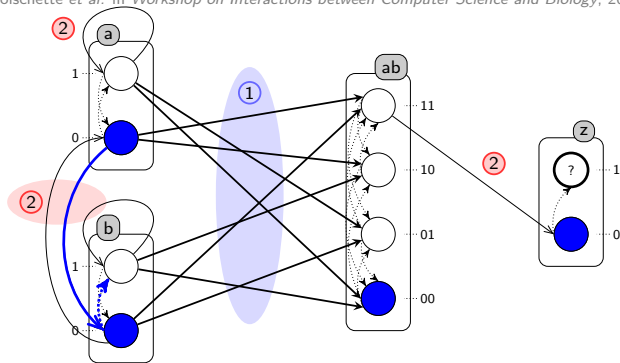
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Canonical Process Hitting

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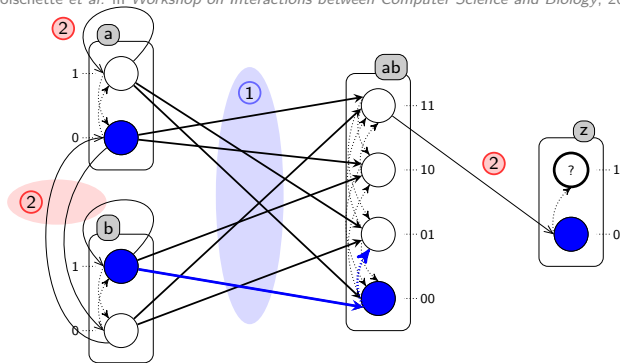
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$$\langle a_0, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{00}, z_0 \rangle \rightarrow \langle a_1, b_0, ab_{10}, z_0 \rangle \rightarrow \langle a_0, b_0, ab_{10}, z_0 \rangle$$

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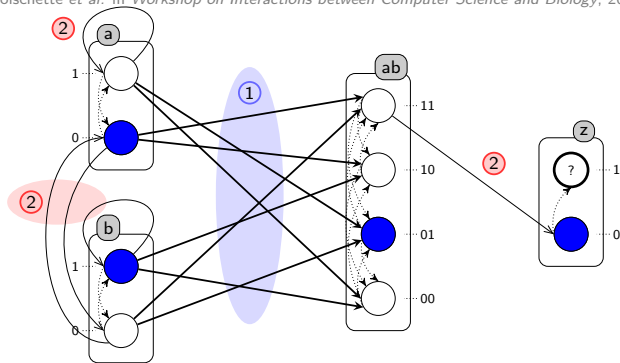
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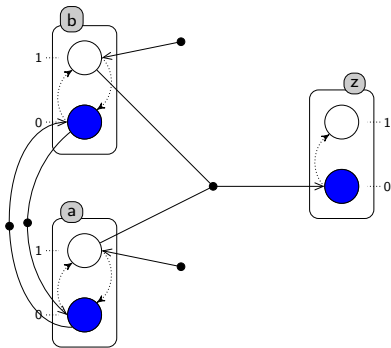


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Canonical Process Hitting with Synchronous Actions



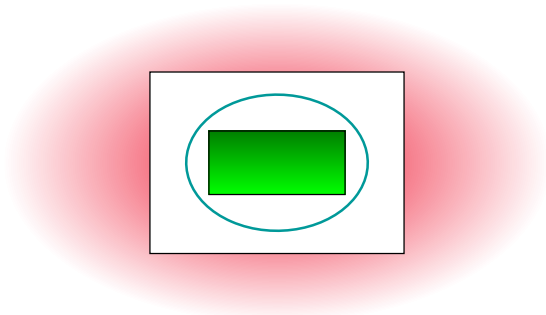
- Equivalent dynamics
- Sub-class of synchronous automata networks
- No priorities (no ill-formed model)
- No interfering updates and less intertwining

Static Analysis of Canonical Process Hitting

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]

Adding priorities restricts the possible dynamics (preemptions)

→ Invalidates the previous under-approximation

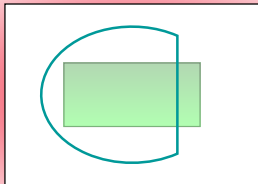


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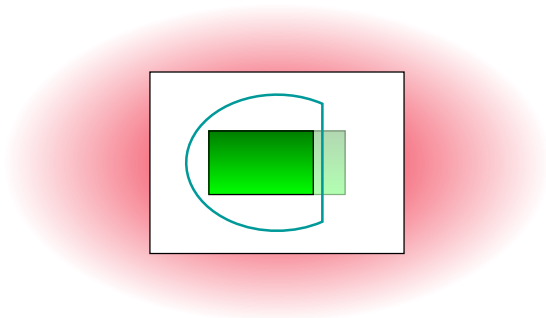


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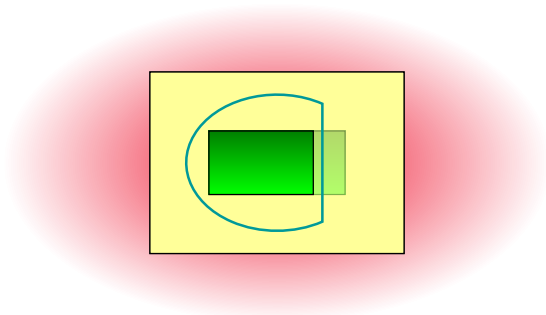


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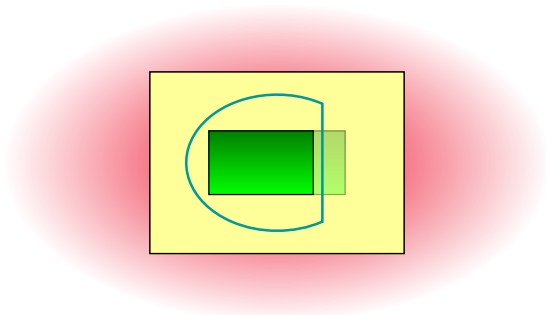


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Similar complexity for a more expressive formalism

→ Still efficient for big models

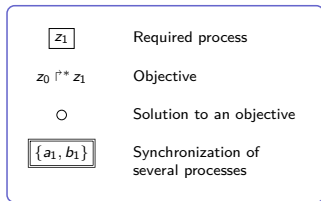
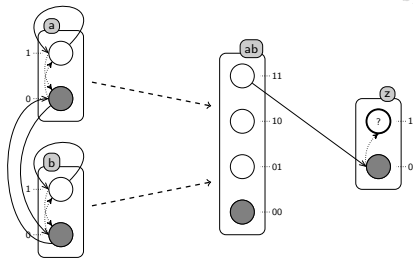
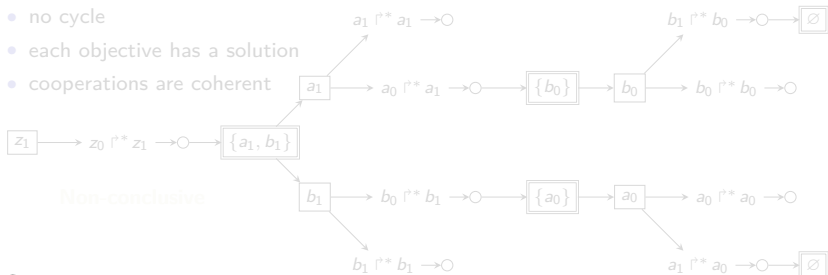
→ Finer under-approximation

Static Analysis of Canonical Process Hitting

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]

Sufficient condition:

- no cycle
- each objective has a solution
- cooperations are coherent

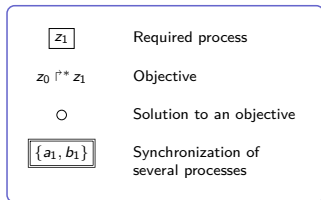
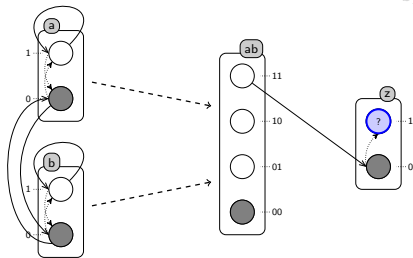
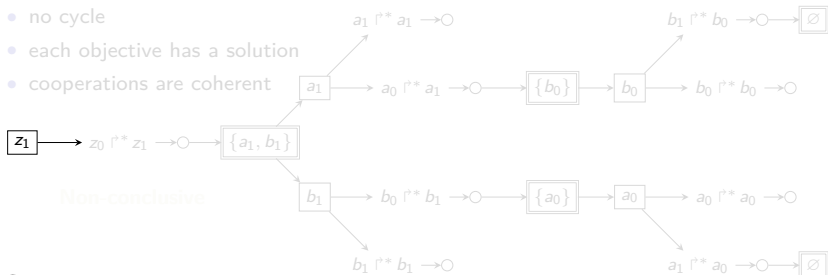


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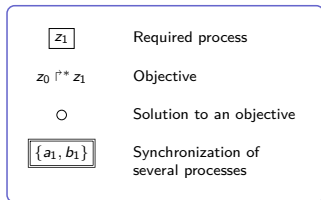
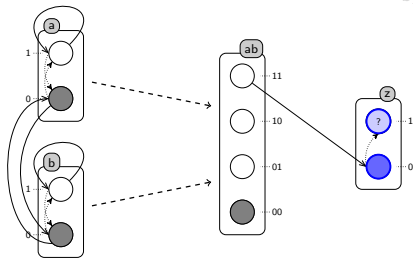
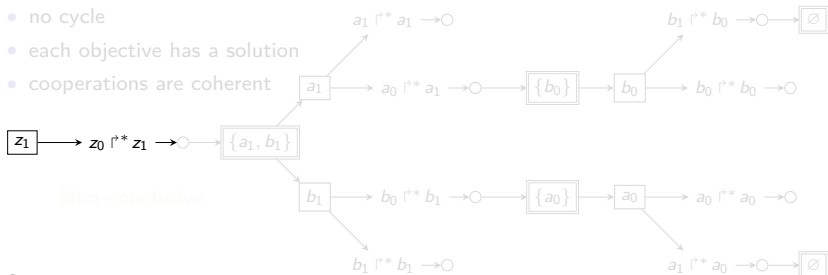


Static Analysis of Canonical Process Hitting

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]

Sufficient condition:

- no cycle
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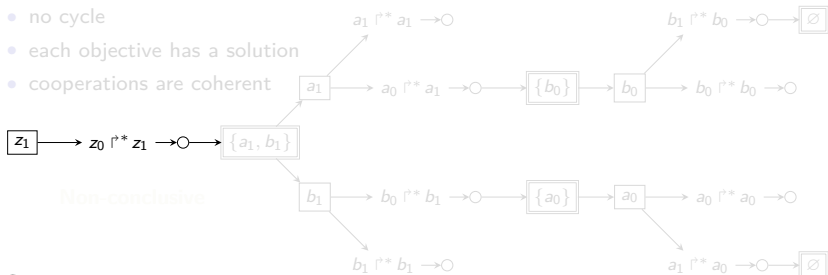


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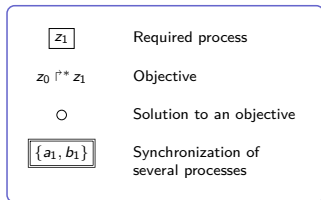
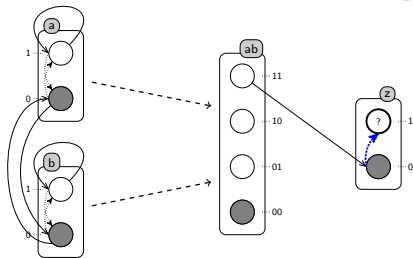
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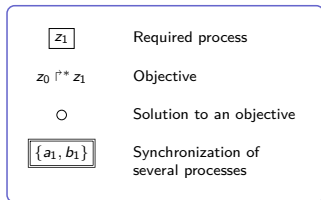
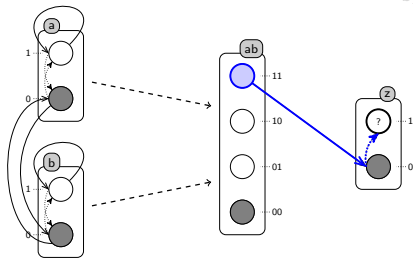
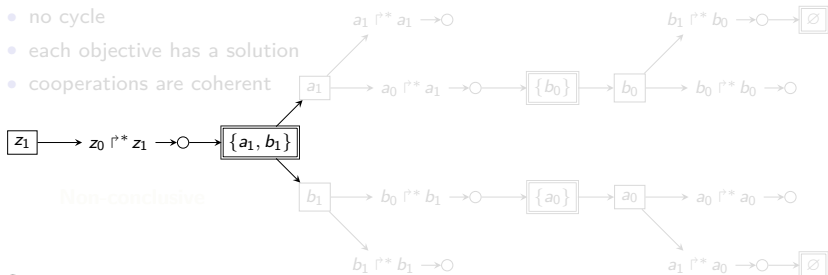


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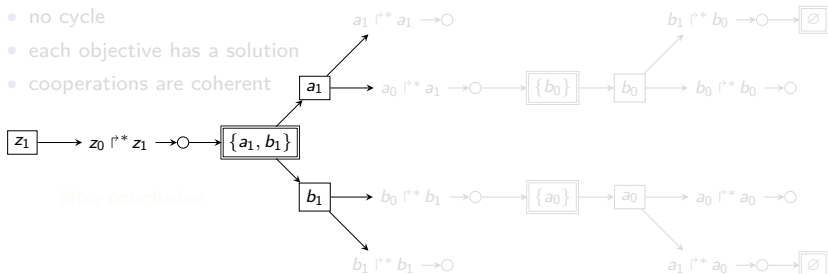


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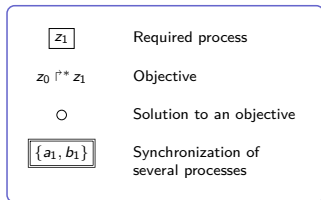
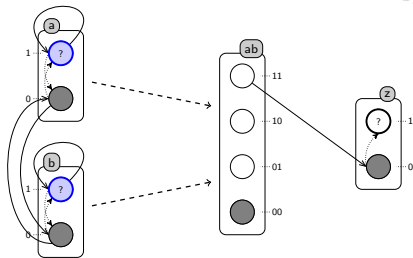
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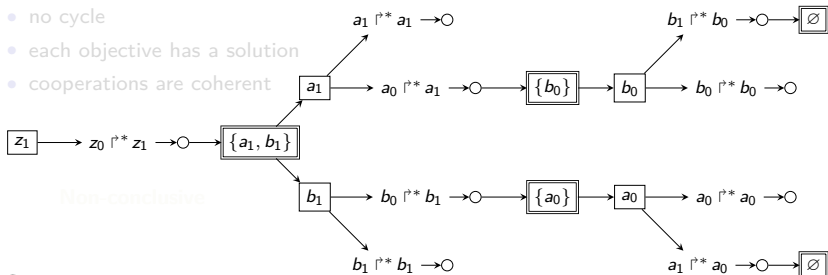


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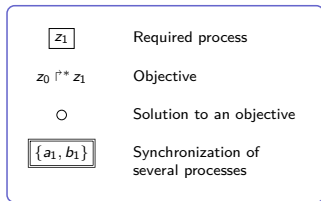
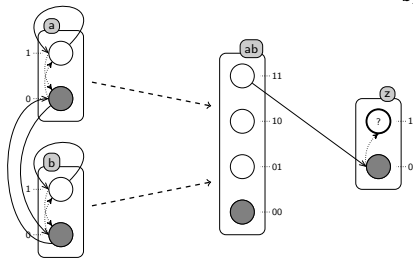
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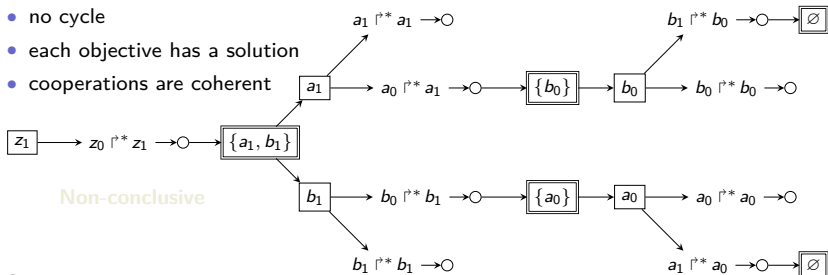


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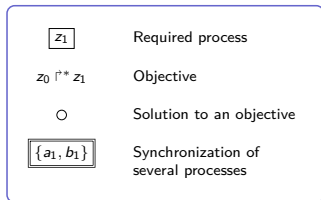
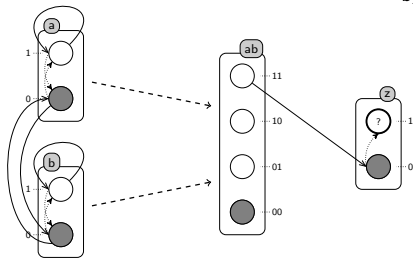
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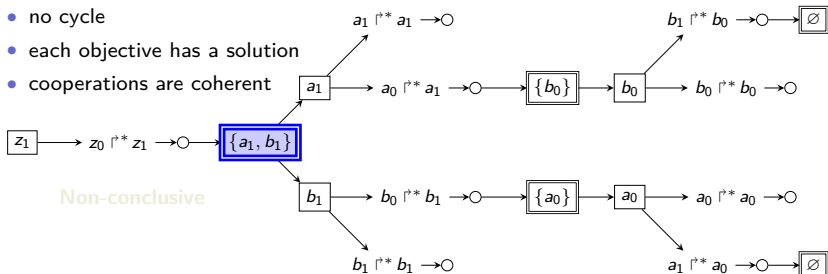


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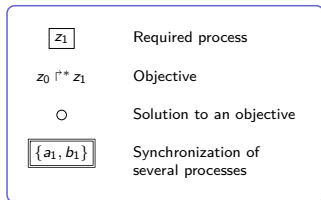
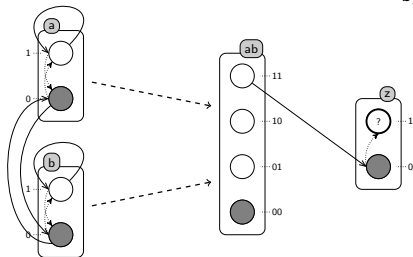
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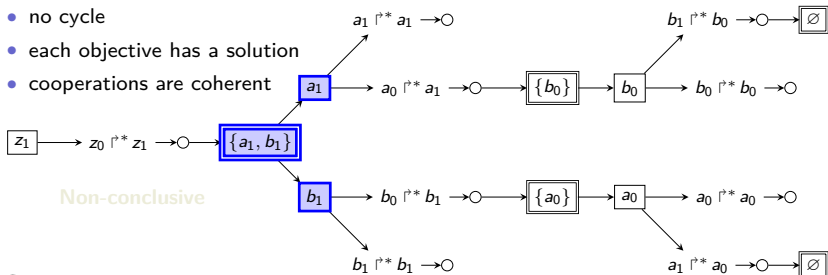


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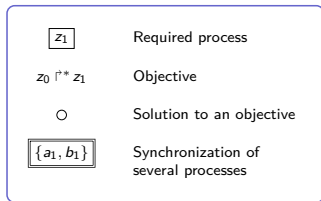
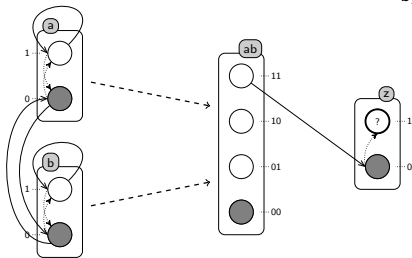
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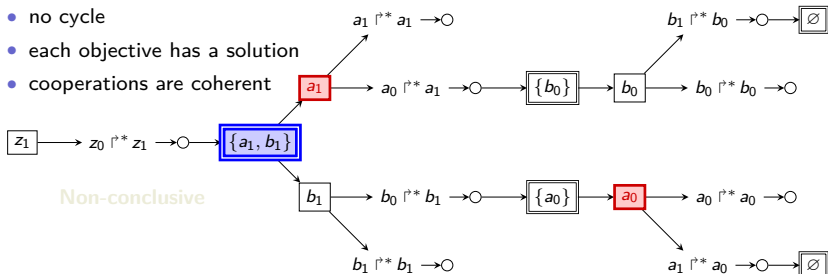


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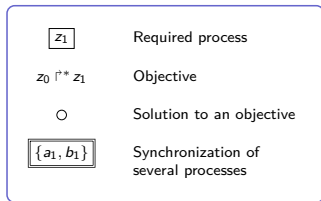
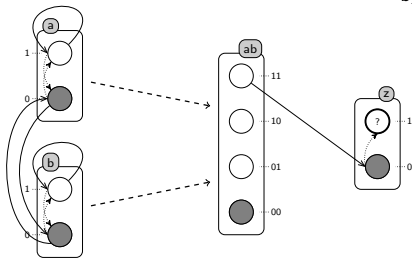
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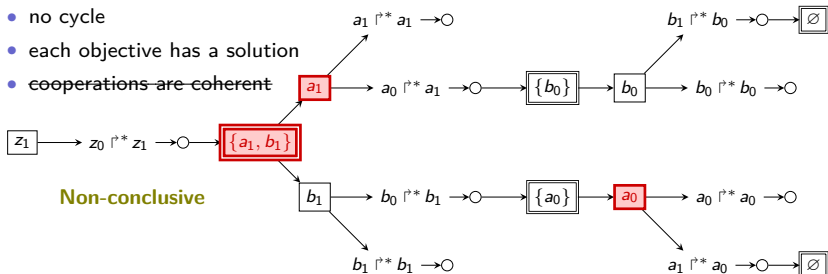


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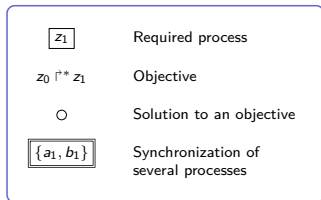
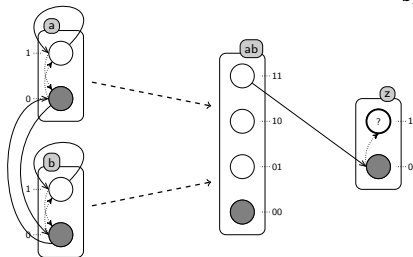
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Non-conclusive



Implementation of the Static Analysis Into PINT

Complexity:

- Computation of the local causality graph:
 - Polynomial in the number of sorts
 - Exponential in the number of processes of each sort
- Analysis of the graph (sufficient condition):
 - Polynomial in the size of the graph

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Makes the study of large networks tractable:

Modèle	Sortes	Processus	Actions	États	libddd ¹	GINsim ²	PINT
egfr20	35	196	670	2^{64}		<1s	0.02s
tcrsig40	54	156	301	2^{73}		∞	0.02s
tcrsig94	133	448	1124	2^{194}	[13min - ∞]		0.03s
egfr104	193	748	2356	2^{320}			0.16s

¹ LIP6/Move [Couvreur *et al.*, *Lecture Notes in Computer Science*, 2002]

² TAGC/IGC [Chaouiya, Naldi, Thieffry, *Methods in Molecular Biology*, 2012]

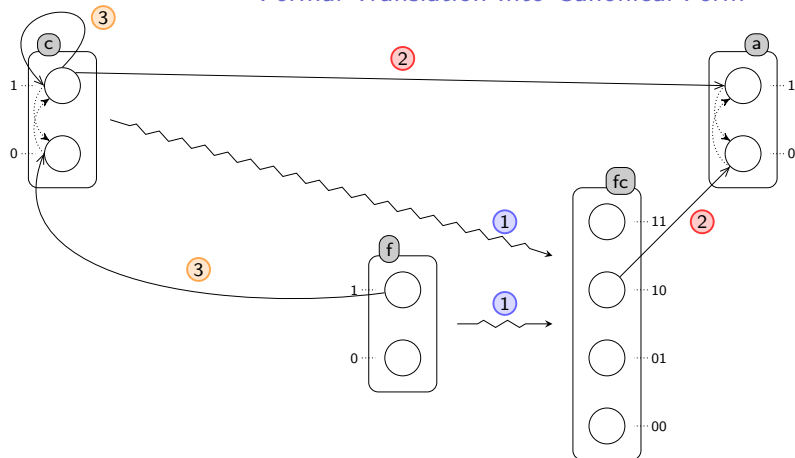
egfr20 : Epithelial Growth Factor Receptor (20 components) [Sahin *et al.*, 2009]

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

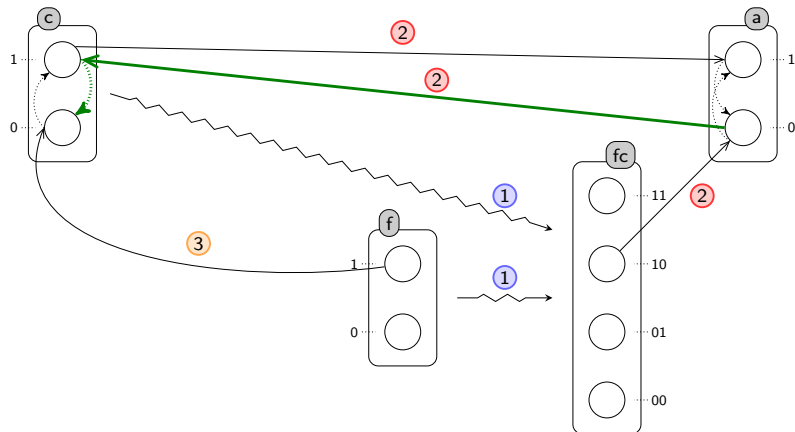
tcrsig40 : T-Cell Receptor (40 composants) [Klamt *et al.*, 2006]

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

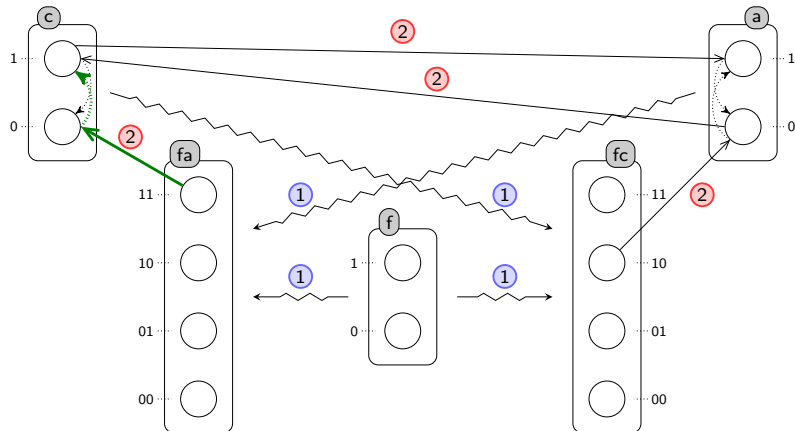
Formal Translation Into Canonical Form



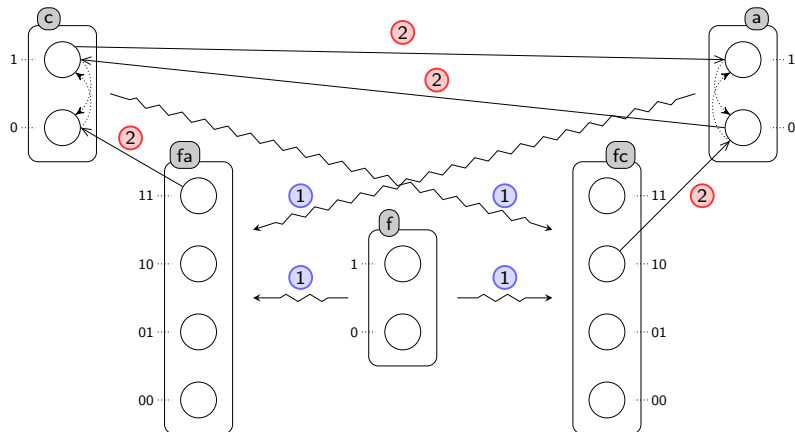
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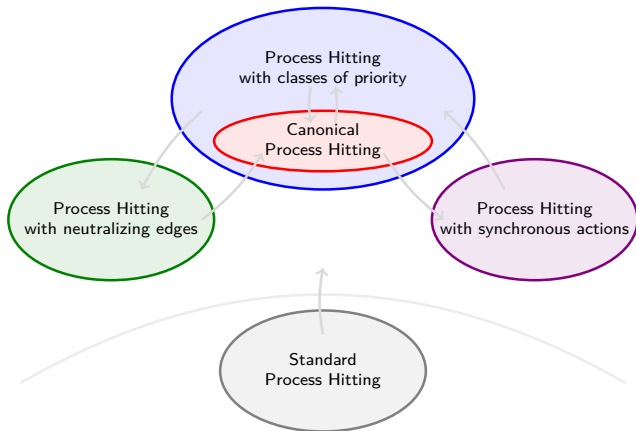
Formal Translation Into Canonical Form



→ Same dynamics (with supplemental cooperative sorts)

→ The canonical form can be computed for all Process Hitting extensions, with classes of priorities, neutralizing edges or synchronous actions

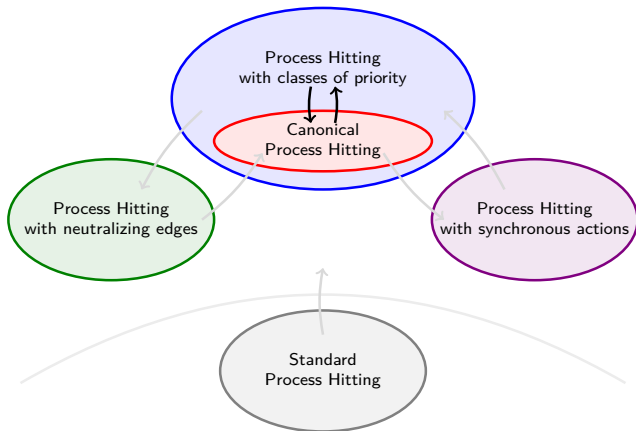
Equivalence Between Process Hitting Extensions



All developed enrichments have the same expressivity

- Expressive power improved
- Can always be translated to the canonical form
- But sometimes at the cost of an exponential translation

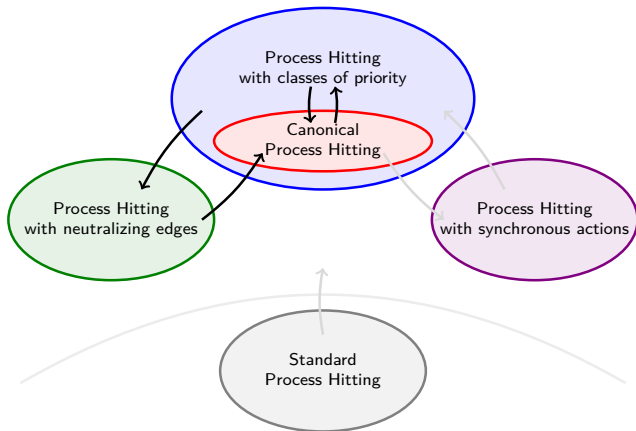
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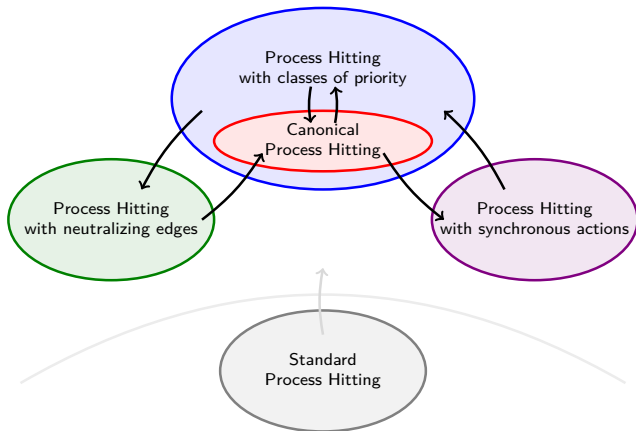
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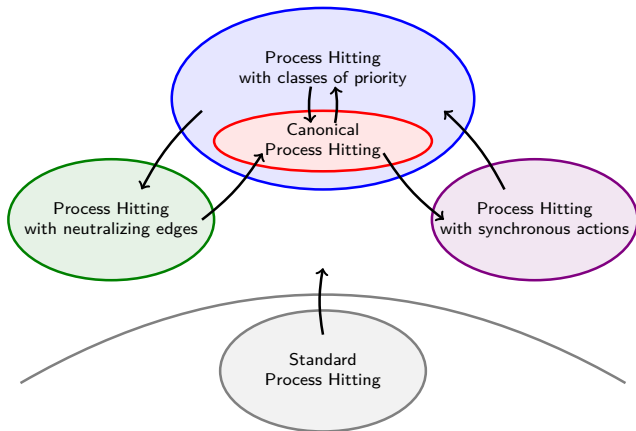
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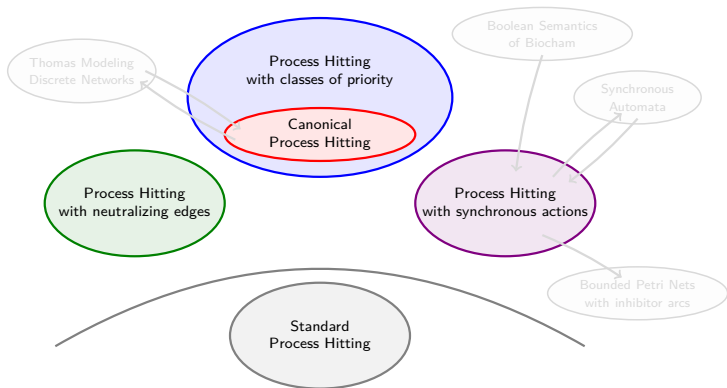
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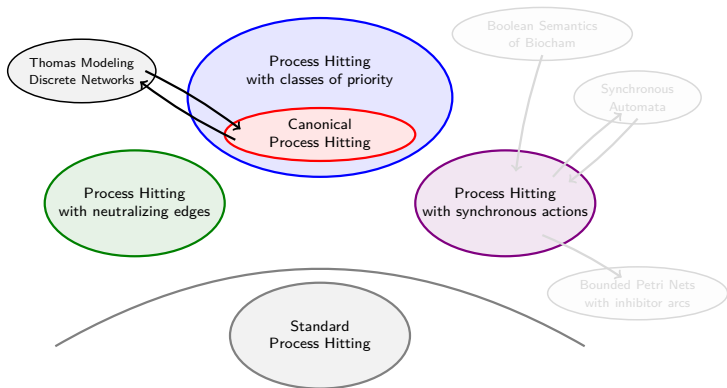
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Translation From and To Other Discrete Models



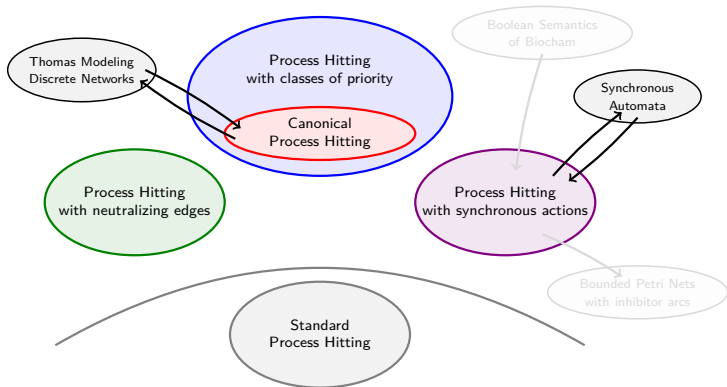
- Equivalence with discrete networks / Thomas modeling
- Equivalence with synchronous automata networks
- Translation towards (bounded) Petri nets with inhibitor arcs
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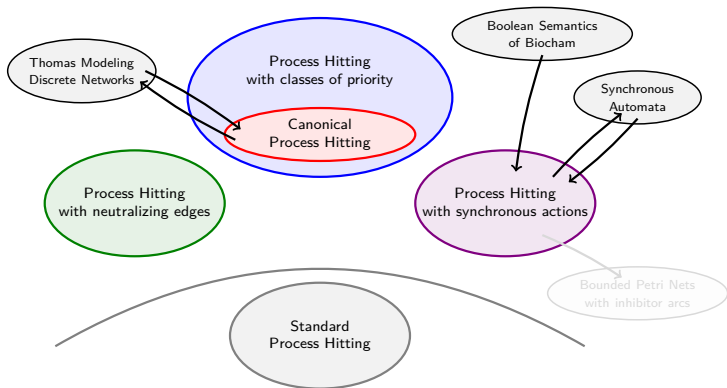
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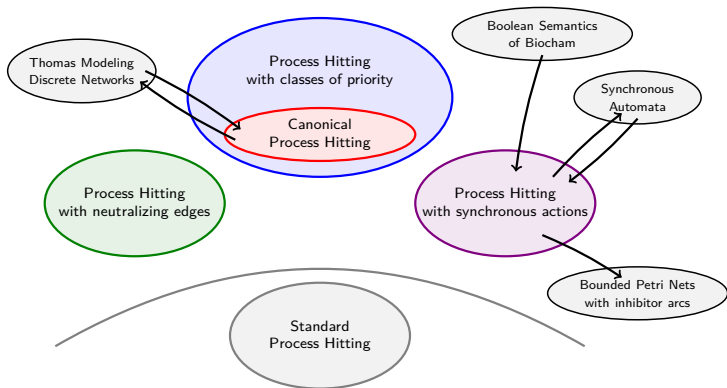
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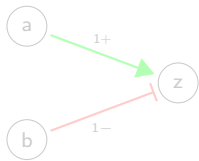
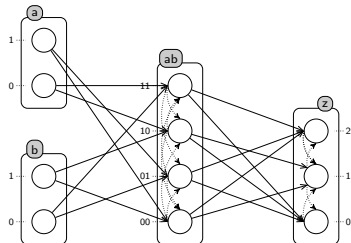
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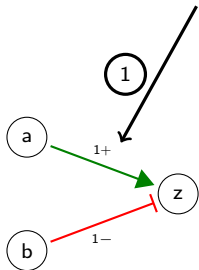
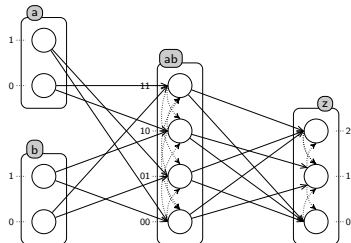
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Inferring a BRN with Thomas' parameters



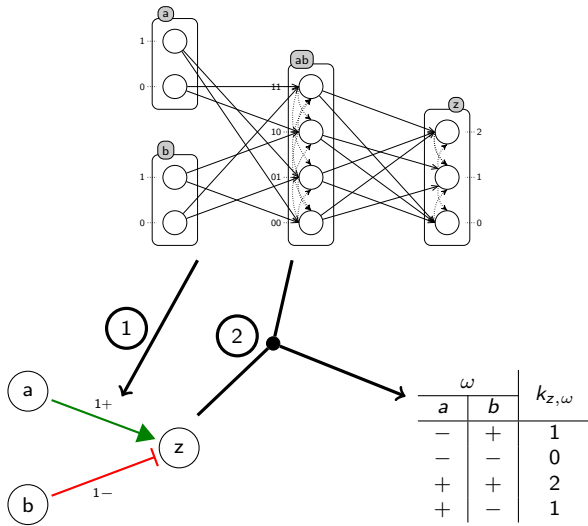
		ω	$k_{z,\omega}$
a	b		
-	+	1	1
-	-	0	0
+	+	2	2
+	-	1	1

Inferring a BRN with Thomas' parameters



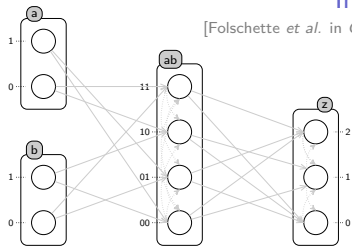
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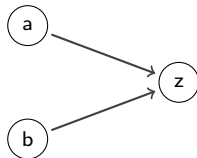
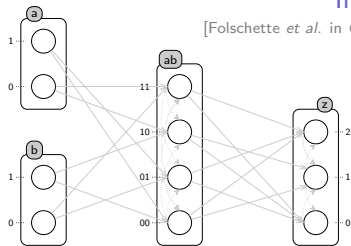
Inferring the Interaction Graph

[Folschette *et al.* in *Computational Methods in Systems Biology*, 2012]



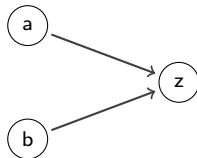
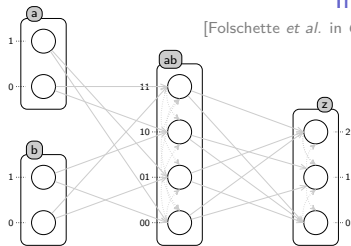
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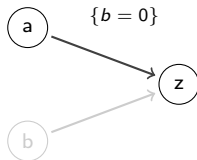
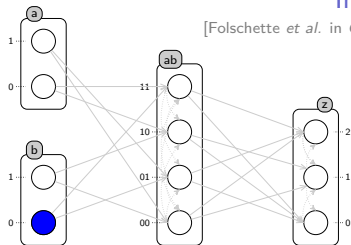
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→ Exhaustive search in all possible configurations

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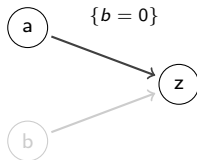
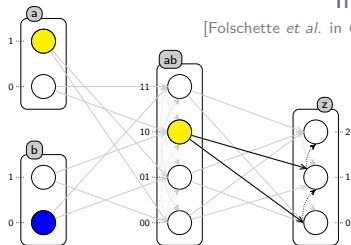


→ Exhaustive search in all possible configurations

1. Pick one regulator [a], and choose an active process for all the others [b_0].

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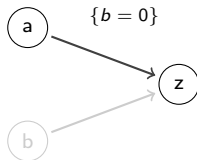
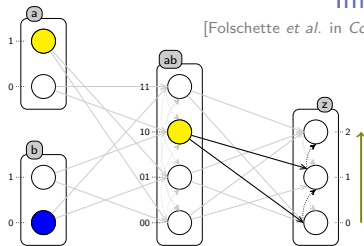


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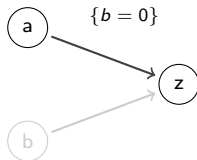
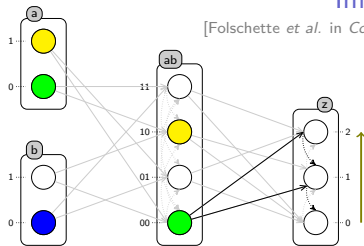


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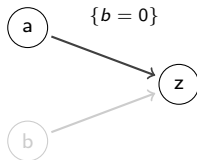
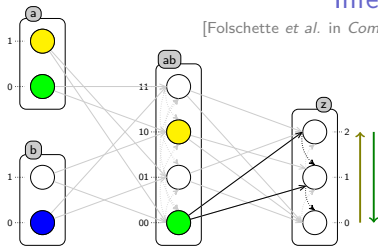


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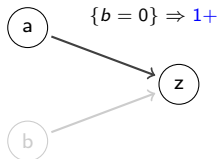
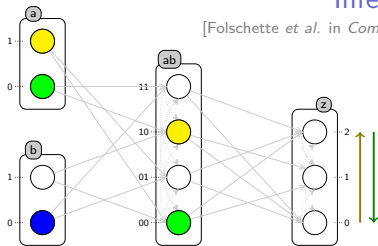


→ **Exhaustive search in all possible configurations**

1. Pick one regulator [**a**], and choose an active process for all the others [**b**].
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Inferring the Interaction Graph

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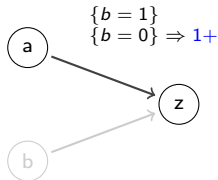
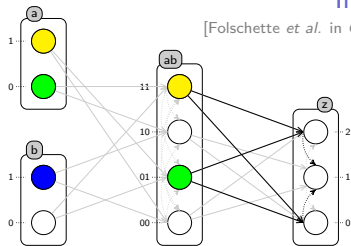


→ Exhaustive search in all possible configurations

1. Pick one regulator [a], and choose an active process for all the others [b_0].
2. Change the active process of the regulator [a_0, a_1] and watch the **evolution**.
3. Conclude locally: $(a_0 \uparrow a_1 \Rightarrow z_0 \uparrow z_2) \Rightarrow$ activation (+) & threshold = 1.

Inferring the Interaction Graph

[Folschette *et al.* in *Computational Methods in Systems Biology*, 2012]

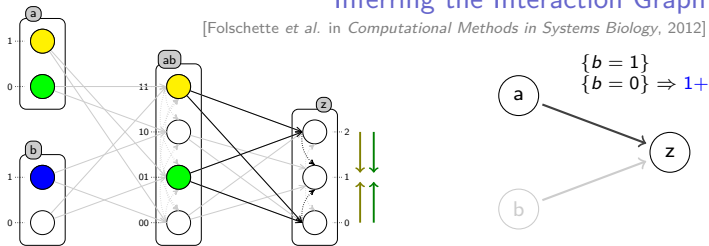


→ Exhaustive search in all possible configurations

1. Pick one regulator [**a**], and choose an active process for all the others [**b**].
2. Change the active process of the regulator [**a**₀, **a**₁] and watch the **evolution**.
3. Conclude locally: (**a**₀ \rightarrow **a**₁ \Rightarrow **z**₀ \rightarrow **z**₂) \Rightarrow activation (+) & threshold = 1.
4. Iterate

Inferring the Interaction Graph

[Folschette *et al.* in *Computational Methods in Systems Biology*, 2012]

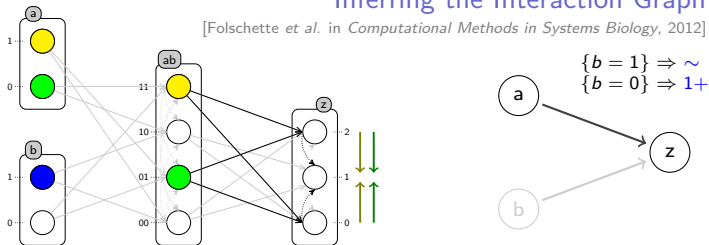


→ Exhaustive search in all possible configurations

1. Pick one regulator $[a]$, and choose an active process for all the others $[b_0]$.
2. Change the active process of the regulator $[a_0, a_1]$ and watch the **evolution**.
3. Conclude locally: $(a_0 \uparrow a_1 \Rightarrow z_0 \uparrow z_2) \Rightarrow$ activation (+) & threshold = 1.
4. Iterate

Inferring the Interaction Graph

[Folschette *et al.* in *Computational Methods in Systems Biology*, 2012]

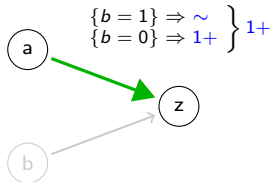
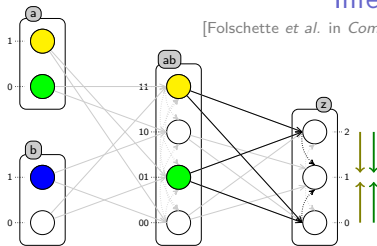


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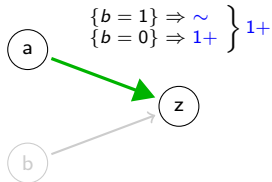
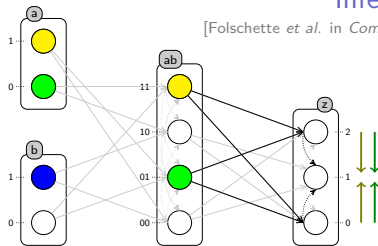


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Inferring the Interaction Graph

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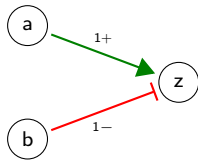
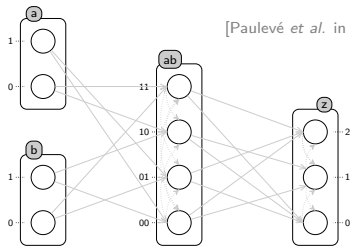
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3. Conclude locally: $(a_0 \uparrow a_1 \Rightarrow z_0 \uparrow z_2) \Rightarrow$ activation (+) & threshold = 1.
4. Iterate and conclude globally.

Problematic cases:

- No focal processes (cycle)
 - Opposite influences (+ & -)
- } \Rightarrow Unsigned edge

Inferring Parameters

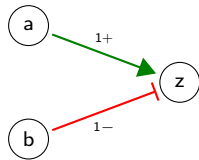
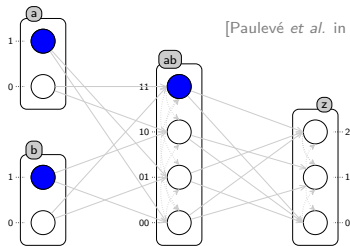
[Paulevé *et al.* in *Transactions on Computational Systems Biology*, 2011]



ω		$k_{z,\omega}$
a	b	
-	+	
-	-	
+	+	
+	-	

Inferring Parameters

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

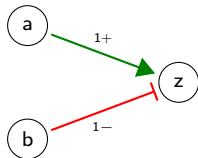
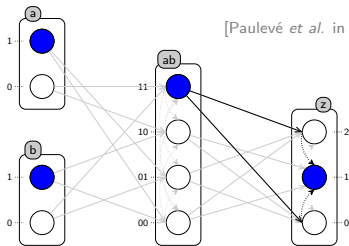


ω		$k_{z,\omega}$
a	b	
-	+	
-	-	
+	+	
+	-	

1. For each configuration of resources $[\omega = \{a^+, b^-\}]$

Infering Parameters

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

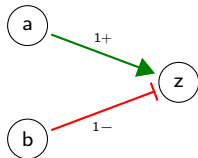
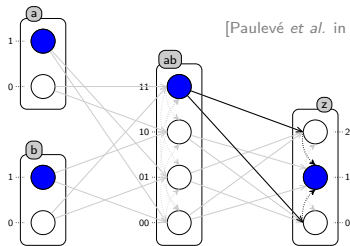


ω		$k_{z,\omega}$
a	b	
-	+	
-	-	
+	+	
+	-	

1. For each configuration of resources find the **focal processes**. $[\omega = \{a^+, b^-\}]$

Inferring Parameters

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

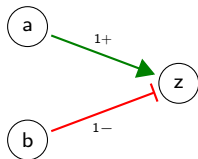
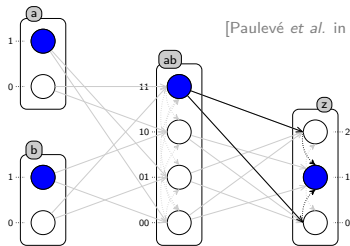


ω		$k_{z,\omega}$
a	b	
-	+	
-	-	
+	+	
+	-	1

- For each configuration of resources $[\omega = \{a^+, b^-\}]$ find the **focal processes**. If possible, conclude. $[k_{z,\{a^+,b^-\}} = 1]$

Inferring Parameters

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



ω		$k_{z,\omega}$
a	b	
-	+	
-	-	
+	+	
+	-	1

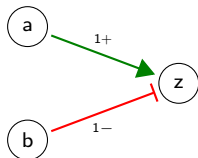
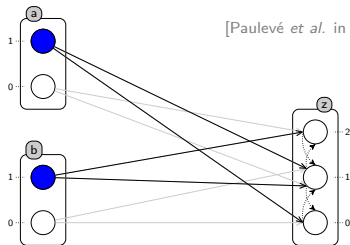
- For each configuration of resources $[\omega = \{a^+, b^-\}]$ find the **focal processes**. If possible, conclude. $[k_{z,\{a^+,b^-\}} = 1]$

Inconclusive cases:

- Behavior cannot be represented as a BRN
- Lack of cooperation (no focal processes)

Inferring Parameters

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



ω		$k_{z,\omega}$
a	b	
-	+	?
-	-	0
+	+	2
+	-	?

- For each configuration of resources $[\omega = \{a^+, b^-\}]$ find the **focal processes**. If possible, conclude. $[k_{z,\{a^+,b^-\}} = 1]$

Inconclusive cases:

- Behavior cannot be represented as a BRN
- Lack of cooperation (no focal processes)

- If some parameters could not be inferred, enumerate all admissible parametrizations, regarding:

- Biological constraints [Bernot *et al.* in *Concurrent Models in Molecular Biology*, 2007]
- The dynamics of the Process Hitting

$$[k_{z,\{a^+,b^-\}} \in \{0; 1; 2\}; k_{z,\{a^-,b^+\}} \in \{0; 1; 2\}]$$

Translation to Thomas Modeling

[Folschette *et al.* in *Computational Methods in Systems Biology*, 2012]

- Two successive inferences: 1) interaction graph; 2) parameters
- Exhaustive analysis of the local dynamics for each regulator
- enumeration of all parametrizations compatible with the dynamics

Complexity:

Linear in the number of genes,

Exponential in the number of regulators of one component

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Complexity:

Linear in the number of genes,

Exponential in the number of regulators of one component

Name	Models			Inference the IG		Inference of parameters	
	Sorts	Processes	Actions	Duration	Edges	Durations	Parameters
egfr20	42	152	399	1s	51	1s	192
tcrsig40	54	156	305	1s	55	1s	143
tcrsig94	133	448	1082	100s	197	1s	578
egfr104	193	744	2304	200s	280	3s	27'496

[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]

General Conclusion

Standard Process Hitting allows to represent biological regulatory networks in an **atomistic** fashion:

- Existing efficient static analysis
- But temporal shift issues
- Limited modeling power

Extensions of the Process Hitting to improve the expressivity:

- Rectification of the temporal shift → Strictly higher expressivity
- Allows to abstract temporal parameters
- New links to other formalisms (Thomas, PN, etc.)

Static analysis of the Canonical Process Hitting:

- Efficient analysis of reachability properties
- Applicable to the extensions at the cost of a translation
- New kind of property: simultaneous activation

New exploitation possibilities:

- Modeling and analysis of full databases
- Study of uncontrollable behaviors or punctual perturbations
- Research of interesting properties (attractors, oscillations, ...)

Improvement of the static analysis:

- Refining in order to reduce the non-conclusiveness
- New methods using by-products such as the local causality graph
- New properties to check (temporal logic, counters, ...)

Enrichment of the modeling power:

- Abstraction of temporal parameters: find properties to avoid Zeno behavior
- Dynamical classes of priorities
- Guarded actions or complex logic gates
- New model checking tools (Hoare logic, ...)

Thank you for your attention

Personal Contributions

Book chapter:

- Loïc Paulevé, Courtney Chancellor, Maxime Folschette, Morgan Magnin, Olivier Roux. [Analyzing Large Network Dynamics with Process Hitting](#), In Luis Farinas del Cerro and Katsumi Inoue, editors: *Logical Modeling of Biological Systems*, 2014.

Journal article:

- Maxime Folschette, Loïc Paulevé, Katsumi Inoue, Morgan Magnin, Olivier Roux. [Constructing Biological Regulatory Networks from Process Hitting models](#), *Theoretical Computer Science*, Vol. 586, 2015.

Conference:

- Maxime Folschette, Loïc Paulevé, Morgan Magnin, Olivier Roux. [Under-approximation of reachability in multivalued asynchronous networks](#), CS2Bio'13, *Electronic Notes in Theoretical Computer Science*, Vol. 299, 2013.

Workshops:

- Maxime Folschette, Loïc Paulevé, Katsumi Inoue, Morgan Magnin, Olivier Roux. [Concretizing the process hitting into biological regulatory networks](#), CMSB'12, *Lecture Notes in Computer Science*, 2012.
- Maxime Folschette, Loïc Paulevé, Katsumi Inoue, Morgan Magnin, Olivier Roux. [Abducing Biological Regulatory Networks from Process Hitting models](#), *ECML-PKDD'12 / LDSSB'12*, 2012.

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- Sohei Ito, Naoko Izumi, Shigeki Hagihara and Naoki Yonezaki. [Qualitative analysis of gene regulatory networks by satisfiability checking of Linear Temporal Logic](#). In 2010 IEEE International Conference on *Bioinformatics and BioEngineering*, pages 232–237, IEEE, 2010.

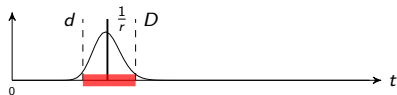
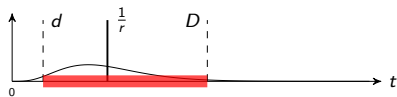
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- Loïc Paulevé, Morgan Magnin, Olivier Roux. [Static analysis of biological regulatory networks dynamics using abstract interpretation](#). *Mathematical Structures in Computer Science*, 2012.
- Gilles Bernot, Franck Cassez, Jean-Paul Comet, Franck Delaplace, Céline Müller, Olivier Roux. [Semantics of Biological Regulatory Networks](#). Proceedings of the First Workshop on Concurrent Models in Molecular Biology, *Electronic Notes in Theoretical Computer Science* 180(3), pages 3–14, 2007.
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- Regina Samaga *et al.* [The Logic of EGFR/ErbB Signaling: Theoretical Properties and Analysis of High-Throughput Data](#). *PLoS Computational Biology*, 5(8), 2009.
- Steffen Klamt *et al.* [A methodology for the structural and functional analysis of signaling and regulatory networks](#). *BMC Bioinformatics*, 7(1), 2006.
- Julio Saez-Rodriguez *et al.* [A Logical Model Provides Insights into T Cell Receptor Signaling](#). *PLoS Computational Biology*, 3(8), 2007.

Stochastic Parameters

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

- Introduction of temporal properties
- Stochastic parameters (r, sa) equivalent to a **firing interval** $[d; D]$

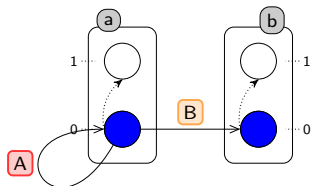
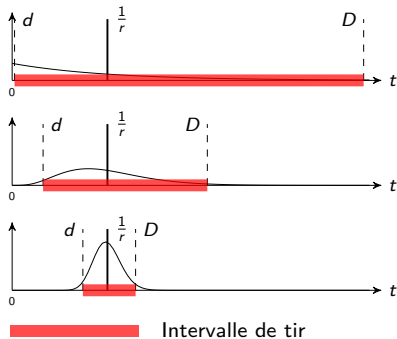


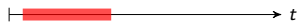
 Intervalle de tir

Stochastic Parameters

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

- Introduction of temporal properties
- Stochastic parameters (r, sa) equivalent to a **firing interval** $[d; D]$


 $a_0 \rightarrow b_0 \xrightarrow{r} b_1 \quad (B)$

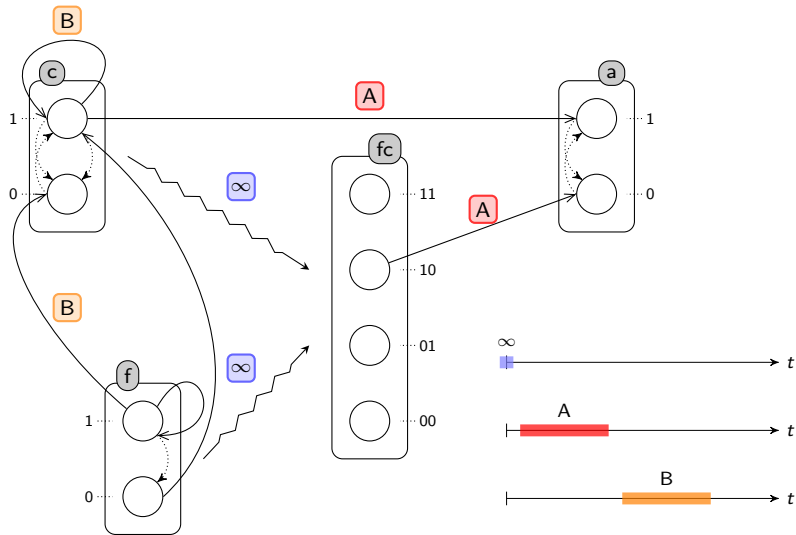
 $a_0 \rightarrow a_0 \xrightarrow{r} a_1 \quad (A)$


→ **Very low probability** to reach b_1

- Simulation → not formal
- *Model-checking* → High complexity for an acceptable precision

Use of Stochastic Parameters

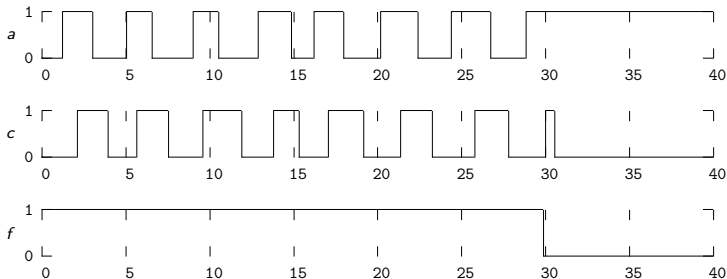
[Paulevé et al. in *Transactions on Computational Systems Biology*, 2011]



Temporal Simulation

[Paulevé (PhD thesis), 2011]

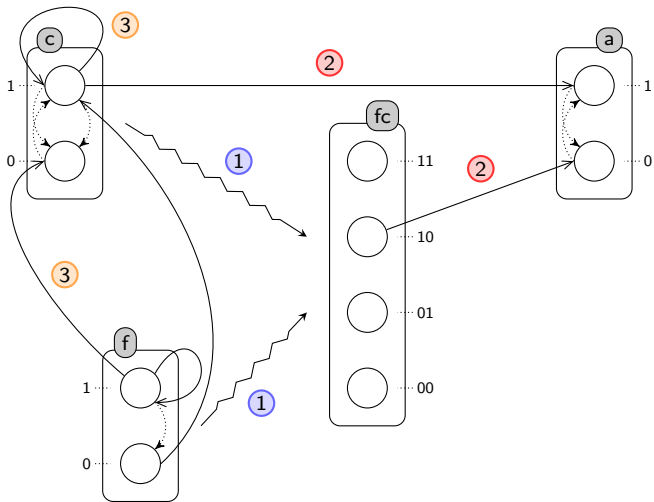
- Simulation with stochastic parameters:



- Other possible analysis: stochastic model checkers (PRISM)
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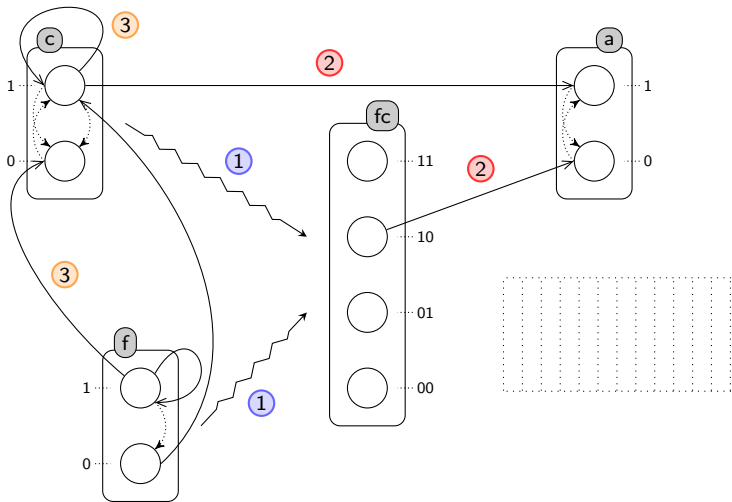
Use of the Classes of Priorities

[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]



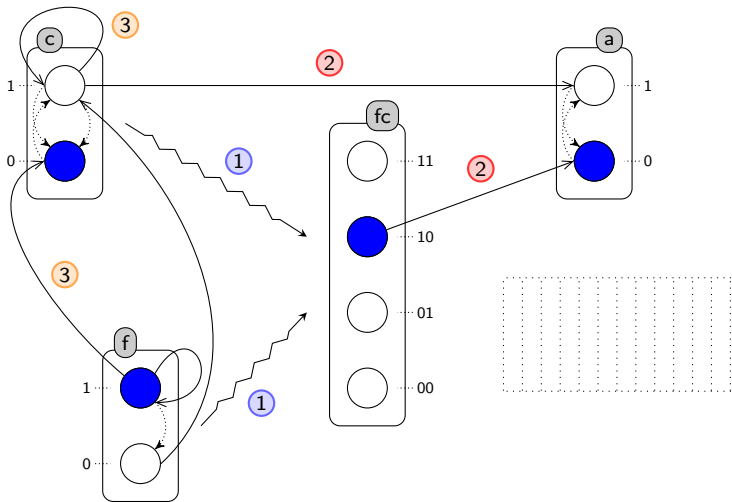
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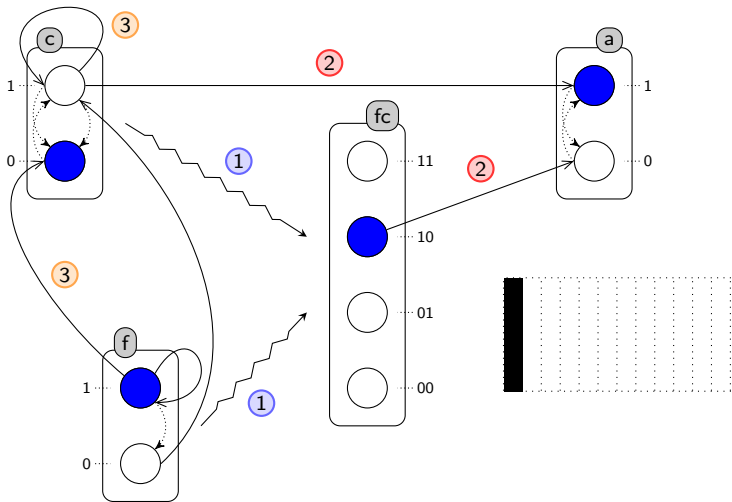
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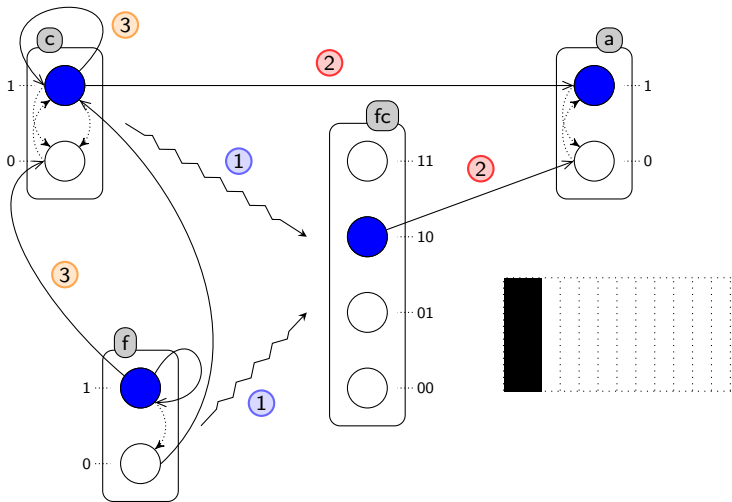
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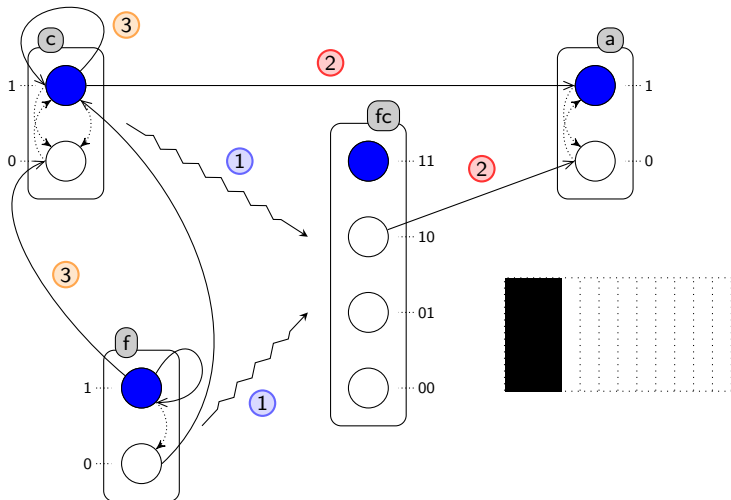
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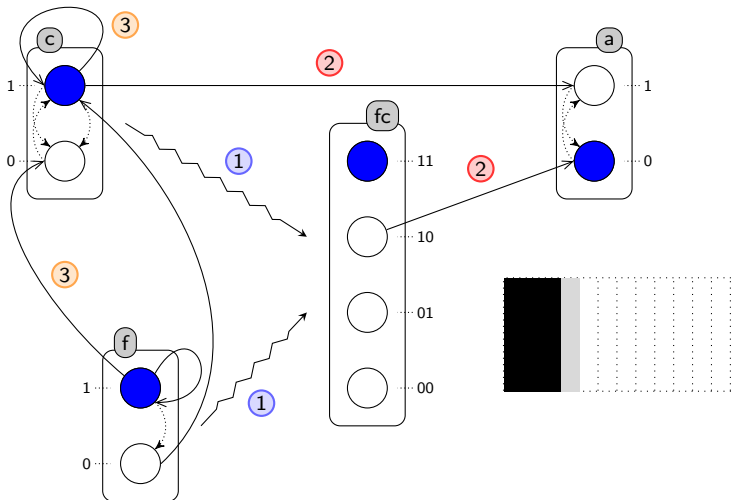
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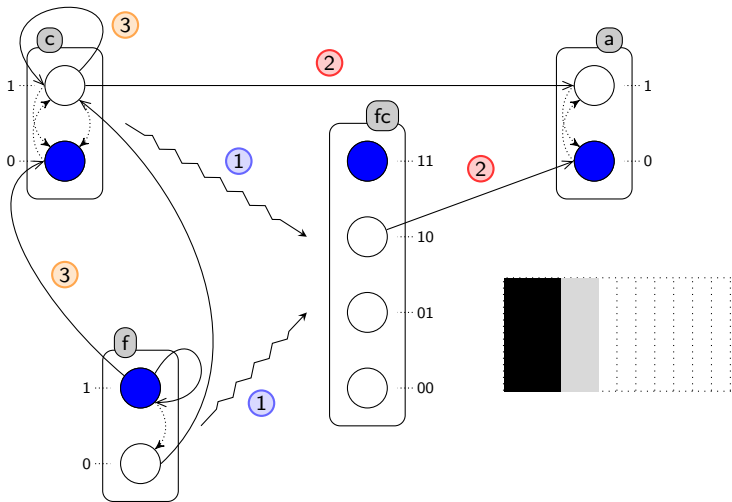
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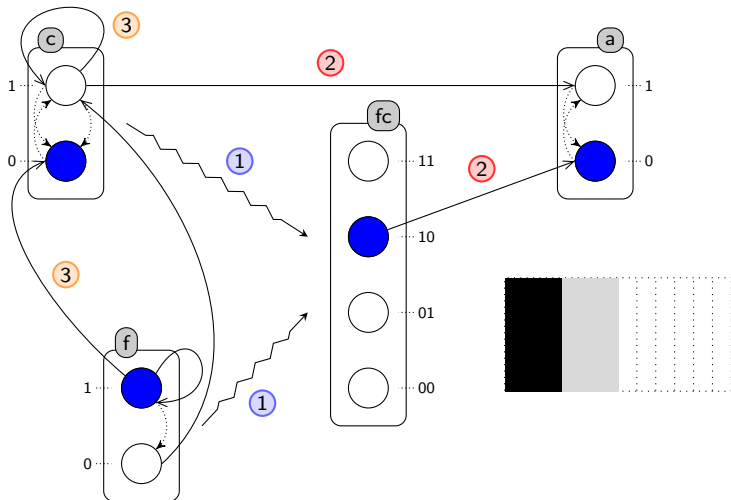
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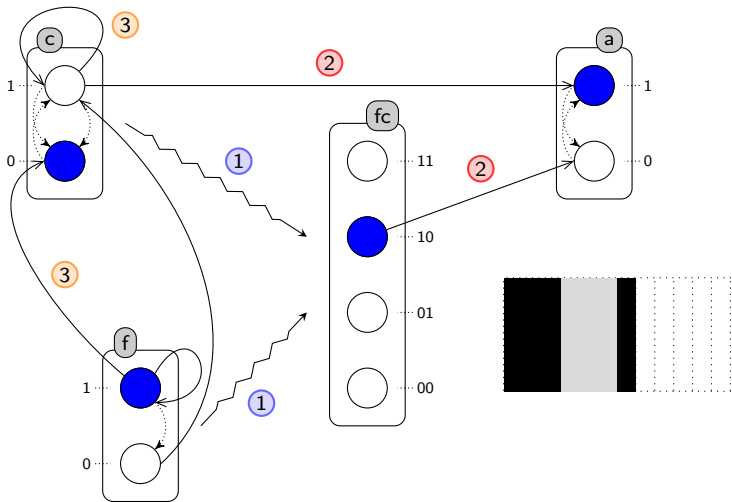
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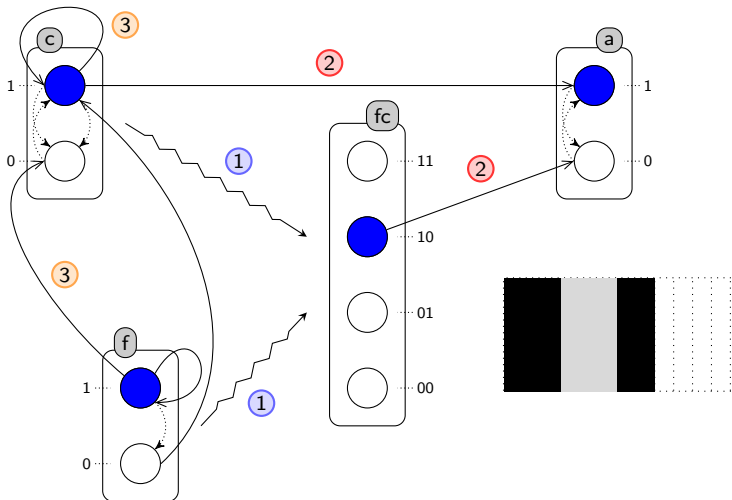
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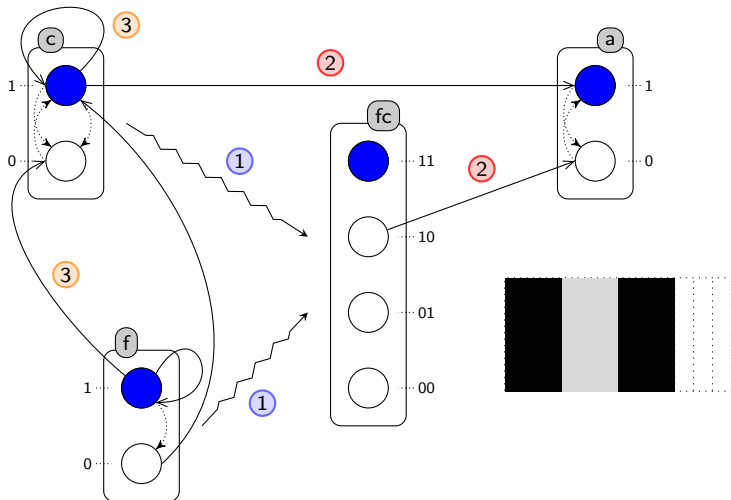
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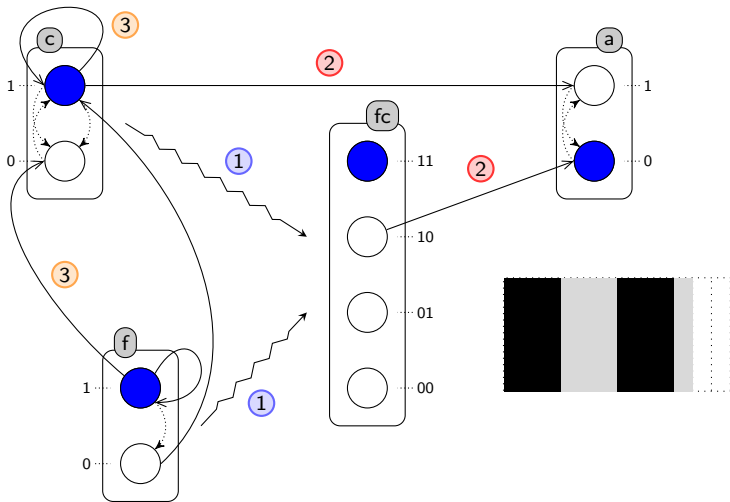
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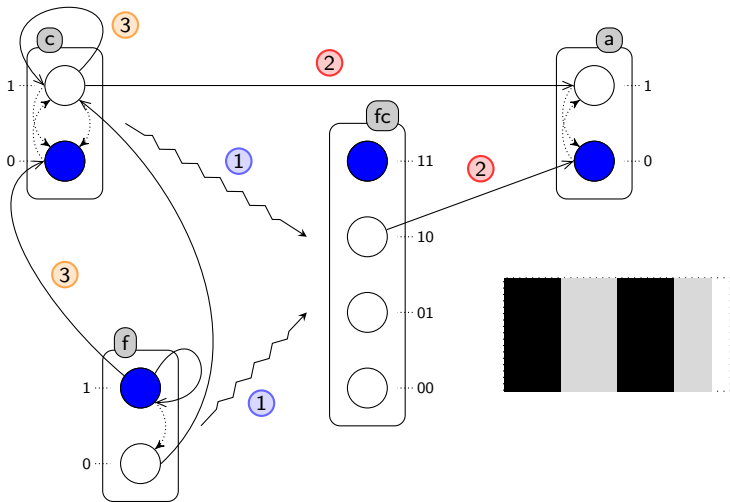
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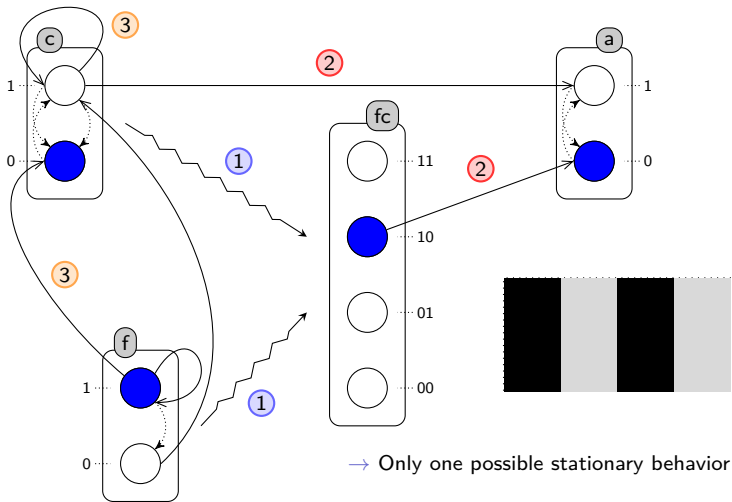
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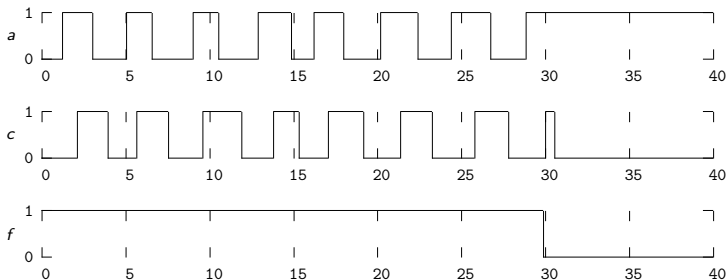
[Folschette et al. in *Workshop on Interactions between Computer Science and Biology*, 2013]



Abstraction of Temporal Parameters

[Paulevé (PhD thesis), 2011]

- Simulation with stochastic parameters:

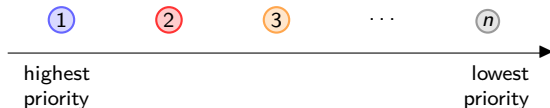


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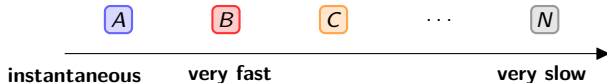
Addition of classes of priorities

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]

- Each action is associated to a discrete priority
- An action is playable only if no other action with higher priority is playable

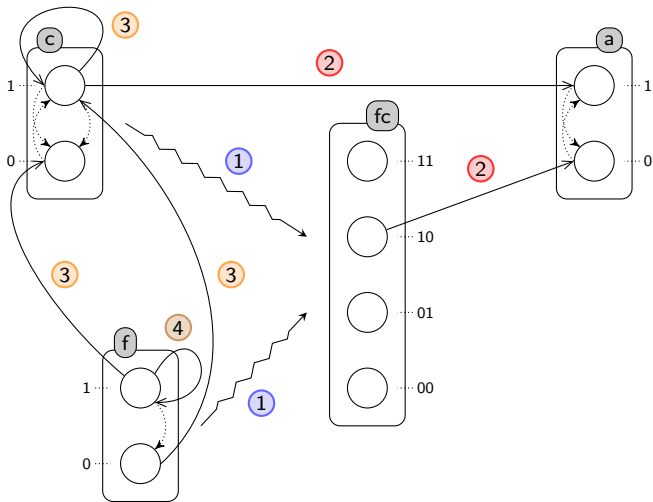


- Allow to model classes of actions with similar speeds or temporal parameters



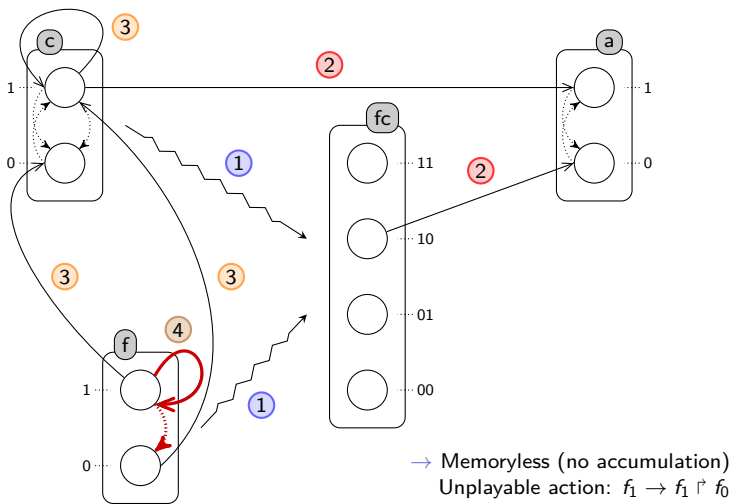
Limitation of the Classes of Priorities

[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



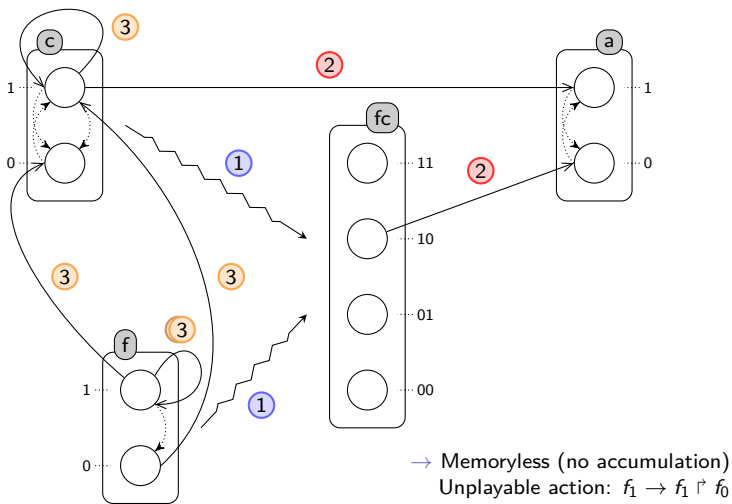
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[Folschette *et al.* in *Workshop on Interactions between Computer Science and Biology*, 2013]



Limitation of the Classes of Priorities

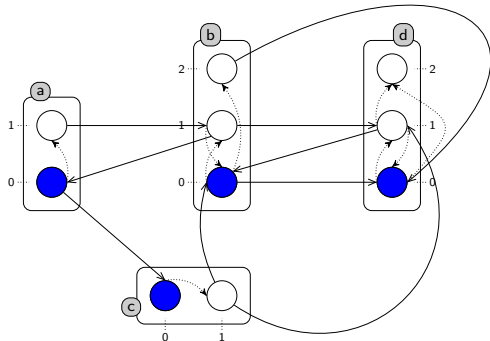
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Static analysis: successive reachability

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

Successive reachability of processes:



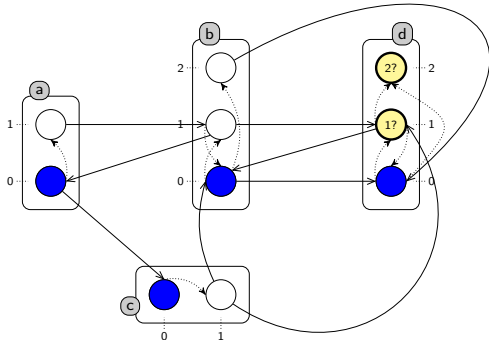
• Initial state

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

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

Successive reachability of processes:



- Initial state
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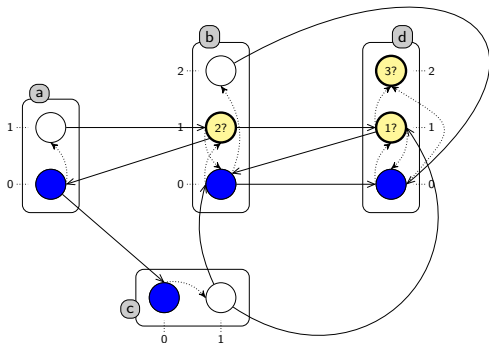
$\langle a_1, b_0, c_0, d_0 \rangle$

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

Static analysis: successive reachability

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

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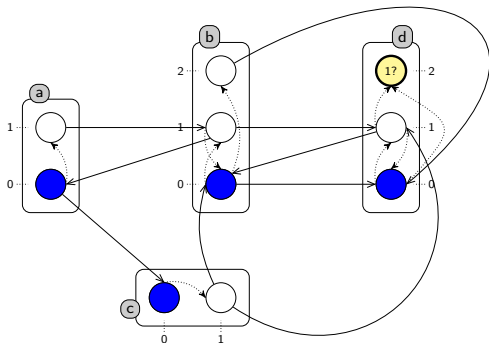
$$[\uparrow d_1 :: \uparrow d_2]$$

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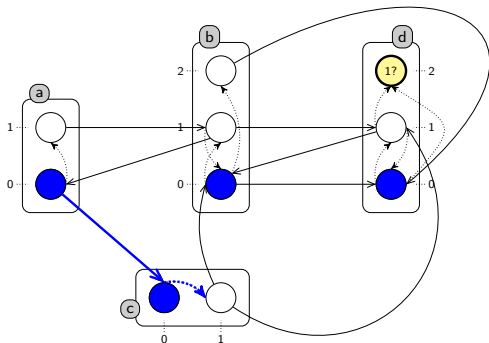
$$[\uparrow d_1 :: \uparrow b_1 :: \uparrow d_2]$$

$$[\uparrow d_2]$$

Static analysis: successive reachability

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$$[\uparrow d_2]$$

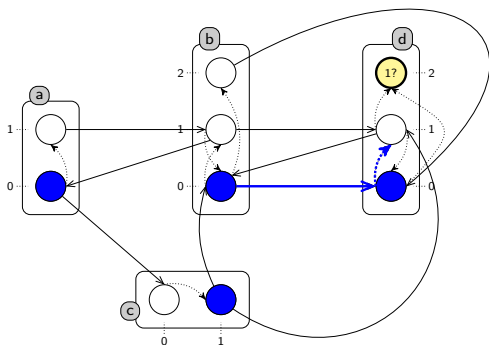
→ Concretization of the objective = scenario

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

Static analysis: successive reachability

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

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- Objectives

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

$$[\uparrow d_1 :: \uparrow b_1 :: \uparrow d_2]$$

$$[\uparrow d_2]$$

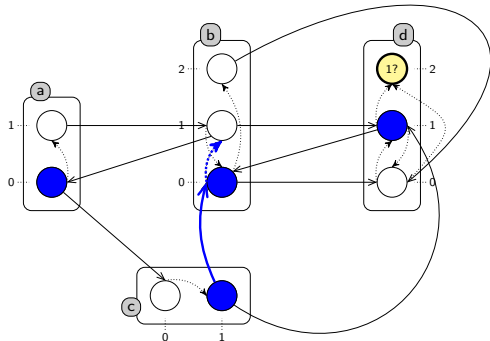
→ Concretization of the objective = scenario

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

Static analysis: successive reachability

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

Successive reachability of processes:



- Initial state

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- Objectives

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

$[\uparrow d_1 :: \uparrow b_1 :: \uparrow d_2]$

$[\uparrow d_2]$

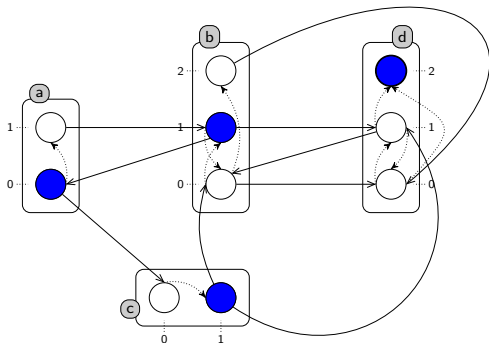
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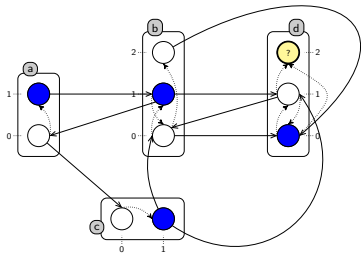
$$[\uparrow d_1 :: \uparrow b_1 :: \uparrow d_2]$$

$$[\uparrow d_2]$$

→ Concretization of the objective = scenario

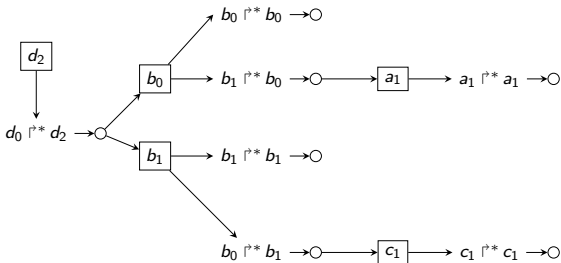
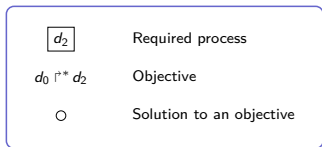
$$a_0 \rightarrow c_0 \uparrow c_1 :: b_0 \rightarrow d_0 \uparrow d_1 :: c_1 \rightarrow b_0 \uparrow b_1 :: b_1 \rightarrow d_1 \uparrow d_2$$

Under-approximation

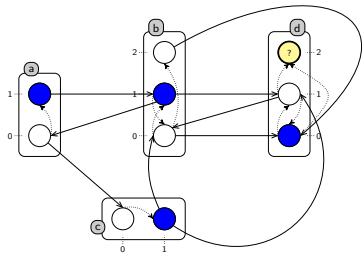


Sufficient condition:

- no cycle
- each objective has a solution



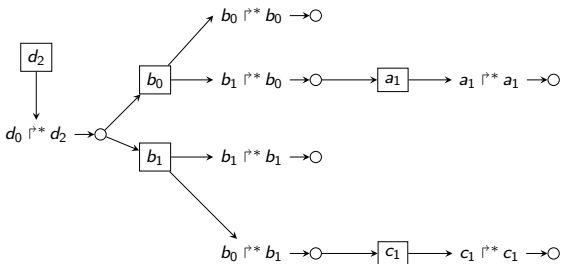
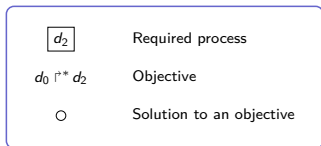
Under-approximation



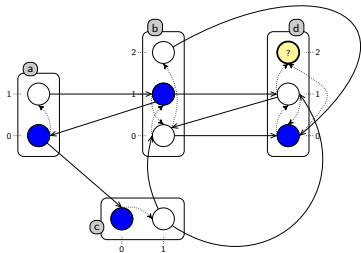
Sufficient condition:

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R is true

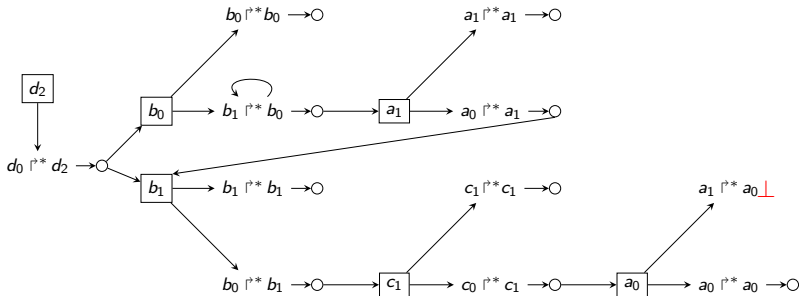


Under-approximation

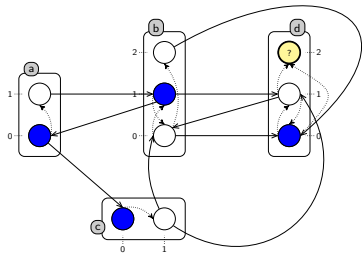


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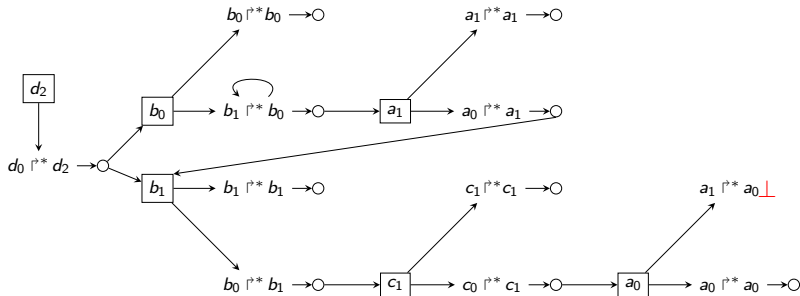
Under-approximation



Sufficient condition:

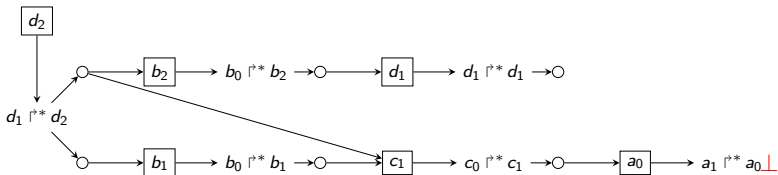
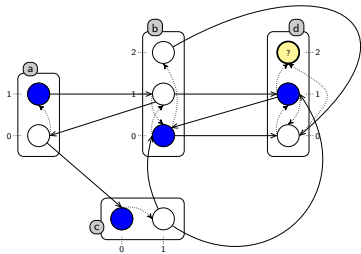
- no cycle
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Inconclusive

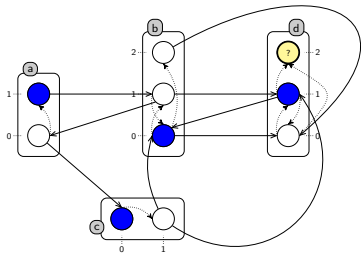


Over-approximation

Necessary condition:



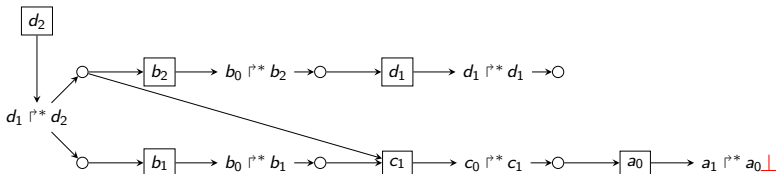
Over-approximation



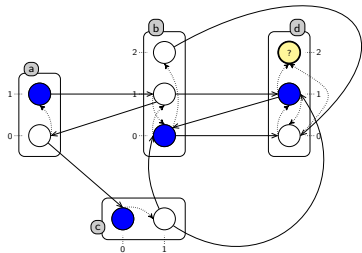
Necessary condition:

There exists a traversal with no cycle

- objective → follow one solution
- solution → follow all processes
- process → follow all objectives



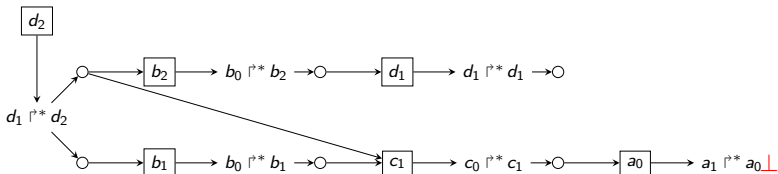
Over-approximation



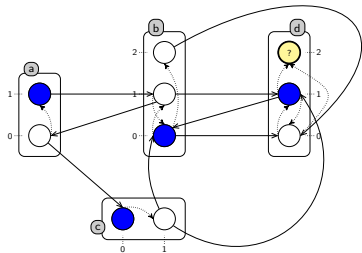
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Over-approximation

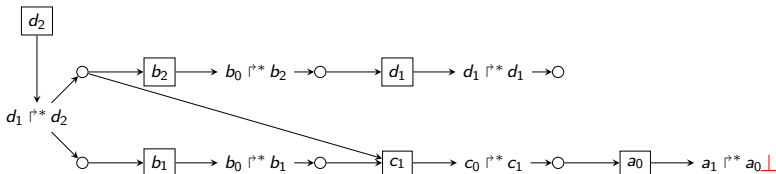


Necessary condition:

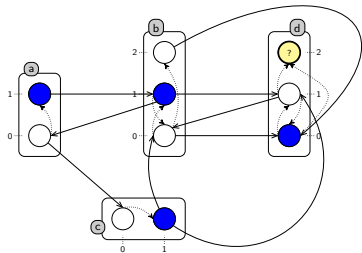
There exists a traversal with no cycle

- objective → follow one solution
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R is false



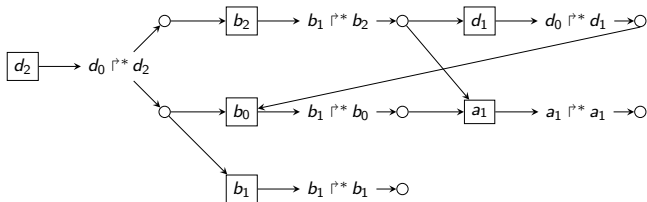
Over-approximation



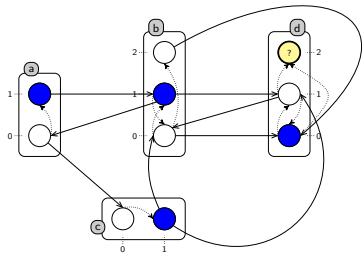
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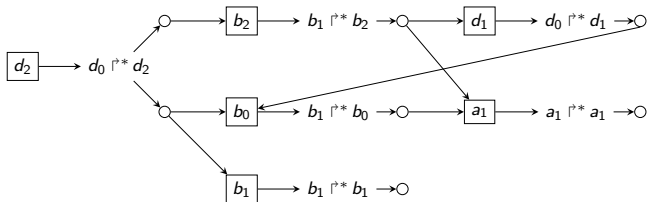


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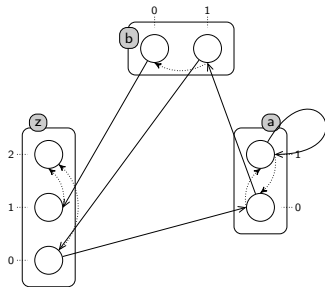


Static Analysis: Fixed Points

[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

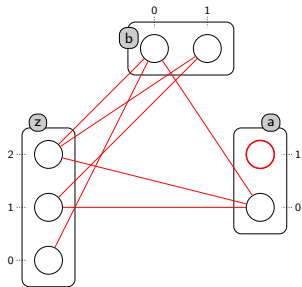
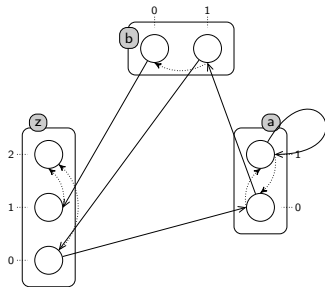


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- Hitless Graph

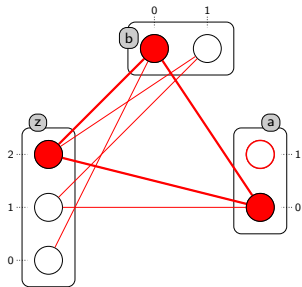
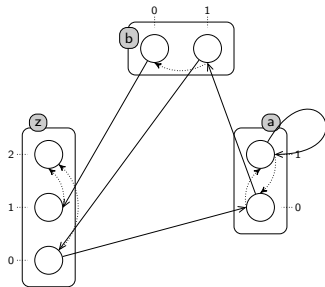


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- Hitless Graph → **n-cliques** = fixed points

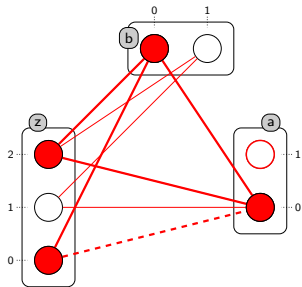
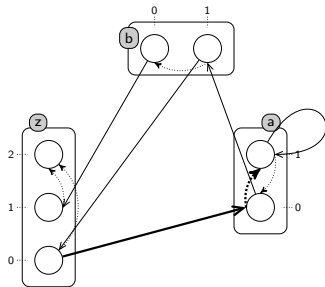


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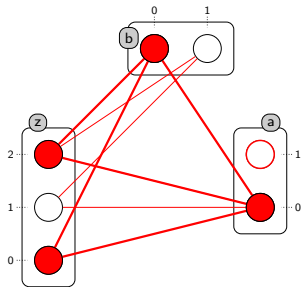
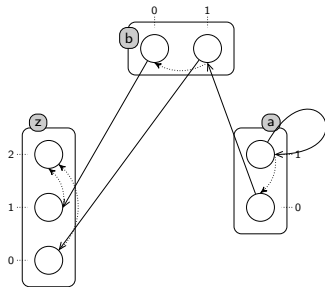


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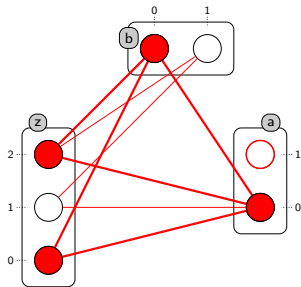
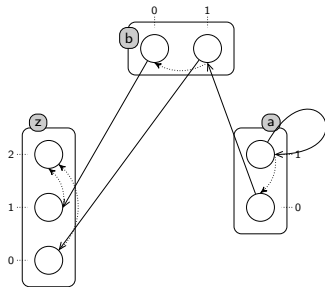


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Exponential complexity w.r.t. the number of sorts