

6^e Séminaire DKM

Static Analysis with Abstract Interpretation for the Verification of Dynamical Properties of Biological Regulatory Networks

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Dymec team IRSET Univ Rennes 1, Inserm

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Bio-informatics?

[De Jong, *Journal of Computational Biology*, 2002]

Bridge between **Biology** and **Computer Science**

Bio-informatics?

[De Jong, *Journal of Computational Biology*, 2002]

Bridge between **Biology** and **Computer Science**

Many fields:


- Sequencing
- Networks
- Simulation
- Experiments
- Databases
- ...

Bio-informatics?

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Bridge between **Biology** and **Computer Science**

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- Sequencing
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 - Differential equations (quantitative)
 - Stochastic/probabilistic (quantitative)
 - Discrete graphs (qualitative)
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 - ...
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Bio-informatics?

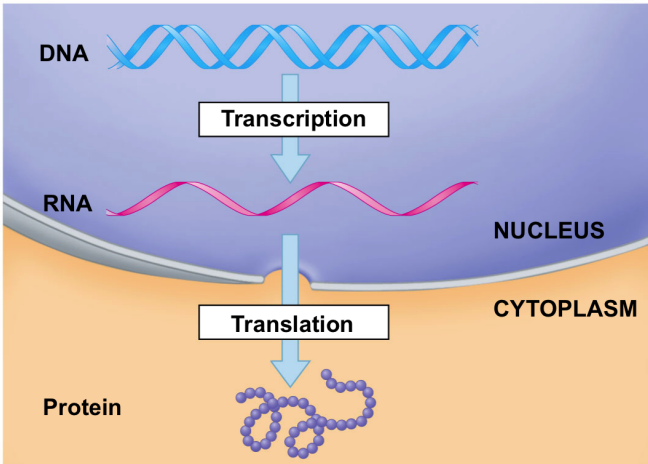
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Bridge between **Biology** and **Computer Science**

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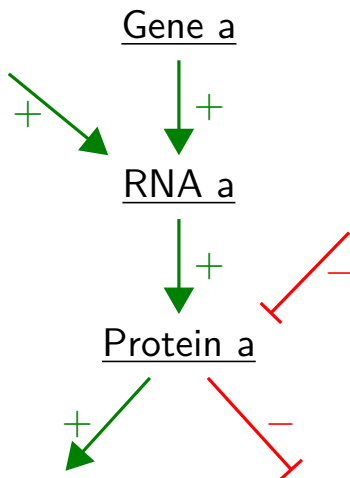
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Abstraction

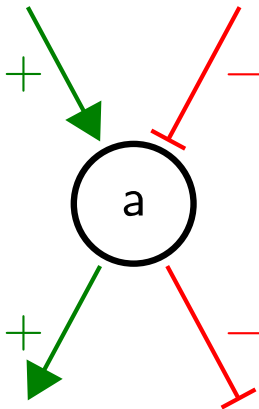


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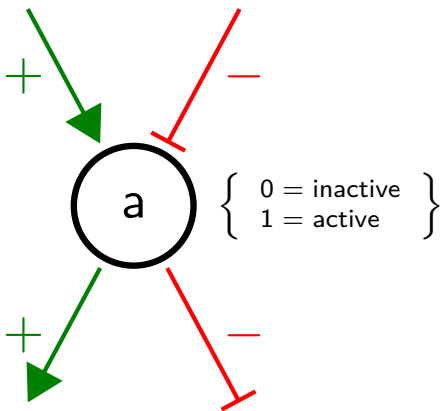
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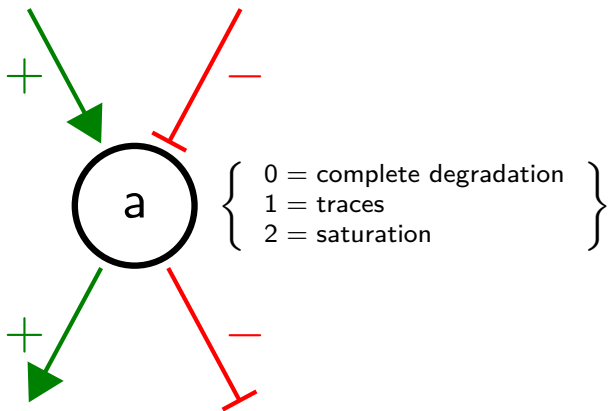
Abstraction



Abstraction

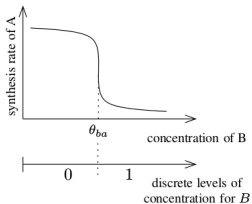


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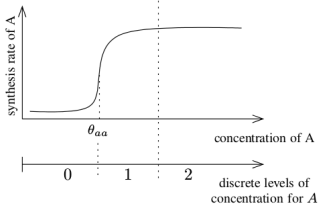
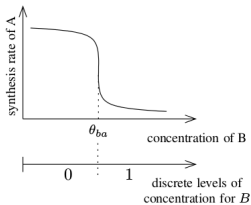
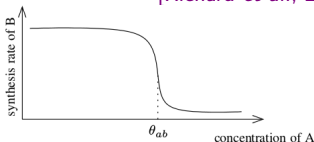
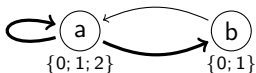
Discretization and Asynchronism

[Richard *et al.*, 2008]



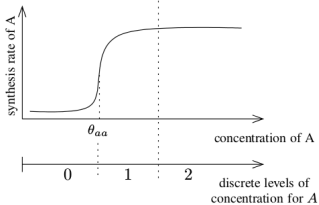
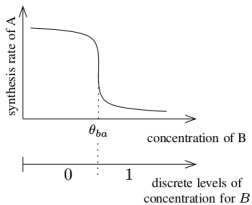
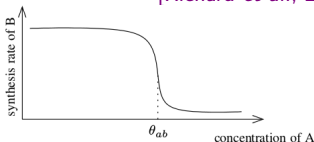
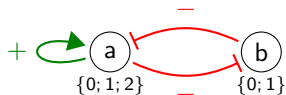
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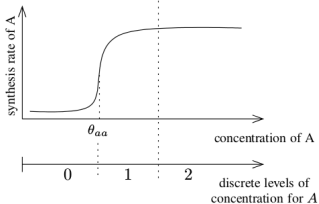
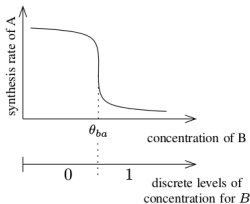
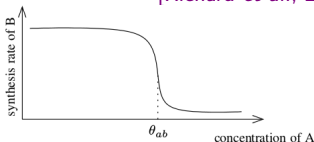
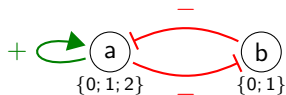
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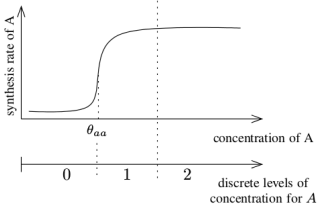
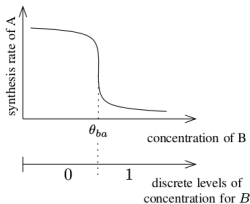
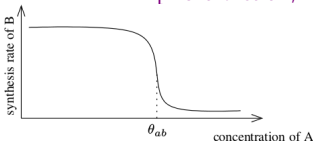
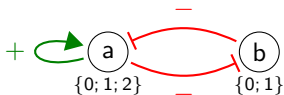
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- Unknown real values of concentrations or continuous activity levels
 → Abstracted as **discrete levels** and thresholds

Discretization and Asynchronism

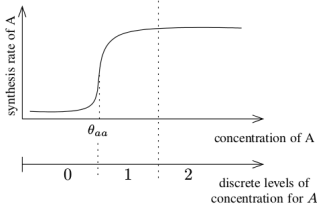
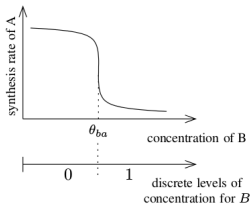
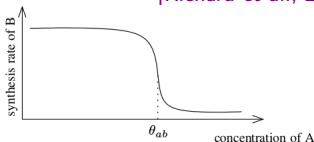
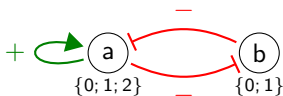
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- Continuous variations of the real values
 → **Unitary** dynamics

Discretization and Asynchronism

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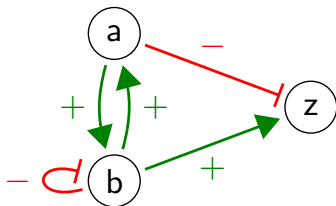


- Unknown real values of concentrations or continuous activity levels
→ Abstracted as **discrete levels** and thresholds
- Continuous variations of the real values
→ **Unitary** dynamics
- Simultaneous crossings of two thresholds never occurs
→ **Asynchronous** dynamics

Modeling of René Thomas

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

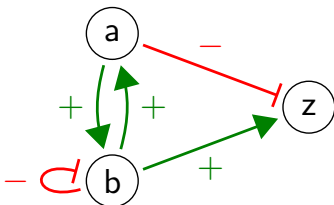
Models of interacting components (genes, proteins, ...)



Modeling of René Thomas

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Models of interacting components (genes, proteins, ...)



Questions:

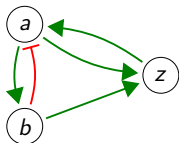
- How does **(z)** **behave**?
- Is it **possible** to make **(a)** inactive?
- If I **knock-out** **(b)**, what changes?

State-graph

The state-graph depicts explicitly the whole dynamics

abz

000	010	001	011
100	110	101	111
200	210	201	211



State-graph

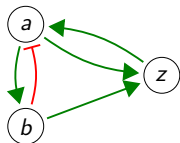
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000 010 001 011

100 110 101 111

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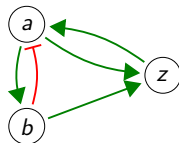
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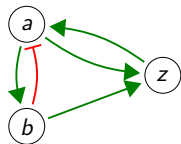
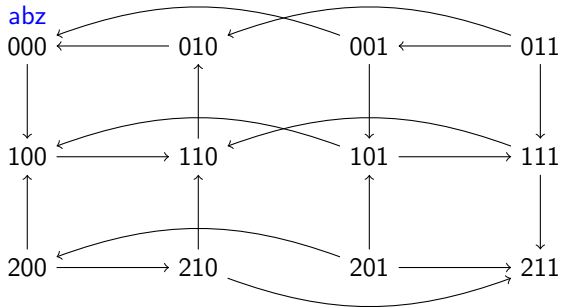
201

211



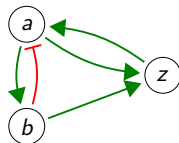
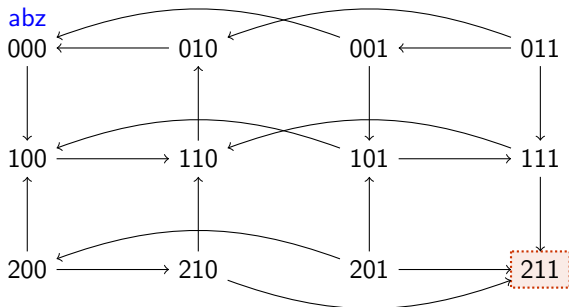
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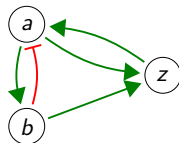
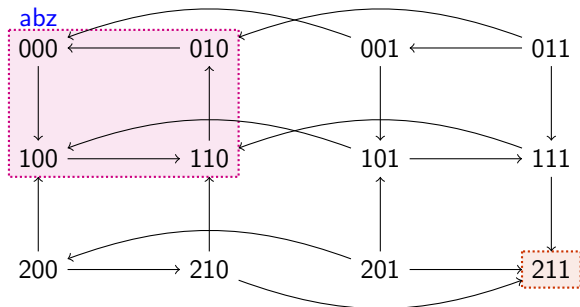
The state-graph depicts explicitly the whole dynamics



- **Stable state** = state with no successors

State-graph

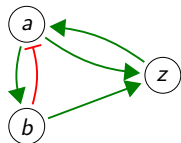
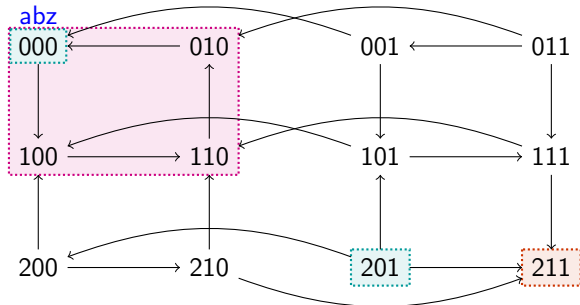
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- **Stable state** = state with no successors
- **Complex attractor** = minimal loop or composition of loops from which the dynamics cannot escape

State-graph

The state-graph depicts explicitly the whole dynamics





- **Stable state** = state with no successors
- **Complex attractor** = minimal loop or composition of loops from which the dynamics cannot escape
- **Reachability** = from **201**, can I reach **000**?



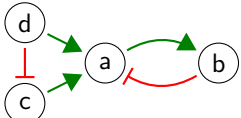
Combinatorial explosion





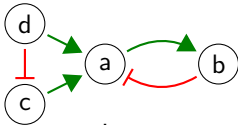
Combinatorial explosion

Model	Possible states
	4
	8



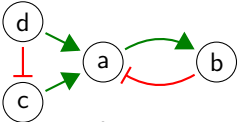
Combinatorial explosion

Model	Possible states
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	8
	16



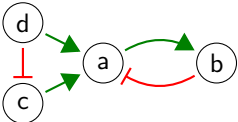
Combinatorial explosion

Model	Possible states
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	8
	16
⋮	⋮
(10)	1024

Combinatorial explosion

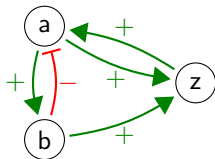
Model	Possible states
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	8
	16
⋮	⋮
(10)	1024
(20)	1048576

Combinatorial explosion

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	16
⋮	⋮
(10)	1024
(20)	1048576
(100)	12676506000000000000000000000000

Conjectures of René Thomas

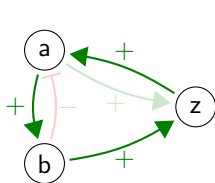
[Thomas, *Num. Methods in the Study of Crit. Phenomena*, 1981]



Conjectures of René Thomas

[Thomas, *Num. Methods in the Study of Crit. Phenomena*, 1981]

- Multiple **stable states** \Rightarrow positive cycle



110

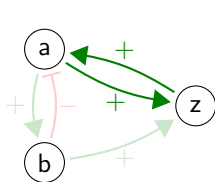
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Proofs: [Remy *et al.*, *Advances in Applied Mathematics*, 2008]
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Conjectures of René Thomas

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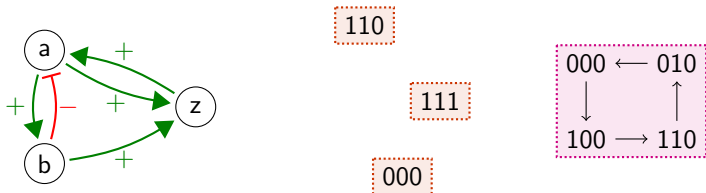


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No positive cycle \Rightarrow **The stable state (if any) is unique**
- Sustained oscillations (**complex attractor**) \Rightarrow negative cycle
No negative cycle \Rightarrow **No complex attractor (only stable states)**

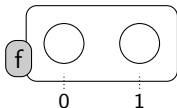
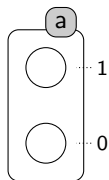
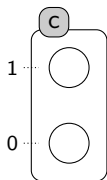


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Asynchronous Automata Networks (AAN)

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

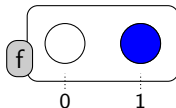
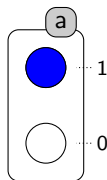
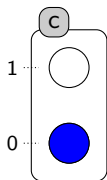
[Folschette et al., *Theoretical Computer Science*, 2015]



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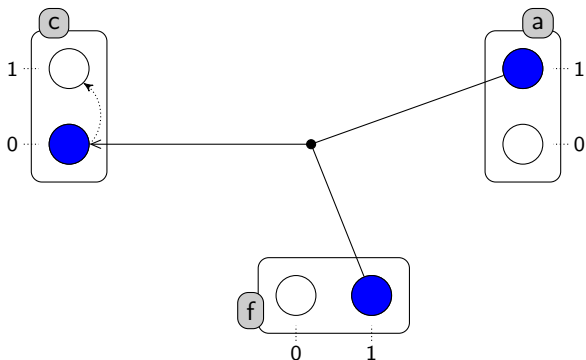
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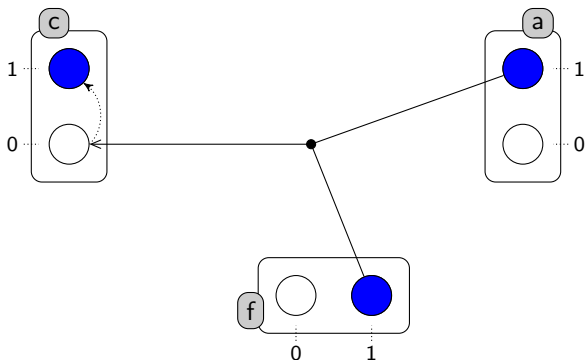
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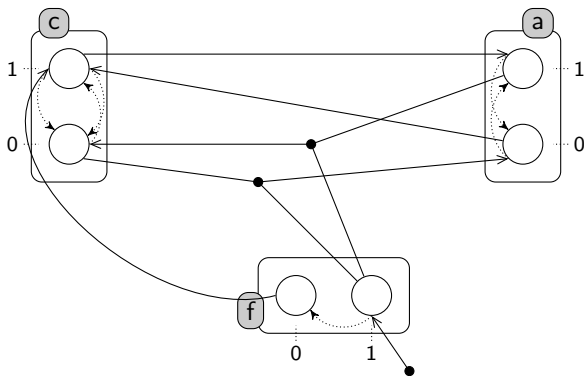


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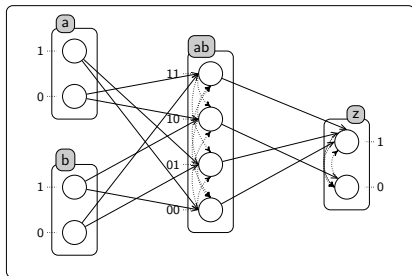
[Folschette et al., *Theoretical Computer Science*, 2015]

Model from [François et al., *Molecular Systems Biology*, 2007]



Translation of AAN models

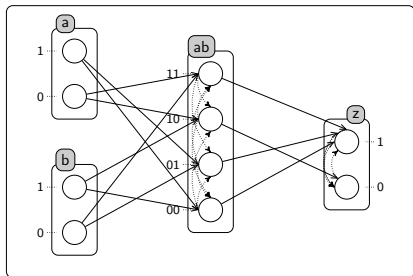
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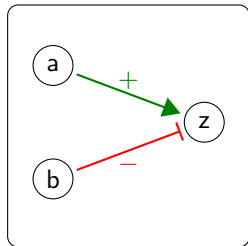
Process Hitting
Efficient but recent

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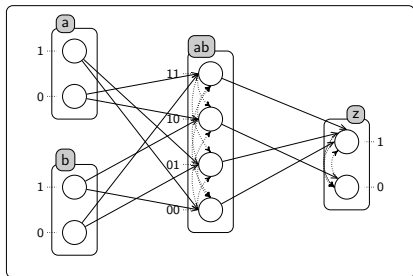
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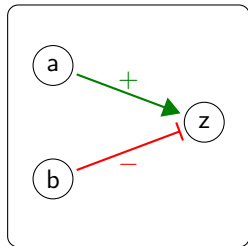
Thomas modeling
Widespread & readable

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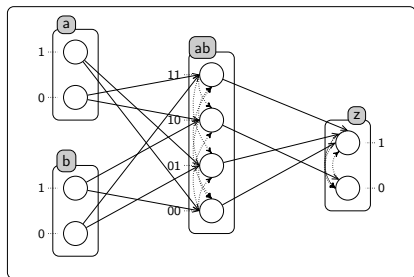
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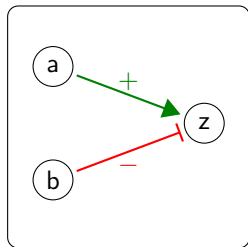
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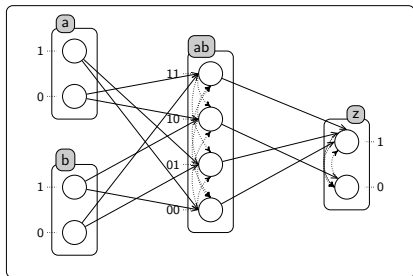
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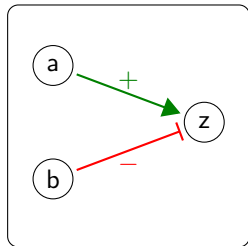
Thomas modeling
Widespread & readable

Towards AANs

[Folschette *et al.*, *CS2Bio*, 2013]



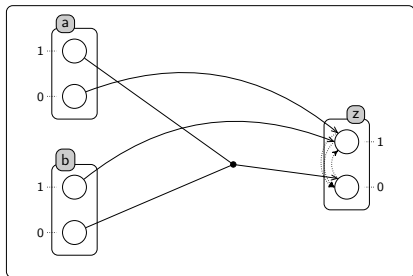
Process Hitting
Loose behavior



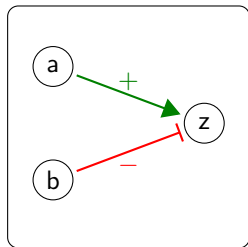
Thomas modeling
Expected behavior

Towards AANs

[Folschette *et al.*, *CS2Bio*, 2013]



AANs
Accurate behavior

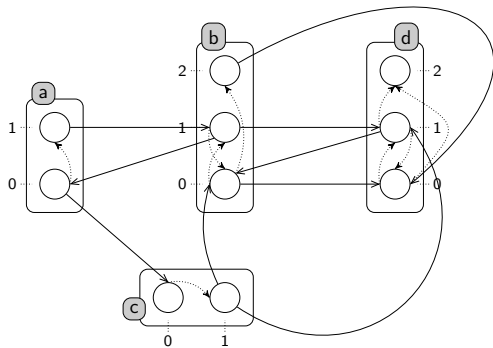


Thomas modeling
Expected behavior

Static analysis: successive reachability

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

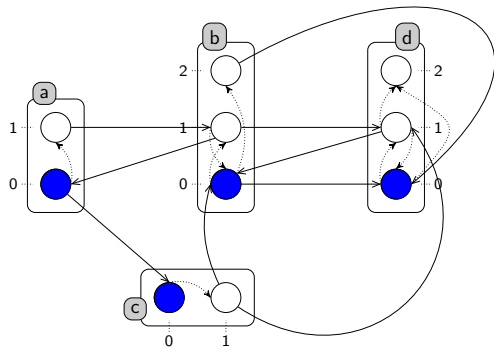
[Folschette et al., *Theoretical Computer Science*, 2015]



Static analysis: successive reachability

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

[Folschette et al., *Theoretical Computer Science*, 2015]



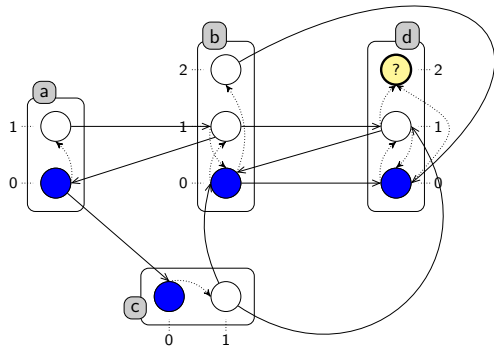
• Initial state

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

Static analysis: successive reachability

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

[Folschette et al., *Theoretical Computer Science*, 2015]



- Initial state

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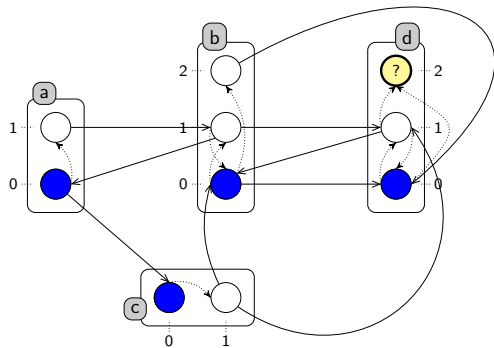
- Objective(s)

$[\uparrow d_2]$

Static analysis: successive reachability

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

[Folschette et al., *Theoretical Computer Science*, 2015]



- Initial state

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

- Objective(s)

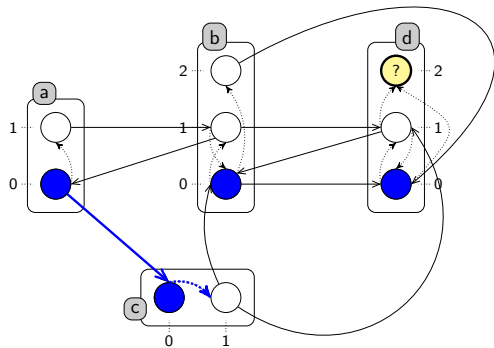
$[\uparrow d_2]$

→ Sequence of actions?

Static analysis: successive reachability

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

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- Initial state

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- Objective(s)

$[\uparrow d_2]$

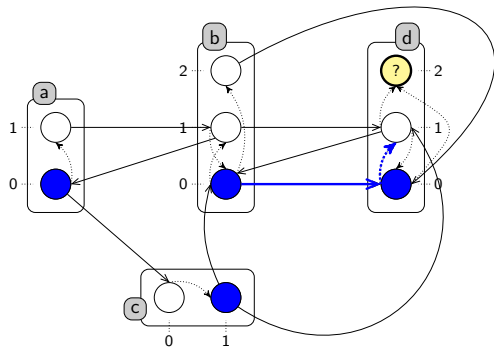
→ Sequence of actions?

$a_0 \rightarrow c_0 \uparrow c_1$

Static analysis: successive reachability

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

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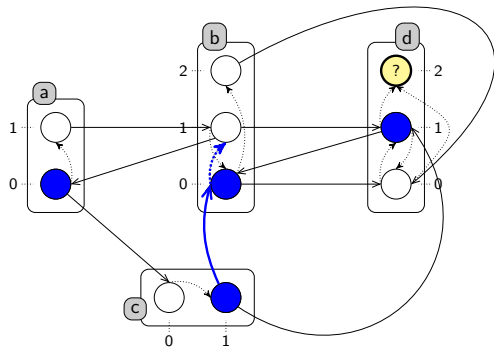
→ Sequence of actions?

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

Static analysis: successive reachability

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

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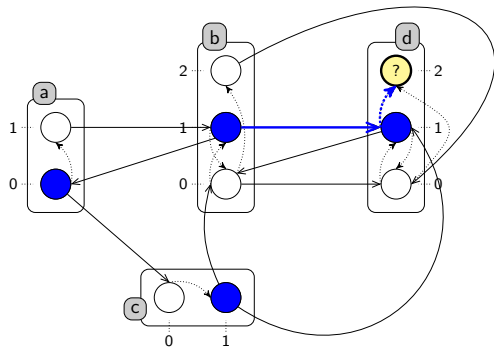
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$a_0 \rightarrow c_0 \uparrow c_1 :: b_0 \rightarrow d_0 \uparrow d_1 :: c_1 \rightarrow b_0 \uparrow b_1$

Static analysis: successive reachability

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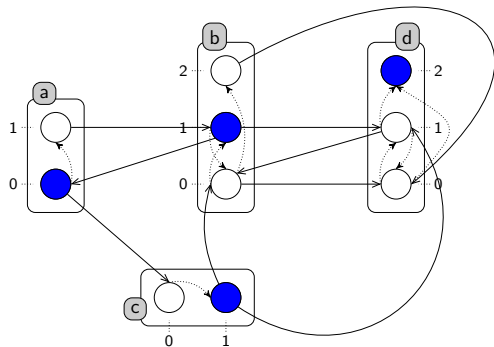
→ Sequence of actions?

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

Static analysis: successive reachability

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- Initial state

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→ Sequence of actions?

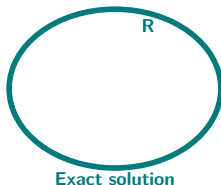
$a_0 \rightarrow c_0 \uparrow c_1 :: b_0 \rightarrow d_0 \uparrow d_1 :: c_1 \rightarrow b_0 \uparrow b_1 :: b_1 \rightarrow d_1 \uparrow d_2$

Approximations of the Dynamics

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

[Folschette *et al.*, *Theoretical Computer Science*, 2015]

- Directly checking **R** is hard (**exponential**)
- Rather check **approximations P** and **Q** so that: $P \Rightarrow R \Rightarrow Q$
so that computing **P** and **Q** is faster (roughly **polynomial**)

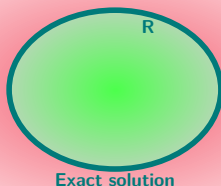


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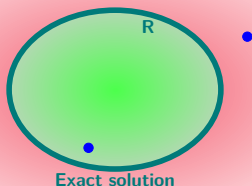


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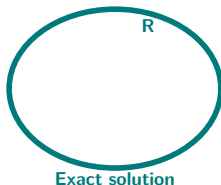


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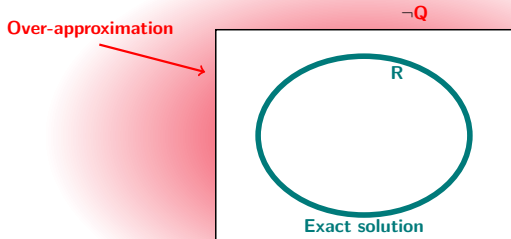


Approximations of the Dynamics

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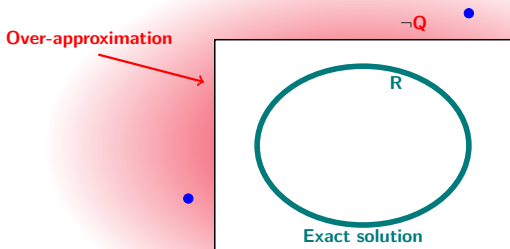


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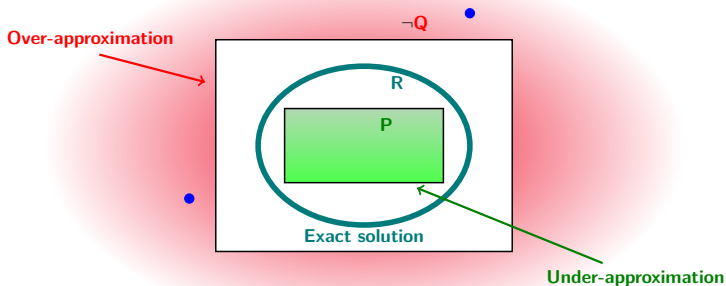


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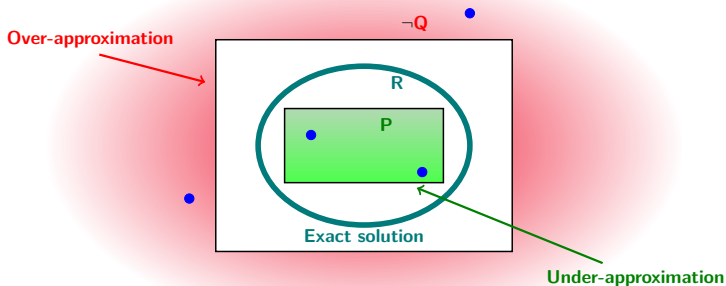


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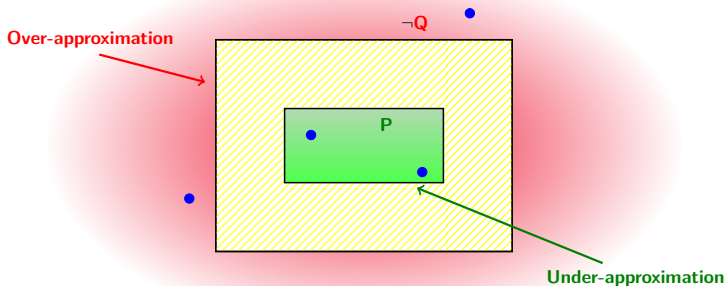


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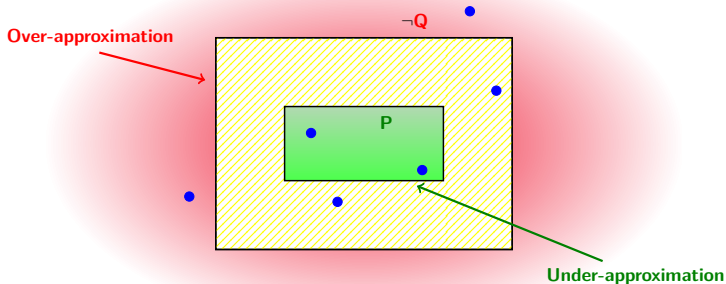


Approximations of the Dynamics

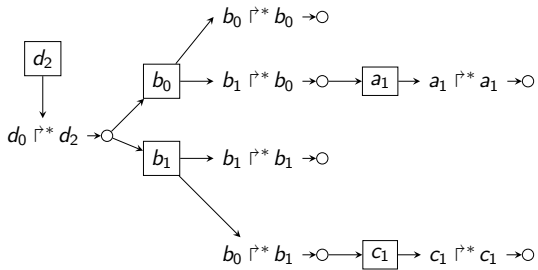
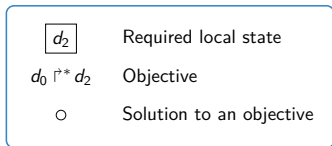
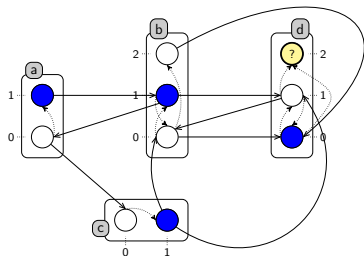
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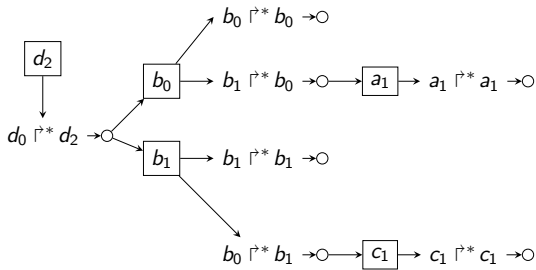
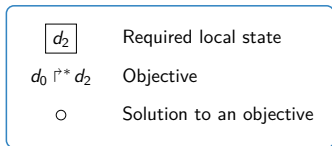
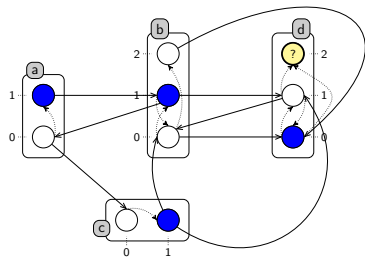
Under-approximation



Under-approximation

Sufficient condition **P**:

- no cycle
- each objective has a solution

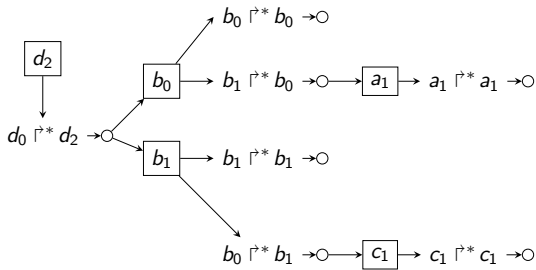
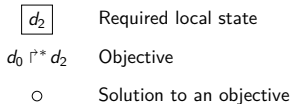
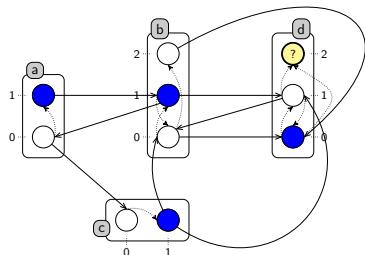


Under-approximation

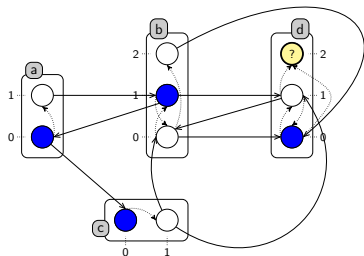
Sufficient condition **P**:

- no cycle
- each objective has a solution

P is true \Rightarrow R is true

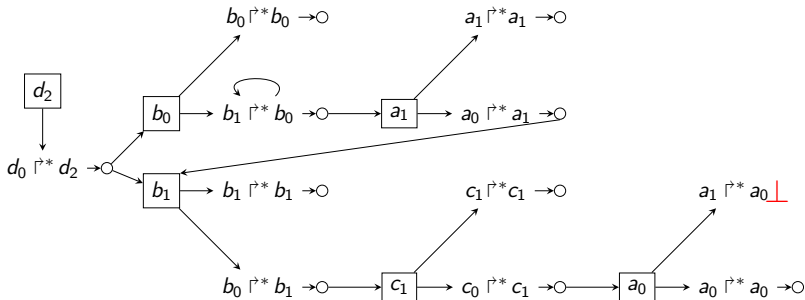


Under-approximation

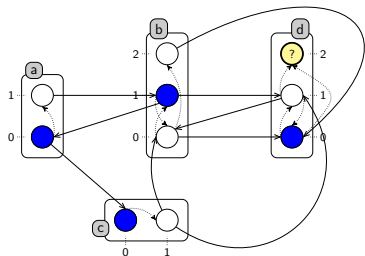


Sufficient condition P:

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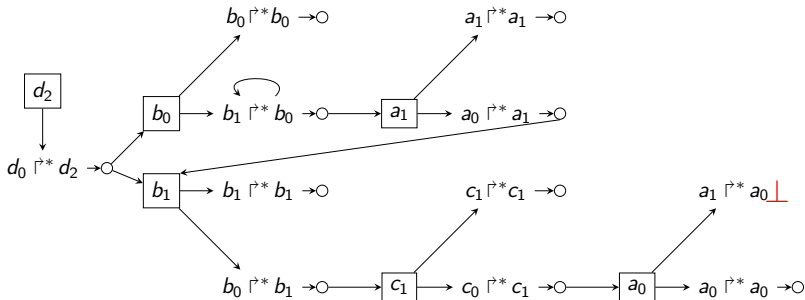
Under-approximation



Sufficient condition **P**:

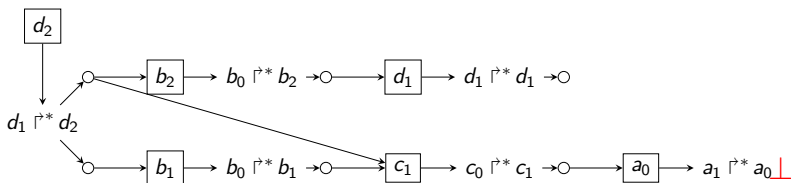
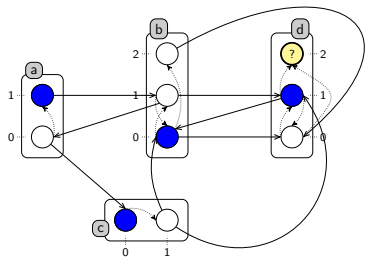
- no cycle
- each objective has a solution

P is false \Rightarrow **Inconclusive**



Over-approximation

Necessary condition **Q**:

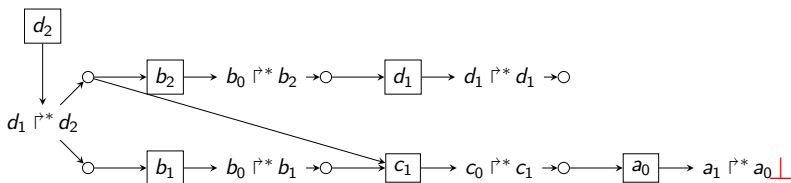
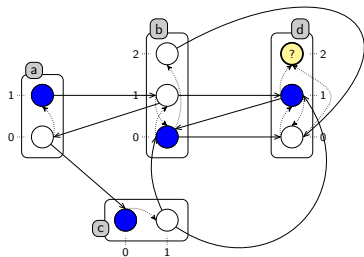


Over-approximation

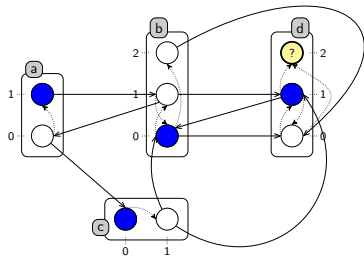
Necessary condition **Q**:

There exists a traversal with no cycle

- objective \rightarrow follow **one** solution
- solution \rightarrow follow **all** local states
- local state \rightarrow follow **all** objectives



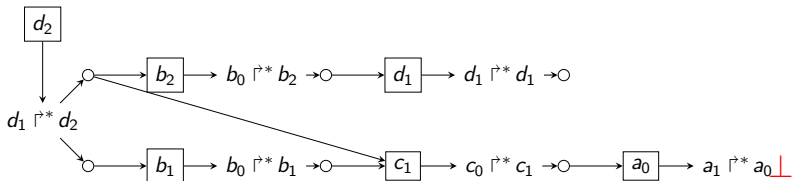
Over-approximation



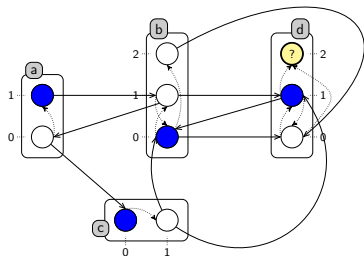
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Over-approximation

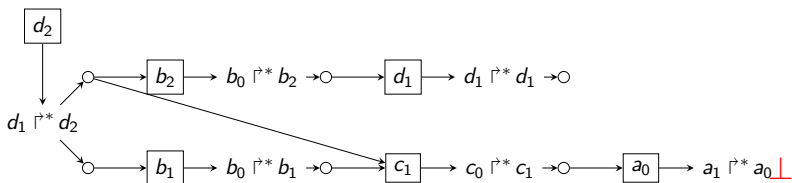


Necessary condition Q:

There exists a traversal with no cycle

- objective \rightarrow follow **one** solution
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- local state \rightarrow follow **all** objectives

Q is false \Rightarrow R is false

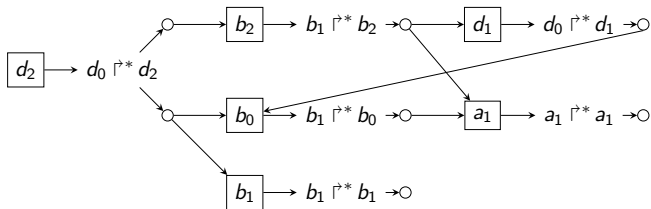
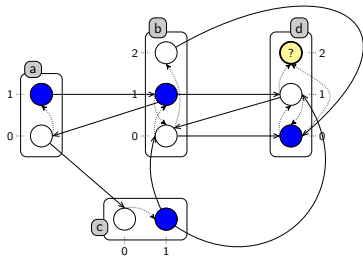


Over-approximation

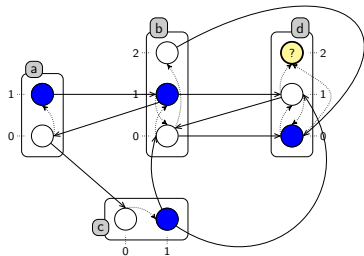
Necessary condition **Q**:

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Over-approximation

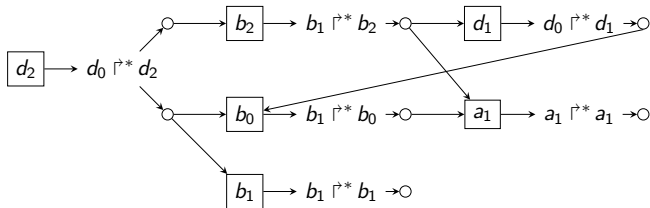


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Q is true \Rightarrow Inconclusive



Results

[Paulevé, *Computational Methods in Systems Biology*, 2017][Folschette *et al.*, *Theoretical Computer Science*, 2015]

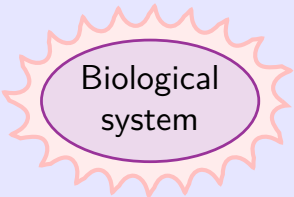
Model	nodes	NuSMV	ITS-reach	Pint
TCell-d	101	2s	0.5s	0.02s
		KO	16min	4.5s
RBE2F	370	KO	KO	0.2s
MAPK	309	KO	KO	48s

- **KO** = Out of memory
- 100% conclusiveness with Pint (no **Inconclusive**)

NuSMV: [Cimatti *et al.*, *CAV*, 2002. <http://nusmv.fbk.eu/>]ITS-reach: [Thierry-Mieg, *TACAS*, 2015. <http://ddd.lip6.fr/itstools.php>]Pint: [Paulevé, *Computational Methods in Systems Biology*, 2017.<http://loicpauleve.name/pint/>]TCell-d: [Abou-Jaoudé *et al.*, *Frontiers in Bioengineering and Biotechnology*, 2015]RBE2F: [Rougnay, *et al.*, *BMC Systems Biology*, 2016]MAPK: [Schoeberl *et al.*, *Nature biotechnology*, 2002]

Experiments *in silico*

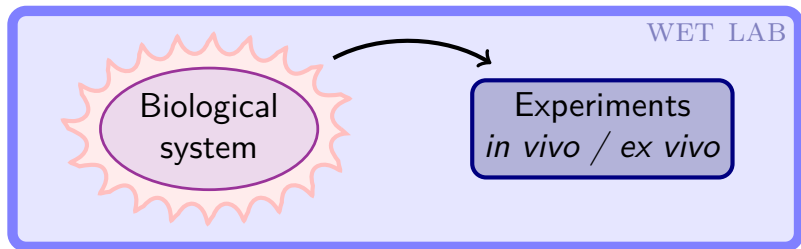
WET LAB



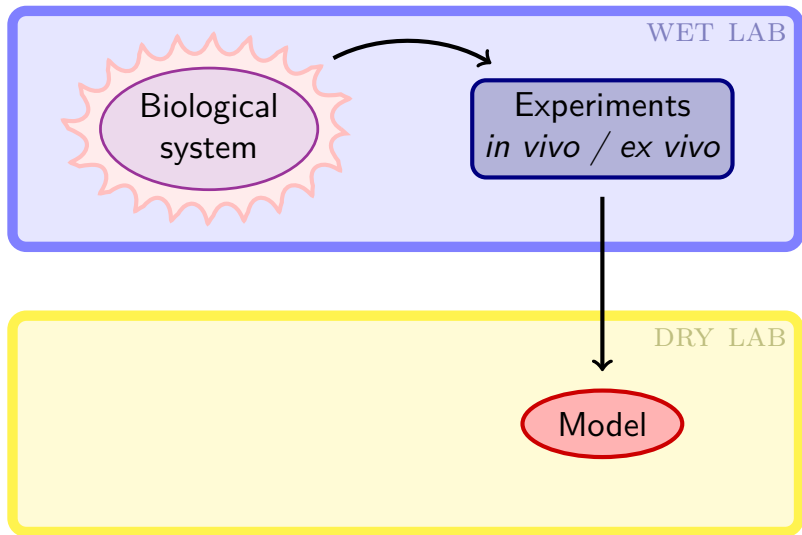
Biological
system

DRY LAB

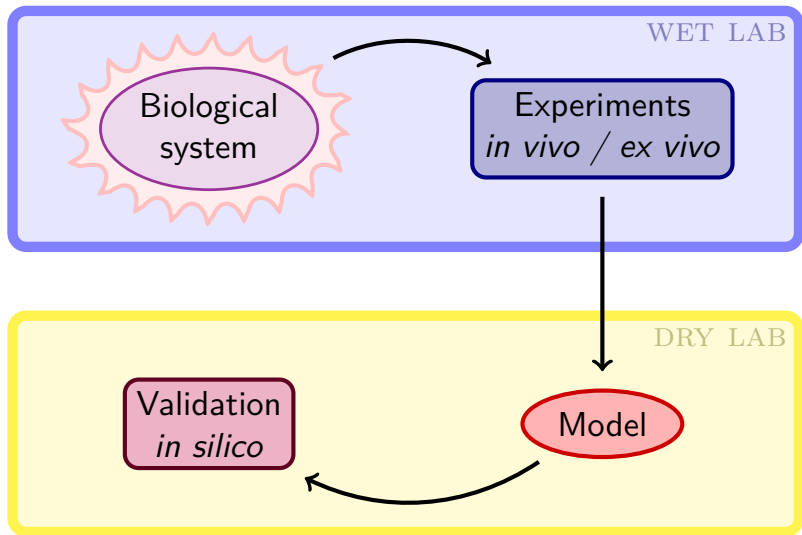
Experiments *in silico*



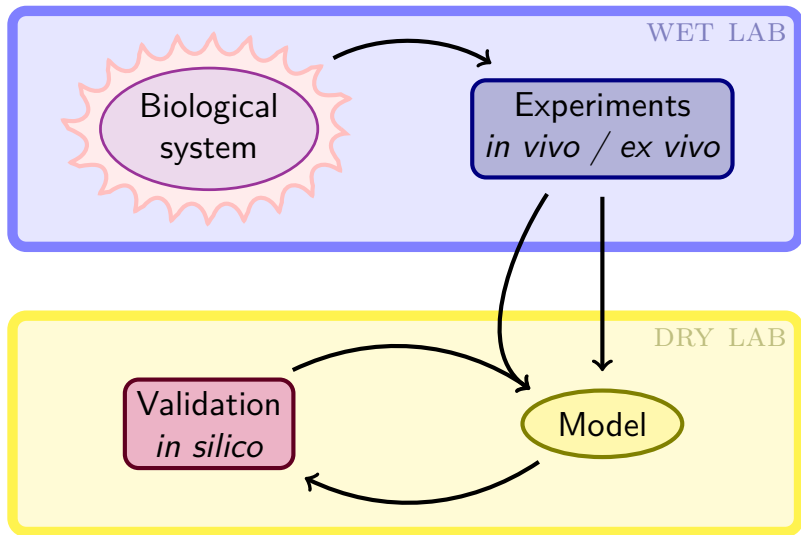
Experiments *in silico*



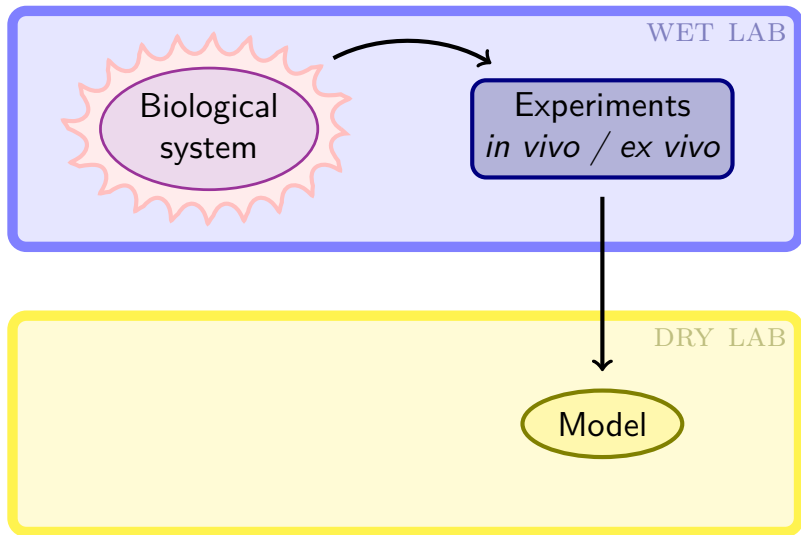
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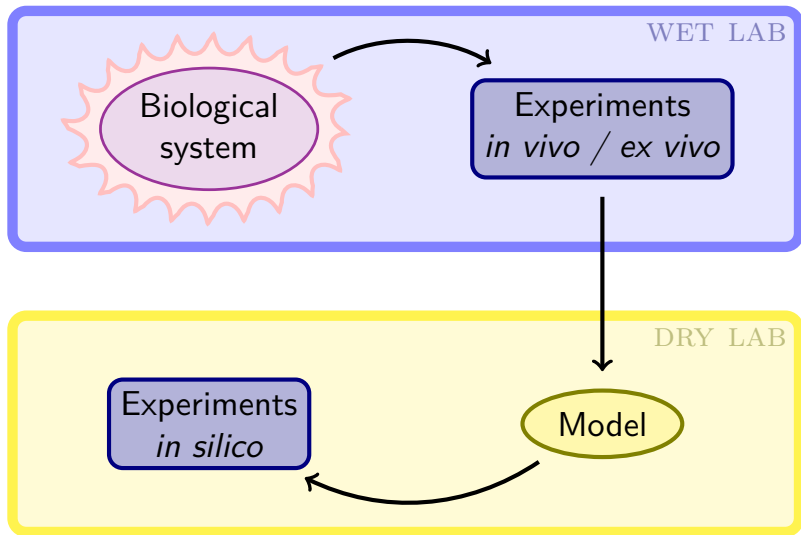
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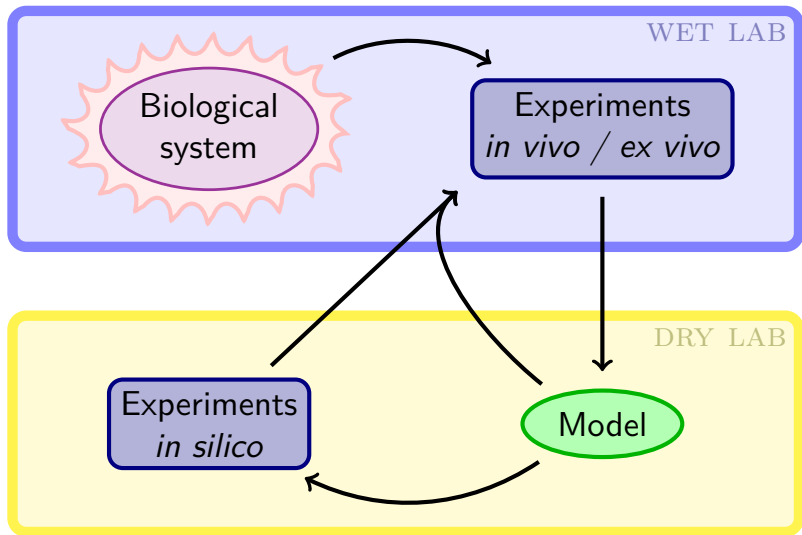
Experiments *in silico*



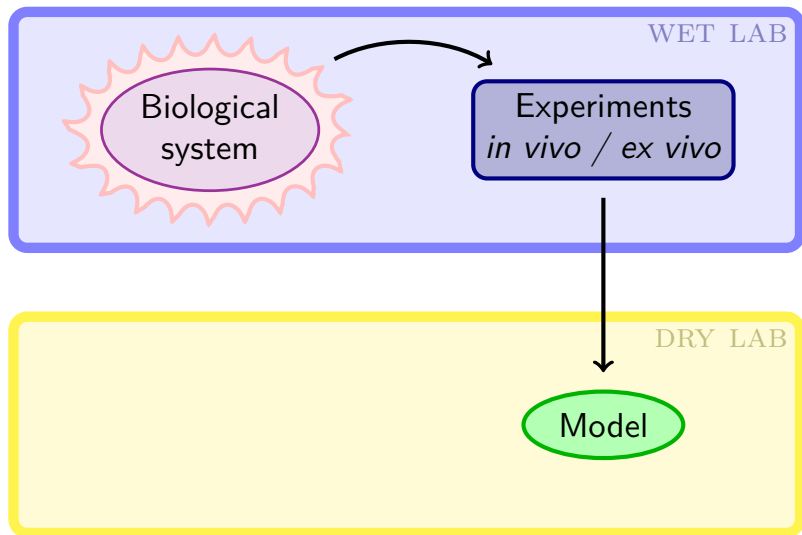
Experiments *in silico*



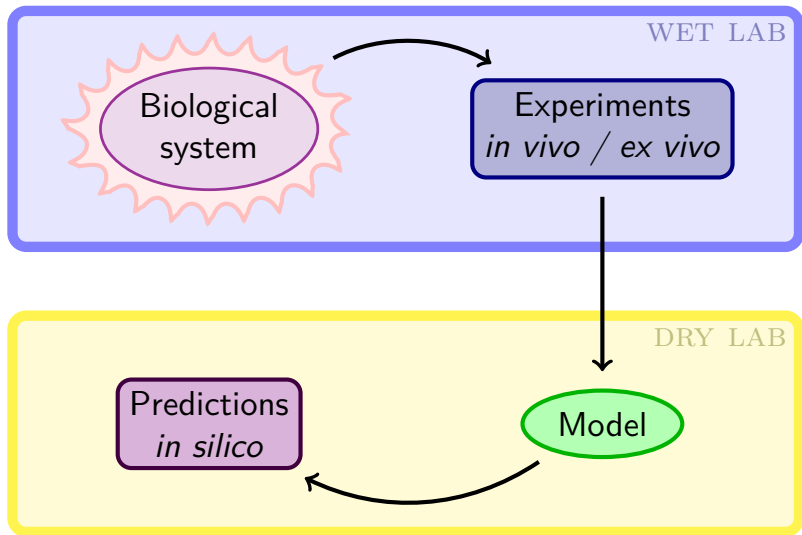
Experiments *in silico*



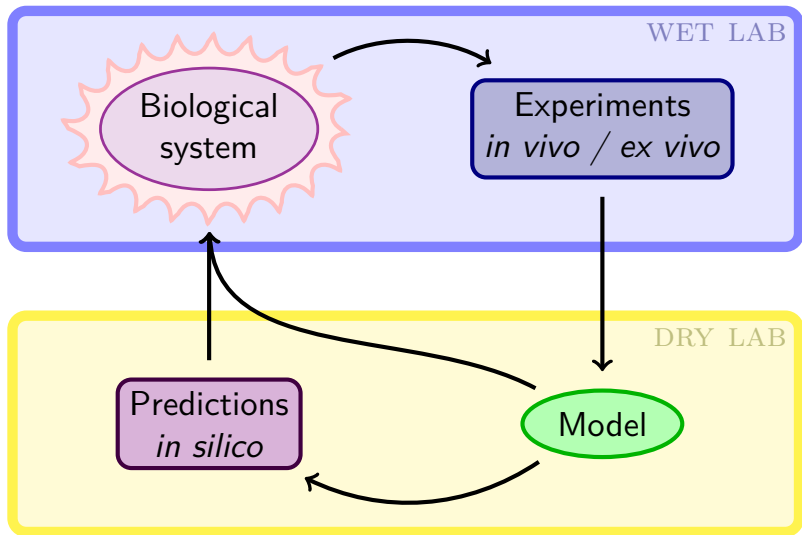
Experiments *in silico*



Experiments *in silico*

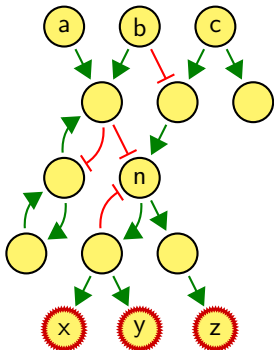


Experiments *in silico*



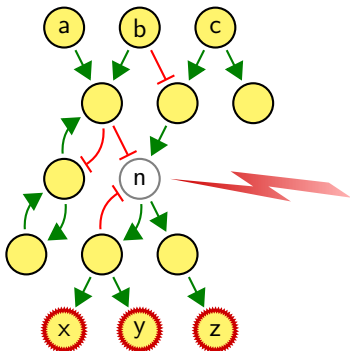
Gene Therapies

Find **therapeutic targets** in complex systems



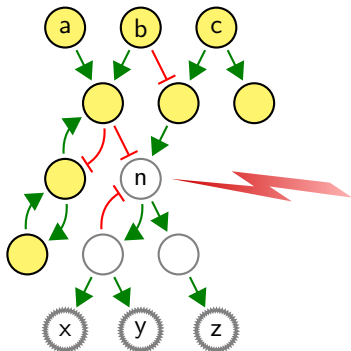
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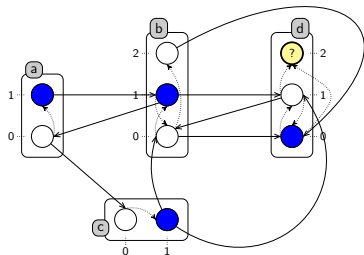
Gene Therapies

Find **therapeutic targets** in complex systems



Back to the Over-approximation

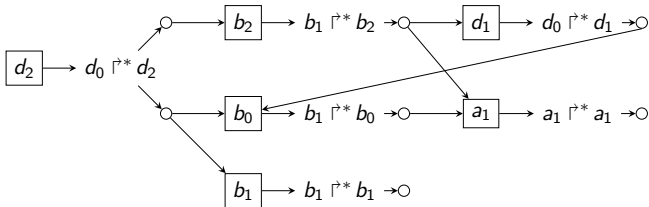
[Paulevé et al., *Computer Aided Verification*, 2013]



Necessary condition **Q**:

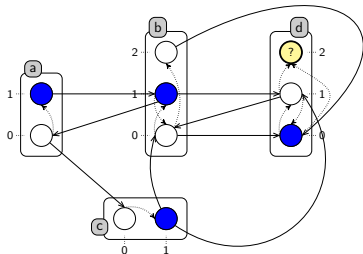
There exists a traversal with no cycle

- objective \rightarrow follow **one** solution
- solution \rightarrow follow **all** local states
- local state \rightarrow follow **all** objectives



Back to the Over-approximation

[Paulevé et al., *Computer Aided Verification*, 2013]

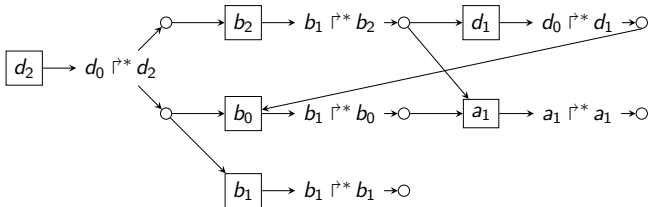


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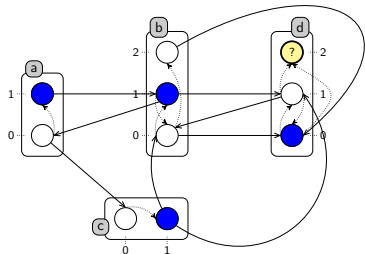
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Q is true \Rightarrow Inconclusive



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[Paulevé et al., *Computer Aided Verification*, 2013]

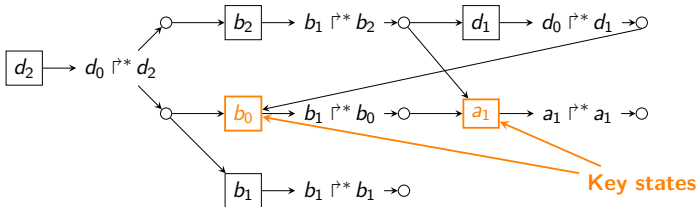


Necessary condition **Q**:

There exists a traversal with no cycle

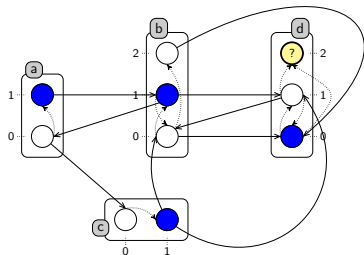
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Back to the Over-approximation

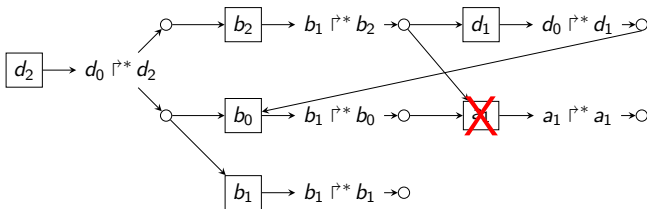
[Paulevé et al., *Computer Aided Verification*, 2013]



Necessary condition **Q**:

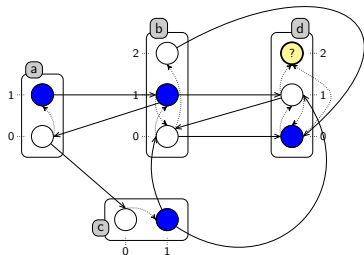
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Back to the Over-approximation

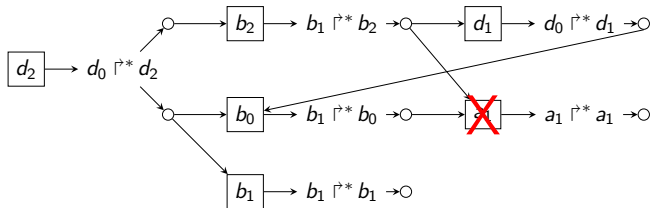
[Paulevé et al., *Computer Aided Verification*, 2013]



Necessary condition **Q**:

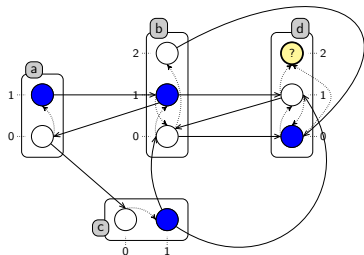
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Back to the Over-approximation

[Paulevé et al., *Computer Aided Verification*, 2013]

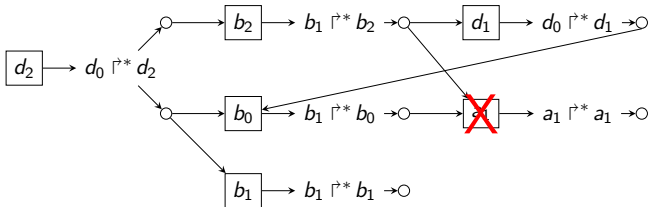


Necessary condition **Q**:

There exists a traversal with no cycle

- objective \rightarrow follow **one** solution
- solution \rightarrow follow **all** local states
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Q is false \Rightarrow R is false



Summary & Conclusion

Modeling of René Thomas for **Regulatory networks**

⇒ How to study its dynamics?

Dynamic analysis

- Classical approach: state-graph computation
- Precise but computational (exponential)
 - ⇒ Large models are intractable

Static analysis

- Much faster (polynomial) but lesser range of results
- Reachability analysis:
 - ⇒ Outperforms classical approaches
 - ⇒ Very few inconclusive cases

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Thank you