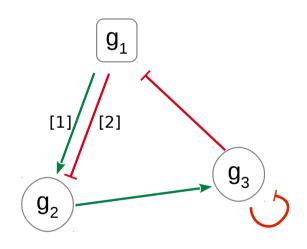
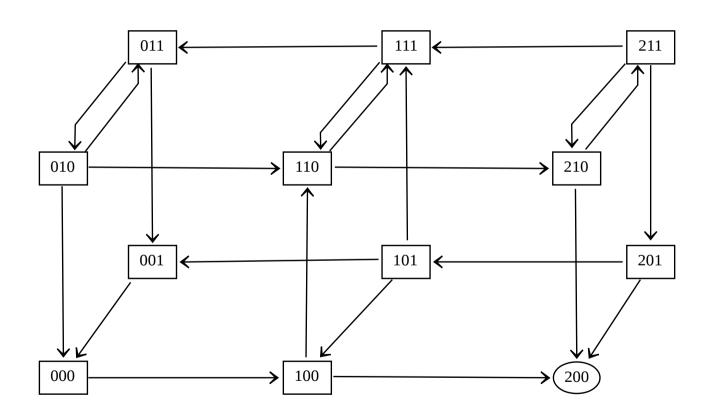
GINsim overview and new features

Logical modeling

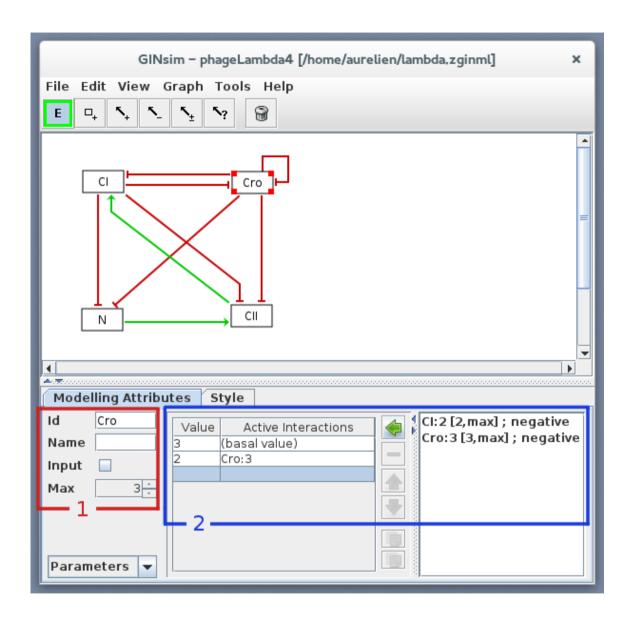


- Nodes: genes, proteins...
 Activity level (Boolean, MV)
- Edges: interactions
 Threshold for MV source
- Logical rules
 next(G3) = G2 and not G3

State Transition Graph



GINsim



Features overview

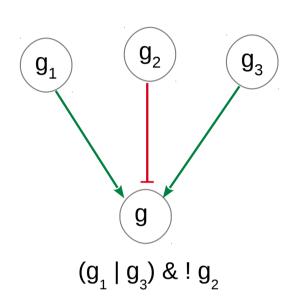
- Graphical User Interface
- Edit the Regulatory Graph
- Simulation: compute the State Transition Graph
- Analysis tools
- Exports

Construct a Regulatory Graph

- Add Components and Interactions
 - Manual layout and visual settings
- Annotations
 - Needs improvements, rely more on SBML standards

- Real model: logical parameters
- Perturbations

Reminder on Logical Parameters



g1	g2	g3	g
0	0	0	0
0	0	1	1
0	1	0	0
0	1	1	0
1	0	0	1
1	0	1	1
1	1	0	0
1	1	1	0

Logical parameters		
Ø (basal value)		
g3		
g2		
g2,g3		
g1		
g1,g3		
g1,g2		
g1,g2,g3		

logical parameter = List of active interactions

1 parameter = 1 line in the truth table

Simulation

- Updating mode
 - (a)synchronous
 - Priority classes
- Selected Initial State(s)
- Apply perturbation
- Regular or "compact" result (Hierarchical graph)

Perturbations

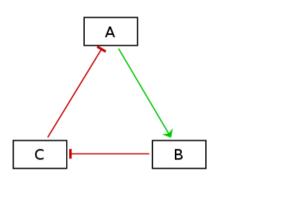
Anything which changes the model:)

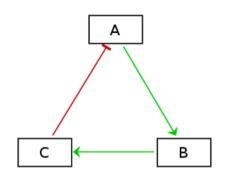
- Fix the value of a component (KO, ectopic expression)
- Restrict a component in a range (multivalued case)
- Remove an interaction
 (block a component only for one of its targets)
- Multiple perturbations

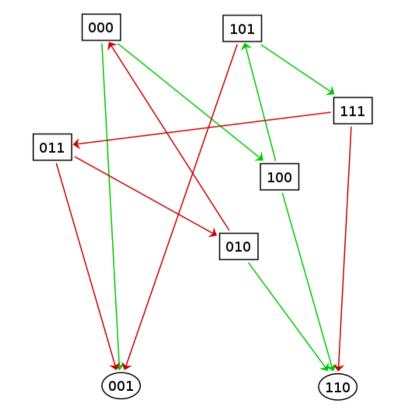
Circuit Analysis

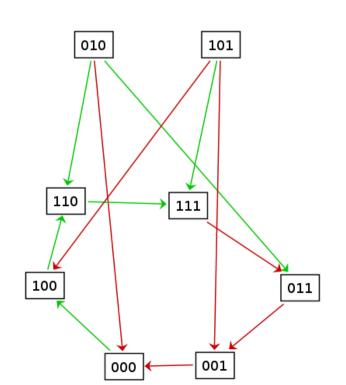
Positive: multiple attractors

Negative: oscillations



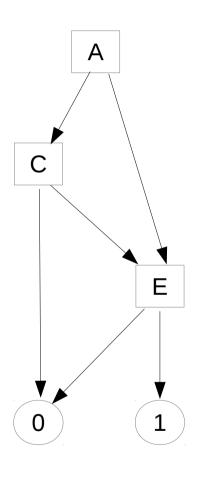






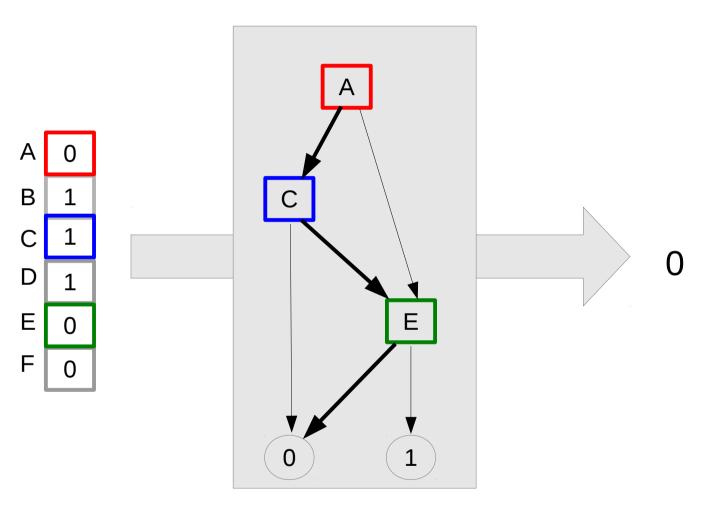
Decision Diagrams (MDD)

(A or C) and E



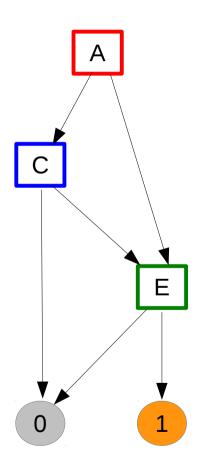
- A,B,C,D,E,F: ordered
- Fast (at most 6 tests, here 3)
- Predictable
- Picking order is hard

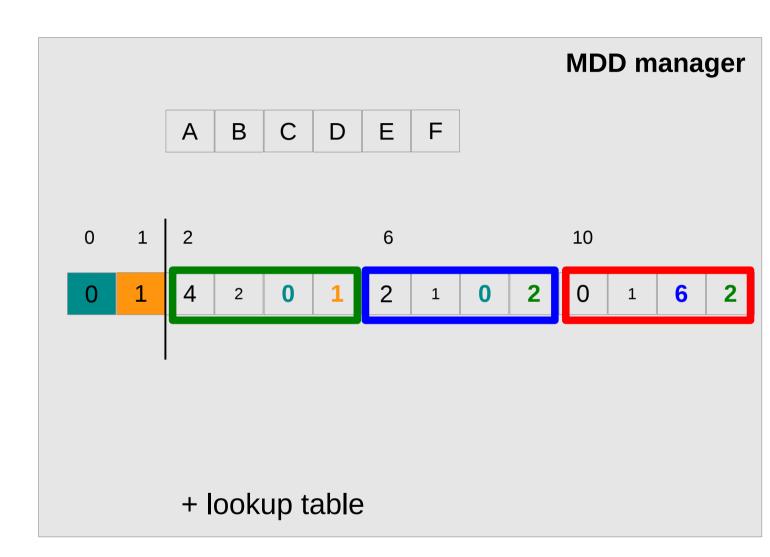
MDD query



Decision Diagrams (MDD)

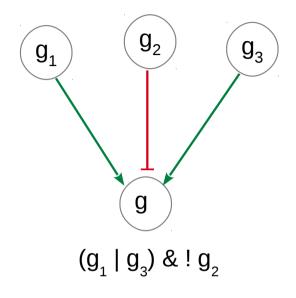
(A or C) and E

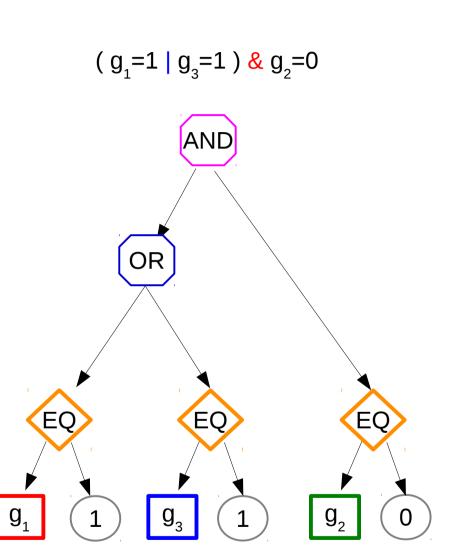




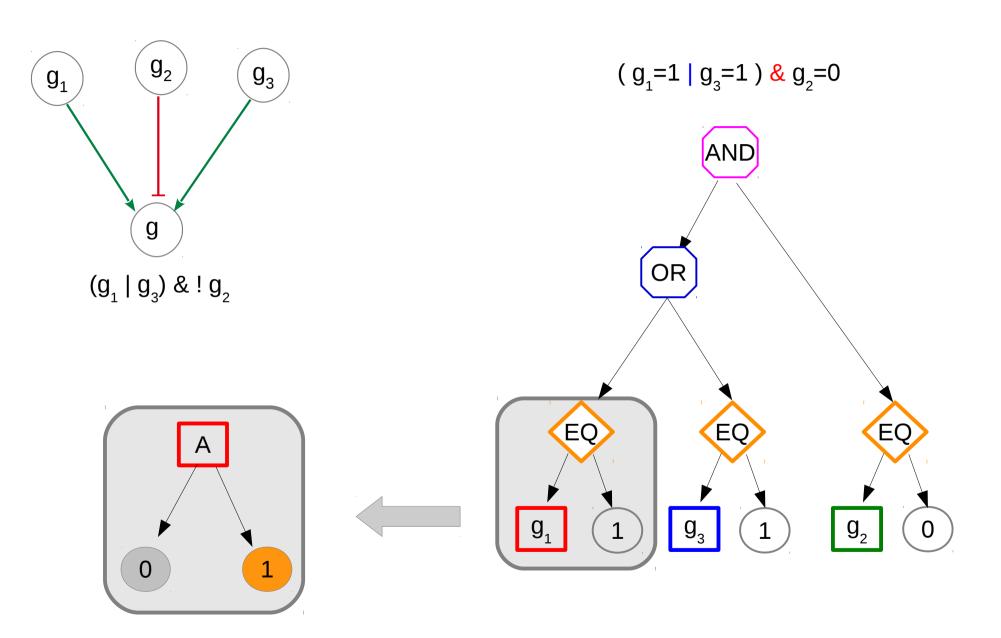
Multi-valued: some variables have more than two children

Functions in SBML-qual (and other)

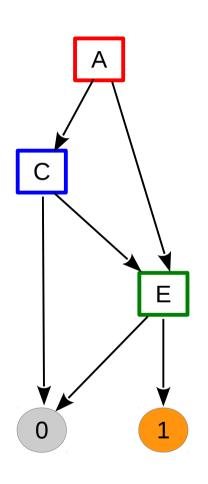




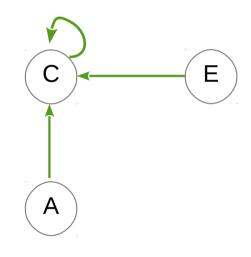
Functions in SBML-qual (and other)



Identification of stable states

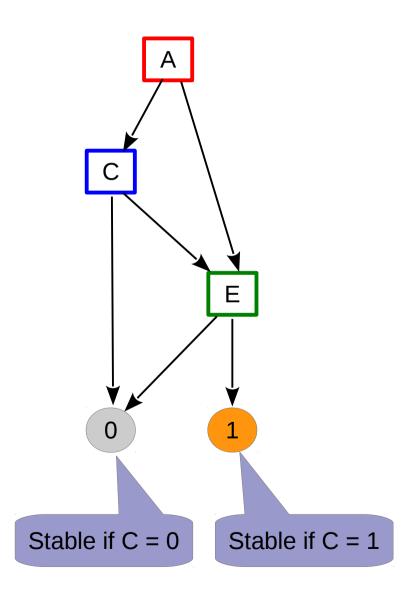


Function for C

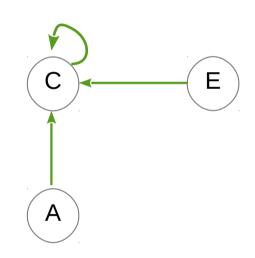


(A | C) & E

Identification of stable states

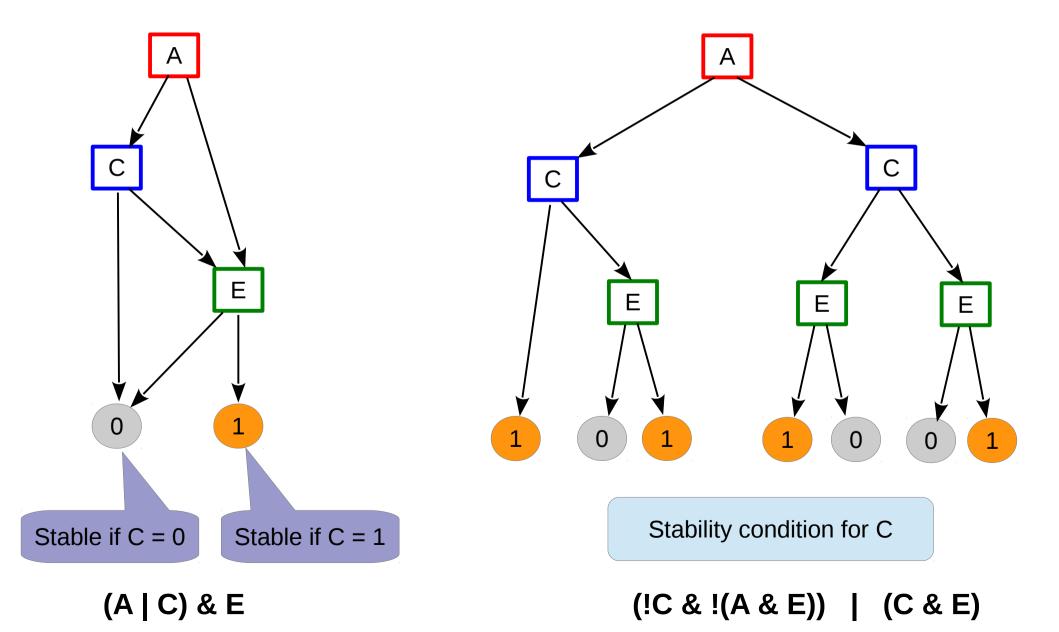


Function for C

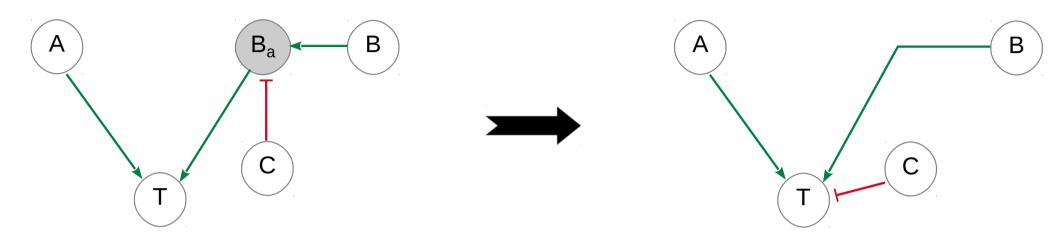


(A | C) & E

Identification of stable states

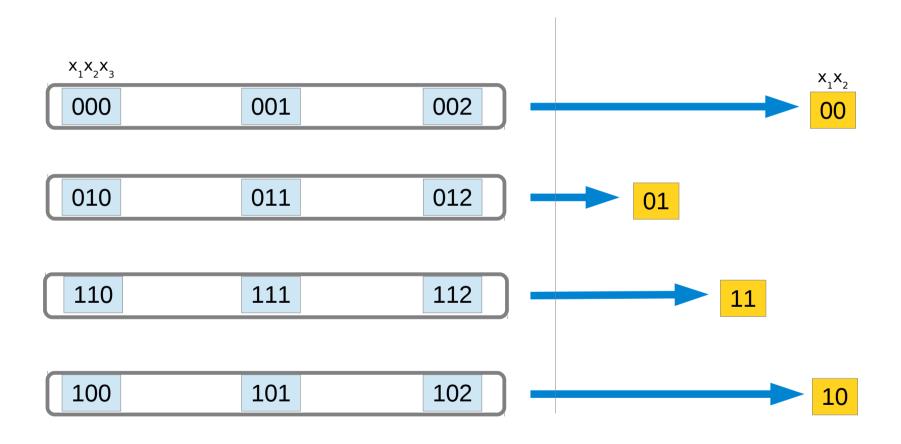


Model reduction

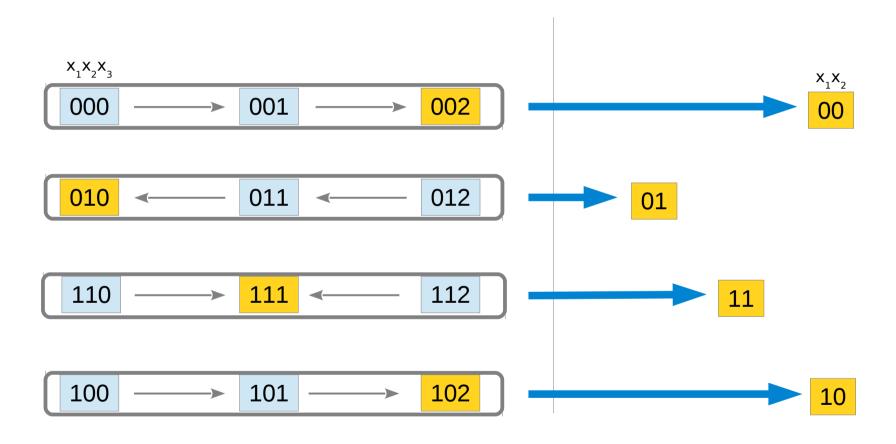


- Construct an explicit model
- Algorithm to "hide" some components
 - Transfer the role of regulators into targets
 - Preserve dynamical properties
 Self-regulated components are protected

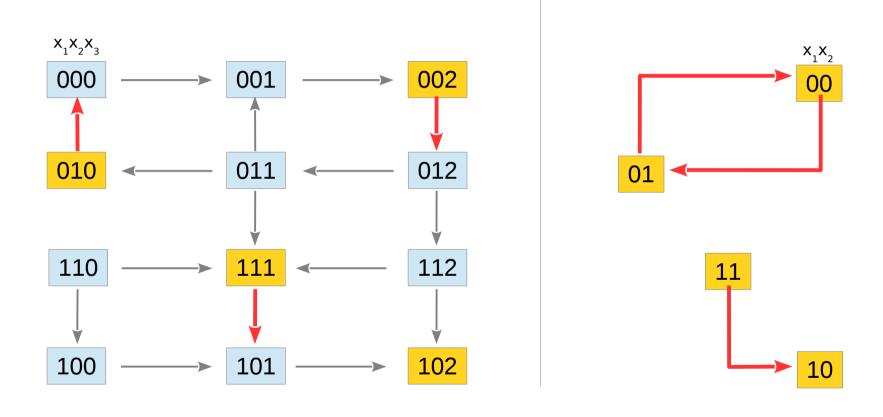
Impact on dynamics



Impact on dynamics



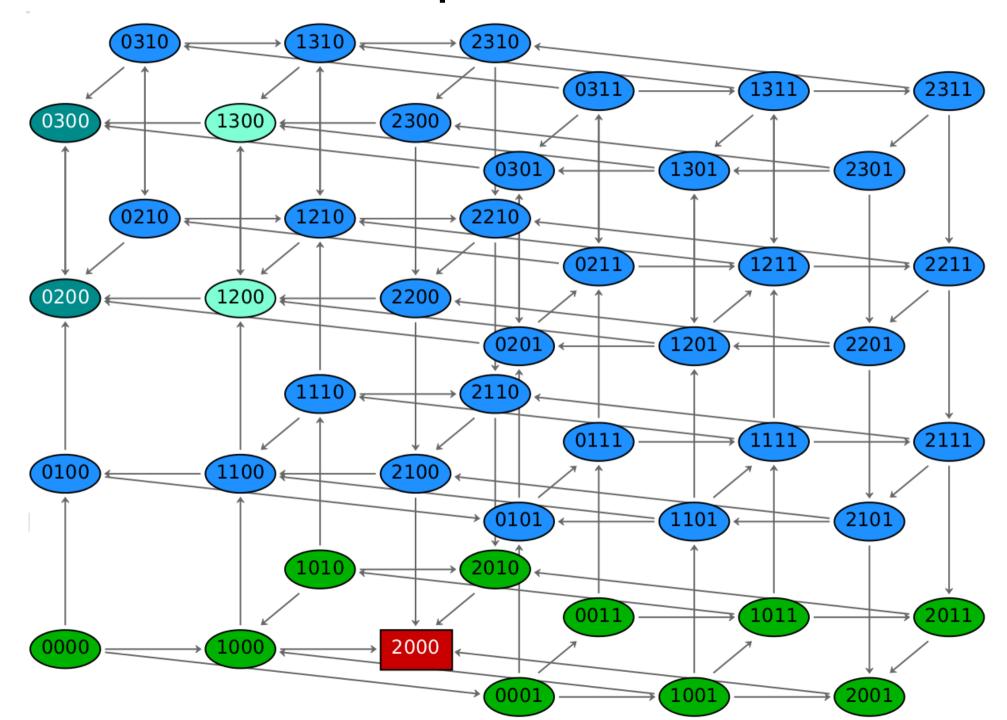
Impact on dynamics



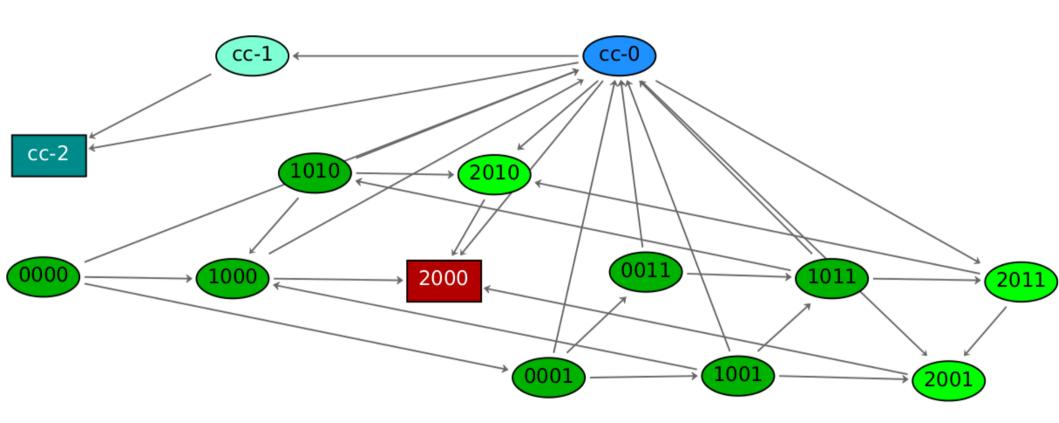
Properties of the reduction

- Dynamics similar to priority classes (hidden = fast)
- Representative states
- Stable states are identical
- Reachability can be lost, not made-up
- Complex attractors are "preserved"
 - Can be split, transient cycles can become terminal
- Some "safe" reductions: no transition lost

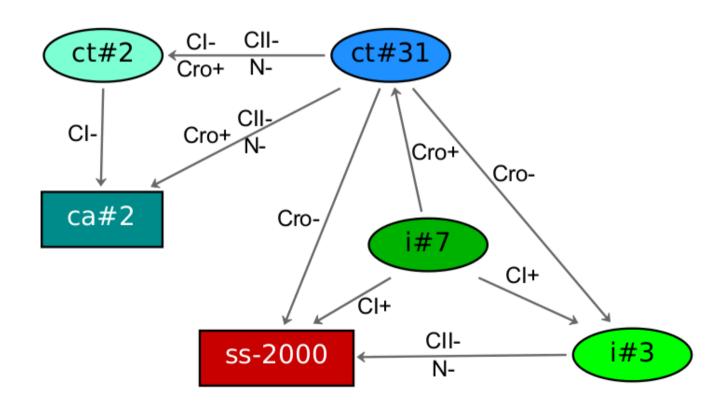
Hierarchical Graph



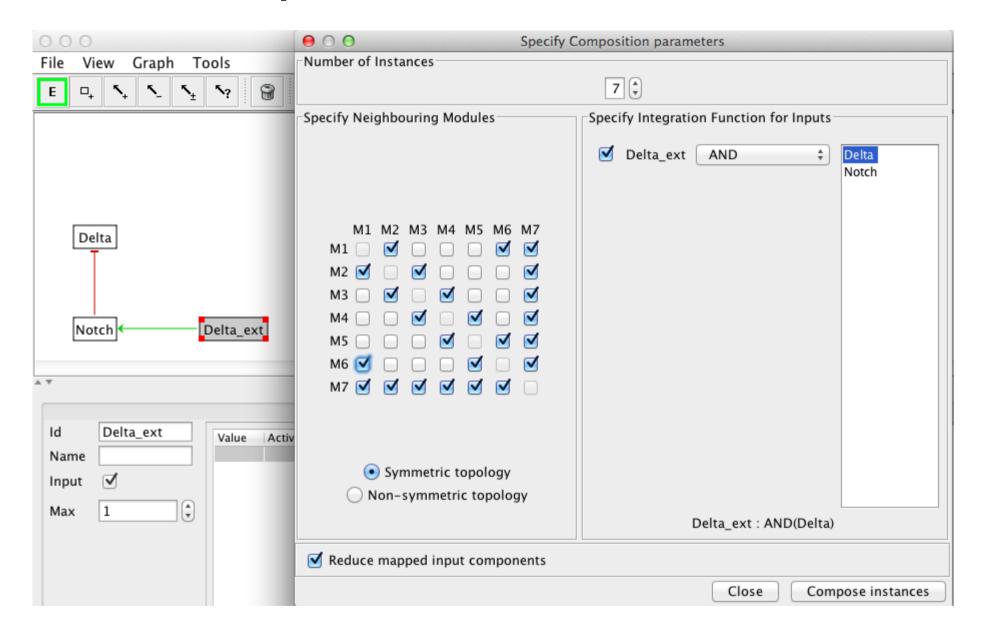
Hierarchical Graph



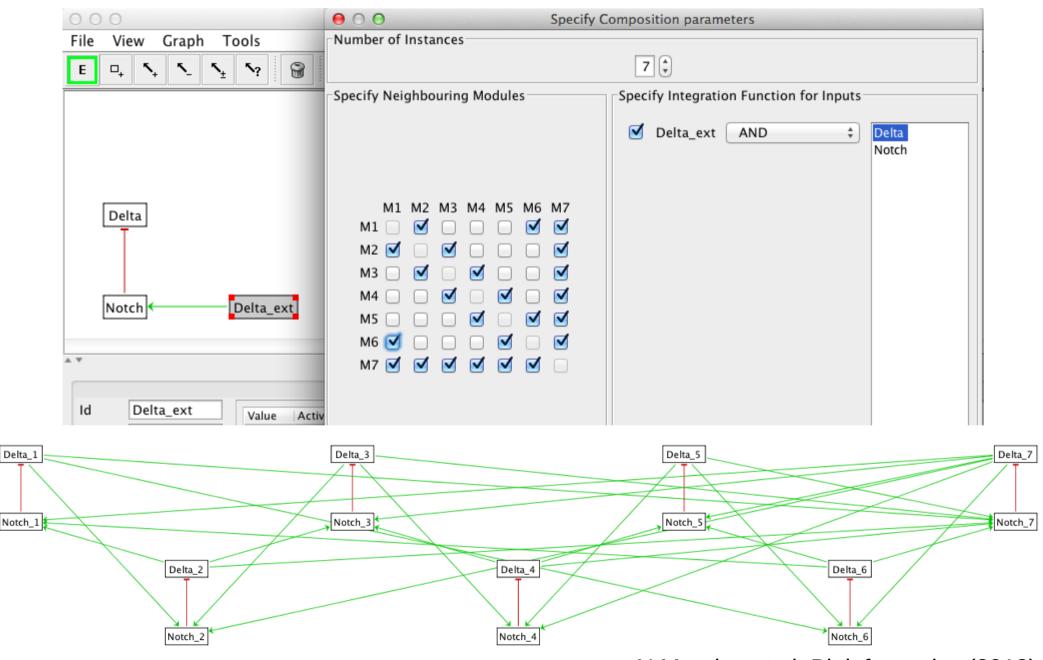
Hierarchical Graph



Model Composition



Model Composition



N Mendes et al. Bioinformatics (2013)

Exports

• Image of the graph (SVG, PNG)

Documentation

Petri net

Model checker

SBML qual

Others: GNA, boolsim

Upcoming in GINsim 3.0

- Large architecture change
 - Backend: Core, Services
 - GUI (core and services)
 - Much improved scripting (using Jython)
- Backend relies on LogicalModel lib
 - Better MDD implementation
- New view canvas and styles
- Imports
 - SBML qual, Truth table, boolsim

Future plans

Improve annotation support

- Function editor
 - Automatic functions
 - Improve hand-crafted functions

Allow external extensions

People











TAGC (INSERM) Marseille, France

People





IGC & INESC Lisbon, PT



IBENS Paris, FR



CIG - UNIL Lausanne, CH