Reduction of Dynamical Systems over Monoids

G. Argyris, A. Lluch Lafuente, A. Leguizamon-Robayo, M. Tribastone, Max Tschaikowski, and Andrea Vandin



18/02/2025

Outline

- A bit of history
- Preliminaries
 - Discrete time systems and Boolean Networks
 - State Space + Dynamics = State Transition Graph
 - Attractors
 - State space explosion
 - T-Cell modelling
- Generalized Forward Bisimulation
- Biological Applications

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Maximal aggregation of polynomial **PNAS** dynamical systems

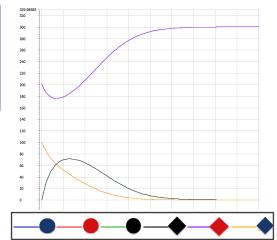
Luca Cardelli, Mirco Tribastone 🔎 🏾 , Max Tschaikowski, and Andrea Vandin 🔎 Authors Info & Affiliations

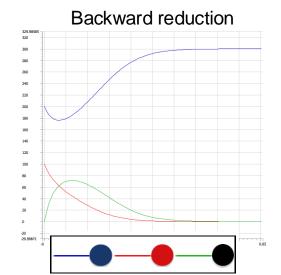
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September 6, 2017 114 (38) 10029-10034 <u>https://doi.org/10.1073/pnas.1702697114</u>

2 linear reductions for non-linear Ordinary Differential Equations (ODEs) Backward Reduction

$$\frac{dx(t)}{dt} = F(x(t)) \qquad x = (x_1, \dots, x_n)$$





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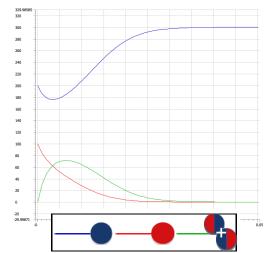
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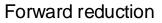
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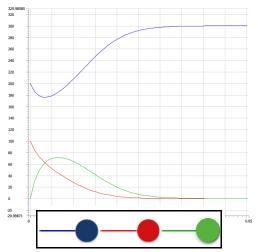
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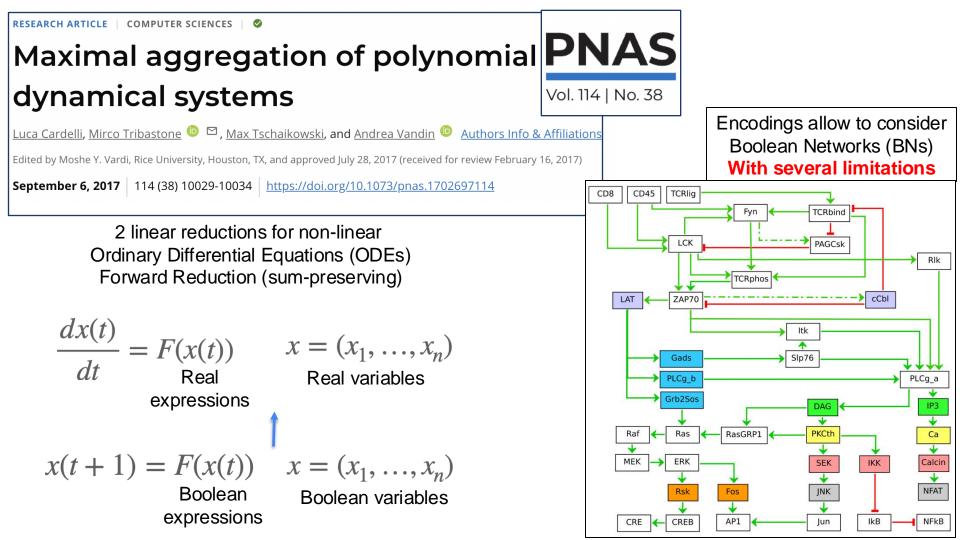
2 linear reductions for non-linear Ordinary Differential Equations (ODEs) Forward Reduction (sum-preserving)

$$\frac{dx(t)}{dt} = F(x(t)) \qquad x = (x_1, \dots, x_n)$$









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Forward bisimulation ODEs: Linear reduction (sum-preserving) of non-linear Ordinary Differential Equations (ODEs)

Minimization of Dynamical Systems over Monoids

Georgios Argyris*, Alberto Lluch Lafuente*, Alexander Leguizamon Robayo[†], Mirco Tribastone[‡], Max Tschaikowski[†], and Andrea Vandin[§],*

Thirty-Eighth Annual ACM/IEEE Symposium on

Logic in Computer Science (LICS)

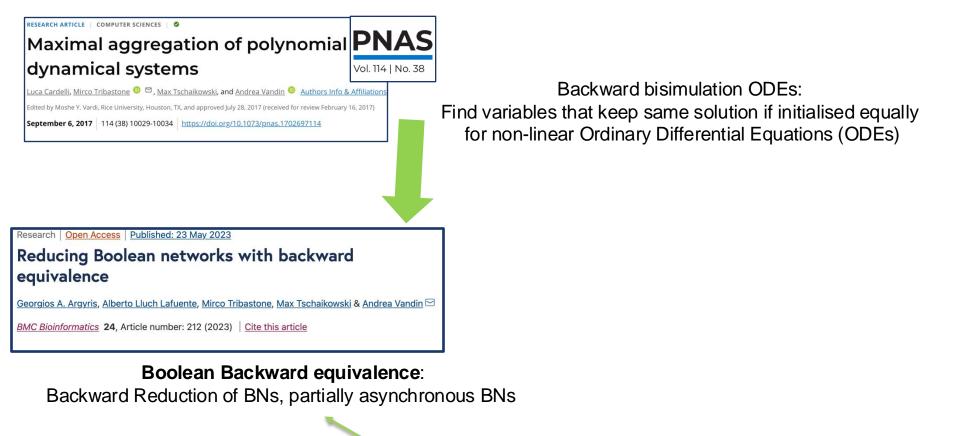
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Generalized Forward bisimulation:

Non-linear reduction (preserving monoids operations) of non-linear ODEs, BNs, Difference Equations,

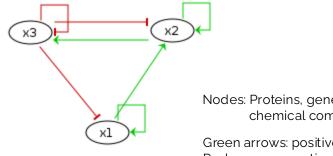
More general reductions

More general family of models



Different family of models

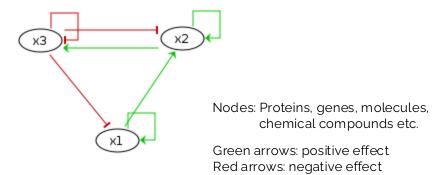
Graphical representation



Nodes: Proteins, genes, molecules, chemical compounds etc.

Green arrows: positive effect Red arrows: negative effect

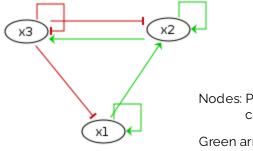
Graphical representation



Boolean Network

$$\begin{array}{rcl} x_1(t+1) &=& \neg x_3(t) \lor x_1(t) \\ x_2(t+1) &=& x_1(t) \lor x_2(t) \lor \neg x_3(t) \\ x_3(t+1) &=& x_2(t) \land \neg x_3(t) \end{array}$$

STG: State Transition Graph

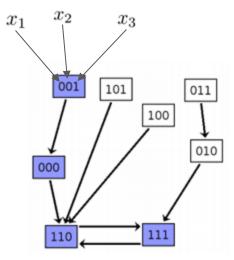


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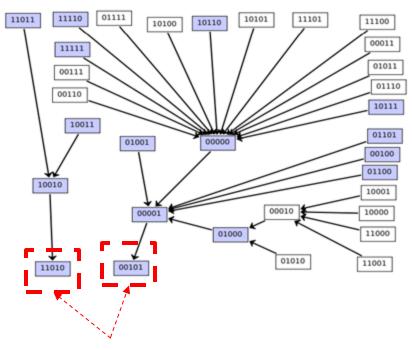
Boolean Network

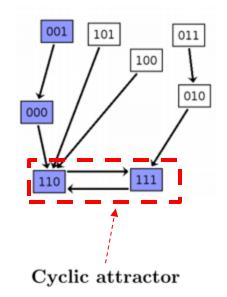
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0: inactive 1: active

Attractors





Steady state attractor

State Space Explosion

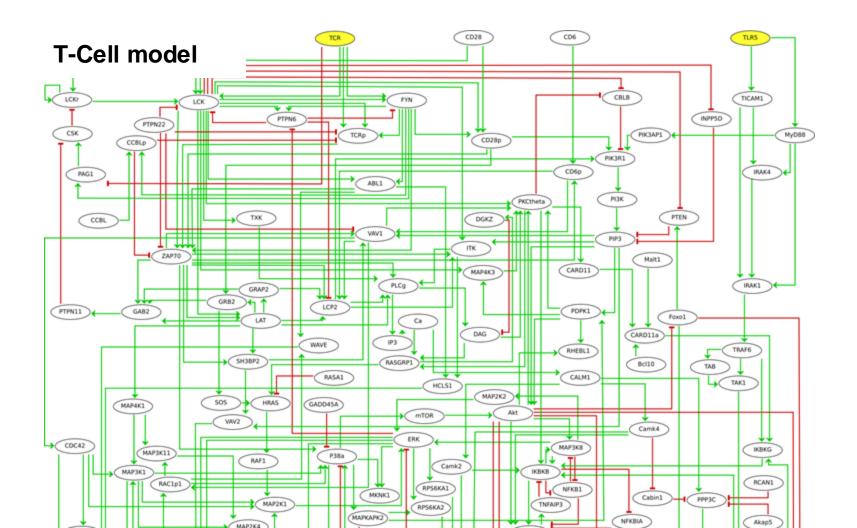


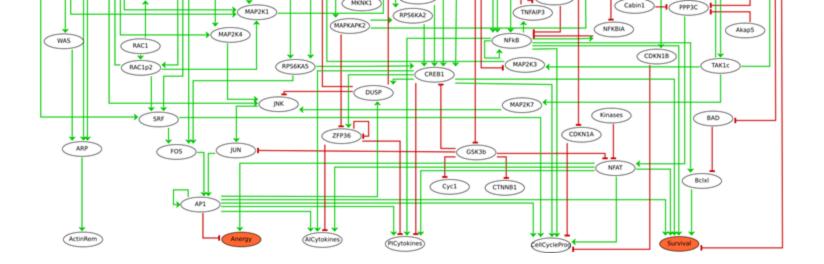
State Space Explosion

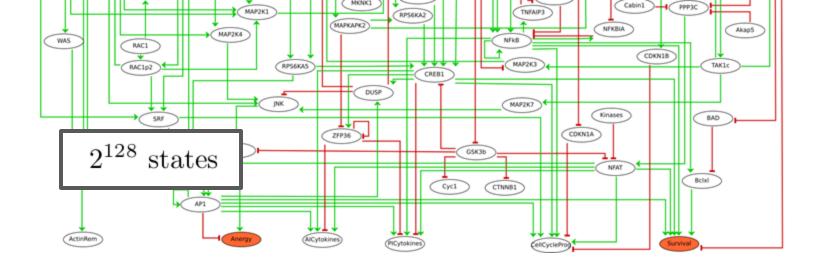


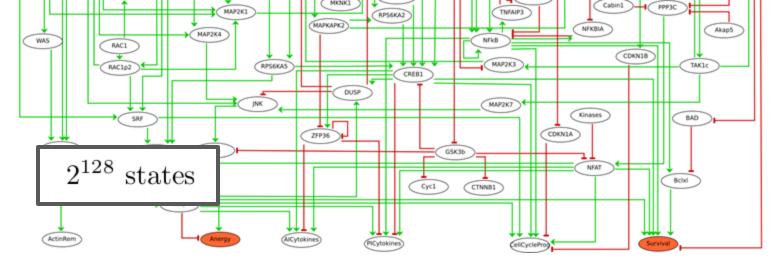
Reduction facilitates:

- STG generation
- Attractor computation
- Control
- ...









Model	Size	Attractors	Analysis (s)		
Original T-Cell	128	-Time Out-			
Reduced T-Cell v1	116	— Time Out—			
Reduced T-Cell v2	98	8	9349.577		
Reduced T-Cell v3	97	8	1103.912		
Reduced T-Cell v4	95	2	29.336		

Experiments with even larger BN: 321 variables

Model	Variables	Attract Count	ors analysis Runtime(s)
Original	321	—Ti	me Out—
Output separated	189	—Time Out—	
01	70	64	0.668
02	33	64	0.325
Maximal	1	1	0.001

• We consider large model (321 variables) by S.Raza, et al:

A logic-based diagram of signalling pathways central to macrophage activation, BMC systems biology, 2008

- Original model could not be analysed
- · Output-separated reduction is still too large, maximal reduction is trivial
- In O1 and O2 we admit to aggregate some outputs

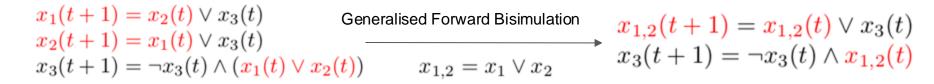
We can perform some analysis of an otherwise not analyzable model

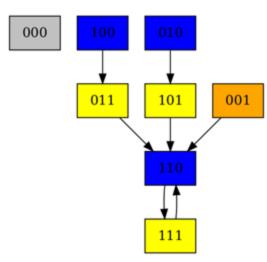
Reductions are useful!

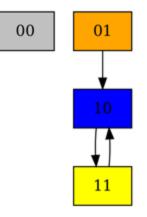
Results on STG generation

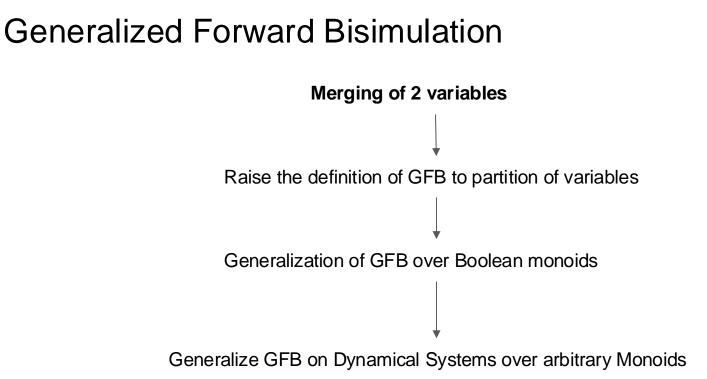
Model		Original model	Input-distinguished Reduced model			Maximal Reduced model		
	Size	$STG \ generation(s)$	Reduction	(s) Size	STG generation(s)	Reduction	(s) Size	STG generation(s)
B7	33	out of memory	0.585	27	out of memory	0.608	25	out of memory
B9	28	out of memory	0.449	25	out of memory	0,416	20	52.8
B10	26	out of memory	0.227	23	457	0.145	4	0.006
B11	24	984	0.243	23	475	0.207	9	0,280
B12	24	987	0.349	21	102	0.121	4	0.050

Example









$$f_{x_1} = x_2 \lor x_3$$

$$f_{x_2} = x_1 \lor x_3$$

$$f_{x_3} = \neg x_3 \land (x_1 \lor x_2)$$

$$\begin{aligned}
f_{x_1} &= x_2 \lor x_3 \\
f_{x_2} &= x_1 \lor x_3 \\
f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\
& & & \\
& & \\
f_{x_1} \lor f_{x_2} &= x_2 \lor x_3 \lor x_1 \lor x_3 = x_1 \lor x_2 \lor x_3 \\
& & \\
f_{x_3} &= \neg x_3 \land (x_1 \lor x_2)
\end{aligned}$$

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f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\
\downarrow \\
f_{x_{1,2}} &= x_3 \lor x_{1,2} \\
f_{x_3} &= \neg x_3 \land x_{1,2}
\end{aligned}$$

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f_{x_1} &= x_2 \lor x_3 \\
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\downarrow \\
f_{x_1} \lor f_{x_2} &= x_2 \lor x_3 \lor x_1 \lor x_3 = x_1 \lor x_2 \lor x_3 = f_{x_1} \lor f_{x_2}[x_1/0, x_2/x_1 \lor x_2] \\
\downarrow \\
f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\
&= f_{x_3}[x_1/0, x_2/x_1 \lor x_2] \\
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&= f_{x_3}[x_1/0, x_3/x_1 \lor x_3$$

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f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\
\downarrow \\
f_{x_1,2} &= x_3 \lor x_{1,2} \\
f_{x_3} &= \neg x_3 \land x_{1,2}
\end{aligned}$$
Identity element of the monoid (\mathbb{B}, \vee)

$$\begin{aligned} f_{x_1} &= x_2 \lor x_3 \\ f_{x_2} &= x_1 \lor x_3 \\ f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\ \hline f_{x_1} \lor f_{x_2} &= x_2 \lor x_3 \lor x_1 \lor x_3 = x_1 \lor x_2 \lor x_3 = f_{x_1} \lor f_{x_2}[x_1/0, x_2/x_1 \lor x_2] \\ \hline f_{x_3} &= \neg x_3 \land (x_1 \lor x_2) \\ \hline f_{x_{1,2}} &= x_3 \lor x_{1,2} \\ f_{x_3} &= \neg x_3 \land x_{1,2} \end{aligned}$$
 Identity element of the monoid (\mathbb{B}, \lor)

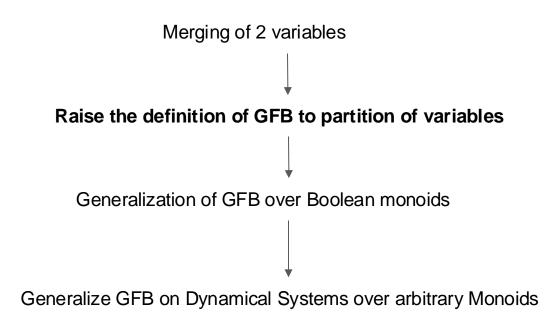
Definition 1. A Boolean network is a pair (X, F) where $X = \{x_1, \ldots, x_n\}$ is a set of variables, and $F = \{f_{x_1}, \ldots, f_{x_n}\}$ is a set of update functions with $f_{x_i} : \mathbb{B}^n \to \mathbb{B}$.

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f_{x_1} &= x_2 \lor x_3 \\
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\downarrow \\
f_{x_{1,2}} &= x_3 \lor x_{1,2} \\
f_{x_3} &= \neg x_3 \land x_{1,2}
\end{aligned}$$

$$f_{x_1} \vee f_{x_2} = f_{x_1} \vee f_{x_2}[x_1/0, x_2/x_1 \vee x_2]$$
$$\bigwedge f_{x_3} = f_{x_3}[x_1/0, x_2/x_1 \vee x_2]$$

Theorem:

- This SMT formula is valid IFF we can aggregate x1 and x2



Definition 2. A partition $P = \{P_1, P_2, \ldots\}$ of the set of variables is a Generalised Forward Bisimulation if and only if the BN can be written in one variable for each block P_i of the partition, representing the disjunction (OR) of the variables belonging to this block.

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$$P = \{\{x_1, x_2\}, \{x_3\}\}$$

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$$f_{x_1} \lor f_{x_2} = f_{x_1} \lor f_{x_2} [x_1/1, x_2/x_1 \lor x_2] \bigwedge f_{x_3} = f_{x_3} [x_1/0, x_2/x_1 \lor x_2]$$

The corresponding SMT formula for the partition

Definition 2. A partition $P = \{P_1, P_2, \ldots\}$ of the set of variables is a Generalised Forward Bisimulation if and only if the BN can be written in one variable for each block P_i of the partition, representing the disjunction (OR) of the variables belonging to this block.

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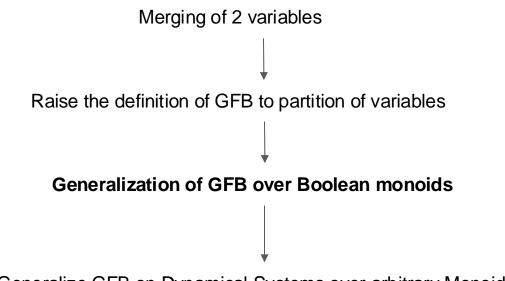
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$$P = \{\{x_1, x_2\}, \{x_3\}\}$$

$$f_{x_1} \vee f_{x_2} = f_{x_1} \vee f_{x_2} [x_1/1, x_2/x_1 \vee x_2] \bigwedge f_{x_3} = f_{x_3} [x_1/0, x_2/x_1 \vee x_2]$$

 $\forall P_i, \forall x_i, x_j \in P_i$ the following formula holds:

$$\bigwedge_{P_i \in P} \left(\bigvee_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} = \bigvee_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} [x_i/0] [x_j/(x_i \lor x_j)] \right)$$



Generalize GFB on Dynamical Systems over arbitrary Monoids

Generalization to Boolean Monoids

 $\forall P_i, \forall x_i, x_j \in P_i$ the following formula holds:

$$\bigwedge_{P_i \in P} \left(\bigvee_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} = \bigvee_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} [x_i/\mathbf{0}] [x_j/(x_i \vee x_j)] \right)$$

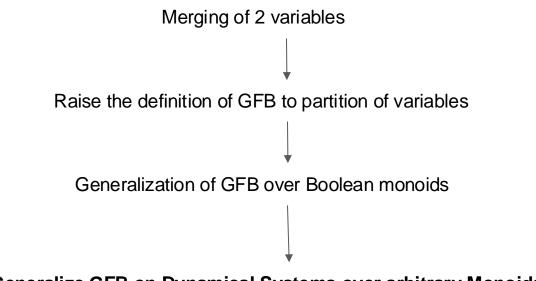
Generalization to Boolean Monoids

 $\forall P_i, \forall x_i, x_j \in P_i$ the following formula holds:

$$\bigwedge_{P_i \in P} \left(\bigvee_{\mathbf{x_k} \in \mathbf{P_i}} f_{x_k} = \bigvee_{\mathbf{x_k} \in \mathbf{P_i}} f_{x_k} [x_i/\mathbf{0}] [x_j/(x_i \lor x_j)] \right)$$

For an arbitrary commutative monoid (\mathbb{B}, \oplus) , the partition P is a Generalised Forward Bisimulation if and only if $\forall P_i, \forall x_i, x_j \in P_i$ the following formula holds:

$$\bigwedge_{P_i \in P} \left(\bigoplus_{x_k \in P_i} f_{x_k} = \bigoplus_{x_k \in P_i} f_{x_k} [x_i / \mathbf{0}_{\bigoplus}] [x_j / (x_i \oplus x_j)] \right)$$



Generalize GFB on Dynamical Systems over arbitrary Monoids

Definition 2. A discrete-time dynamical system (DS) is a pair (X, F) where $X = \{x_1, \ldots, x_n\}$ is a set of variables, and $F = \{f_{x_1}, \ldots, f_{x_n}\}$ is a set of update functions with $f_{x_i} : \mathbb{M}^n \to \mathbb{M}$ being the update function of variable x_i .

For an arbitrary commutative monoid (\mathbb{M}, \oplus) , the partition P is a Generalised Forward Bisimulation if and only if $\forall P_i, \forall x_i, x_j \in P_i$ the following formula holds:

$$\bigwedge_{P_i \in P} \left(\bigoplus_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} = \bigoplus_{\boldsymbol{x_k} \in \boldsymbol{P_i}} f_{\boldsymbol{x_k}} [x_i / \mathbf{0_{\bigoplus}}] [x_j / (x_i \oplus x_j)] \right)$$

$$(\mathbb{M}, \oplus) = (\mathbb{R}, +)$$

 $(\mathbb{M}, \oplus) = (\mathbb{R}, \cdot)$

+ studied before, while * is new. Example: Lotka-Volterra model

$$\partial_t v_{x_1} = v_{x_1} (1 - v_{x_2} v_{x_3})$$

$$\partial_t v_{x_2} = v_{x_2} (1 - v_{x_1})$$

$$\partial_t v_{x_3} = v_{x_3} (1 - v_{x_1})$$

$$f_{x_1}(s) = s_{x_1} + \tau s_{x_1}(1 - s_{x_2}s_{x_3})$$

$$f_{x_2}(s) = s_{x_2} + \tau s_{x_2}(1 - s_{x_1})$$

$$f_{x_3}(s) = s_{x_3} + \tau s_{x_3}(1 - s_{x_1})$$

that yield for $(\mathbb{M},\oplus) = (\mathbb{R},\cdot)$ the nonlinear reduction:

$$\partial_t v_{x_1} = v_{x_1} (1 - v_{x_2} v_{x_3})$$
$$\partial_t (v_{x_2} v_{x_3}) = 2v_{x_1} v_{x_2} (1 - v_{x_1})$$

$$(\mathbb{M}, \oplus) = (\mathbb{Z}_n, \min)$$
$$(\mathbb{M}, \oplus) = (\mathbb{Z}_n, \max)$$

Multivalued Networks

$$x_1(t+1) = \begin{cases} 2 & \text{if } (1 \le x_1(t) < 2) \lor ((x_3(t) \ge 1) \land (x_1(t) \ge 1)) \\ 1 & \text{if } (x_1(t) < 1) \land (x_3(t) \ge 1) \\ 0 & \text{otherwise} \end{cases}$$

$$x_2(t+1) = \begin{cases} 1 & \text{if } x_1(t) \ge 1\\ 0 & \text{otherwise} \end{cases}$$
$$x_3(t+1) = \begin{cases} 1 & \text{if } x_2(t) \ge 1\\ 0 & \text{otherwise} \end{cases}$$

Computation of the largest Bisimulation

Algorithm 1: Compute the largest GFB that refines the initial partition \mathcal{X}_R for a DS (X, F).

```
Result: Largest GFB \mathcal{H} that refines \mathcal{X}_{R}
\mathcal{H} \leftarrow \mathcal{X}_R;
while true do
       \mathcal{H}' \leftarrow \emptyset:
       for H \in \mathcal{H} do
             R \leftarrow \{(x_i, x_j) \in H \times H : \text{if } x_i \neq x_j, \}
          then \Psi_{x_i,x_j}^{\mathcal{H}} and \Psi_{x_j,x_i}^{\mathcal{H}}};
\mathcal{H}' \leftarrow \mathcal{H}' \cup (H/R);
        end
        if \mathcal{H} = \mathcal{H}' then
                return \mathcal{H};
        else
                                                                                                                 \Psi_{x_i,x_j}^{\mathcal{X}_R} \equiv \bigwedge_{C \in \mathcal{X}_R} \left( \bigoplus_{x_k \in C} f_{x_k} = \bigoplus_{x_k \in C} f_{x_k} [x_i/0_{\oplus}] [x_j/(x_i \oplus x_j)] \right)
            \mathcal{H} \leftarrow \mathcal{H}';
        end
end
```

Experiments with GinSim & BioModels repositories of BNs

Do we get reductions in practice?

- We consider all 29 BN with outputs from 2 repo GinSim & BioModels
- · Reduction ratio: reduced variables / original variables
- Moderate reduction power:

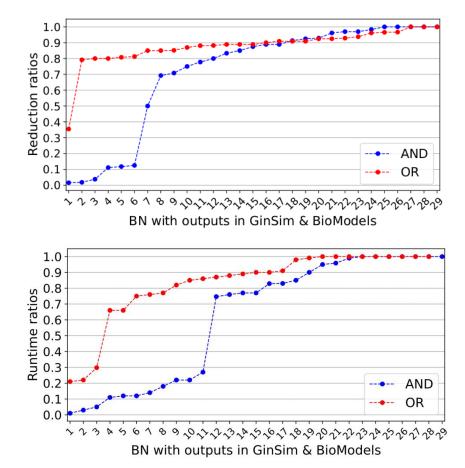
For AND: 9 reductions have size less than 70% of original

· Are these reductions useful?

Yes, these reductions are useful

- We have run attractor analysis on the 29*3 models
- · Runtime ratio: runtime reduced model / runtime reduced
- For AND, 11 models can be analysed faster

In less than 30% of the time of the original ones



Experiments: Non-linear reduction of ODEs and Difference Eq.

Do we get non-linear reductions in practice?

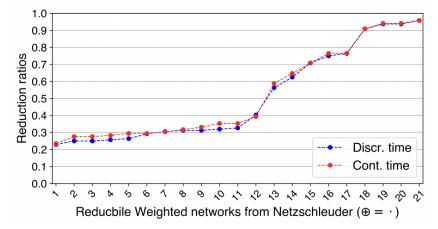
- We consider 72 weighted networks up to 200 nodes
 From https://networks.skewed.de/
- We consider 2 dynamical interpretation for the adjacency matrix A

Discrete-time: x(t + 1) = A(x(t))Continuous-time: $\frac{dx(t)}{dt} = A(x(t))$

- · Reduction ratio: original variables / reduced variables
- Good reduction power:

We provide the 21 reducible models

12 models have less than 40% of the original number of variables



- Randomized polynomial time reduction algorithm for $(\mathbb{M},\oplus)=(\mathbb{R},\cdot)$
- Deterministic version suffers from exponential complexity and did not scale

Future Work

. . .

- On-the-fly computation of GFB
- Extension to hybrid dynamical systems
- Reduction of dynamical systems over arbitrary functions

How do we reduce?

• GFB is implemented in the ERODE tool

