



SCHOOL
FOR ADVANCED
STUDIES
LUCCA

QUANTITATIVE ABSTRACTIONS FOR COLLECTIVE ADAPTIVE SYSTEMS

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Based on joint work with
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SFM'16 - Bertinoro

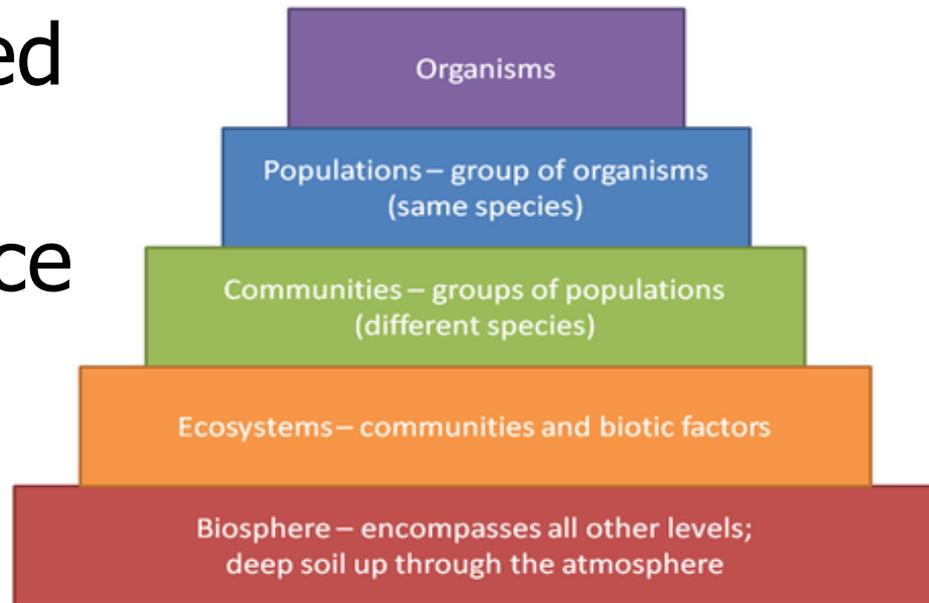
24 June 2016

- CAS are collections of entities interacting with each other and the environment in such a way that the overall behavior cannot be understood by analyzing each agent in isolation
- Modeling CAS raises challenges:
 - The overall behavior requires building the “product space” of the individual state spaces
 - **State explosion** makes the analysis unfeasible in real-world situations

- Focus on **quantitative** properties of CAS
- Standard techniques for quantitative analysis do not scale with large populations of individuals
(see e.g. the lectures of Nicolas/Luca and Jane/Michele)
- **Abstractions** are more compact representations that preserve some of the original behavior
(see e.g. Vashti's lecture for spatial abstractions)

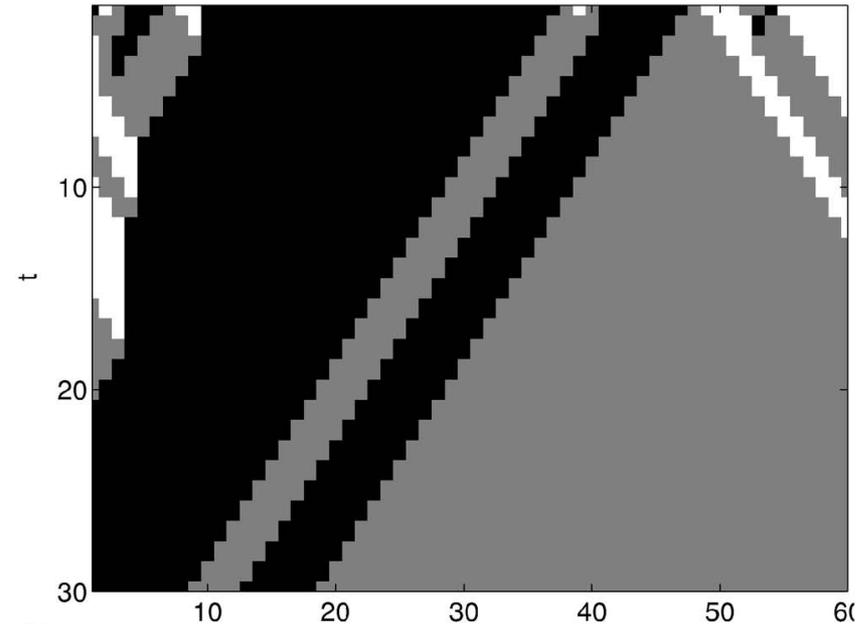
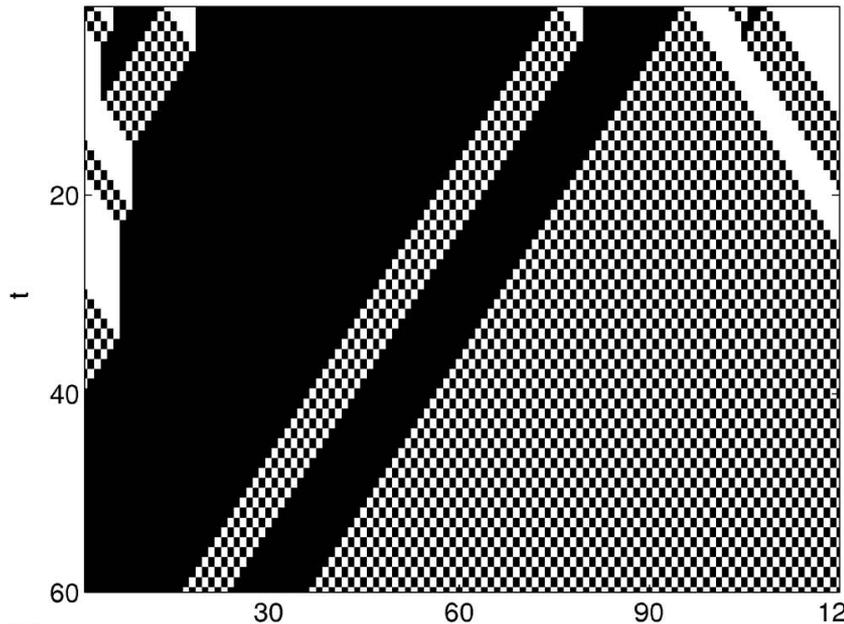
Motivating examples

- **Ecology** is a prime domain of (natural) CAS
 - Populations of individuals interact with each other and adapt to the external environment
 - Different kinds of individuals may have conflicting objectives (e.g., predators vs preys)
- Abstractions are needed to cope with multiple scales in time and space



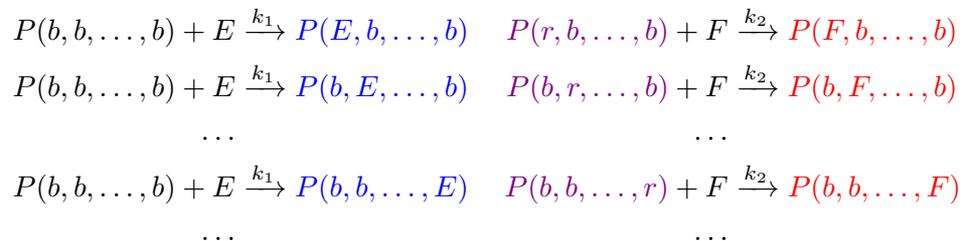
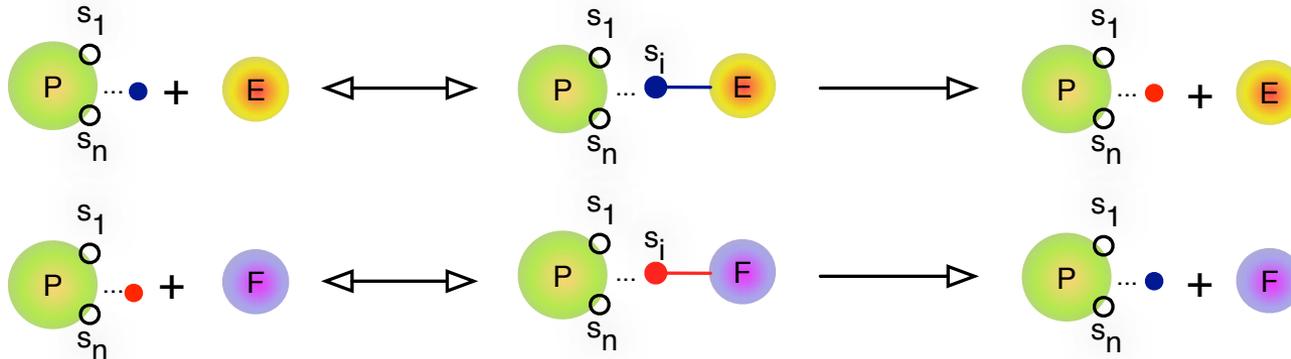
Motivating examples

- In physics, cellular automata are a basic model based on interaction rules between simple neighboring agents (see Vashti's lecture)
- Abstraction recover overall dynamics ignoring low-level details



Motivating examples

- In systems biology, combinatorial explosion arises from the mechanistic modeling of protein interaction networks



- Ordinary differential equations (ODEs) are popular in CAS modeling:
 - Ecology, epidemiology: populations of individuals
 - Systems biology: concentrations of complexes
 - Control engineering: pressure, temperature,...
 - Computer science:
 - Transient probability distribution of a Markov chain is described by a (large) linear ODE system
 - **Fluid approximations** provide more compact (typically non-linear) ODE models of Markov population processes [Hillston'05]

1. Brief intro to ODEs
2. Abstraction through **ODE reduction**
(orthogonal to other approaches that interpolate ODEs as PDEs for spatial limits, see e.g. Vashti's lecture)
 - Symbolic differential equivalences
 - (Structural) bisimulations for reaction networks
3. Perspectives and open challenges
4. Case studies with **ERODE** (A. Vandin)

ODEs: minimal introduction

First-order explicit system of ordinary differential equations

$$\frac{dx_1(t)}{dt} = f_1(x_1(t), \dots, x_n(t))$$

$$\frac{dx_2(t)}{dt} = f_2(x_1(t), \dots, x_n(t))$$

...

$$\frac{dx_n(t)}{dt} = f_n(x_1(t), \dots, x_n(t))$$

$$\dot{x}_1 = f_1(x)$$

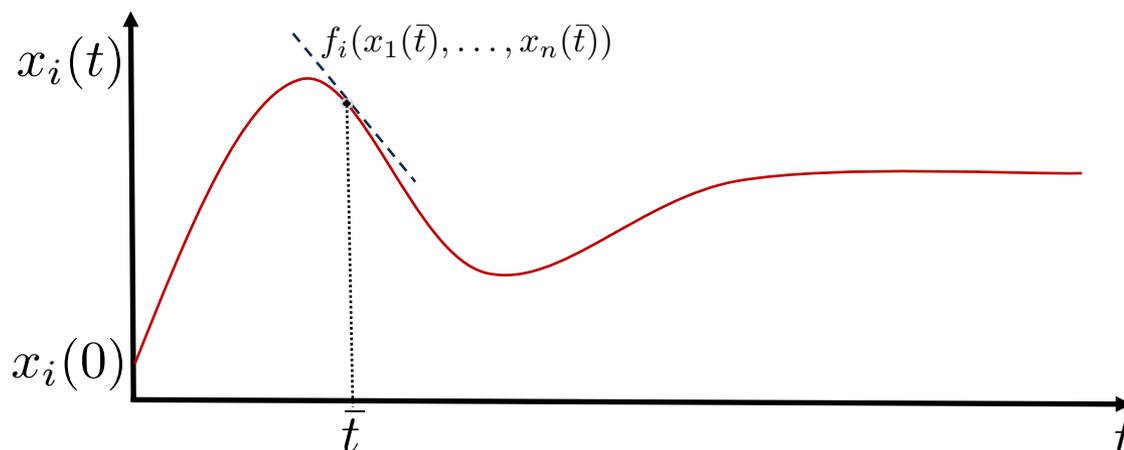
$$\dot{x}_2 = f_2(x)$$

...

$$\dot{x}_n = f_n(x)$$

also written

Initial value problem:
Find the trajectories $x_i(t)$ that satisfy the ODEs when starting from $x_i(0)$



First-order explicit system of ordinary differential equations

$$\frac{dx_1(t)}{dt} = f_1(x_1(t), \dots, x_n(t))$$

$$\frac{dx_2(t)}{dt} = f_2(x_1(t), \dots, x_n(t))$$

...

$$\frac{dx_n(t)}{dt} = f_n(x_1(t), \dots, x_n(t))$$

also written

$$\dot{x}_1 = f_1(x)$$

$$\dot{x}_2 = f_2(x)$$

...

$$\dot{x}_n = f_n(x)$$

Solution (exists and is unique in our models):

$$\frac{dx_i(t)}{dt} \approx \frac{x_i(t + \Delta t) - x_i(t)}{\Delta t}$$

$$x_i(t + \Delta t) \approx x_i(t) + \Delta t \cdot f_i(x_1(t), \dots, x_n(t))$$

First-order explicit system of ordinary differential equations

$$\frac{dx_1(t)}{dt} = f_1(x_1(t), \dots, x_n(t))$$

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...

$$\frac{dx_n(t)}{dt} = f_n(x_1(t), \dots, x_n(t))$$

also written

$$\dot{x}_1 = f_1(x)$$

$$\dot{x}_2 = f_2(x)$$

...

$$\dot{x}_n = f_n(x)$$

$$x_i(t + \Delta t) \approx x_i(t) + \Delta t \cdot f_i(x_1(t), \dots, x_n(t))$$

- In many cases, n can be very large (e.g., order of millions)
- Numerical solution may become computationally prohibitive

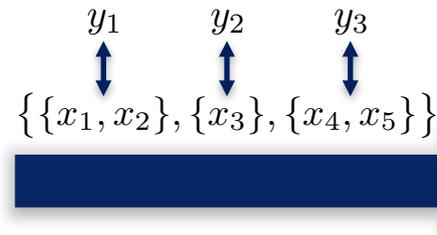
A lower dimensional ODE that preserves “some” of the original dynamics

$$\begin{array}{ccc}
 \dot{x}_1 = f_1(x) & m \ll n & \dot{y}_1 = g_1(y) \\
 \dot{x}_2 = f_2(x) & \longrightarrow & \dots \\
 \dots & \text{Nonlinear ODEs} & \\
 \dot{x}_n = f_n(x) & \text{Automatic Scalable} & \dot{y}_m = g_m(y) \\
 & \text{Exact} &
 \end{array}$$

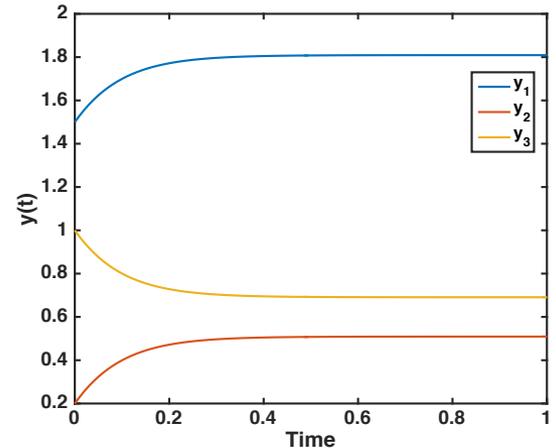
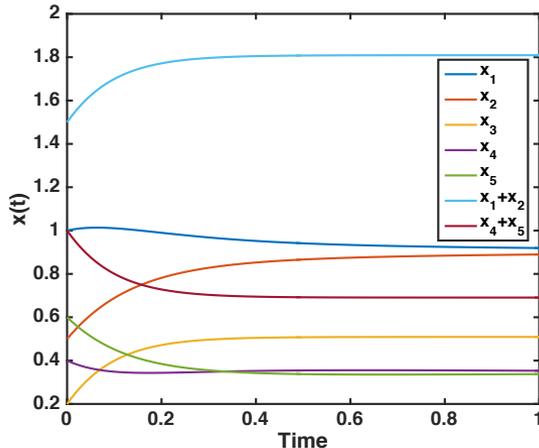
Forward equivalence

A partition of the variables yielding an equation for each block (sum of variables)

$$\begin{aligned}\dot{x}_1 &= -x_1 + x_2 - 3x_1x_3 + 4x_4 \\ \dot{x}_2 &= +x_1 - x_2 - 3x_2x_3 + 4x_5 \\ \dot{x}_3 &= -3x_1x_3 + 4x_4 - 3x_2x_3 + 4x_5 \\ \dot{x}_4 &= +3x_1x_3 - 4x_4 \\ \dot{x}_5 &= +3x_2x_3 - 4x_5\end{aligned}$$



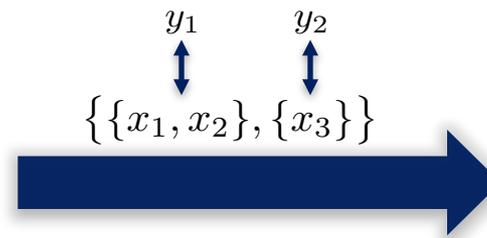
$$\begin{aligned}\dot{y}_1 &= -3y_1y_2 + 4y_3 \\ \dot{y}_2 &= -3y_1y_2 + 4y_3 \\ \dot{y}_3 &= +3y_1y_2 - 4y_3\end{aligned}$$



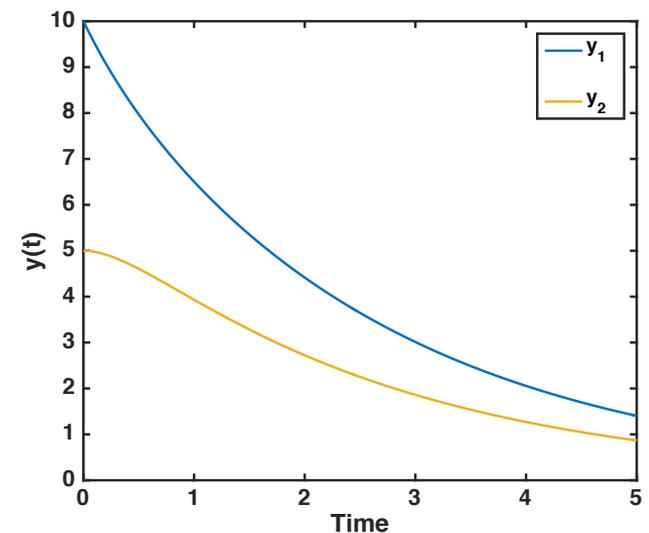
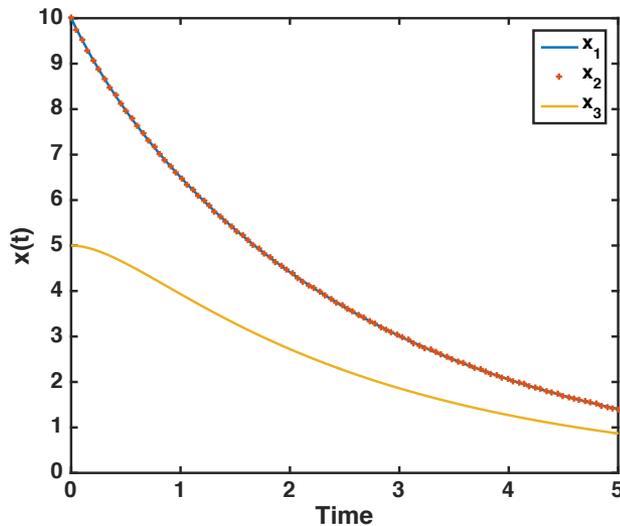
Backward equivalence

Equivalent variables have the same solutions at all time points

$$\begin{aligned}\dot{x}_1 &= -\min(x_1, x_2) + x_3 \\ \dot{x}_2 &= -\min(x_1, x_2) + x_3 \\ \dot{x}_3 &= +\min(x_1, x_2) - 2x_3\end{aligned}$$



$$\begin{aligned}\dot{y}_1 &= -y_1 + y_2 \\ \dot{y}_2 &= +y_1 - 2y_2\end{aligned}$$



IDOL: Intermediate Drift-oriented Language [POPL'16]

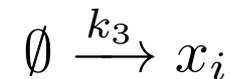
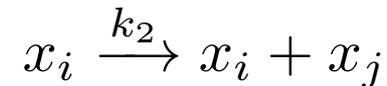
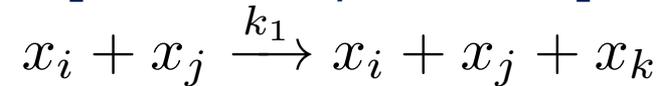
$$p ::= \varepsilon \mid \dot{x}_i = f, p$$

$$f ::= n \mid x_i \mid f + f \mid f \cdot f \mid f^{\frac{1}{m}}$$

- ODEs covered:
 - Polynomials of any degree
 - Rational expressions
 - Minima/maxima
 - ...
- Forward/backward equivalences are **fully characterized**
- Symbolic partition refinement via an **SMT encoding**

Reaction Networks

[CONCUR'15, TACAS'16]



- Multivariate polynomials of degree **at most two**
- Bisimulations over the "species" of the reaction network
- Forward bisimulation is a **sufficient condition** only
- Backward bisimulation fully characterized
- **Polynomial** partition refinement

Language-driven reasoning

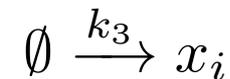
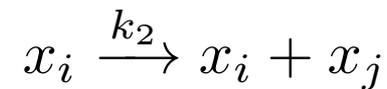
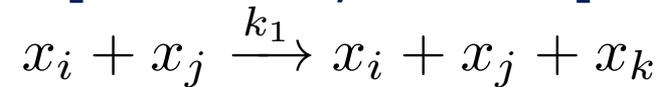
IDOL: Intermediate Drift-oriented
Language [POPL'16]

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Reaction Networks

[CONCUR'15, TACAS'16]



Scalability

Expressiveness/Completeness

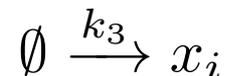
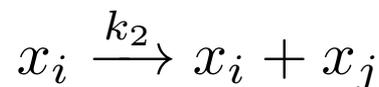
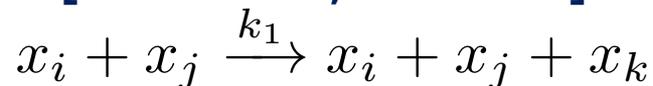
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Reaction Networks

[CONCUR'15, TACAS'16]



This lecture:

- Forward equivalence
- **Backward equivalence**

- **Forward bisimulation**
- Backward bisimulation

- Basic idea:
 - An assignment (x_1, \dots, x_n) is **uniform** on a partition of variables if it has equal values for equivalent variables.
 - $(x_1, x_2, x_3) = (1, 1, 0)$ is uniform on $\{\{x_1, x_2\}, \{x_3\}\}$
 - **Theorem:** A partition of variables is a backward equivalence iff for any uniform assignment its derivative is also uniform
 - Encode this condition in first-order logic!

Model

$$\dot{x}_1 = -\min(x_1, x_2) + x_3$$

$$\dot{x}_2 = -\min(x_1, x_2) + x_3$$

$$\dot{x}_3 = +\min(x_1, x_2) - 2x_3$$

Candidate partition

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

Equivalence condition (quantifier free)

$$\phi := (x_1 = x_2) \implies -\min(x_1, x_2) + x_3 = -\min(x_1, x_2) + x_3$$

SMT check

$$\text{sat}(\neg\phi) = \text{false}$$

Algorithm. Compute the largest equivalence that refines a given partition of variables.

1. SMT check
2. If **sat** get witness and split partition preserving its uniformity. Goto 1.
3. If **unsat** the current partition is the coarsest refinement. End.

$$\dot{x}_1 = -\min(x_1, x_2) + x_3$$

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$$\dot{x}_3 = +\min(x_1, x_2) - 2x_3$$

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



$$f((1, 1, 1)) = (0, 0, -1)$$

sat



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

unsat

Algorithm. Compute the largest equivalence that refines **a given partition of variables**.

The freedom in choosing the initial partition is useful:

- The largest equivalence can be obtained by initializing the algorithm with the trivial singleton partition
- Other partitions may be used to keep variables distinct (e.g., if they are known to start from different initial conditions)

$$\dot{x}_1 = -\min(x_1, x_2) + x_3$$

$$\dot{x}_2 = -\min(x_1, x_2) + x_3$$

$$\dot{x}_3 = +\min(x_1, x_2) - 2x_3$$

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



$$f((1, 1, 1)) = (0, 0, -1)$$

sat



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

unsat

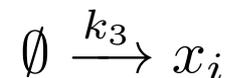
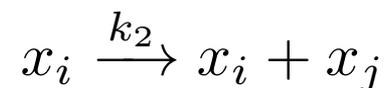
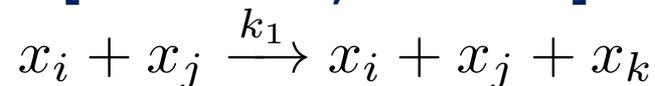
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Reaction Networks

[CONCUR'15, TACAS'16]

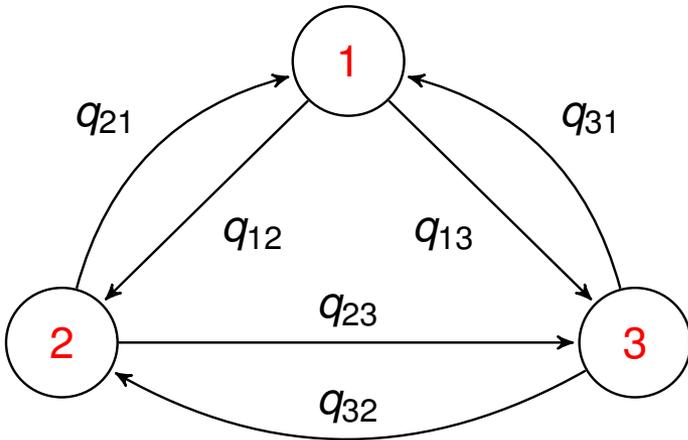


- Forward equivalence
- Backward equivalence

- Forward bisimulation
- Backward bisimulation

Analogy: Markov chain lumping

Transition diagram



Transition matrix

$$Q = \begin{bmatrix} -(q_{12} + q_{13}) & q_{12} & q_{13} \\ q_{21} & -(q_{21} + q_{23}) & q_{23} \\ q_{31} & q_{32} & -(q_{31} + q_{32}) \end{bmatrix}$$

Equations of motion (linear ODE system)

$$\frac{d\pi_i(t)}{dt} = \underbrace{q_{ii}\pi_i(t)}_{\text{flux out}} + \sum_{j \neq i} \underbrace{q_{ji}\pi_j(t)}_{\text{flux in}}$$

Ordinary lumpability

- Set $Z = \{1, \dots, n\}$ the state space of a CTMC with matrix $Q = (q_{ij})_{1 \leq i, j \leq n}$
- A partition $X = \{X_1, \dots, X_N\}$ of Z is **ordinarily lumpable** if for any pair of blocks I, J and any two states $i_1, i_2 \in I$

$$q_{i_1 J} = q_{i_2 J}, \quad q_{i J} := \sum_{j \in X_J} q_{ij}$$

- These common values form the **lumped CTMC**

Ordinary lumpability

A special case of forward equivalence:

- Let $\pi(t) = (\pi_1(t), \dots, \pi_n(t))$ be the solution of the original CTMC
- Let $\hat{\pi}(t) = (\hat{\pi}_1(t), \dots, \hat{\pi}_N(t))$ be the solution of the lumped CTMC
- Set $\Pi_{X_i}(t) := \sum_{j \in X_i} \pi_j(t)$
- Then we have

$$\hat{\pi}_i(0) = \Pi_{X_i}(0) \implies \hat{\pi}_i(t) = \Pi_{X_i}(t)$$

Example

Idle

Think time

Working

Service

$$Q = \begin{matrix} & \begin{matrix} (I, I) & (I, W) & (W, I) & (W, W) \end{matrix} \\ \begin{matrix} (I, I) \\ (I, W) \\ (W, I) \\ (W, W) \end{matrix} & \begin{bmatrix} -2\lambda & \lambda & \lambda & 0 \\ \mu & -(\mu + \lambda) & 0 & \lambda \\ \mu & 0 & -(\mu + \lambda) & \lambda \\ 0 & \mu/2 & \mu/2 & -\mu \end{bmatrix} \end{matrix}$$

$$Q_{\mathcal{N}} = \begin{matrix} & \begin{matrix} (2, 0) & (1, 1) & (0, 2) \end{matrix} \\ \begin{matrix} (2, 0) \\ (1, 1) \\ (0, 2) \end{matrix} & \begin{bmatrix} -2\lambda & 2\lambda & 0 \\ \mu & -(\mu + \lambda) & \lambda \\ 0 & \mu & -\mu \end{bmatrix} \end{matrix}$$

(Symmetry reduction for Markov chains)

Ordinary lumpability

- The criterion

$$q_{i_1 J} = q_{i_2 J}, \quad q_{i J} := \sum_{j \in X_J} q_{ij}$$

is **structural** but it implies aggregation at the ODE level

- Idea: Can we find an analogous structural criterion for a more general class of ODE systems?

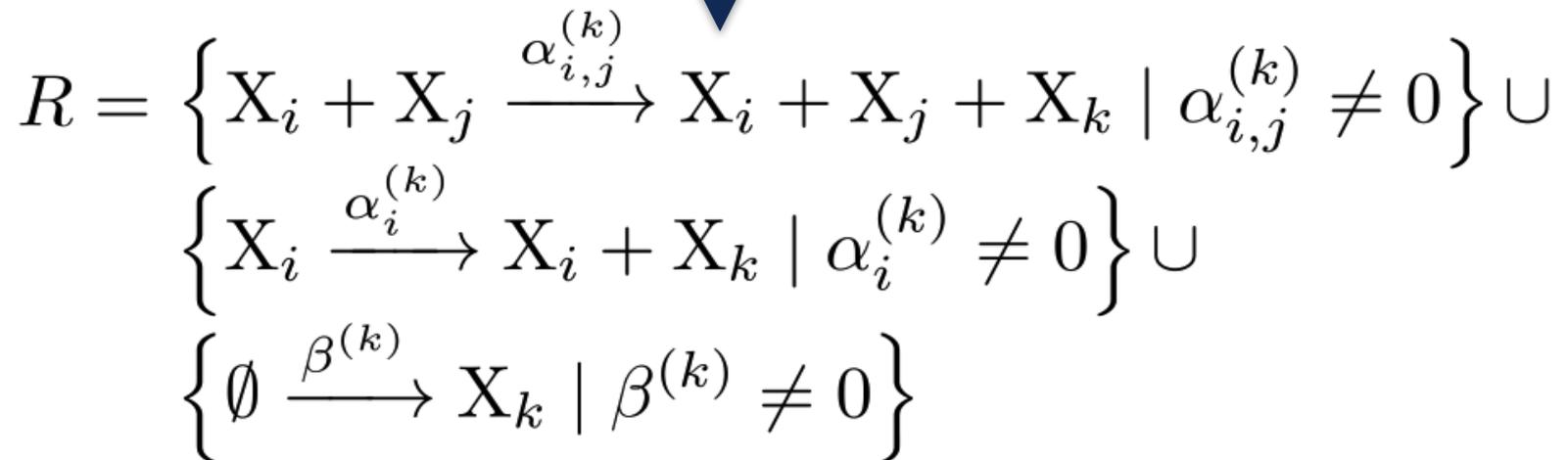
ODEs via reaction networks

- Defined for reaction networks (RN) with at most two reagents in each reaction:

$$\dot{V}_k = \sum_{1 \leq i, j \leq n} \boxed{\alpha_{i,j}^{(k)} \cdot V_i \cdot V_j} + \sum_{1 \leq i \leq n} \boxed{\alpha_i^{(k)} \cdot V_i} + \boxed{\beta^{(k)}}$$



through mass-action semantics



Based on quantities from the **RN syntax**

$$\mathbf{crr}[X, \rho] := (\rho(X) + 1) \sum_{X+\rho \xrightarrow{\alpha} \pi \in R} \alpha, \quad \mathbf{pr}(X, Y, \rho) := (\rho(X) + 1) \sum_{X+\rho \xrightarrow{\alpha} \pi \in R} \alpha \cdot \pi(Y)$$

$$\mathbf{pr}[X, H, \rho] := \sum_{Y \in H} \mathbf{pr}(X, Y, \rho)$$

For X, Y in a block, for all blocks H and partners ρ :

$$\mathbf{crr}[X, \rho] = \mathbf{crr}[Y, \rho] \quad \text{and} \quad \mathbf{pr}[X, H, \rho] = \mathbf{pr}[Y, H, \rho]$$

 It corresponds to ordinary lumpability for RNs that represent a Markov chain

Bisimulations: algorithm

Initial partition

$$\{\{X_1, X_2, X_3, X_4, X_5\}\}$$

After pre-partitioning for **crr**

$$\{\{X_1, X_2, X_4, X_5\}, \{X_3\}\}$$

$$\mathbf{crr}[X_1, \emptyset] = 1 \quad \mathbf{crr}[X_1, X_3] = 3$$

$$\mathbf{crr}[X_2, \emptyset] = 1 \quad \mathbf{crr}[X_2, X_3] = 3$$

$$\mathbf{crr}[X_3, \emptyset] = 0 \quad \mathbf{crr}[X_3, X_3] = 0$$

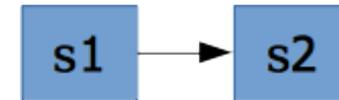
$$\mathbf{crr}[X_4, \emptyset] = 1 \quad \mathbf{crr}[X_4, X_3] = 3$$

$$\mathbf{crr}[X_5, \emptyset] = 1 \quad \mathbf{crr}[X_5, X_3] = 3$$

$$\begin{array}{l} X_1 \xrightarrow{1} X_2 \\ X_2 \xrightarrow{1} X_1 \\ X_4 \xrightarrow{1} 2X_1 + X_3 \\ X_5 \xrightarrow{1} 2X_2 + X_3 \\ X_1 + X_3 \xrightarrow{3} X_4 \\ X_2 + X_3 \xrightarrow{3} X_5 \\ X_4 + X_3 \xrightarrow{3} X_5 \\ X_5 + X_3 \xrightarrow{3} X_4 \end{array}$$

Current partition:

$$\{\{X_1, X_2, X_4, X_5\}, \{X_3\}\}$$



Partitioning according to s1 we get:

$$\{\{X_3\}, \{X_1, X_2\}, \{X_4, X_5\}\}$$

$$\mathbf{pr}[X_1, s1, \emptyset] = 1$$

$$\mathbf{pr}[X_2, s1, \emptyset] = 1$$

$$\mathbf{pr}[X_4, s1, \emptyset] = 2$$

$$\mathbf{pr}[X_5, s1, \emptyset] = 2$$

$$\begin{aligned} X_1 &\xrightarrow{1} X_2 \\ X_2 &\xrightarrow{1} X_1 \\ X_4 &\xrightarrow{1} 2X_1 + X_3 \\ X_5 &\xrightarrow{1} 2X_2 + X_3 \end{aligned}$$

$$X_1 + X_3 \xrightarrow{3} X_4$$

$$X_2 + X_3 \xrightarrow{3} X_5$$

$$X_4 + X_3 \xrightarrow{3} X_5$$

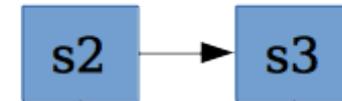
$$X_5 + X_3 \xrightarrow{3} X_4$$

Second iteration

Current partition:

$$\{\{X_3\}, \{X_1, X_2\}, \{X_4, X_5\}\}$$

Candidate splitters:



No refinement is obtained for s2

$$\mathbf{pr}[X_1, s2, \emptyset] = 0 \quad \mathbf{pr}[X_1, s2, X_3] = 0$$

$$\mathbf{pr}[X_2, s2, \emptyset] = 0 \quad \mathbf{pr}[X_2, s2, X_3] = 0$$

$$\mathbf{pr}[X_4, s2, \emptyset] = 1 \quad \mathbf{pr}[X_4, s2, X_3] = 0$$

$$\mathbf{pr}[X_5, s2, \emptyset] = 1 \quad \mathbf{pr}[X_5, s2, X_3] = 0$$

$X_1 \xrightarrow{1} X_2$
$X_2 \xrightarrow{1} X_1$
$X_4 \xrightarrow{1} 2X_1 + X_3$
$X_5 \xrightarrow{1} 2X_2 + X_3$
$X_1 + X_3 \xrightarrow{3} X_4$
$X_2 + X_3 \xrightarrow{3} X_5$
$X_4 + X_3 \xrightarrow{3} X_5$
$X_5 + X_3 \xrightarrow{3} X_4$

Third iteration

Current partition:

$$\{\{X_3\}, \{X_1, X_2\}, \{X_4, X_5\}\}$$

Candidate splitters:

s3



No refinement is obtained for s3

$$\mathbf{pr}[X_1, s3, \emptyset] = 0 \quad \mathbf{pr}[X_1, s3, X_3] = 3$$

$$\mathbf{pr}[X_2, s3, \emptyset] = 0 \quad \mathbf{pr}[X_2, s3, X_3] = 3$$

$$\mathbf{pr}[X_4, s3, \emptyset] = 0 \quad \mathbf{pr}[X_4, s3, X_3] = 3$$

$$\mathbf{pr}[X_5, s3, \emptyset] = 0 \quad \mathbf{pr}[X_5, s3, X_3] = 3$$

$$\begin{aligned} X_1 &\stackrel{1}{\rightarrow} X_2 \\ X_2 &\stackrel{1}{\rightarrow} X_1 \\ X_4 &\stackrel{1}{\rightarrow} 2X_1 + X_3 \\ X_5 &\stackrel{1}{\rightarrow} 2X_2 + X_3 \\ X_1 + X_3 &\stackrel{3}{\rightarrow} X_4 \\ X_2 + X_3 &\stackrel{3}{\rightarrow} X_5 \\ X_4 + X_3 &\stackrel{3}{\rightarrow} X_5 \\ X_5 + X_3 &\stackrel{3}{\rightarrow} X_4 \end{aligned}$$

Time Complexity: $O(mn \log n)$

Third iteration

Current partition:

$$\{\{X_3\}, \{X_1, X_2\}, \{X_4, X_5\}\}$$

Candidate splitters:

s3



No refinement is obtained for s3

$$\mathbf{pr}[X_1, s3, \emptyset] = 0 \quad \mathbf{pr}[X_1, s3, X_3] = 3$$

$$\mathbf{pr}[X_2, s3, \emptyset] = 0 \quad \mathbf{pr}[X_2, s3, X_3] = 3$$

$$\mathbf{pr}[X_4, s3, \emptyset] = 0 \quad \mathbf{pr}[X_4, s3, X_3] = 3$$

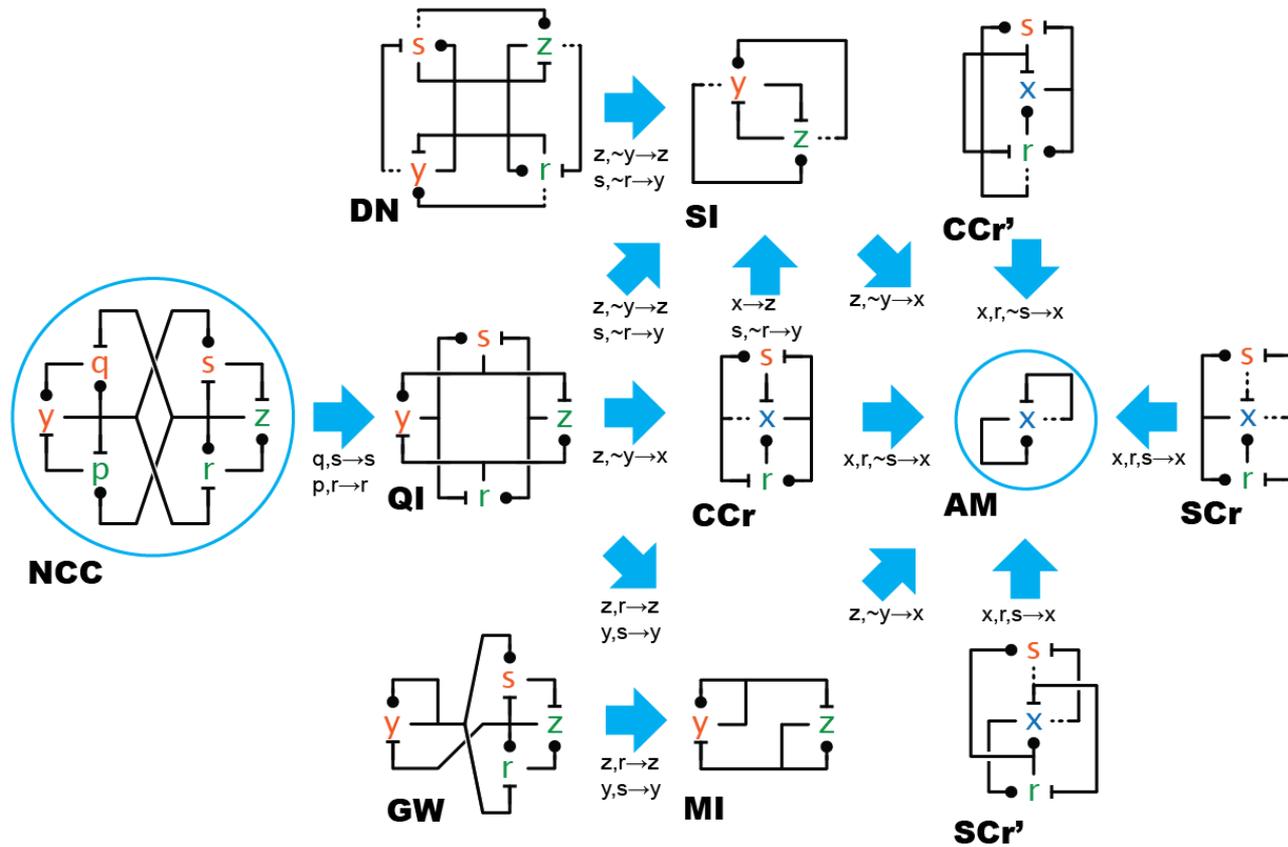
$$\mathbf{pr}[X_5, s3, \emptyset] = 0 \quad \mathbf{pr}[X_5, s3, X_3] = 3$$

$$\begin{aligned} X_1 &\xrightarrow{1} X_2 \\ X_2 &\xrightarrow{1} X_1 \\ X_4 &\xrightarrow{1} 2X_1 + X_3 \\ X_5 &\xrightarrow{1} 2X_2 + X_3 \\ X_1 + X_3 &\xrightarrow{3} X_4 \\ X_2 + X_3 &\xrightarrow{3} X_5 \\ X_4 + X_3 &\xrightarrow{3} X_5 \\ X_5 + X_3 &\xrightarrow{3} X_4 \end{aligned}$$

Based on [Derisavi et al., 2003]
and [Valmari & Franceschinis, 2010]

Case study: adaptation as evolution

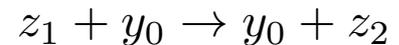
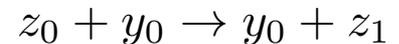
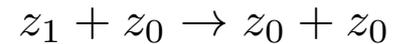
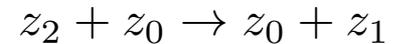
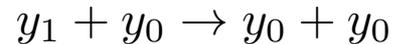
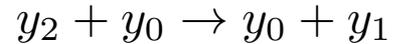
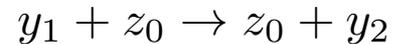
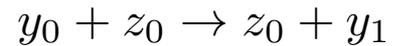
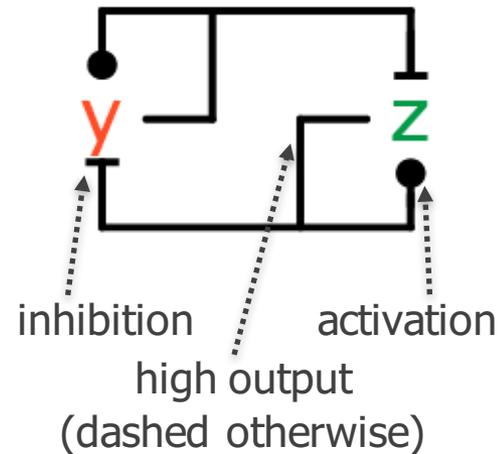
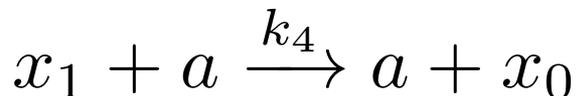
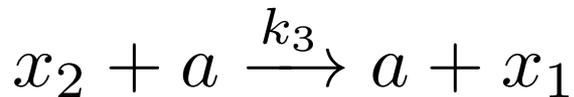
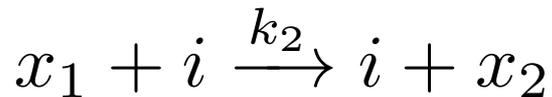
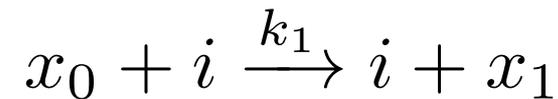
"Zoo" of influence networks



From [Cardelli'14]

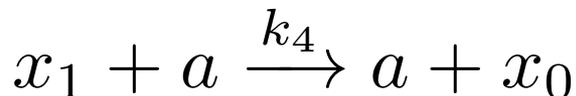
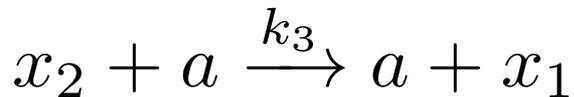
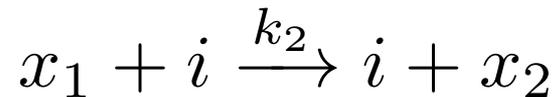
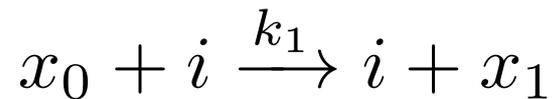
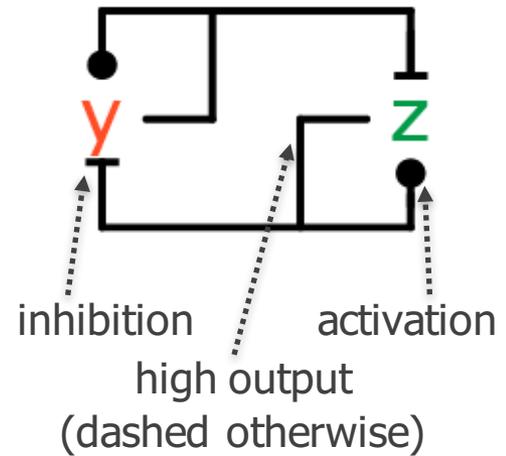
- Each node x corresponds to a triplet of chemical species x_0, x_1, x_2
- Each triplet gives rise to four chemical reactions

high interm. low



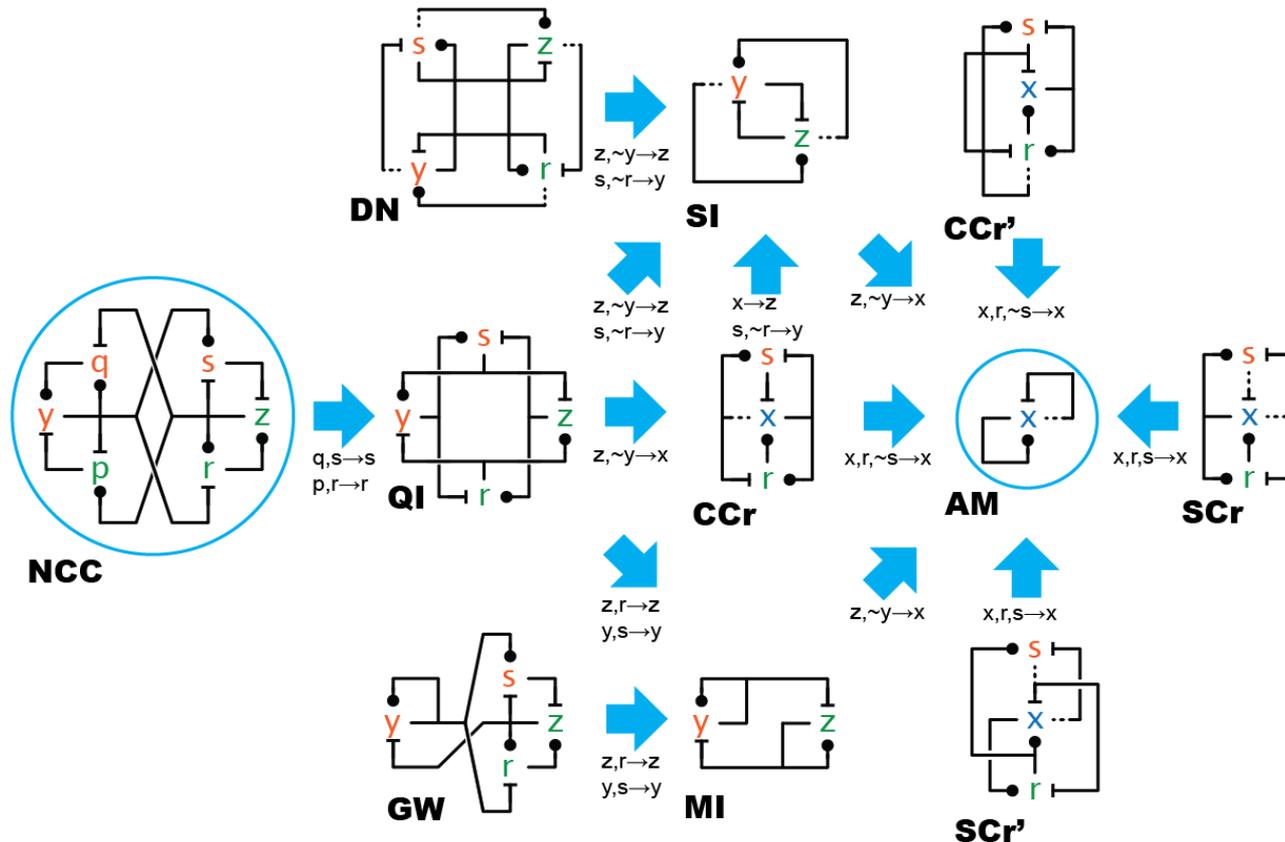
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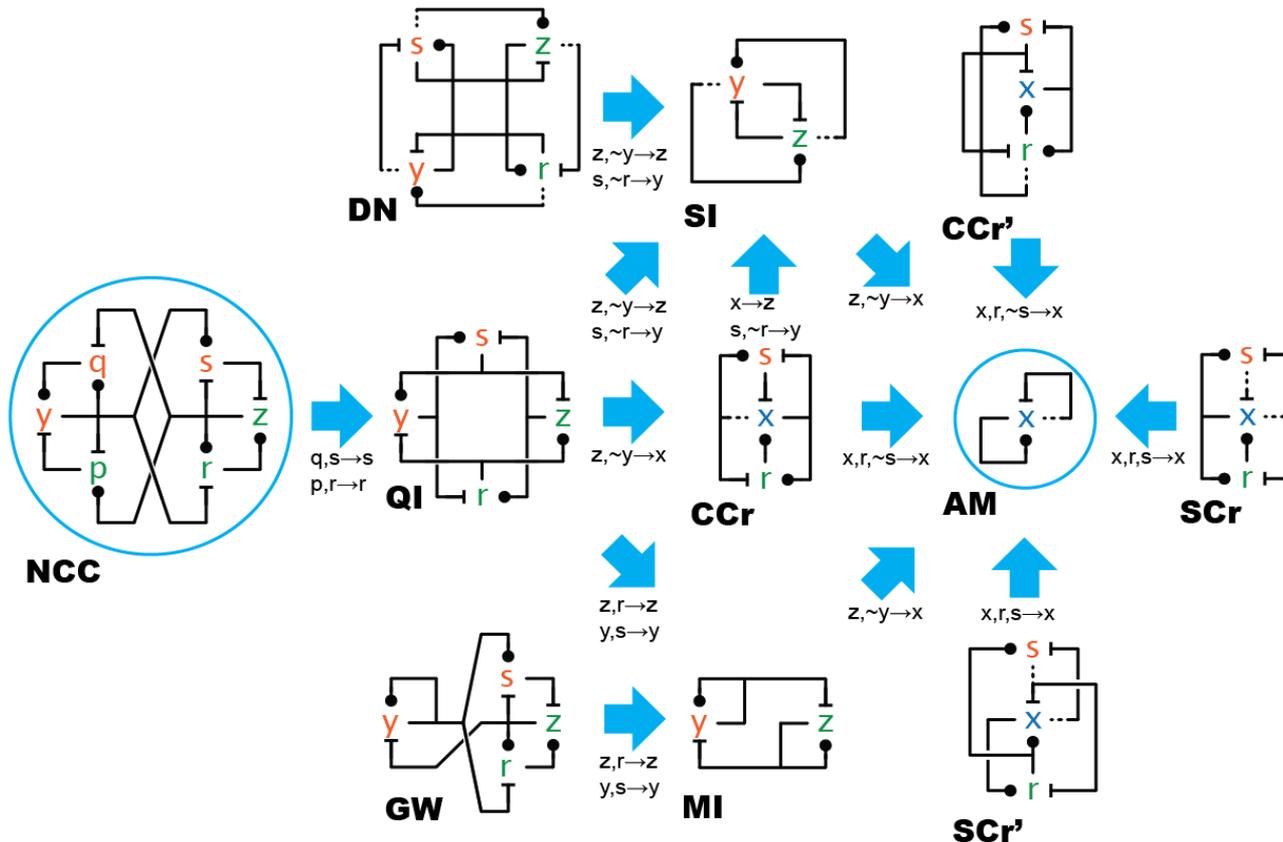


$$\begin{aligned} \frac{dX_0(t)}{dt} = & -k_1 X_0(t) I(t) + \\ & + k_4 X_1(t) A(t) + \\ & + \dots \end{aligned}$$

mass-action semantics
(degree-two polynomials)

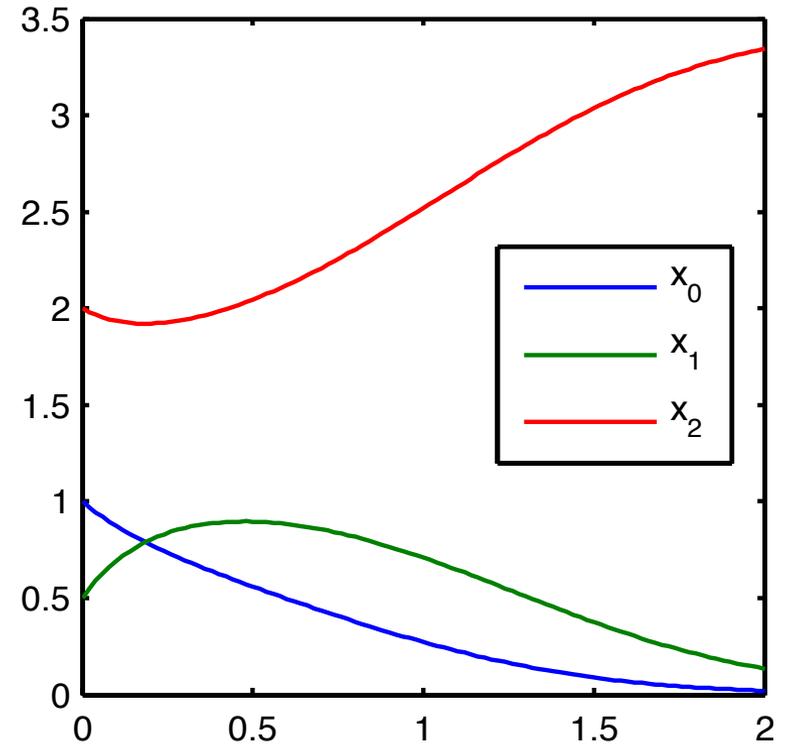
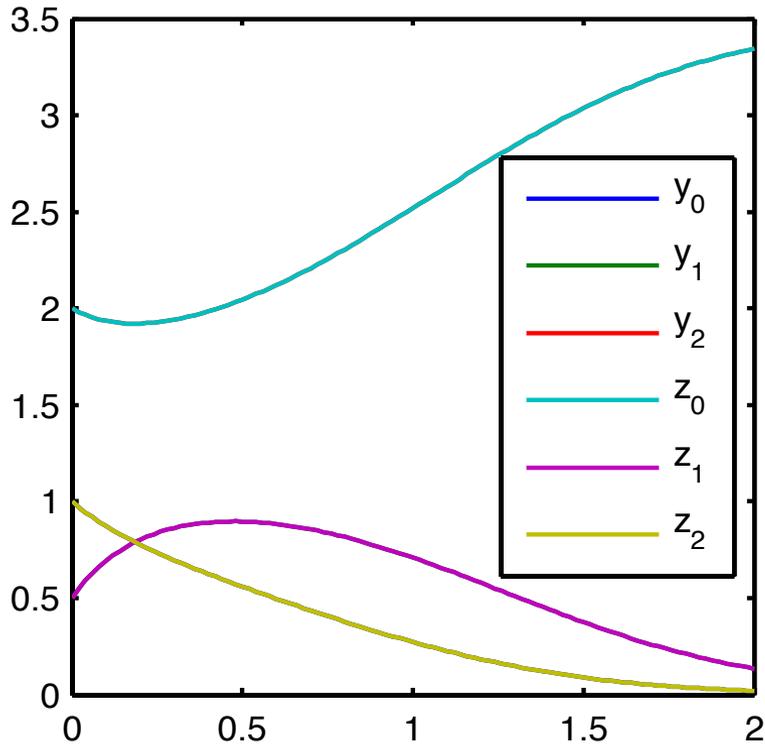


- Emulation is a mapping between species of two influence networks such that related species have equal solutions at all time points

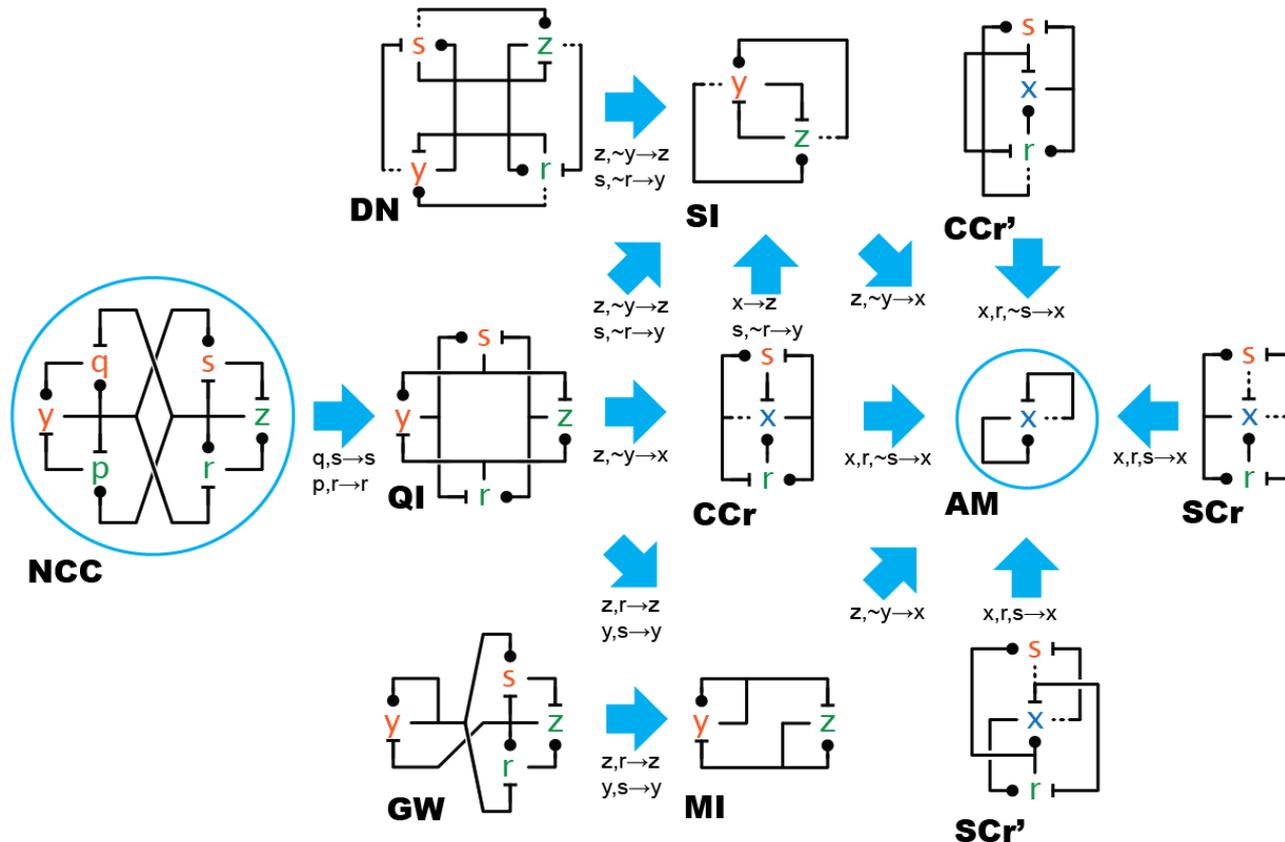


- For example $z, \sim y \rightarrow x$ for MI/AM means

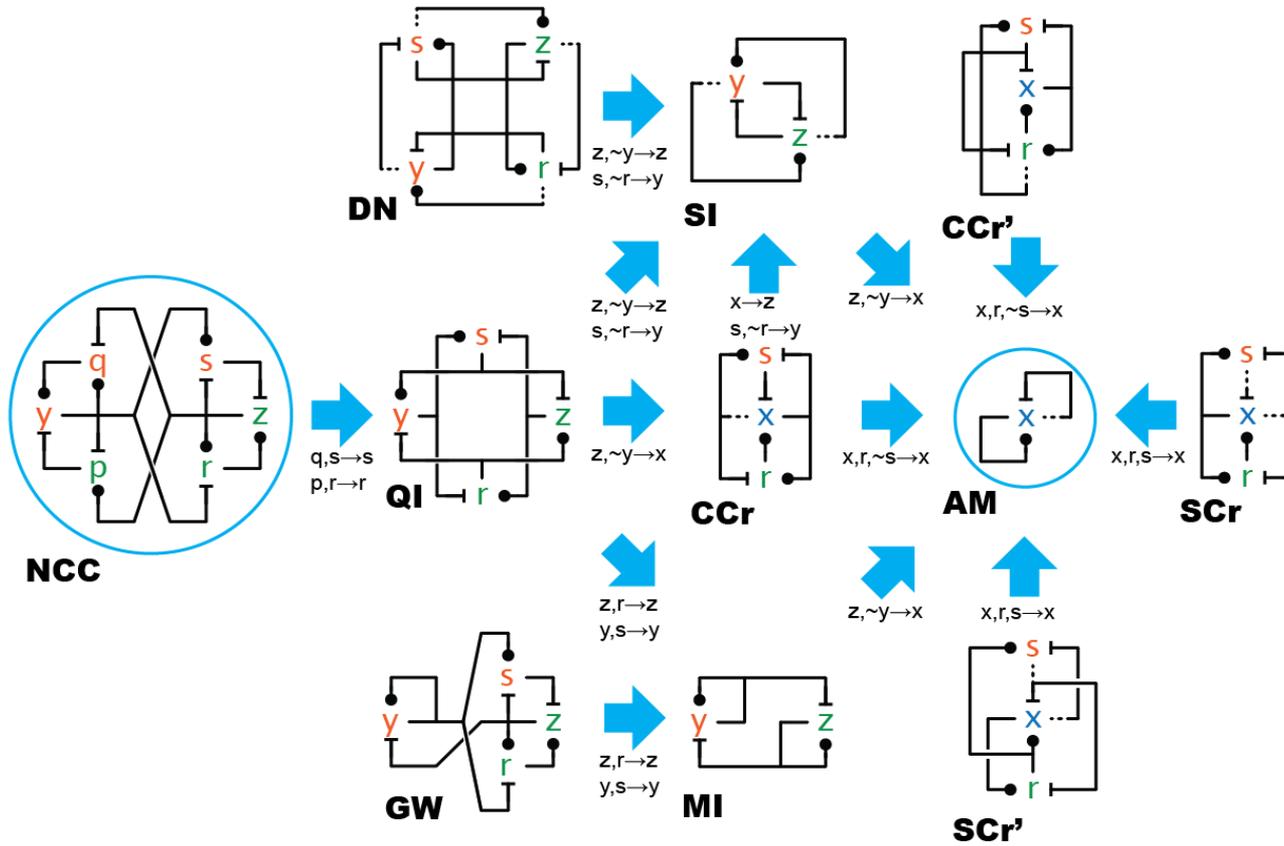
$$z_0, y_2 \rightarrow x_0, z_2, y_0 \rightarrow x_2, z_1, y_1 \rightarrow x_1$$



- For example $z, \sim y \rightarrow x$ for MI/AM means
 $z_0, y_2 \rightarrow x_0, z_2, y_0 \rightarrow x_2, z_1, y_1 \rightarrow x_1$



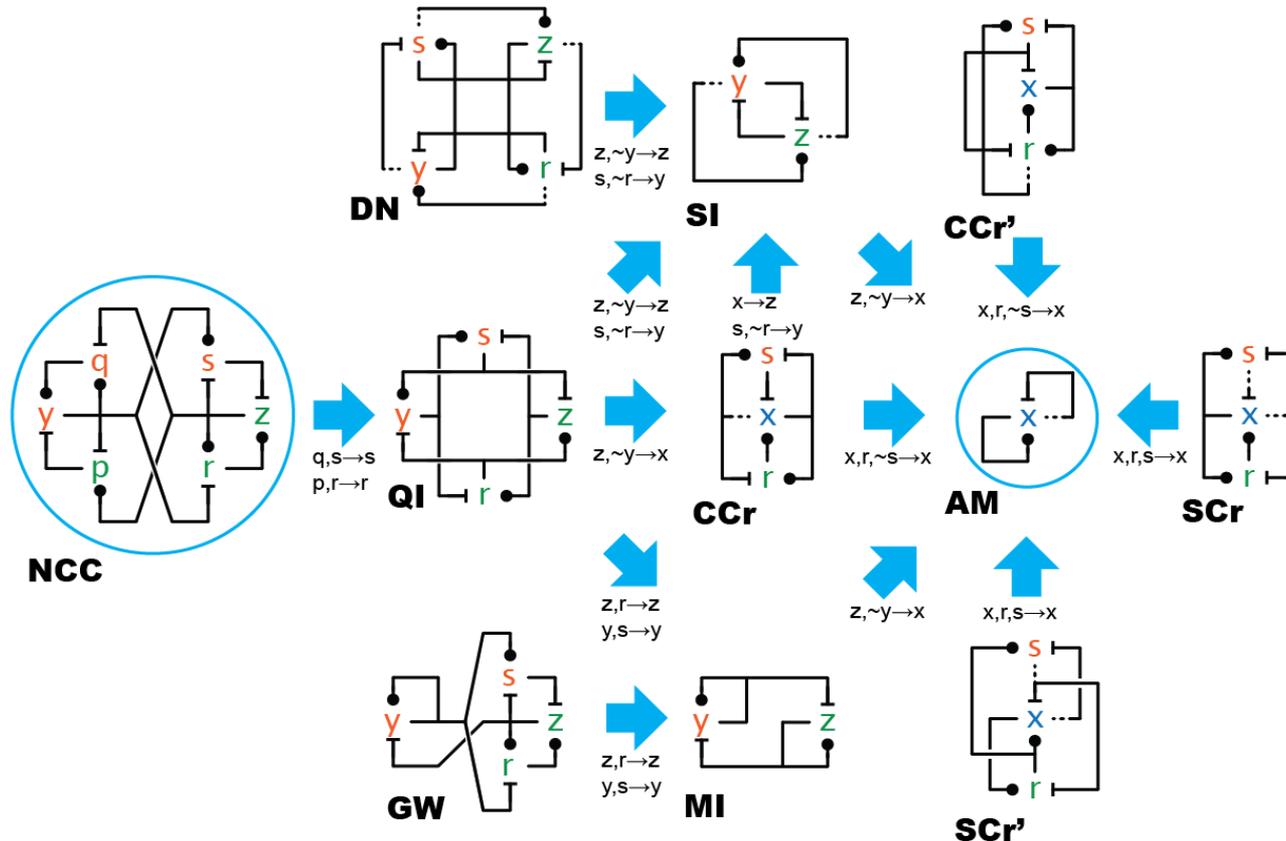
- This can be discovered automatically by computing the largest backward bisimulation on the **union chemical reaction network**



- Largest backward bisimulation:

$$\left\{ \left\{ z_0, y_2, x_0 \right\}, \left\{ z_2, y_0, x_2 \right\}, \left\{ z_1, y_1, x_1 \right\} \right\}$$

Analysis with differential equivalences



- Backward bisimulations found with mass-action assumptions carry over to other kinetic assumptions (Hill kinetics, checked with backward differential equivalence)

Numerical results

Original Model			Forward bisimulation		Forward equivalence	
<i>ID</i>	<i>Reactions</i>	<i>Vars</i>	<i>Vars</i>	<i>Time</i>	<i>Vars</i>	<i>Time</i>
M1	8620	745	745	0.65 s	105	> 2h
M2	3680	354	354	0.28 s	105	~ 1 h
M3	4944	411	411	0.13 s	47	10 min
M4	3477	348	348	0.25 s	215	~1.5 h

[POPL'16]

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[POPL'16]

- Forward bisimulation may miss reductions

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[POPL'16]

- Forward bisimulation may miss reductions
- But forward equivalence is significantly more time consuming

Numerical results

Original Model			Forward bisimulation		Backward bisimulation	
<i>ID</i>	<i>Reactions</i>	<i>Vars</i>	<i>Vars</i>	<i>Time</i>	<i>Vars</i>	<i>Time</i>
CRN1	3,538,944	262,146	222	7.49 s	222	12 s
CRN5	194,054	14,531	10,855	0.40 s	6,634	0.6 s
CRN13	24	18	18	4 ms	7	4 ms
AFF2	8,814,880	1,270,433	160,951	~ 10 min	639,509	~ 3 min

[TACAS'16]

Numerical results

Original Model			Forward bisimulation		Backward bisimulation	
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[TACAS'16]

- Bisimulation algorithms scale well (original CRN1 could not be solved on our machines)

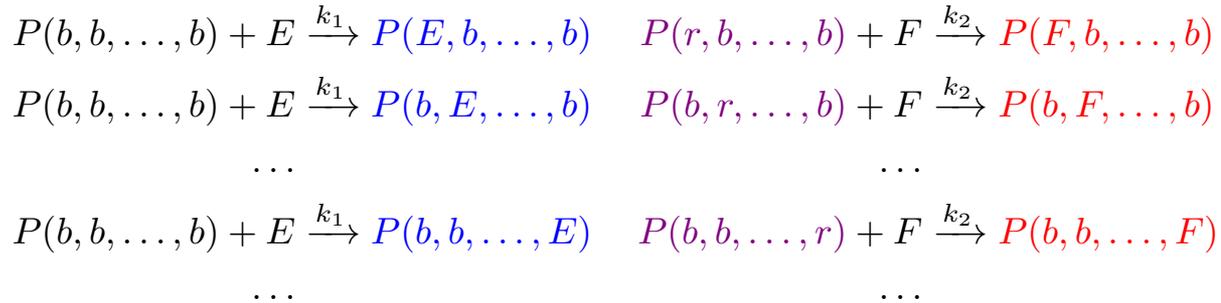
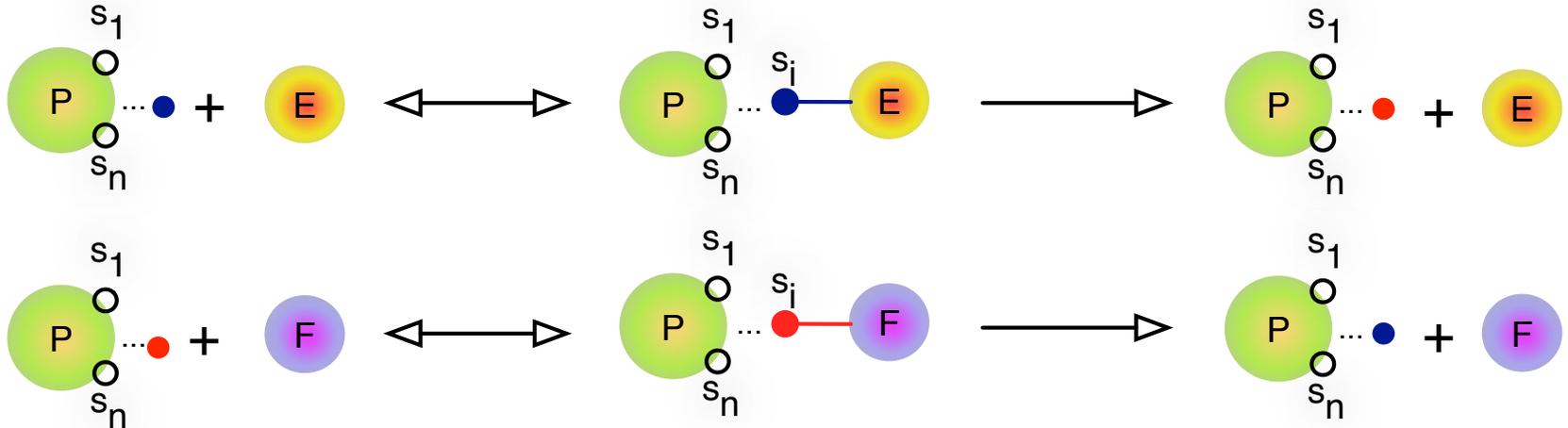
Numerical results

Original Model			Forward bisimulation		Backward bisimulation	
<i>ID</i>	<i>Reactions</i>	<i>Vars</i>	<i>Vars</i>	<i>Time</i>	<i>Vars</i>	<i>Time</i>
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[TACAS'16]

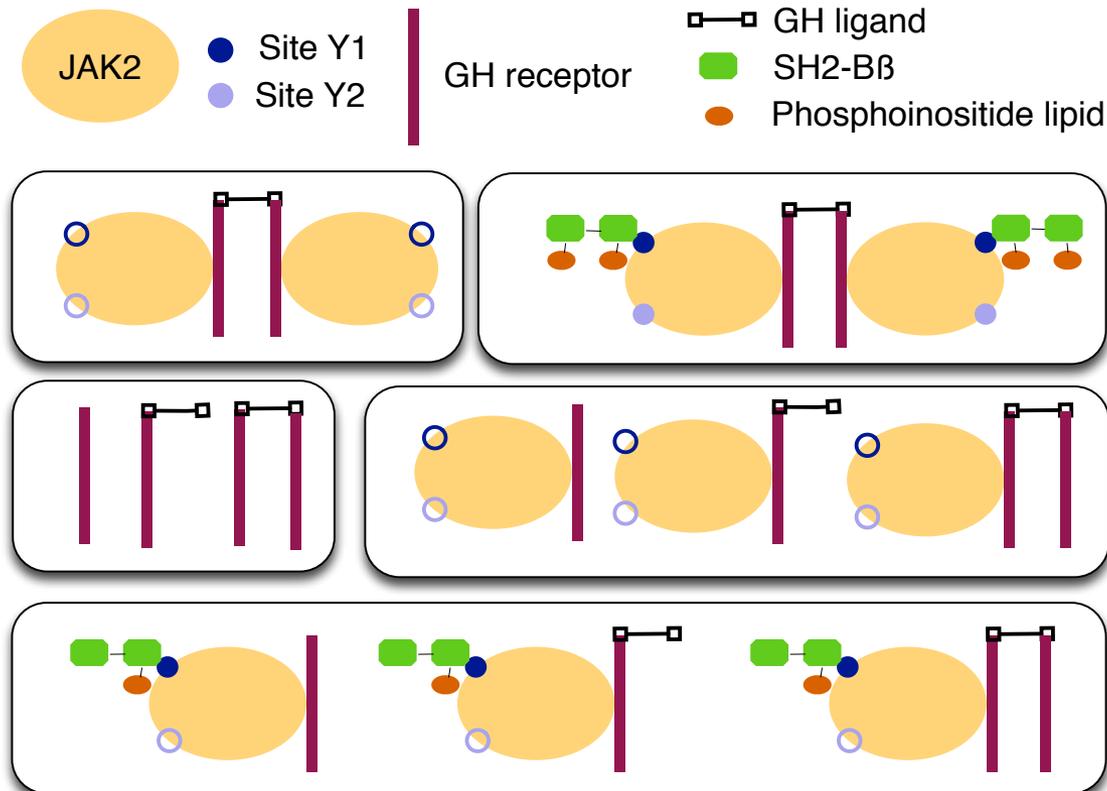
- Bisimulation algorithms scale well
(original CRN1 could not be solved on our machines)
- Forward and backward bisimulation are not comparable

Physical interpretations



- Symmetry reduction in protein interaction networks

Physical interpretations



[Barua et al. '09]

- Endocytosed complexes are equivalent when they have the same structure up to the conformation of the GH ligand

Tool support: ERODE

The screenshot displays the ERODE software interface. On the left, a Package Explorer shows a project structure with folders for 'ERODE', 'Examples', and 'ExampleODE_BDE ode'. The main area contains two code editors. The left editor shows the 'ExampleODE' model with parameters (r1, r2), initial conditions (Au, Ap, B), and a set of ordinary differential equations (ODEs) for species Au, Ap, B, AuB, and ApB. The right editor shows the 'ExampleRN' model with similar parameters and initial conditions, but with a different set of reactions. Below the code editors is a console window showing the output of the simulation, including a welcome message and a goodbye message with the completion time. On the right side, a plot window titled 'simulateODE(tEnd=1.0) ExampleRN - ODE solutions - All species/variables' shows the concentration of various species over time from 0 to 1.0. The plot includes curves for Au, Ap, B, AuB, and ApB, with Au and Ap decreasing and B, AuB, and ApB increasing over time.

Importing the model ExampleRN from the editor
 Read parameters: 2, read species: 5, read reactions: 6, read reagents: 6, read products: 6.

Simulating the ODEs of the crn with name ExampleRN ... completed. Time necessary 0.001 (s).

```
*****
*****
***** Welcome to ERODE [29/01/2016 09-30-21-084] *****
*****
*****
***** Goodbye from ERODE [29/01/2016 09-30-21-084] *****
*****
***** Completed at time [29/01/2016 09-30-21-331] *****
*****
```

- Equivalences allow to automatically reduce large systems of nonlinear ODE **exactly**
 - Encoding into SMT for general case: complete but slower (although it can be made more efficient)
 - Efficient partition refinement for multivariate polynomials of degree at most two:
 - Quite a large class on its own (contains affine systems and mass-action CRNs)
 - Sometimes nonlinear systems are handled by first expanding into such a class of polynomials

- Still insisting on **exact reductions**:
 - Extend bisimulation results to arbitrary-degree polynomials
 - Go beyond partition refinement? It is not possible to encode arbitrary constraints on the initial partition to be refined [LICS'16]
 - For the forward case, go beyond sum-of-variables? Arbitrary linear transformations may give further compressions

- **Approximate variants** are highly desired
 - Problem is how to compute error bounds a priori, without solving the original model first
 - Some techniques for nonlinear systems have been developed **but**
 1. No algorithm is available to compute candidate partition [DSN'13, TAC'16, Bortolussi & Gast'16]
 2. Bounds tend to be loose because only part of the information about the structure of the system is exploited [DSN'13, TAC'16]

Some related work

- Fragmentation/lumpability in Kappa [Danos/Feret]: domain specific
- Exact and ordinary lumpability for Markov chains [Buchholz]: special case of ODE equivalences
- Lumping algorithms for Markov chains [Derisavi et al., Valmari & Franceschinis]: special cases of minimization algorithms for forward and backward RN bisimulation
- Exact lumpability in CRNs [Li & Rabitz]: no algorithm available; forward bisimulation special case
- Exact bisimulations for control systems [Pappas]: preservation of the controllability subspace
- Model order reduction (MOR) techniques [Antoulas]: mostly for linear systems, approximate without error bounds

References (1/2)

- G. Li, and H. Rabitz: *A general analysis of exact lumping in chemical kinetics*. **Chemical Engineering Science** 44 (1989) 1413–1430
- P. Buccholz: *Exact and Ordinary Lumpability in Finite Markov Chains*. **Journal of Applied Probability**, 31 59–75 (1994)
- S. Derisavi,, H. Hermanns, W. Sanders: *Optimal state-space lumping in Markov chains*. **Inf. Process. Lett.** 87 (2003) 309–315
- G. J. Pappas: *Bisimilar linear systems*. **Automatica**, 39(12):2035–2047, 2003.
- A. Antoulas: *Approximation of Large-Scale Dynamical Systems*. Advances in Design and Control. SIAM, 2005.
- J. Hillston: *Fluid Flow Approximation of PEPA Models*. **QEST 2005**
- D. Barua, J. R. Faeder, and J. M. Haugh: *A bipolar clamp mechanism for activation of jak-family protein tyrosine kinases*. **PLoS Computational Biology**, 5(4), 2009
- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine: *Abstracting the differential semantics of rule-based models: Exact and automated model reduction*. **LICS 2010**

- A.Valmari, G Franceschinis: Simple $O(m \log n)$ time Markov Chain lumping. **TACAS 2010**
- G. Iacobelli, M. Tribastone: *Lumpability of Fluid Models with Heterogeneous Agent Types*. **DSN 2013**
- L. Cardelli: *Morphisms of reaction networks that couple structure to function*. **BMC Systems Biology**, 2014
- L. Cardelli, M. Tribastone, M. Tschaikowski, A. Vandin: *Forward and backward bisimulations for chemical reaction networks*. **CONCUR 2015**
- L. Cardelli, M. Tribastone, M. Tschaikowski, A. Vandin: *Symbolic computation of differential equivalences*, **POPL 2016**
- L. Cardelli, M. Tribastone, M. Tschaikowski, A. Vandin. *Efficient syntax-driven lumping of differential equations*, **TACAS 2016**
- L. Cardelli, M. Tribastone, M. Tschaikowski, A. Vandin. *Comparing Chemical Reaction Networks: A Categorical and Algorithmic Perspective*, **LICS 2016**
- M. Tschaikowski, M. Tribastone. *Approximate reduction of heterogeneous models with differential hulls*, **Transactions on Automatic Control**, 2016
- L. Bortolussi and N. Gast: *Mean Field Approximation of Uncertain Stochastic Models*. **DSN 2016**