Molecules as Automata

Representing Biochemical Systems as Collectives of Interacting Automata

Luca Cardelli

Microsoft Research

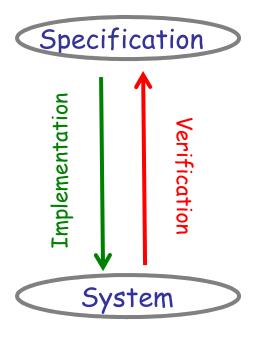
WADT, Pisa, 2008-06-14

http://LucaCardelli.name

Formal Methods vs. Scientific Method

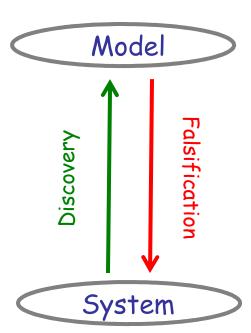
Direct Engineering

Reverse Engineering



<- Abstract ->

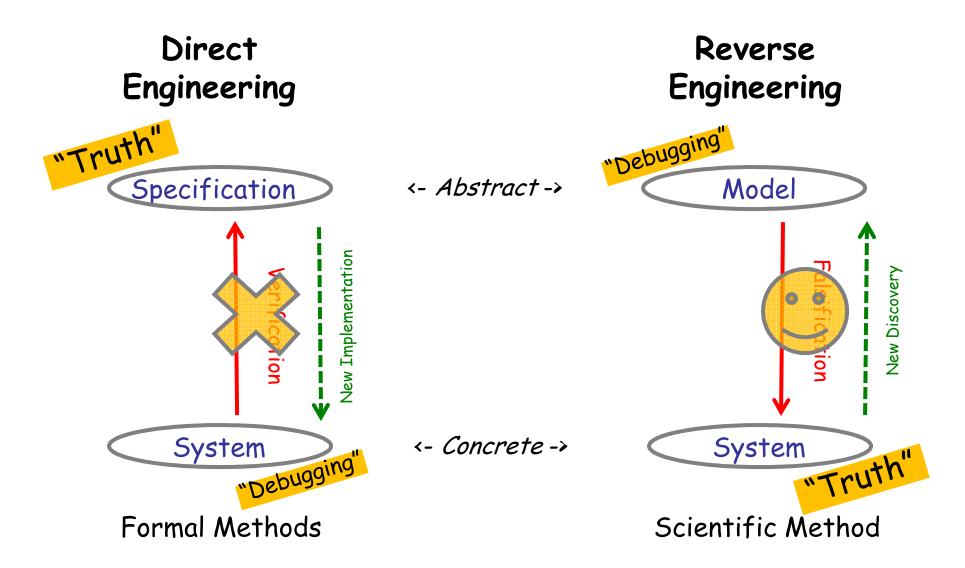
<- Concrete ->



Formal Methods

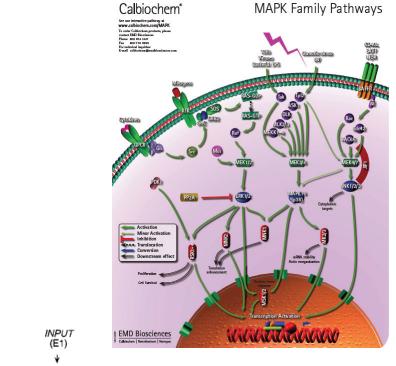
Scientific Method

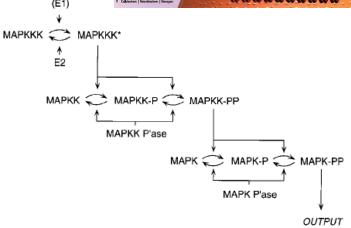
Formal Methods vs. Scientific Method



Motivation: Cells Compute

- No survival without computation!
 - Finding food
 - Avoiding predators
- How do they compute?
 - Unusual computational paradigms.
 - Proteins: do they work like electronic circuits?
 - Genes: what kind of software is that?
- Signaling networks
 - Clearly "information processing"
 - They are "just chemistry": molecule interactions
 - But what are their principles and algorithms?
- Complex, higher-order interactions
 - MAPKKK = MAP Kinase Kinase: that which operates on that which operates on that which operates on protein.
- General models of biological computation
 - What are the appropriate ones?

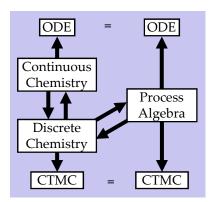




<u>Ultrasensitivity in the mitogen-activated protein cascade,</u> Chi-Ying F. Huang and James E. Ferrell, Jr., 1996, <u>Proc.</u> <u>Natl. Acad. Sci. USA</u>, 93, 10078-10083.

Aims

- Connections between modeling approaches
 - Connecting the discrete/concurrent/stochastic/molecular approach
 - to the continuous/sequential/deterministic/population approach
- Connecting syntax with semantics
 - Syntax = model presentation (equations/programs/diagrams/blobs etc.)
 - Semantics = state space (generated by the syntax)



- Ultimately, connections between analysis techniques
 - We need (and sometimes have) good semantic techniques to analyze state spaces (e.g. calculus, but also increasingly modelchecking)
 - But we need equally good syntactic techniques to structure complex models (e.g. compositionality) and analyze them (e.g. process algebra)

(Macro-) Molecules as (Interacting) Automata

• Concurrent

Asynchronous

• Stochastic

Stateful

Discrete

Interacting

(math is based on processes, not functions)

(no global clock)

(or nondeterministic)

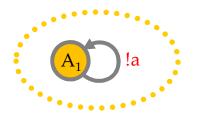
(e.g. phosphorylation state)

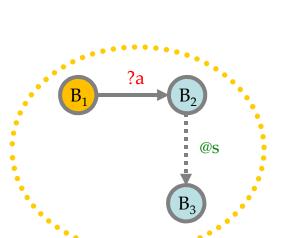
(transitions between states)

(an "interaction" can be pretty much anything you want that changes molecular state)

Based on work on process algebra and biological modeling;
 see references in related papers.





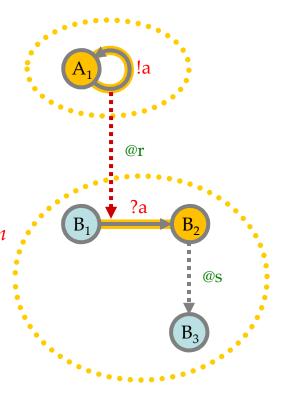


- A_1 is a state
- is a *channel* i.e. a named *interaction interface* (e.g. a surface patch)
- ?,! indicate any *complementarity* of interaction (e.g. charge)
- ?a, !a indicate complementary actions,
- @r, @s are rates



Kinetic laws:

Two complementary actions may result in an interaction.



 A_1 is a state

is a *channel* i.e. a named *interaction interface* (e.g. a surface patch)

?,! indicate any *complementarity* of interaction (e.g. charge)

?a, !a indicate *complementary actions*, joined by an interaction arrow ••••

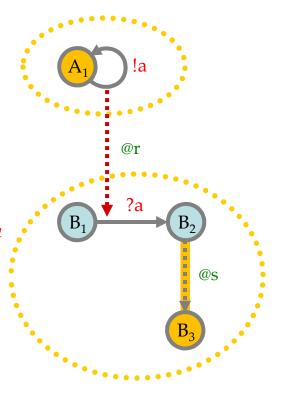
@r, @s are rates



Kinetic laws:

Two complementary actions may result in an interaction.

A decay may happen spontaneously.



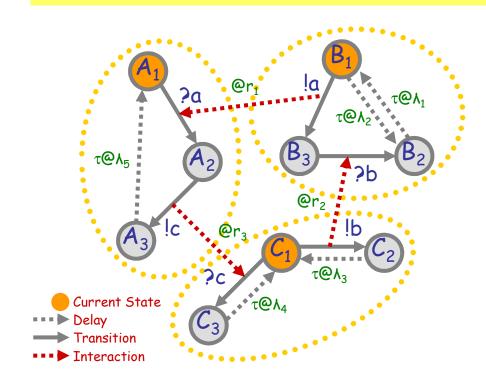
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?,! indicate any *complementarity* of interaction (e.g. charge)

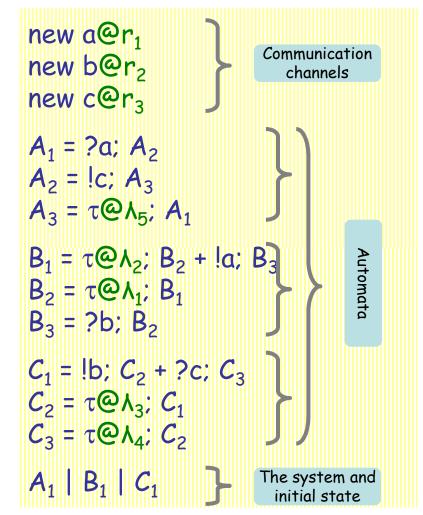
?a, !a indicate *complementary actions*, joined by an interaction arrow ••••

@r, @s are rates

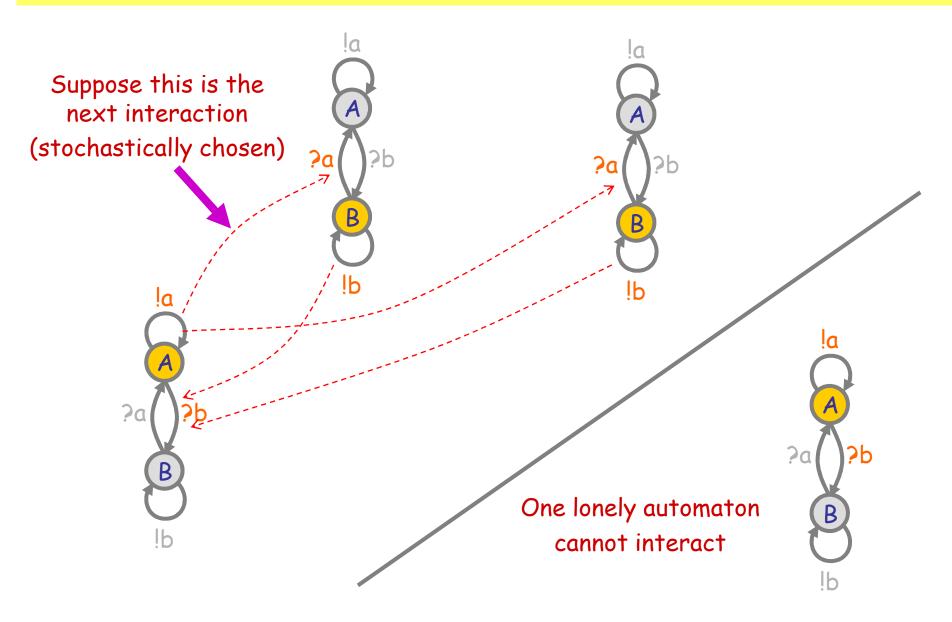


Interactions have rates. Actions DO NOT have rates.

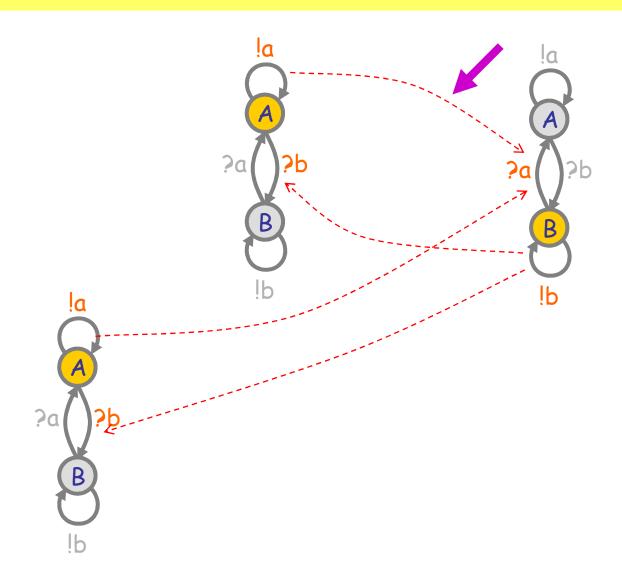
The equivalent process algebra model



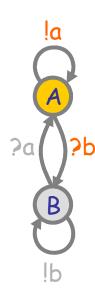
Interactions in a Population

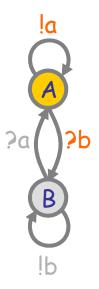


Interactions in a Population



Interactions in a Population



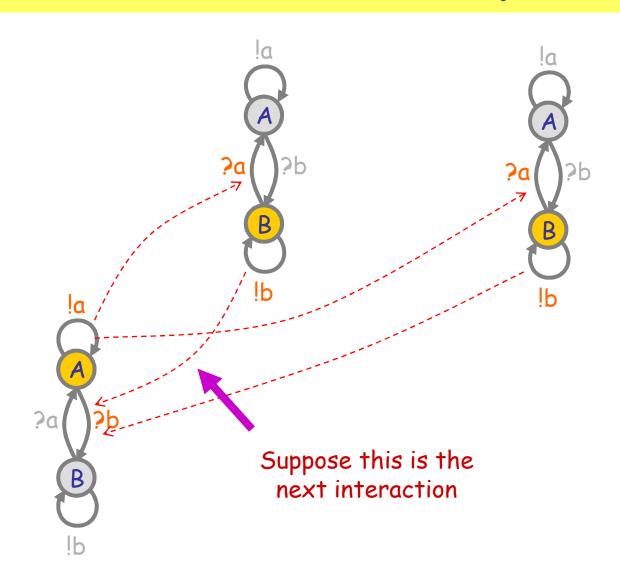






All-A stable population

Interactions in a Population (2)



Interactions in a Population (2)





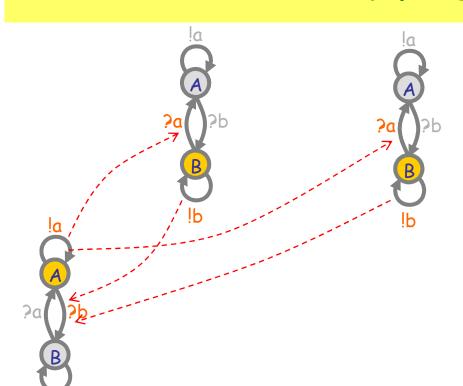




All-B stable population

Nondeterministic population behavior ("multistability")

CTMC Semantics



• r A R CTMC

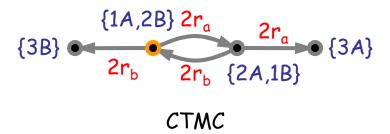
(homogeneous) Continuous Time Markov Chain

- directed graph with no self loops
- nodes are system states
- arcs have transition rates

Probability of holding in state A:

$$Pr(H_A>t) = e^{-rt}$$

in general, $Pr(H_A > t) = e^{-Rt}$ where R is the sum of all the exit rates from A



Stochastic Automata Collectives

• "Collective":

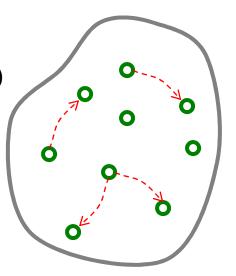
- A large set of interacting finite state automata:
 - Not quite language automata ("large set")
 - Not quite cellular automata ("interacting" but not on a grid)
 - Not quite process algebra ("collective behavior")
 - Cf. multi-agent systems and swarm intelligence



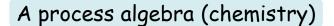
- Interactions have rates
 - Not quite discrete (hundreds or thousands of components)
 - Not quite continuous (non-trivial stochastic effects)
 - Not quite hybrid (no "switching" between regimes)



- Which is a large set of stochastically interacting molecules/proteins
- Are proteins finite state and subject to automata-like transitions?
 - Let's say they are, at least because:
 - Much of the knowledge being accumulated in Systems Biology is described as state transition diagrams [Kitano].



Chemistry vs. Automata



r:
$$A + B \rightarrow_{k1} C + D$$

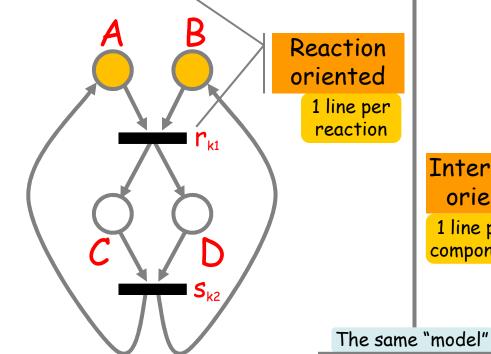
s: $C + D \rightarrow_{k2} A + B$

$$S: C + D \rightarrow_{\bowtie} A + B$$

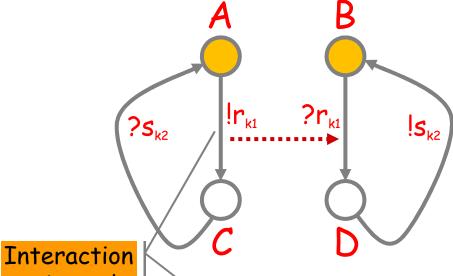
Does A become C or D?

Maps to

a CTMC



A different process algebra (automata)



oriented

1 line per component

Maps to

a CTMC

$$A = !r_{ki}; C$$

$$C = ?s_{k2}; A$$

$$B = ?r_{kl}; D$$

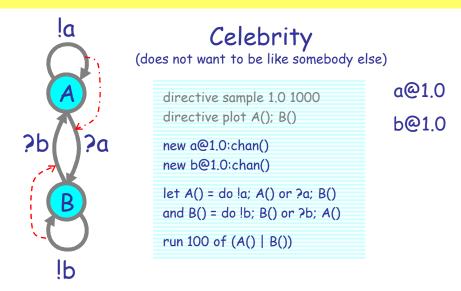
$$D = !s_{k2}; B$$

A Petri-Net-like representation. Precise and dynamic but not modular, scalable, or maintainable.

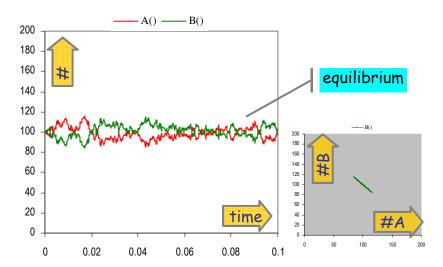
A compositional graphical representation (precise, dynamic and modular) and the corresponding calculus.

Groupies and Celebrities

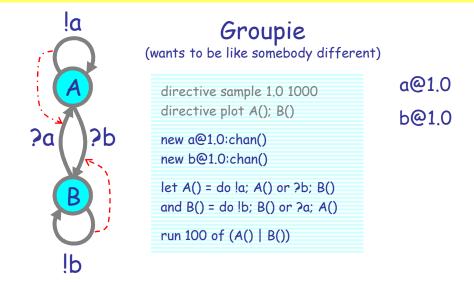
Groupies and Celebrities



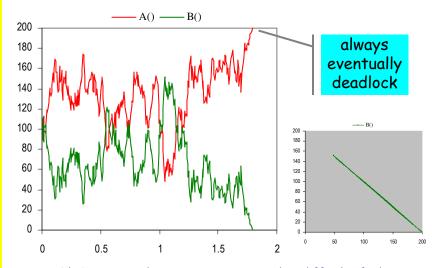
A stochastic collective of celebrities:



Stable because as soon as a A finds itself in the majority, it is more likely to find somebody in the same state, and hence change, so the majority is weakened.



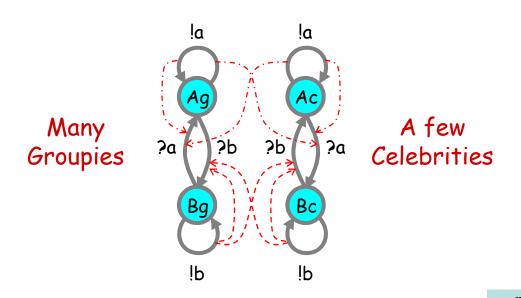
A stochastic collective of groupies:



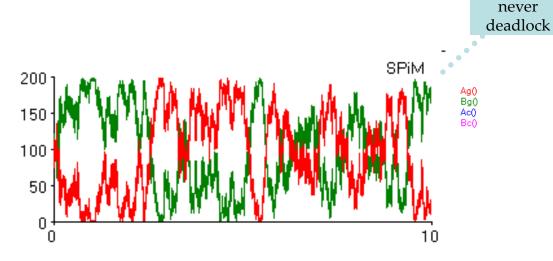
Unstable because within an A majority, an A has difficulty finding a B to emulate, but the few B's have plenty of A's to emulate, so the majority may switch to B. Leads to deadlock when everybody is in the same state and there is nobody different to emulate.

Both Together

A way to break the deadlocks: Groupies with just a few Celebrities



directive sample 10.0 directive plot Aq(); Bq(); Ac(); Bc() new a@1.0:chan() new b@1.0:chan() let Ac() = do!a; Ac() or ?a; Bc()and Bc() = do !b; Bc() or ?b; Ac() let Ag() = do!a; Ag() or?b; Bg()and Bg() = do!b; Bg() or ?a; Ag()run 1 of Ac()



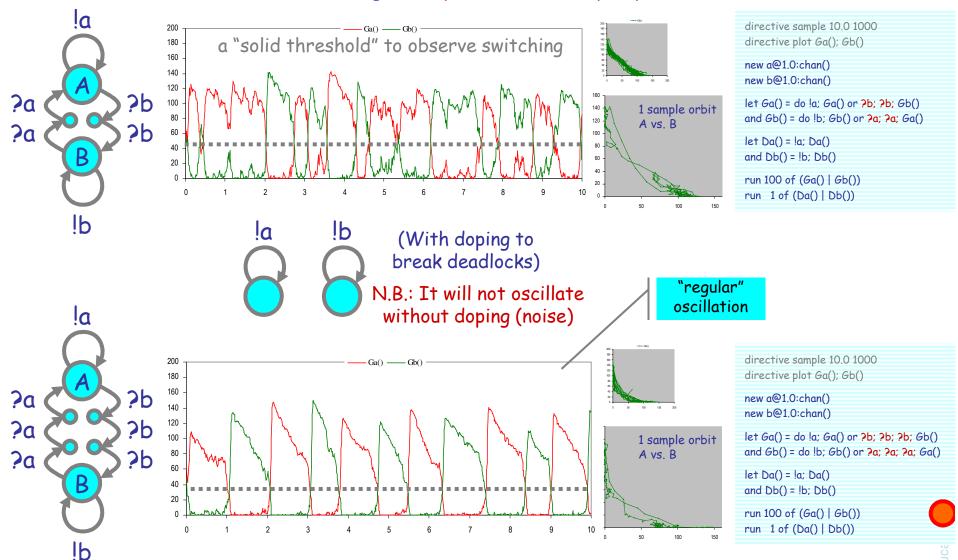
A tiny bit of "noise" can make a huge difference

run 100 of (Ag() | Bg())

Regularity can arise not far from chaos

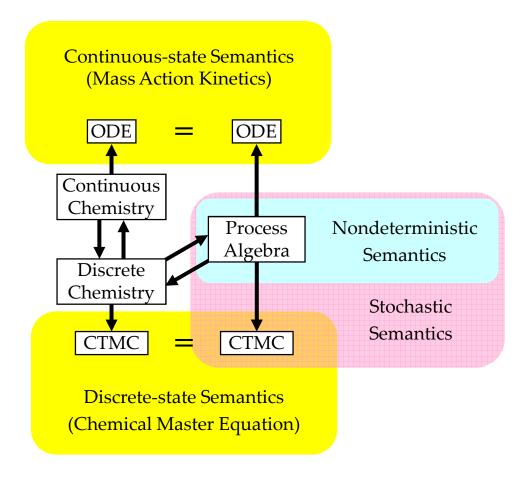
Hysteric Groupies

We can get more regular behavior from groupies if they "need more convincing", or "hysteresis" (history-dependence), to switch states.



Semantics of Collective Behavior

The Two Semantic Sides of Chemistry

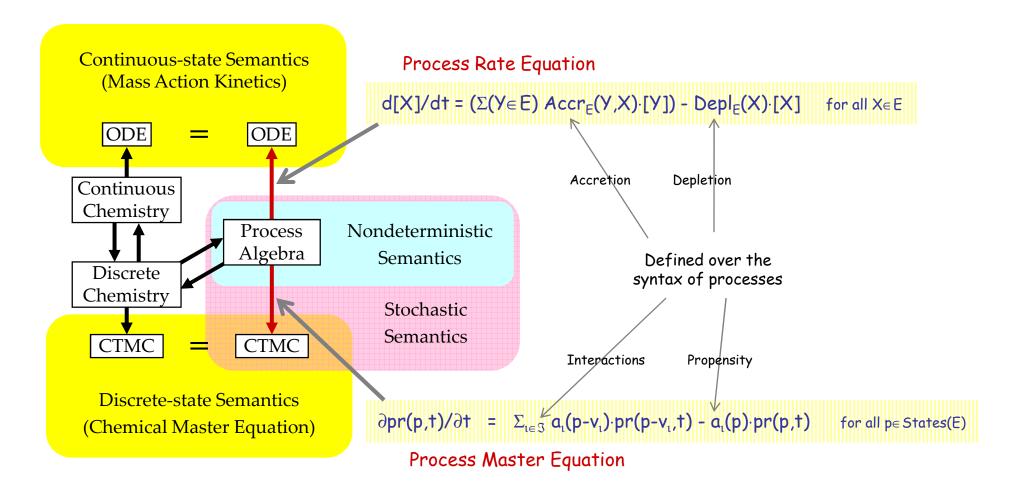


These diagrams commute via appropriate maps.

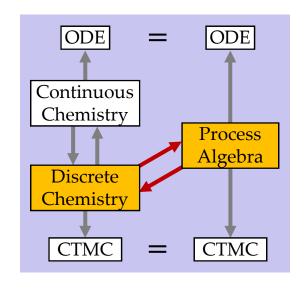
L. Cardelli: "On Process Rate Semantics" (TCS)

L. Cardelli: "A Process Algebra Master Equation" (QEST'07)

Quantitative Process Semantics



Stochastic Processes & Discrete Chemistry



Chemical Reactions

$$A \rightarrow^{r} B_1 + ... + B_n (n \ge 0)$$

$$A_1 + A_2 \rightarrow^r B_1 + ... + B_n$$
 (n≥0)

$$A + A \rightarrow^r B_1 + ... + B_n$$
 (n≥0)

Unary Reaction d[A]/dt = -r[A]

Exponential Decay

Hetero Reaction $d[A_i]/dt = -r[A_1][A_2]$ Mass Action Law

Homeo Reaction $d[A]/dt = -2r[A]^2$

Mass Action Law

(assuming $A \neq B_i \neq A_j$ for all i,j)

No other reactions!

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The chemical Langevin equation

Daniel T. Gillespiea) Research Department, Code 4T4100D, Naval Air Warfare Center, China Lake, California 93555

Genuinely trimolecular reactions do not physically occur in dilute fluids with any appreciable frequency. Apparently trimolecular reactions in a fluid are usually the combined result of two bimolecular reactions and one monomolecular reaction, and involve an additional short-lived species.

Chapter IV: Chemical Kinetics

[David A. Reckhow, CEE 572 Course]

... reactions may be either elementary or nonelementary. Elementary reactions are those reactions that occur exactly as they are written, without any intermediate steps. These reactions almost always involve just one or two reactants. ... Non-elementary reactions involve a series of two or more elementary reactions. Many complex environmental reactions are non-elementary. In general, reactions with an overall reaction order greater than two, or reactions with some non-integer reaction order are non-elementary.

THE COLLISION THEORY OF **REACTION RATES**

www.chemguide.co.uk

The chances of all this happening if your reaction needed a collision involving more than 2 particles are remote. All three (or more) particles would have to arrive at exactly the same point in space at the same time, with everything lined up exactly right, and having enough energy to react. That's not likely to happen very often!

Trimolecular reactions:

$$A + B + C \rightarrow^{r} D$$

the measured "r" is an (imperfect) aggregate of e.g.:

$$A + B \leftrightarrow AB$$

$$AB + C \rightarrow D$$

Enzymatic reactions:

$$S \stackrel{E}{\longrightarrow} P$$

the "r" is given by Michaelis-Menten (approximated steady-state) laws:

$$E + S \leftrightarrow ES$$

$$FS \rightarrow P + F$$

Reactions have rates. Molecules do not have rates.

Chemical Ground Form (CGF)

E ::= 0 : X=M, E

 $M ::= 0 : \pi; P \oplus M$

P ::= 0 : X | P

 $\pi ::= \tau_{(r)} : ?a_{(r)} : !a_{(r)}$

CGF ::= E,P

Reagents

Molecules

Solutions

Actions (delay, input, output)

Reagents plus Initial Conditions

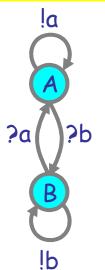
A stochastic subset of CCS

(no values, no restriction)

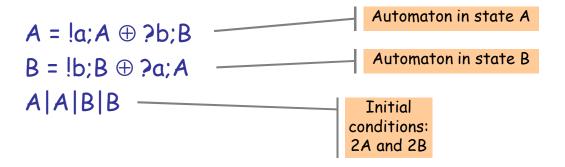
Interacting Automata + dynamic forking

(To translate chemistry to processes we need a bit more than interacting automata: we may have "+" on the right of \rightarrow , that is we may need "|" after π .)

⊕ is stochastic choice (vs. + for chemical reactions)
 O is the null solution (P|O = O|P = P)
 and null molecule (M⊕O = O⊕M = M)
 Each X in E is a distinct species
 Each name a is assigned a fixed rate r: a_(r)

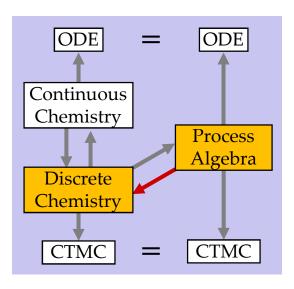


Ex: Interacting Automata (= finite-control CGFs: they use "|" only in initial conditions):

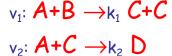


From Reagents to Reactions (by example)

Interacting	Discrete Chemistry
initial states $A \mid A \mid \mid A$	initial quantities #A ₀
A @r A'	A→r A'
A ?a A' B !a B'	A+B ⊶ ^r A'+B'
?a A !a	A+A→2r A'+A"



From Reactions to Reagents (by example)



Interaction Matrix

$$v_3: C \rightarrow k_3 E+F$$

$$v_4$$
: $F+F \rightarrow k_4$ B





1: Fill the matrix by columns:

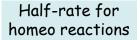
Degradation reaction v_i : $X \rightarrow k_i P_i$ add τ ; P_i to $\langle X, v_i \rangle$.

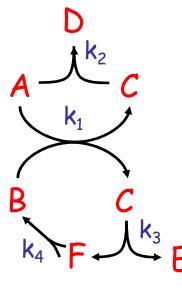
Hetero reaction v_i : X+Y $\rightarrow k_i P_i$ add ?; P_i to $\langle X, v_i \rangle$ and !;0 to $\langle Y, v_i \rangle$

Homeo reaction v_i : $X+X \rightarrow k_i P_i$ add ?; P_i and !;0 to $\langle X, v_i \rangle$

channels and rates (1 per reaction)

	v _{1(k1)}	$V_{2(k2)}$	V _{3(k3)}	$V_{4(k4/2)}$
Α	?;(C C)	? ;D		
В	!;0			
С		!;0	τ;(E F)	
D				
Е				
F				?;B !;0





2: Read the result by rows:

$$A = v_{1(k1)}; (C|C) \oplus v_{2(k2)}; D$$

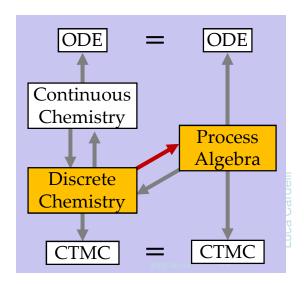
 $B = !v_{1(k1)}; O$

 $C = v_{2(k2)}; 0 \oplus \tau_{k3}; (E|F)$

D = 0

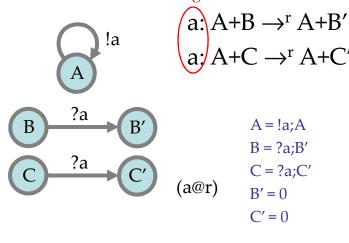
E = 0

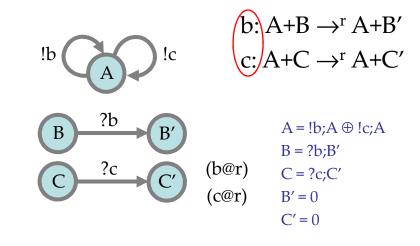
 $F = v_{4(k4/2)}; B \oplus v_{4(k4/2)}; 0$



Entangled vs Detangled







Entangled: Two reactions on one channel

Detangled: Two reactions on two separate channels

We need a semantics of automata that identifies automata that have the "same chemistry".

No process algebra equivalence is like this!

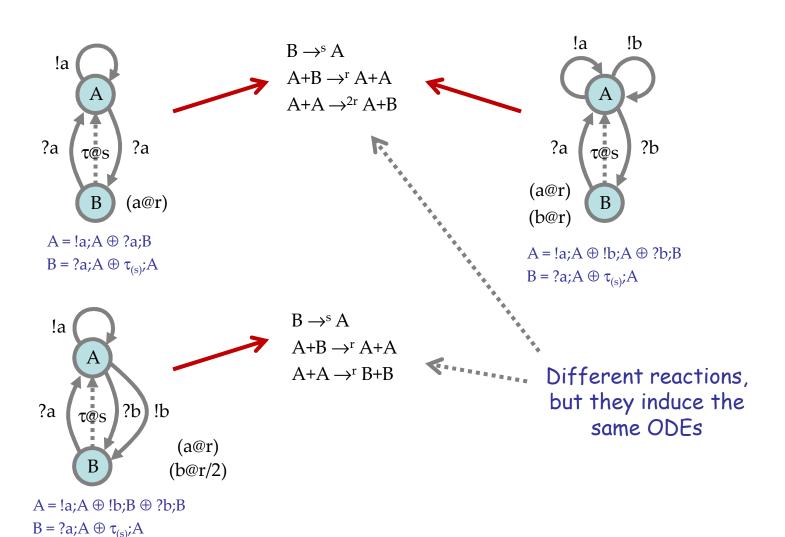
Entangled automata lead to more compact models than in chemistry.

Detangled automata are in simple correspondence with chemistry.

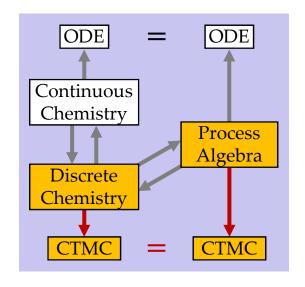
Same Semantics

Could chemistry itself be that semantics?

No: different sets of reactions can have the same behavior!



Discrete-State Semantics



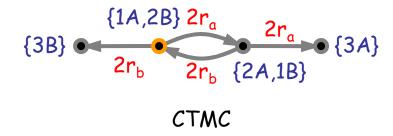
Discrete Semantics of Reactions

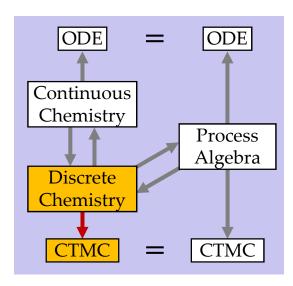
Syntax:

$$A+B \rightarrow^{r} A+A$$
 $A+B \rightarrow^{r} B+B$
 $A+B+B$

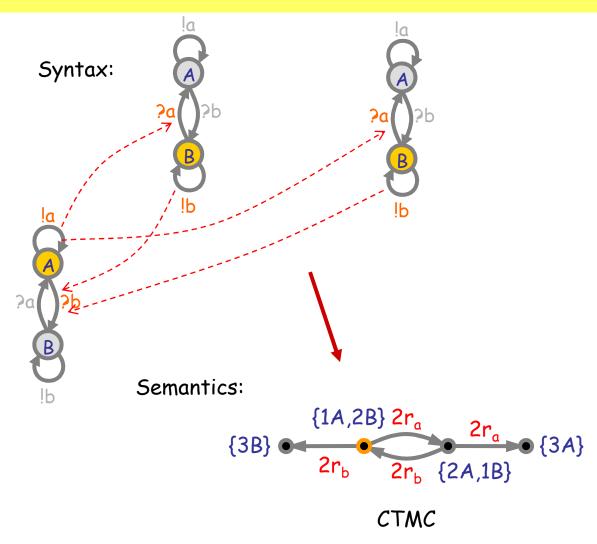


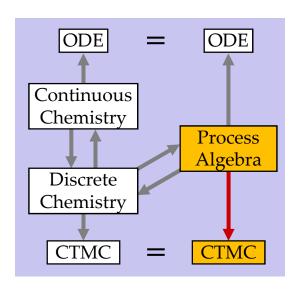
Semantics:





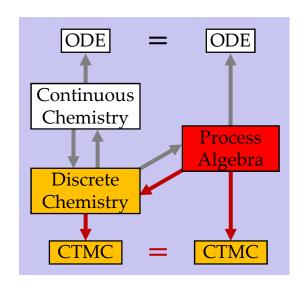
Discrete Semantics of Reagents

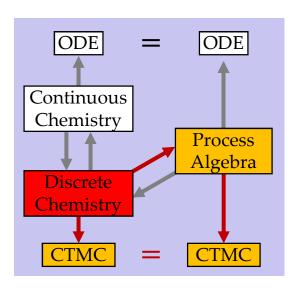




Discrete State Equivalence

- Def: m is equivalent CTMC's (isomorphic graphs with same rates).
- Thm: E *∞* Ch(E)
- Thm: *C* ≈ Pi(*C*)





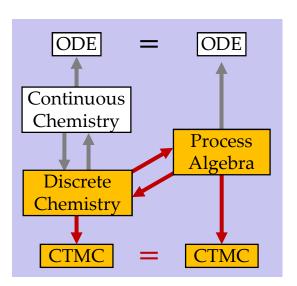
- For each E there is an $E' \approx E$ that is detangled (E' = Pi(Ch(E)))
- For each E in automata form there is an an E' \approx E that is detangled and in automata form (E' = Detangle(E)).

Process Algebra = Discrete Chemistry

This is enough to establish that the process algebra is really faithful to the chemistry.

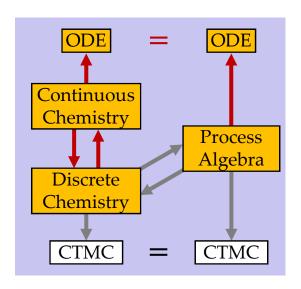
But CTMC are not the "ultimate semantics" because there are still questions of when two different CTMCs are actually equivalent (e.g. "lumping").

The "ultimate semantics" of chemistry is the *Chemical Master Equation* (derivable from the Chapman-Kolmogorov equation of the CTMC).



Continuous-State Semantics

(short version)



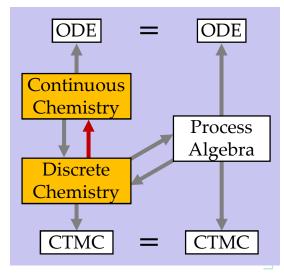
The Gillespie^(?) Conversion

Discrete Chemistry	Continuous Chemistry	$\gamma = N_A V$:M ⁻¹
initial quantities $\#A_0$	initial concentration $[A]_0$	ns with [A] ₀ =#	$^{\prime}A_{0}/\gamma$
A ⊶ A'	$A \rightarrow^k A'$	with $k = r$:s ⁻¹
A+B ⊶ ^r A'+B'	$A+B \rightarrow^k A'+B'$	with $k = r\gamma$:M ⁻¹ s ⁻¹
A+A ⊶ ^r A'+A"	$A+A \rightarrow^k A'+A''$	with $k = r\gamma/2$.:M ⁻¹ s ⁻¹

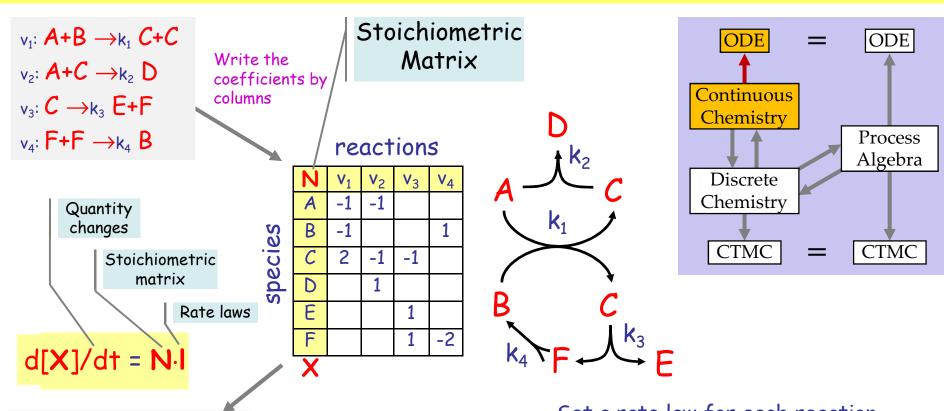
V = interaction volume N_A = Avogadro's number

Think
$$\gamma = 1$$
 i.e. $V = 1/N_A$

 $M = mol \cdot L^{-1}$ molarity (concentration)



From Reactions to ODEs (Law of Mass Action)



$$d[A]/dt = -I_1 - I_2$$

 $d[B]/dt = -I_1 + I_4$
 $d[C]/dt = 2I_1 - I_2 - I_3$
 $d[D]/dt = I_2$
 $d[E]/dt = I_3$
 $d[F]/dt = I_3 - 2I_4$

Read the concentration changes from the rows

E.g.
$$d[A]/dt = -k_1[A][B] - k_2[A][C]$$

Set a rate law for each reaction (Degradation/Hetero/Homeo)



X: chemical species

[-]: quantity of molecules

I: rate laws

k: kinetic parameters

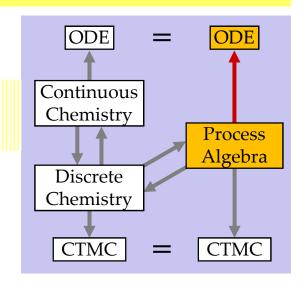
N: stoichiometric matrix

Processes Rate Equation

Process Rate Equation for Reagents E in volume γ

$$d[X]/dt = (\Sigma(Y \in E) Accr_{E}(Y,X)\cdot[Y]) - Depl_{E}(X)\cdot[X]$$
for all $X \in E$

"The change in process concentration (!!) for X at time t is:
the sum over all possible (kinds of) processes Y of:
the concentration at time t of Y
times the accretion from Y to X
minus the concentration at time t of X
times the depletion of X to some other Y"



$$Depl_{E}(X) =$$

$$\Sigma$$
(i: E.X.i= τ _(r);P) r +

$$\Sigma$$
(i: E.X.i= $a_{(r)}$;P) $r\gamma$ ·OutsOn_E(a) +

$$\Sigma$$
(i: E.X.i=! $a_{(r)}$;P) $r\gamma$ ·InsOn_E(a)

$$Accr_{F}(Y, X) =$$

$$\Sigma$$
(i: E.Y.i= τ _(r);P) #X(P)·r +

$$\Sigma$$
(i: E.Y.i= $a_{(r)}$:P) $\#X(P)$ ·r γ ·OutsOn_E(a) +

$$\Sigma$$
(i: E.Y.i=! $a_{(r)}$;P) #X(P)·r γ ·InsOn_E(a)

InsOn_E(a) =
$$\Sigma(Y \in E)$$
 #{Y.i | E.Y.i=?a_(r);P}·[Y]
OutsOn_E(a) = $\Sigma(Y \in E)$ #{Y.i | E.Y.i=!a_(r);P}·[Y]

$$X = \tau_{(r)}; 0 \rightarrow d[X]/dt = -r[X]$$

$$X = 2a_{(r)};0$$
 $d[X]/dt = -r\gamma[X][Y]$

$$Y = !a_{(r)};0$$
 $d[Y]/dt = -r\gamma[X][Y]$

$$X = 2a_{(r)};0 \longrightarrow d[X]/dt = -2r\gamma[X]^2$$

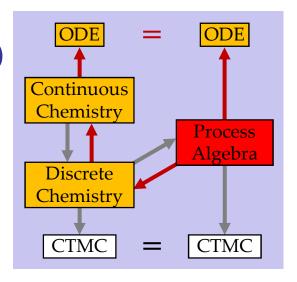
 $\oplus !a_{(r)};0$

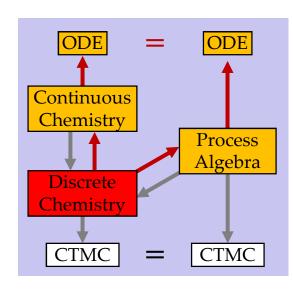
Continuous State Equivalence

Def: ≈ is equivalence of polynomials over the field of reals.

• Thm: E ≈ Cont(Ch(E))

• Thm: $Cont(C) \approx Pi(C)$

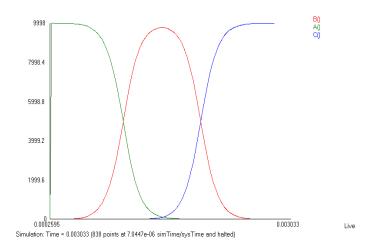




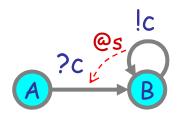
- For each E there is an $E' \approx E$ that is detangled (E' = Pi(Ch(E)))
- For each E in automata form there is an an E' ≈ E that is detangled and in automata form (E' = Detangle(E)).

Exercise: Making Waves

Build me a population like this:



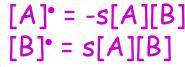
Nonlinear Transition (NLT)

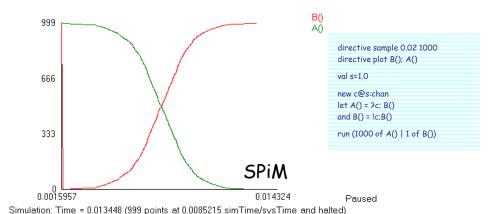


$$A = ?c_{(s)};B$$

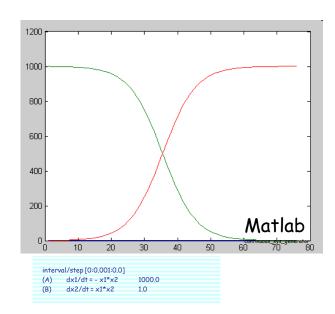
$$B = !c_{(s)};B$$

$$A+B \rightarrow^{s} B+B$$

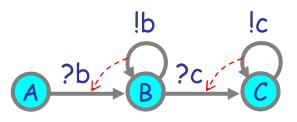




N.B.: needs at least 1 B to "get started".



Two NLTs: Bell Shape



 $[B]^{\bullet} = [B]([A]-[C])$

directive sample 0.0025 1000 directive plot B(); A(); C()

new b@1.0:chan new c@1.0:chan

let A() = ?b; B()

and B() = do !b;B() or ?c; C()

and C() = !c; C()

run ((10000 of A()) | B() | C())

 $A = ?b_{(1)};B$

B = $!b_{(1)};B \oplus ?c_{(1)};C$ C = $!c_{(1)};C$

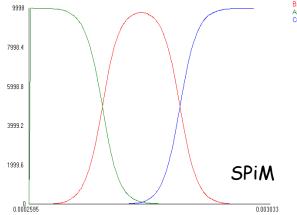
 $A+B \rightarrow^1 B+B$

 $B+C \rightarrow^1 C+C$

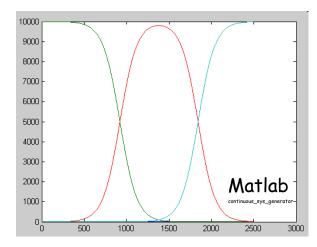
 $[A]^{\bullet} = -[A][B]$

 $[B]^{\bullet} = [A][B] - [B][C]$

 $[C]^{\bullet} = [B][C]$

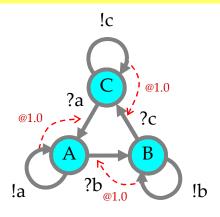


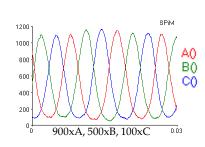
Simulation: Time = 0.003033 (838 points at 7.0447e-06 simTime/sysTime and halted)



inter	val/step [0:0.000001:0.0025]	
(A)	dx1/dt = -x1*x2	10000.0
(B)	dx2/dt = x1*x2 - x2*x3	1.0
(C)	dx3/dt = x2*x3	1.0

NLT in a Cycle: Oscillator (unstable)





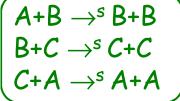
directive sample 0.03 1000
directive plot A(); B(); C()

new a@1,0:chan new b@1,0:chan new c@1,0:chan let A() = do la; A() or ?b; B()
and B() = do lb; B() or ?c; C()
and C() = do lc; C() or ?a; A()

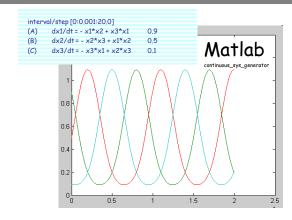
run (900 of A() | 500 of B() | 100 of C())

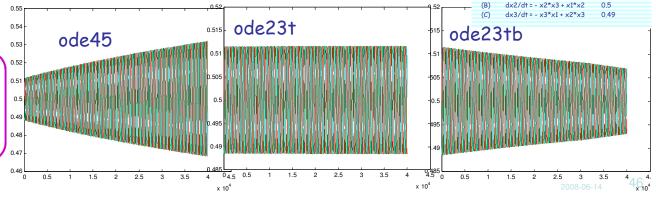
interval/step [0:0.01:400.0] (A) dx1/dt = - x1*x2 + x3*x1

```
A = !a_{(s)}; A \oplus ?b_{(s)}; B
B = !b_{(s)}; B \oplus ?c_{(s)}; C
C = !c_{(s)}; C \oplus ?a_{(s)}; A
```

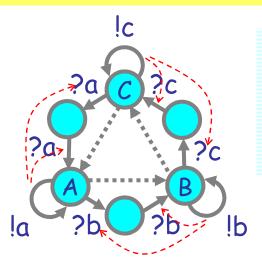








Oscillator (stable)



directive sample 0.1 1000 directive plot A1(); A2(); A3()

val r=1.0 val s=1.0

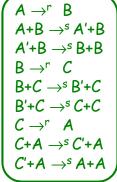
new a1@s:chan new a2@s:chan new a3@s:chan
let A1() = do !a1;A1() or delay@r;A2() or ?a2; ?a2; A2()
and A2() = do !a2;A2() or delay@r;A3() or ?a3; ?a3; A3()
and A3() = do !a3;A3() or delay@r;A1() or ?a1; ?a1; A1()

run 1000 of A1()

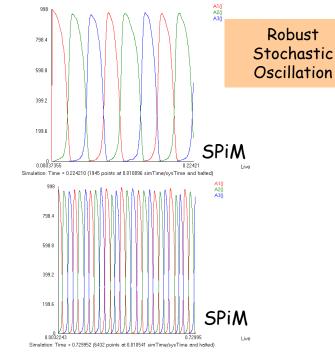
N.B. this does not deadlock!

 $A = !a_{(s)}; A \oplus \tau_r; B \oplus ?b_{(s)}; A'$ $A' = ?b_{(s)}; B$ $B = !b_{(s)}; B \oplus \tau_r; C \oplus ?c_{(s)}; B'$ $B' = ?c_{(s)}; C$ $C = !c_{(s)}; C \oplus \tau_r; A \oplus ?a_{(s)}; C'$ $C' = ?a_{(s)}; A$

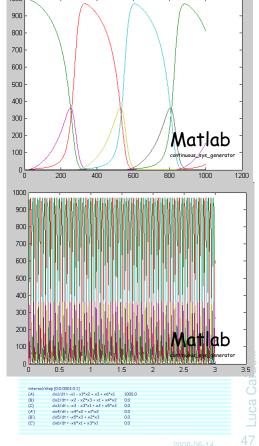
Sustained
Determinisitic
Oscillation



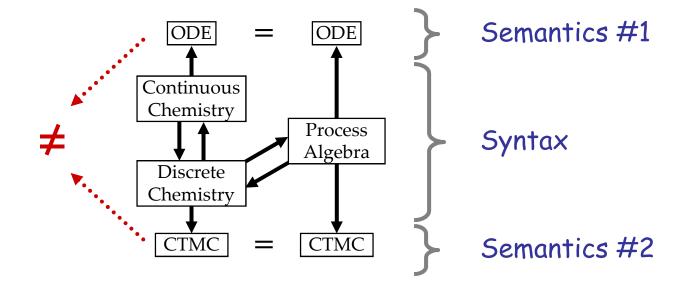
1000 C 900 -8+B 700 -600 -+C 40 -300 -100 -



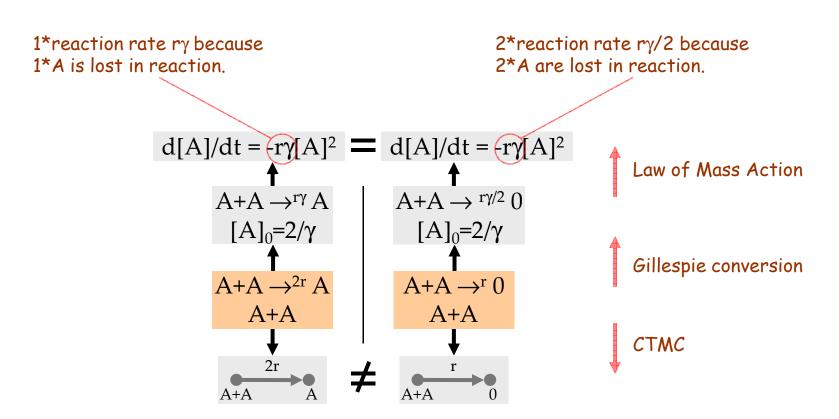
[A]* = -r[A]-s[A][B]+r[C]+s[C'][A]
[B]* = -r[B]-s[B][C]+r[A]+s[A'][B]
[C]* = -r[C]-s[C][A]+r[B]+s[B'][C]
[A']* = -s[A'][B] + s[A][B]
[B']* = -s[B'][C] + s[B][C]
[C']* = -s[C'][A] + s[C][A]



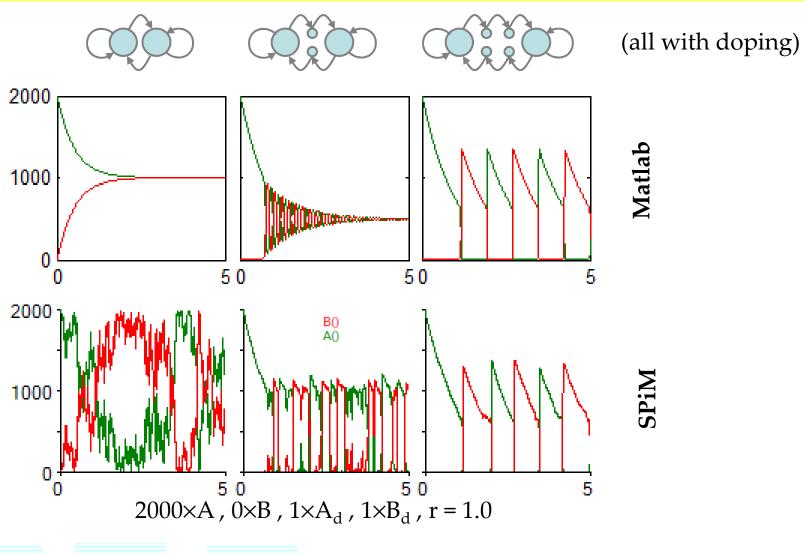
GMA ≠ CME



$A+A \rightarrow^{2r} A =? A+A \rightarrow^{r} 0$



Continuous vs. Discrete Groupies



directive sample 5.0 1000 directive plot Ik(); A() new 86 10 chard) new 86 10 chard) left B(); A() new 86 10 chard) left A() = do let A() or 7b; 7b; 8f) and 8f) = do let A() or 7b; 7b; 7b] left A() = let A() = let A() left A() = let A() left A() = let A() left A() = let A() let let A

directive sample 5.0 1000
directive plot filt; A()
directive plot filt; A()
level at 10 f.ch.ch.up)
neve bit 10.ch.un)
let A() a du 1x, A() or 70, 70, 70, 70, 70
let A() a du 1x, A() or 70, 70, 70, 70, 70
let A() = 1x, A()
and 8() = 50, 8()
un 2000 of A()
un 2000 of A()
un 2000 of A()

Groupe ODEs - Groupies.mat [0:0.001:5:0] r=1.0 k=1.0 A dx1/dt= -(x1-x2), 2000.0 B dx2/dt= (x1-x2), 0.0 Groupe ODEs - Groupies Hysteric 1 mat [00.0015.0] r=1.0 k=1.0 A dx/d+sz4**A-3**dx4**A-2000.0 A dx2/d+sx4**A-3**dx5*x4*x2, 0.0 8 dx3/d+sx4**x2*dx4*x3*x2*, 0.0 8 dx4/d+sx4**x3*x4**x4*, 0.0 Groupe ODEs - Groupies Hysteric 2:met

[00.0015.0] =1.0 k=1.0

A dxt/ds-tx**-6x3*-xix-tx6, 2000.0

A dxt/ds-tx**-6x3*-xix-tx6, 2000.0

A dxt/ds-tx**-6x3*-xix-tx6-xix-2, 0.0

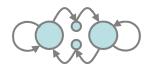
A dxt/ds-tx3*-xix-tx6-xix-xix, 0.0

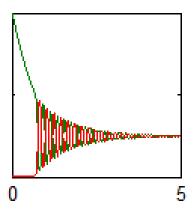
B dxt/ds-tx3*-xix-tx6-xix-xix, 0.0

B dxt/ds-tx3*-xix-tx6-xix-xix, 0.0

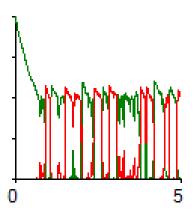
B dxt/ds-tx3*-xix-tx6-xix-xix, 0.0

Scientific Predictions



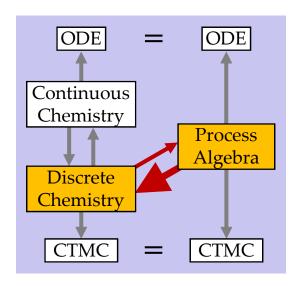


After a while, all 4 states are almost equally occupied.

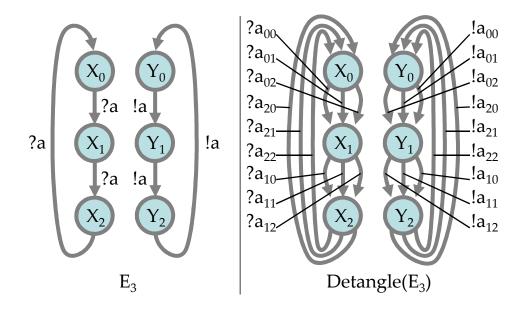


The 4 states are almost never equally occupied.

Model Compactness



Entangled vs detangled



(closely related to $Pi(Ch(E_3))$)

n² Scaling Problems

- E_n has 2n variables (nodes) and 2n terms (arcs).
- $Ch(E_n)$ has 2n species and n^2 reactions.

- The stoichiometric matrix has size $2n \cdot n^2 = 2n^3$.
- The ODEs have 2n variables and 2n(n+n) = 4n² terms (number of variables times number of accretions plus depletions when sums are distributed)

E3

$$X_0 = ?a_{(r)}; X_1$$

 $X_1 = ?a_{(r)}; X_2$
 $X_2 = ?a_{(r)}; X_0$
 $Y_0 = !a_{(r)}; Y_1$
 $Y_1 = !a_{(r)}; Y_2$
 $Y_2 = !a_{(r)}; Y_0$

$Ch(E_3)$

$a_{00}: X_0 + Y_0 \rightarrow^r X_1 + Y_1$
$a_{01}: X_0 + Y_1 \rightarrow^r X_1 + Y_2$
$a_{02}: X_0 + Y_2 \rightarrow^r X_1 + Y_0$
$a_{10}: X_1 + Y_0 \rightarrow^r X_2 + Y_1$
$a_{11}: X_1+Y_1 \rightarrow^r X_2+Y_2$
$a_{12}: X_1 + Y_2 \rightarrow^r X_2 + Y_0$
$a_{20}: X_2 + Y_0 \rightarrow^r X_0 + Y_1$
$a_{21}: X_2 + Y_1 \rightarrow^r X_0 + Y_2$
$a_{22}\text{: }X_2\text{+}Y_2\to^r X_0\text{+}Y_0$

Stoichiometric $Matrix(Ch(E_3))$

	a ₀₀	a ₀₁	a ₀₂	a ₁₀	a ₁₁	a ₁₂	a ₂₀	a ₂₁	a ₂₂
X _o	-1	-1	-1				+1	+1	+1
X_1	+1	+1	+1	-1	-1	-1			
X_2				+1	+1	+1	-1	-1	-1
Y ₀	-1		+1	-1		+1	-1		+1
Y ₁	+1	-1		+1	-1		+1	-1	
y ₂		+1	-1		+1	-1		+1	-1

ODE(E₃)

$$\begin{aligned} &d[X_0]/dt = -r[X_0][Y_0] - r[X_0][Y_1] - r[X_0][Y_2] + r[X_2][Y_0] + r[X_2][Y_1] + r[X_2][Y_2] \\ &d[X_1]/dt = -r[X_1][Y_0] - r[X_1][Y_1] - r[X_1][Y_2] + r[X_0][Y_0] + r[X_0][Y_1] + r[X_0][Y_2] \\ &d[X_2]/dt = -r[X_2][Y_0] - r[X_2][Y_1] - r[X_2][Y_2] + r[X_1][Y_0] + r[X_1][Y_1] + r[X_1][Y_2] \\ &d[Y_0]/dt = -r[X_0][Y_0] - r[X_1][Y_0] - r[X_2][Y_0] + r[X_0][Y_2] + r[X_1][Y_2] + r[X_2][Y_2] \\ &d[Y_1]/dt = -r[X_0][Y_1] - r[X_1][Y_1] - r[X_2][Y_1] + r[X_0][Y_0] + r[X_1][Y_0] + r[X_2][Y_0] \\ &d[Y_2]/dt = -r[X_0][Y_2] - r[X_1][Y_2] - r[X_2][Y_2] + r[X_0][Y_1] + r[X_1][Y_1] + r[X_2][Y_1] \end{aligned}$$

On the Computational Power of Biochemstry

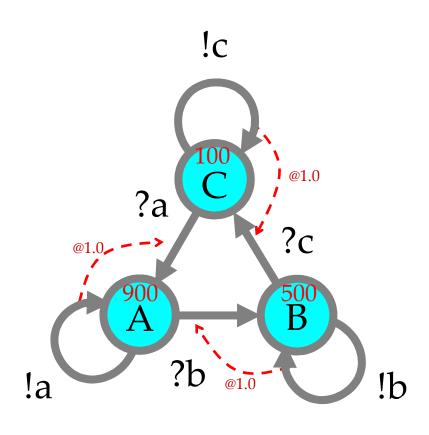
joint work with

Gianluigi Zavattaro

University of Bologna

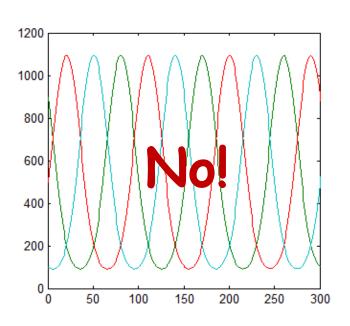
in: Algebraic Biology '08

Can this program halt?



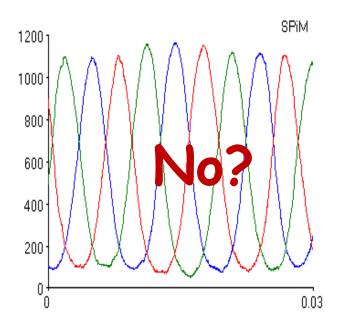
c:
$$B+C \rightarrow C+C$$

"Experimantal evidence"



Continuous-State Simulation

interval/step [0:0.0001:0.03] (A) dx1/dt = -x1*x2 + x3*x1 900.0 (B) dx2/dt = -x2*x3 + x1*x2 500.0 (C) dx3/dt = -x3*x1 + x2*x3 100.0



Discrete-State Simulation

directive sample 0.03 1000
directive plot A(); B(); C()

new a@1.0:chan new b@1.0:chan new c@1.0:chan let A() = do !a; A() or ?b; B()
and B() = do !b; B() or ?c; C()
and C() = do !c; C() or ?a; A()

run (900 of A() | 500 of B() | 100 of C())

But in a longer simulation...



Discrete-State Simulation 0A + 1500B + 0C

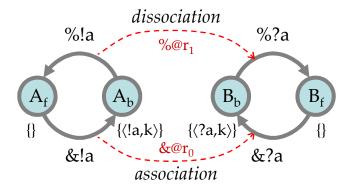
Is termination decidable in Chemistry?

- Three notations for "basic chemistry":
 - FSRN: Finite Stochastic Reaction Networks (finite systems of stochastic chemical reactions)
 - CGF: our process algebra (CTCM-equivalent to FSRN).
 - Place-Transition Petri nets.
- Answer: termination (reachability) in Chemistry is decidable!
 - FSRNs are not Turing-powerful (Soloveichik et al. Computation with Finite Stochastic Chemical Reaction Networks. In Nat. Computing. 2008).
 - Termination in CGF (weather a given molecule could be produced) can be reduced to termination in place-transition Petri Nets, where it (reachability) is decidable.
- Hence, basic chemistry is NOT Turing-complete!
 - (Although the full story is a bit more subtle.)

Biochemistry = Interaction + Complexation

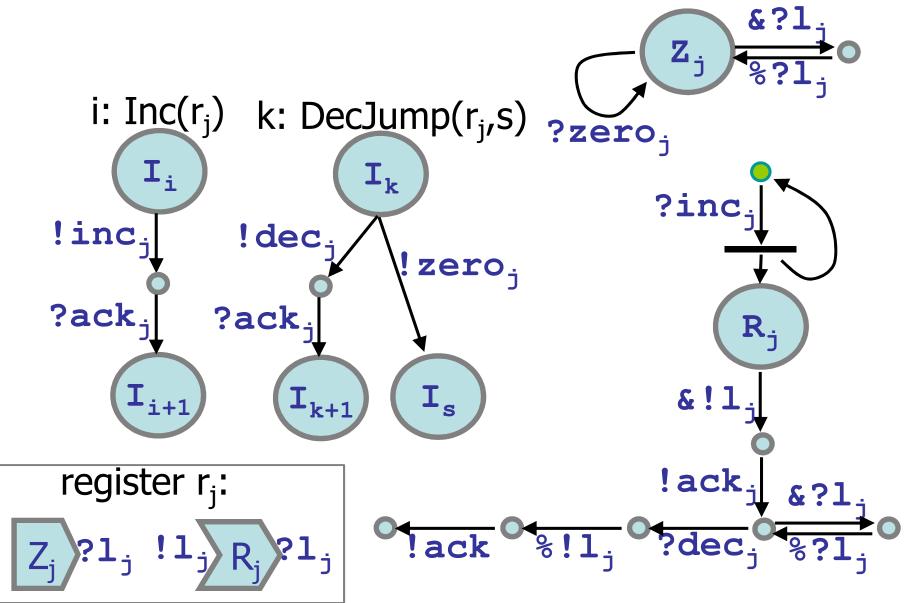


• Complexation is what proteins "do", in contrast to simpler chemicals.



• Leading to a process algebra that we call the Biochemical Ground Form (BGF).

RAM encoding in BGF



Expressiveness of Biochemistry

- Basic chemistry (FSRN, or CGF) is not Turing-complete
- Biochemistry (FSRN + complexation, or BGF) is Turing-complete.
- More powerful process algebras of course are Turing complete
 - They (e.g. π -calculus) include BGF, but they also have mechanisms that are not directly biologically justifiable.
 - In BGF we have in a sense the minimal biologically-inspired extension of FSRN, and it is already Turing-complete.
- Intrinsic to biochemistry (but not to simple chemistry) is at least one Turing-complete mechanism.

Conclusions

Conclusions

Compositional modeling languages

- Accurate (at the "appropriate" abstraction level).
- Manageable (so we can scale them up by composition).
- Executable (stochastic simulation).

Analysis techniques

- Mathematical techniques: Markov theory,
 Chemical Master Equation, and Rate Equation
- Computing techniques: Abstraction and Refinement, Model Checking, Causality Analysis.

Many lines of extensions

- Parametric processes for model factorization
- Ultimately, rich process-algebra based modeling languages.

Quantitative techniques

- Important in the "real sciences".