

On Switches and Oscillators

Program Equivalence in Biology?

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Outline

- Some questions that nature has (apparently) answered:

<http://www.bioch.ox.ac.uk/aspsite/index.asp?pageid=593>

- Building 'good' bistable systems
- Building 'switches' (switchable bistable system)
- Building switches with hysteresis (needed for good oscillators)
- Building 'limit cycle' oscillators that do not dampen or diverge
- Building robust oscillators that resist parameter variations

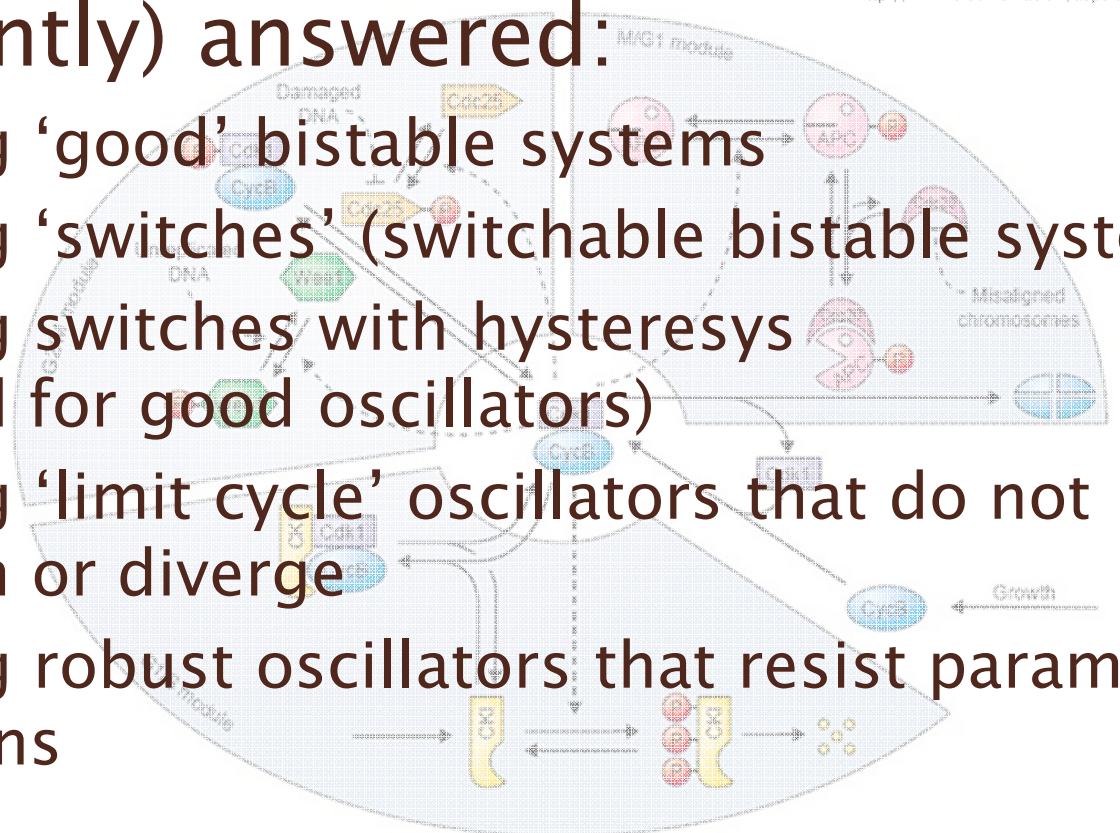


Figure 1: Cell cycle regulation of cyclin dependent kinase (Cdk1) Cyclin-B (CycB) complex. The active Cdk1/CycB dimer can be inactivated by binding to an inhibitor (CKI) or by phosphorylation of the kinase subunit by Wee1. The inhibitory phosphate group is removed by Cdc25 phosphatase (Cdc25). Cdk1/CycB can also be inactivated by proteolysis of its cyclin partner, mediated by the anaphase-promoting complex (APC) in combination with Cdc20

Outline

- Subject to ‘chemical constraints’
 - Not all reactions can be easily implemented
 - Not all molecules can perform all functions
- The ‘logical’ solutions
 - Need to be adapted due to chemical constraints
 - Can we then still recognize them (if they exist)?

Switches

The Cell Cycle Switch

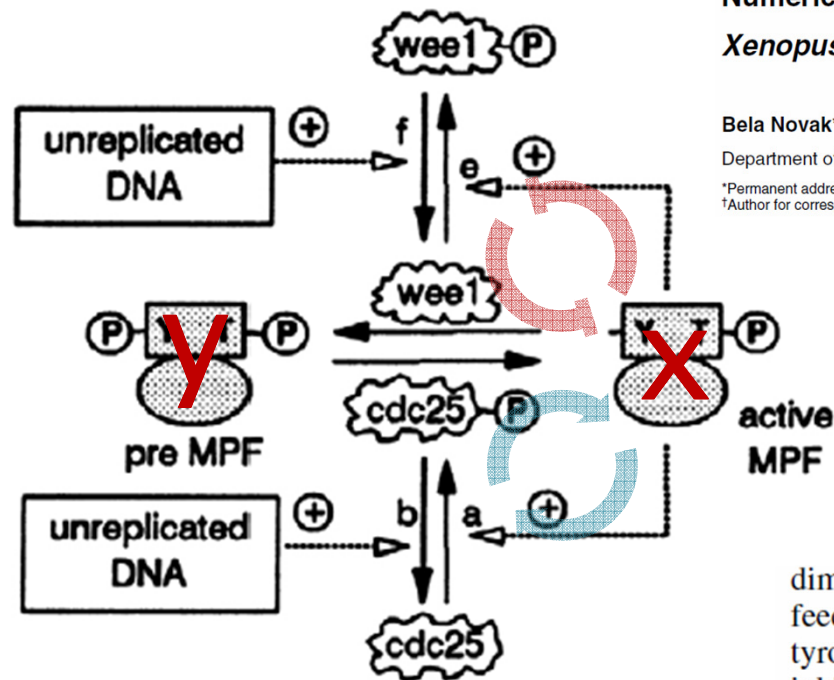
Journal of Cell Science 106, 1153-1168 (1993)
 Printed in Great Britain © The Company of Biologists Limited 1993

Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos

Bela Novak* and John J. Tyson†

Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24060-0406, USA

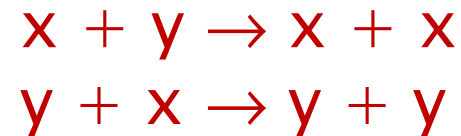
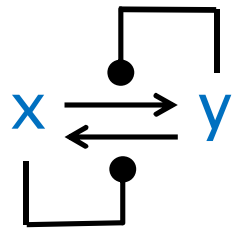
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 †Author for correspondence



dimers is left off the diagram to keep it simple.) (B) Positive feedback loops. Active MPF stimulates its own production from tyrosine-phosphorylated dimers by activating Cdc25 and inhibiting Wee1. We suspect that these signals are indirect, but intermediary enzymes are unknown and we ignore them in this paper. The signals from active MPF to Wee1 and Cdc25 generate an autocatalytic instability in the control system. We indicate also an 'external' signal from unreplicated DNA to Wee1 and Cdc25, which can be used to control the efficacy of the positive feedback loops. The letters a, b, e and f are used to label the rate constants for these reactions in Fig. 2. (C) Negative feedback loop. Active

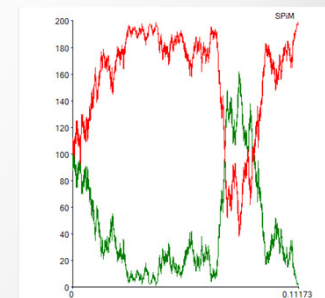
Direct Competition

- x catalyzes the transformation of y into x
- y catalyzes the transformation of x into y



- This system is bistable, but
 - Convergence to a stable state is slow (a random walk).
 - *Any* perturbation of a stable state can initiate a random walk to the other stable state.
 - With 100 molecules of x and y, convergence is quick, but with 10000 molecules, even at the same concentration (adjusting the rate) you will wait for a long time.

```
Simulation sample 0.0002  
10000  
end of 1000  
New variables added  
New equations added  
M1: x1 =  
M2: x2 =  
M3: x3 =  
M4: x4 =  
M5: x5 =  
M6: x6 =  
M7: x7 =  
M8: x8 =  
M9: x9 =  
M10: x10 =
```



Approximate Majority

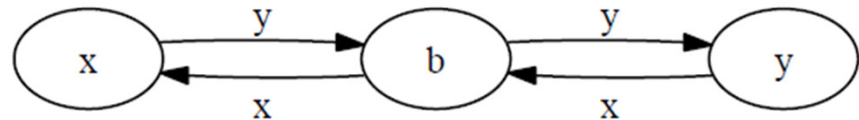
- A fundamental ‘population protocol’
 - Agents in a population start in state x or state y .
 - A pair of agents is chosen randomly at each step, they interact and change state.
 - The whole population must eventually agree on a majority value (x or y) with probability 1.

Dana Angluin · James Aspnes · David Eisenstat

A Simple Population Protocol for Fast Robust Approximate Majority

We analyze the behavior of the following population protocol with states $Q = \{b, x, y\}$. The state b is the **blank** state. Row labels give the initiator's state and column labels the responder's state.

	x	b	y
x	(x, x)	(x, x)	(x, b)
b	(b, x)	(b, b)	(b, y)
y	(y, b)	(y, y)	(y, y)



Properties

- Using martingales, we show that with high probability,
 - The number of state changes before converging is $O(n \log n)$
 - The total number of interactions before converging is $O(n \log n)$
 - The final outcome is correct if the initial disparity is $\omega(\sqrt{n \log n})$
- This algorithm is the fastest possible
 - Must wait $\Omega(n \log n)$ steps in expectation for all agents to interact

[Angluin et al.]

“Parallel time” is the number of steps divided by the number of agents. Hence the algorithm terminates with high probability in $O(\log n)$.

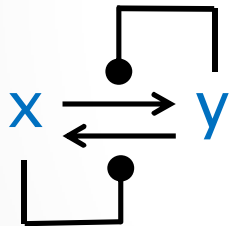
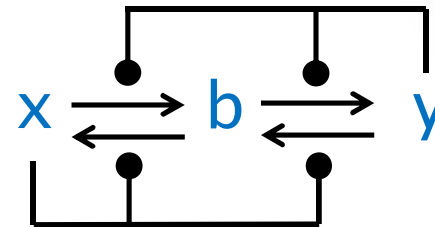
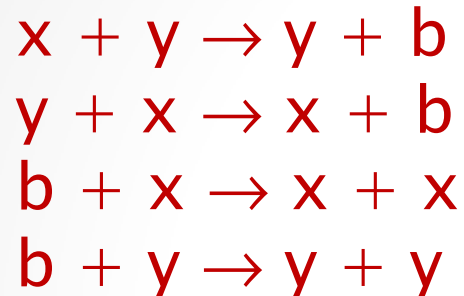
N.B. this holds even if the x,y populations are initially of equal size!

vs. Stochastic Chemistry

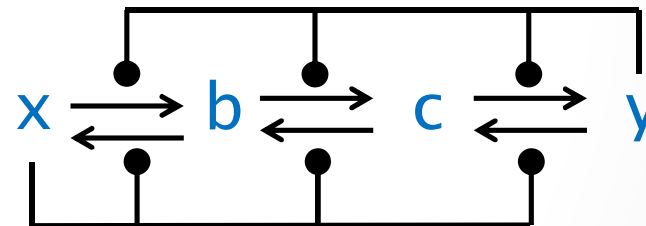
- Chemical systems as distributed systems
 - What can they compute?
 - What can we say about their dynamics?
- Replace “agent” with “molecule” \Rightarrow Chemical Master Equation (modulo details)
- Objection: in real life, some pairs of agents are more likely to interact than others
 - Agents in the same state are interchangeable
 - In a **well-stirred** chemical mixture, reaction *types* occur with the right probabilities (Gillespie, Physica A 1992)

[Angluin et al.]

Chemical Implementation

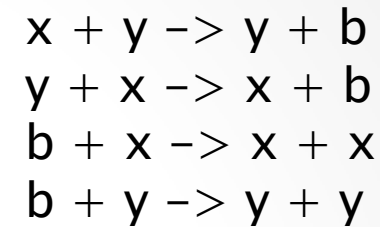


- This too is a bistable system, but:
- It converges slowly, by a random walk, hence $O(n^2)$.
 - It is unstable: any random fluctuation from an all-x or all-y state can send it (by a random walk) to the other state.

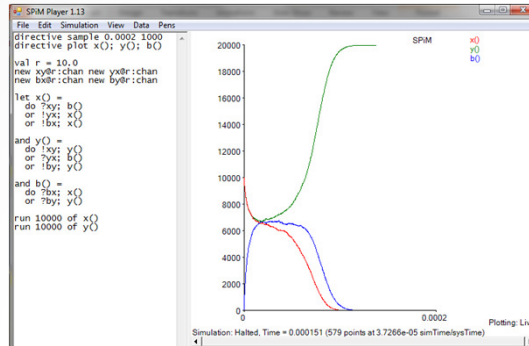


This one gives no significant improvement over the above.

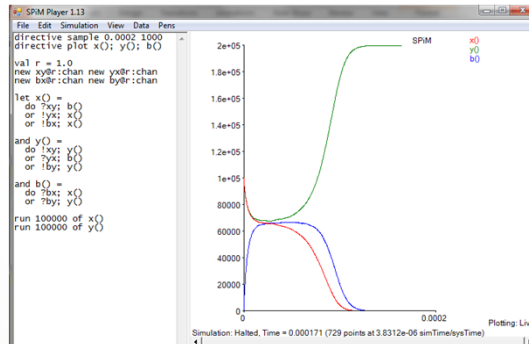
Majority of $x=y$ (CRN)



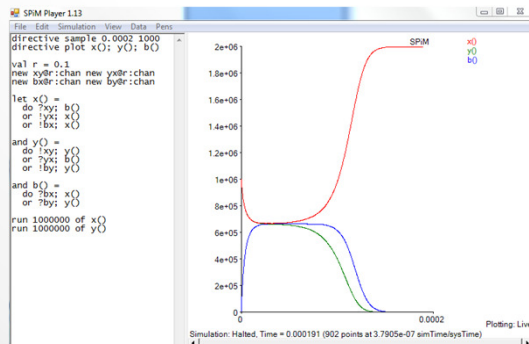
20k molecules, rate 10.0/s



200k molecules, rate 1.0/s (same concentration)



2000k molecules, rate 0.1/s (same concentration)



Gillespie simulation of the chemical reactions in SPiM.

- 10x more molecules at same concentration (i.e. lower rate) converge in 'comparable' time.
- Not shown: 10x more molecules in same volume, (i.e. higher concentration) converge 10x faster.

N.B. a deterministic (ODE) simulation with $x=y$ would not converge at all!

```

directive sample 0.0002 1000
directive plot x(); y(); b()

val r = 10.0
new xy@r:chan new yx@r:chan

new bx@r:chan new by@r:chan

let x() =
do ?xy; b()
or !yx; x()
or !bx; x()

and y() =
do !xy; y()
or ?yx; b()
or !by; y()

and b() =
do ?bx; x()
or ?by; y()

run 10000 of x()
run 10000 of y()
    
```

```

directive sample 0.0002 1000
directive plot x(); y(); b()

val r = 1.0
new xy@r:chan new yx@r:chan

new bx@r:chan new by@r:chan

let x() =
do ?xy; b()
or !yx; x()
or !bx; x()

and y() =
do !xy; y()
or ?yx; b()
or !by; y()

and b() =
do ?bx; x()
or ?by; y()

run 100000 of x()
run 100000 of y()
    
```

```

directive sample 0.0002 1000
directive plot x(); y(); b()

val r = 0.1
new xy@r:chan new yx@r:chan

new bx@r:chan new by@r:chan

let x() =
do ?xy; b()
or !yx; x()
or !bx; x()

and y() =
do !xy; y()
or ?yx; b()
or !by; y()

and b() =
do ?bx; x()
or ?by; y()

run 1000000 of x()
run 1000000 of y()
    
```

Bistable Element

- I had rediscovered (but not analyzed so well) the same system, while looking for a memory circuit.
- The point here was not computing majority, but switching easily and quickly and stably: it's a switch.

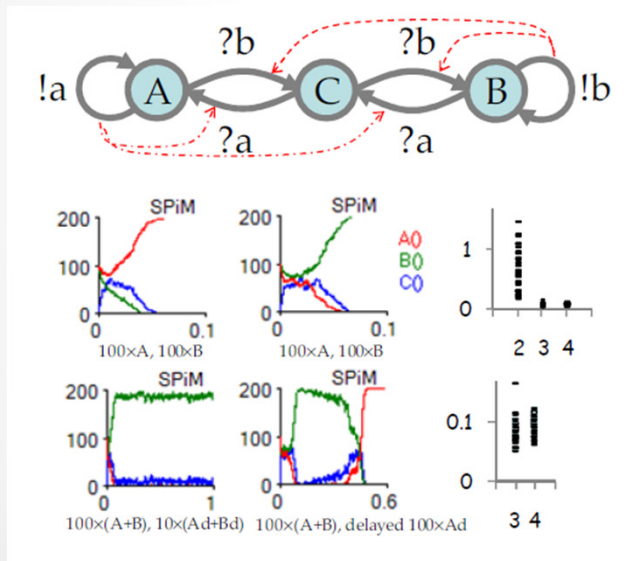
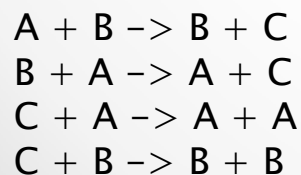


Figure 34 Memory Elements

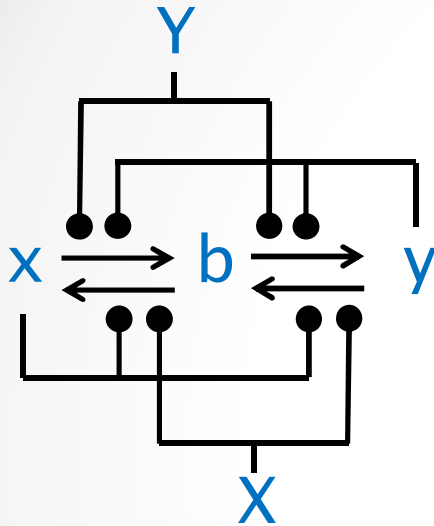


Artificial Biochemistry. Luca Cardelli

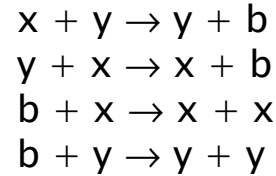
©2009 In A. Condon, D. Harel, J.N. Kok, A. Salomaa, E. Winfree (Eds.) *Algorithmic Bioprocesses*. Springer 2009. DOI: 10.1007/978-3-540-88869-7_22. ISBN: 978-3-540-88868-0. Auxiliary Materials: Simulations, Figures.

In Figure 34 we show a modified version of the groups, obtained by adding an intermediate state shared by the two state transitions. This automaton has very good memory properties. The top-left and top-center plots show that it is in fact spontaneously bistable. The bottom-left plot shows that it is stable in presence of sustained 10% fluctuations produced by doping automata. The bottom-center plot shows that, although resistant to perturbations, it can be switched from one state to another by a signal of the same magnitude as the stability level: the switching time is comparable to the stabilization time. In addition, this circuit reaches stability 10 times faster than the original groups: the top-right plot shows the convergence times of 30 runs each of the original groups with 2 states, the current automaton with 3 states, and a similar automaton (not shown) with 4 states that has two middle states in series. The bottom-right plot is a detailed view of the same data, showing that the automaton with 4 states is not significantly faster than the one with 3 states. Therefore, we have a stable and fast memory element.

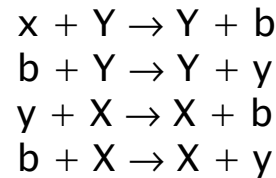
As a Flip-Flop



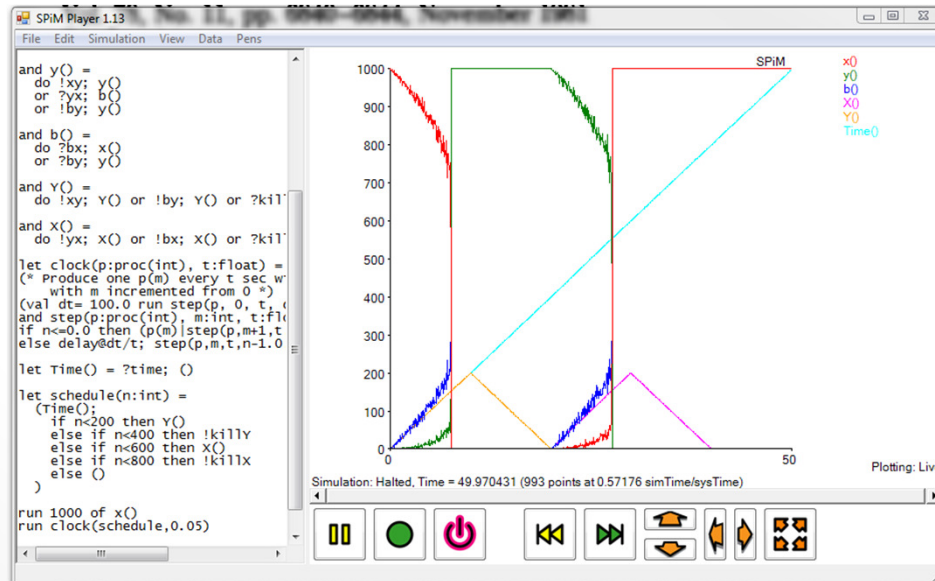
Outputs x,y:



Inputs X,Y:



Can be switched by external (catalytic) signals that are only 20% of the x,y levels.



```
directive sample 50.0 1000
directive plot x0; y0; b0; X0; Y0; Time()

val r = 1.0
new xy@r:chan new yx@r:chan
new bx@r:chan new by@r:chan
new killX:chan new killY:chan
new time:chan

let x() =
do ?xy; b()
or !yx; x()
or !bx; x()

and y() =
do !xy; y()
or ?yx; b()
or !by; y()

and b() =
do ?bx; x()
or ?by; y()

and Y() =
do !xy; Y() or !by; Y() or ?killY; ()

and X() =
do !yx; X() or !bx; X() or ?killX; ()

let clock(p:proc(int), t:float) =
(* Produce one p(m) every t sec with precision dt,
with m incremented from 0 *)
(val dt= 100.0 run step(p, 0, t, dt, dt))
and step(p:proc(int), m:int, t:float, n:float, dt:float) =
if n<=0.0 then (p(m))step(p,m+1,t,dt,dt)
else delay@dt/t; step(p,m,t,n-1.0,dt)

let Time() = ?time; ()

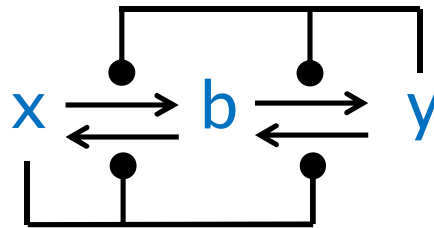
let schedule(n:int) =
(Time());
if n<200 then Y()
else if n<400 then !killY
else if n<600 then X()
else if n<800 then !killX
else ()

run 1000 of x()
run clock(schedule,0.05)
```

Init: 1000 x
Y growing from 0
(t=0) to 200
(t=200) then back
to 0 (t=400)
X growing from 0
(t=400) to 200
(t=600) then back
to 0 (t=800).

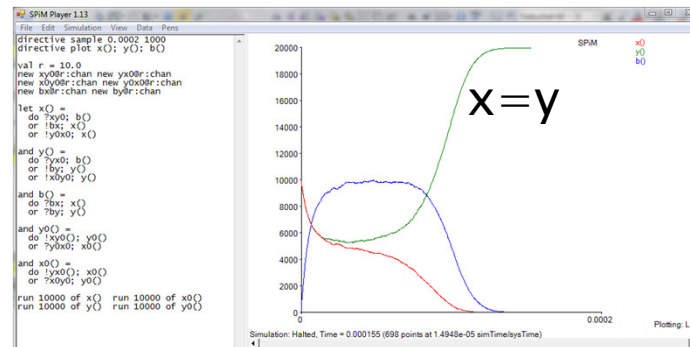
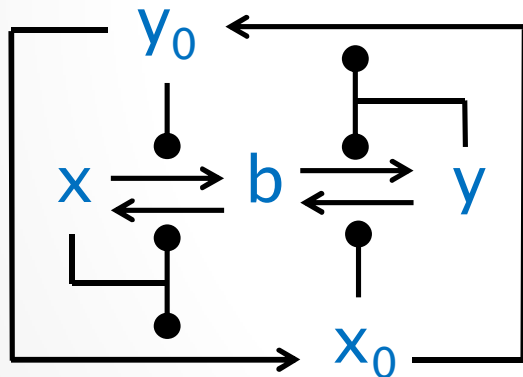
Chemical Constraints

- This circuit is ‘chemically demanding’
 - It requires x molecules to be ‘next’ to y molecules because they interact directly
 - It requires both x and y to be catalysts, and in fact autocatalysts, and in fact each–other’s autocatalyst!



Program Transformations

- An example of relaxing those constraints
 - This circuit works just as well as the original, but it no longer requires x to be 'next' to y . They no longer interact directly. Instead, they interact through an additional x_0 - y_0 equilibrium.



```
directive sample 0.0002 1000
directive plot x0; y0; b0

val r = 10.0
new xy0@r:chan new yx0@r:chan
new x0y0@r:chan new y0x0@r:chan
new bx@r:chan new by@r:chan

let x0 =
do ?xy0; b0
or !bx; x0
or !y0x0; x0
and y0 =
do ?yx0; b0
or !by; y0
or !x0y0; y0
and b0 =
do ?bx; x0
or ?by; y0
and y00 =
do !xy00; y00
or !y0x0; x00
and x00 =
do !yx00; x00
or !x0y0; y00

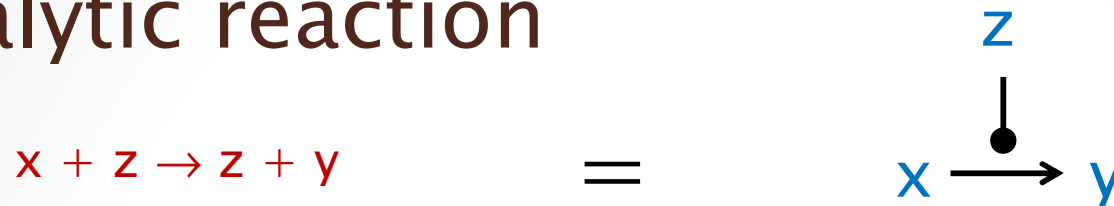
run 5000 of x0 run 5000 of x00
run 5000 of y0 run 5000 of y00
```

Program Transformations

- Another example of relaxing constraints
 - Invent an Approximate Majority network that requires only x to be a catalyst. How?
 - Enter the **Cell Cycle** switches...

Some Notation

- Catalytic reaction



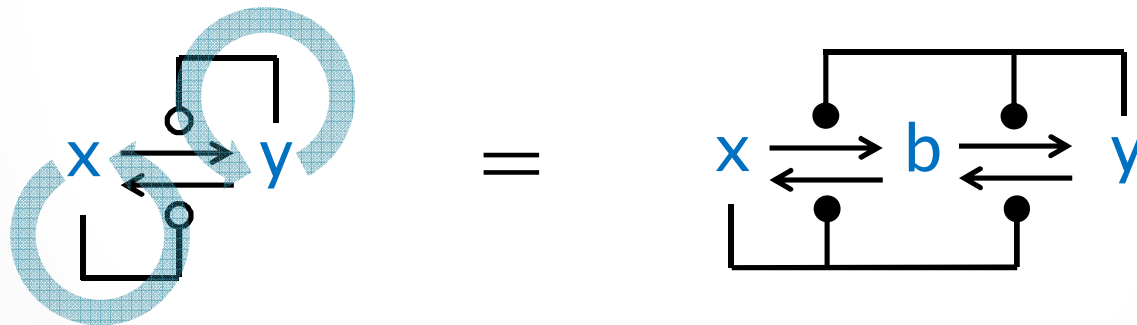
- Non-linear reaction



The hollow circle may represent any ‘non-linear’ reaction (e.g. enzymatic, hill) in addition to this ‘double-phosphorylation’ network, which however is the standard interpretation here.

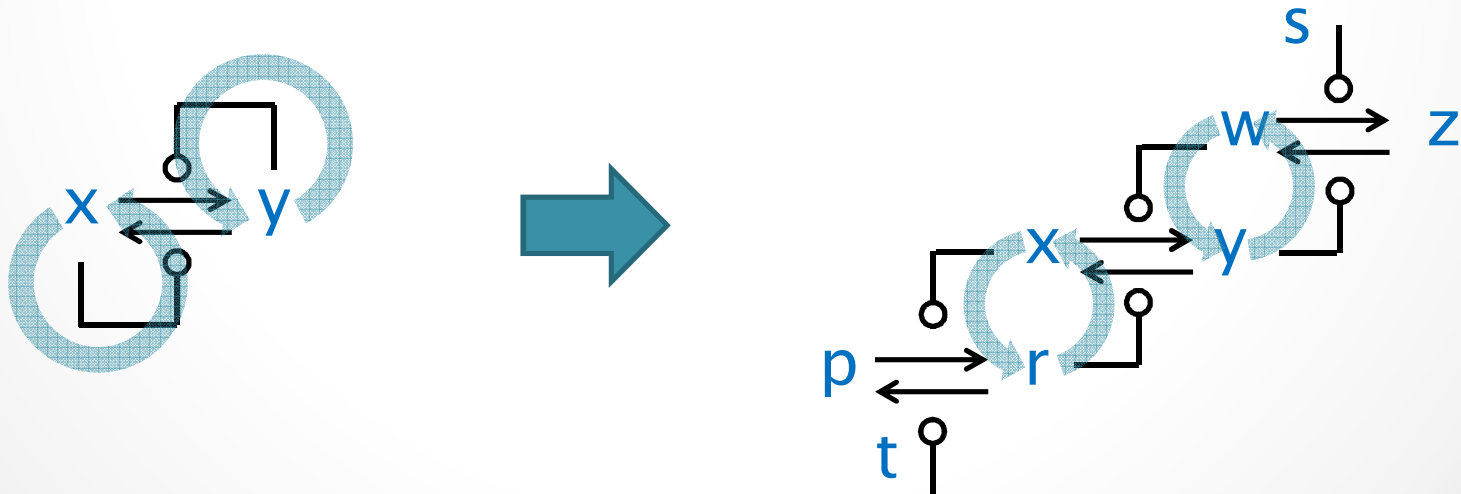
Zero-Input Switches

- ‘Zero-input switch’ = majority circuit: just working off the initial conditions.
- Step 1: the original AM Network



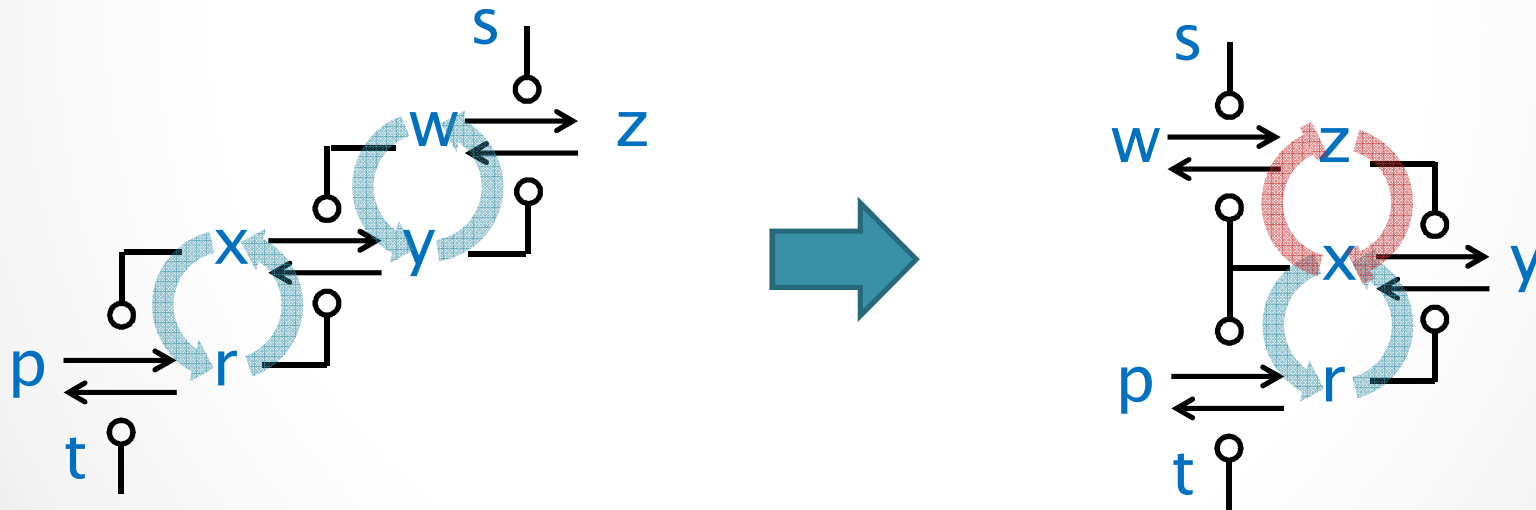
Zero-Input Switches

- Step 2: remove auto-catalysis
 - By introducing intermediate species w , r .
 - Here w breaks the y auto-catalysis, and r breaks the x auto-catalysis, while preserving the feedbacks.
 - w and r need to 'relax back' (to z and t) when they are not catalyzed: s and t provide the back pressure.



Zero-Input Switches

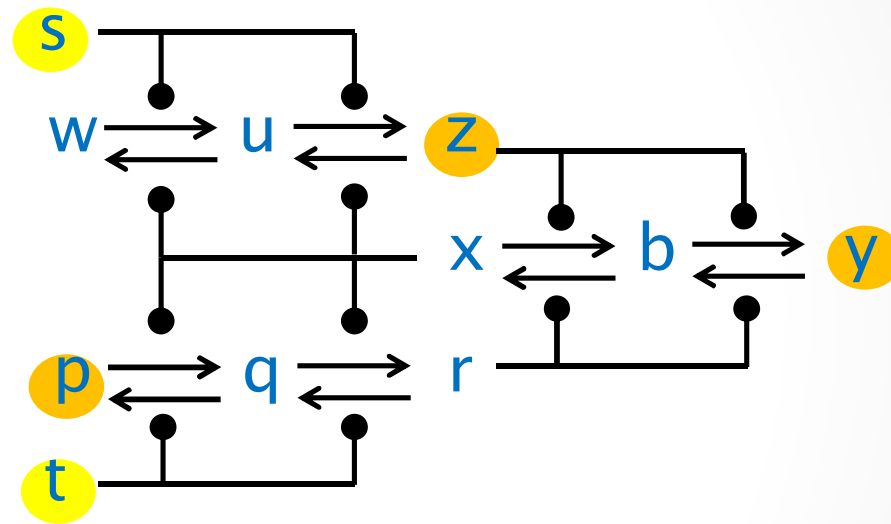
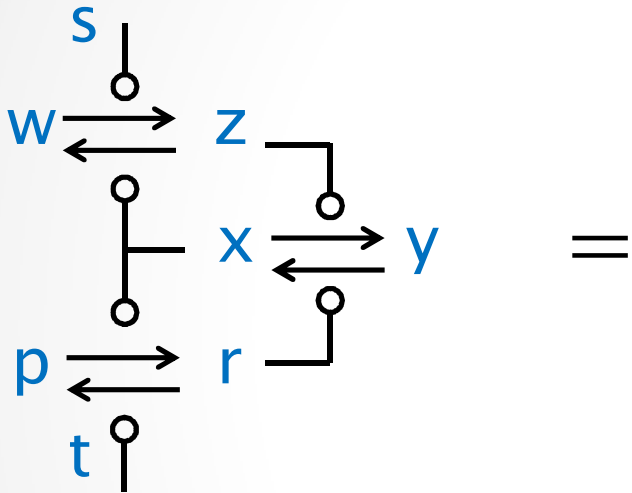
- Step 3: transform a double-positive loop on y into a double-negative loop on x .
 - Instead of y (actively) activating itself through w , we have z activating y (which is passive). To counteract, now x has to switch from inhibiting y to inhibiting z .



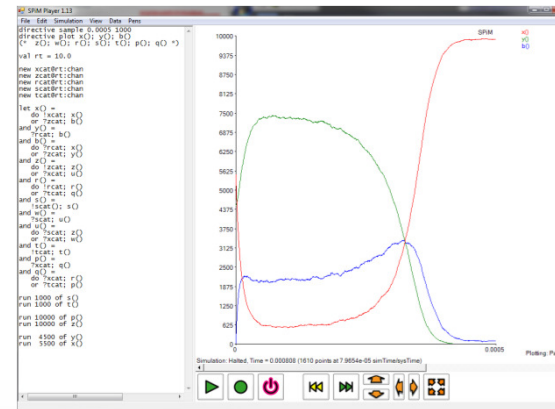
- So that y no longer catalyzes anything.

Zero-Input Switches

- Still an AM circuit



(Although the equal-likelihood outcome here is around 4500 y vs 5500 x, and there are other parameters)



```
directive sample
0.0005 1000
directive plot x(): y():
b()
(* z(): w(): r(): s(): t():
p(): q(): *)
```

```
val rt = 10.0
```

```
new xcat@rt:chan
new zcat@rt:chan
new rcat@rt:chan
new scat@rt:chan
new tcat@rt:chan
```

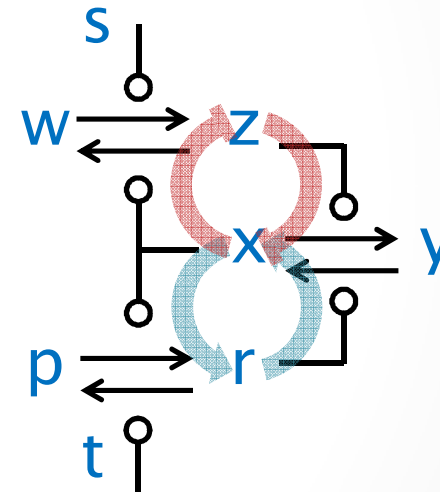
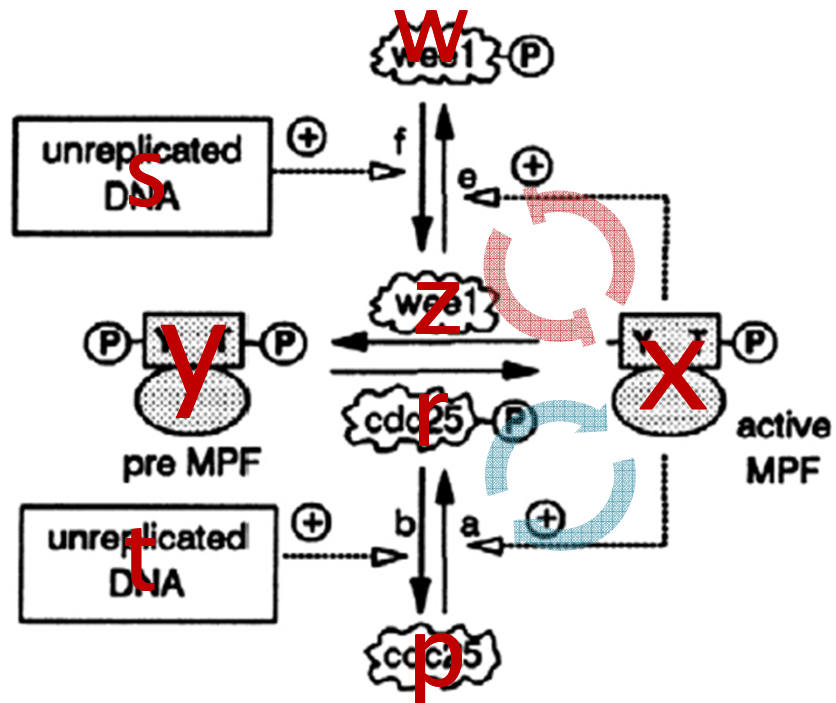
```
let x() =
do !xcat; x()
or ?zcat; b()
and y() =
?rcat; b()
and b() =
do ?rcat; x()
or ?zcat; y()
and z() =
do !zcat; z()
or ?xcat; u()
and r() =
do !rcat; r()
or ?tcat; q()
and s() =
!scat(); s()
and w() =
?scat; u()
and u() =
do ?scat; z()
or ?xcat; w()
and t() =
!tcat; t()
and p() =
?xcat; q()
and q() =
do ?xcat; r()
or ?tcat; p()
```

```
run 1000 of s()
run 1000 of t()
```

```
run 10000 of p()
run 10000 of z()
```

```
run 4500 of y()
run 5500 of x()
```

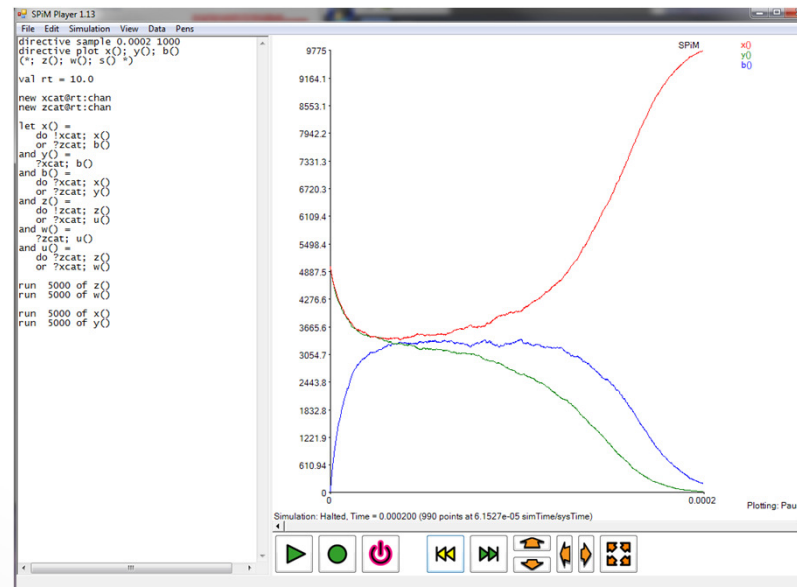
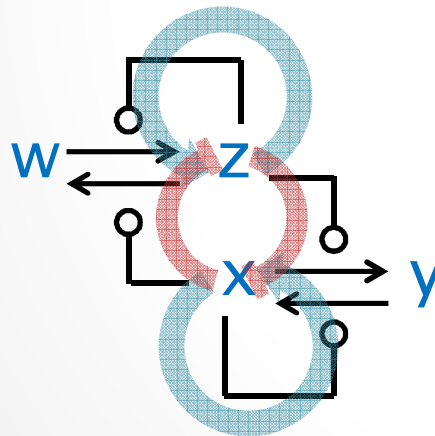
The Cell Cycle Switch



Zero-Input Switches

- Other designs

- A version with no external bias (s,t) where y is still non-catalytic and x and z are self-catalytic.
- Both x and z have an 'inactive' form, y and w, although the both are double catalysts.



```
directive sample 0.0002 1000
directive plot x0; y0; b0
(*; z0; w0; s0 *)
```

```
val rt = 10.0
```

```
new xcat@rt:chan
new zcat@rt:chan
```

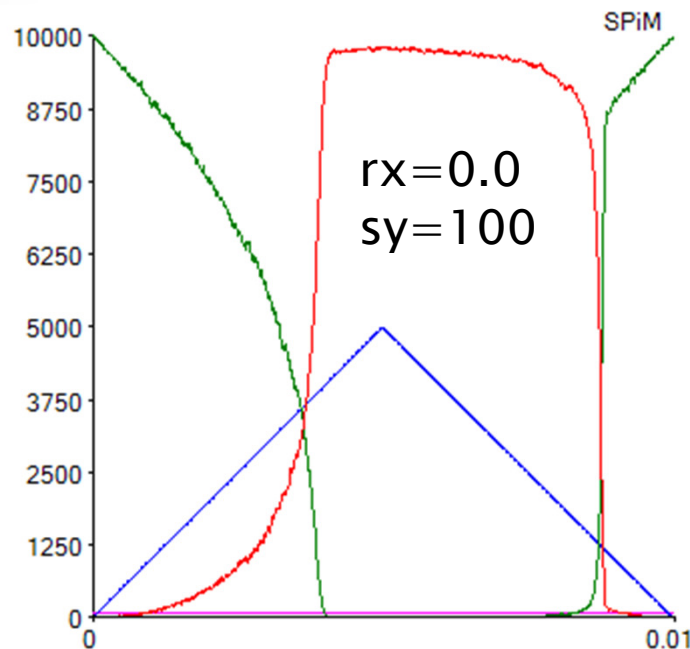
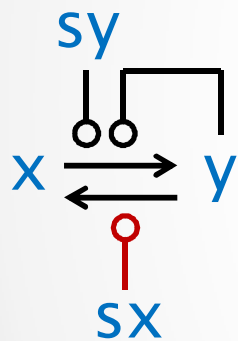
```
let x() =
do ?xcat: x()
or ?zcat: b()
and y() =
?zcat: b()
and b() =
do ?xcat: x()
or ?zcat: y()
and z() =
do ?zcat: z()
or ?xcat: u()
and w() =
?zcat: u()
and u() =
do ?zcat: z()
or ?xcat: w()
```

```
run 5000 of z()
run 5000 of w()
```

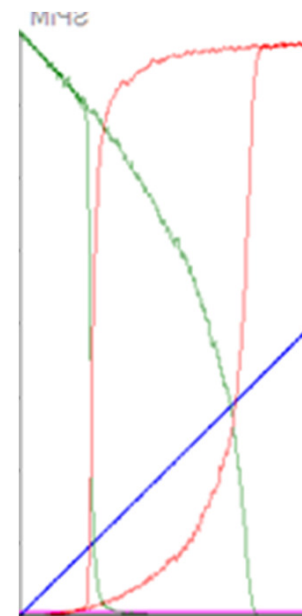
```
run 5000 of x()
run 5000 of y()
```

One-Input Switches

- Hysteresis in AM-like switches



x0
y0
sx0
sy0



```
directive sample 0.01 1000
directive plot x0; y0; sx0; sy0 (* b0; *)

val rt = 10.0
new xcat@rt:chan
new ycat@rt:chan
new sxcat@rt:chan new sxkill:chan
new sycat@rt:chan new sykill:chan

let x0 =
  do ?ycat; b0
  or ?sycat; b0
and y0 =
  do !ycat; y0
  or ?sxcac; b0
and b0 =
  do ?sxcac; x0
  or ?ycat; y0
  or ?sycat; y0

and sy0 = do !sycat; sy0 or ?sykill; ()
and sx0 = do !sxcat; sx0 or ?sxkill; ()

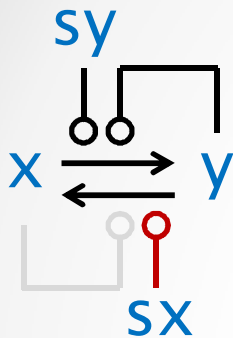
run 10000 of y0
run 100 of sy0

let clock(p:proc(int), t:float) =
  (* Produce one p(m) every t sec with precision
  dt,
  with m incremented from 0 *)
  (val dt= 100.0 run step(p, 0, t, dt, dt))
  and step(p:proc(int), m:int, t:float, n:float,
  dt:float) =
  if n<=0.0 then (p(m))step(p,m+1,t,dt,dt)
  else delay@dt/t; step(p,m,t,n-1.0,dt)

let schedule(n:int) =
  if n < 5000 then sx0
  else if n < 10000 then !sxkill;()
  else ()

run clock(schedule,0.000001)
```

One-Input Switches



```

directive sample 0.02 1000
directive plot x0; y0; sx0; sy0 (* b0; *)

val rt = 10.0
val rx = 1.0
new xcat@rx:chan
new ycat@rt:chan
new sxcat@rt:chan new sxkill:chan
new sycat@rt:chan new sykill:chan

let x() =
do lxcat: x0
or ?ycat: b0
or ?syat: b0
and y() =
do lycat: y0
or ?xcat: b0
or ?sxcat: b0
and b() =
do ?xcat: x0
or ?sxcat: x0
or ?ycat: y0
or ?syat: y0

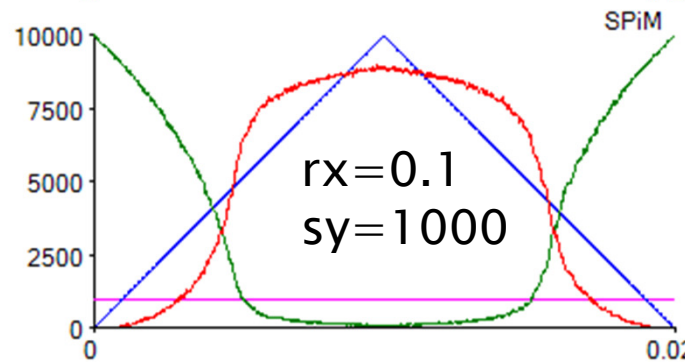
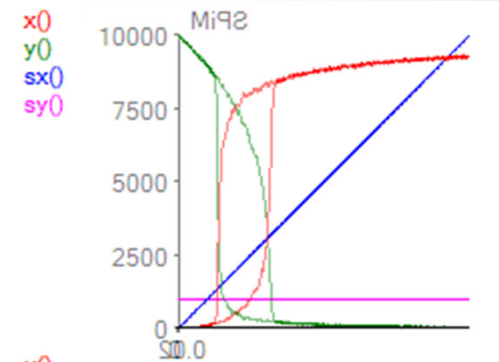
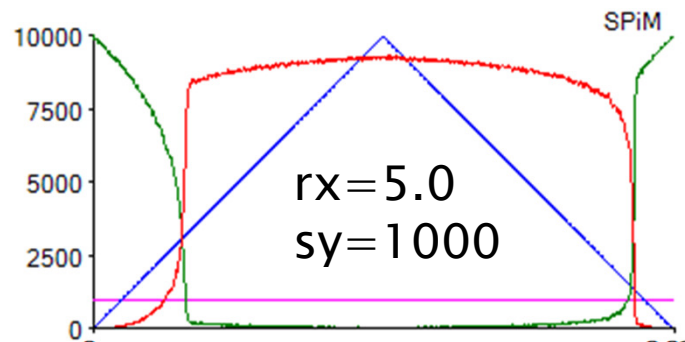
and sy() = do lsycat: sy0 or ?sykill: 0
and sx() = do lsxcat: sx0 or ?sxkill: 0

run 10000 of y0
run 1000 of sy0

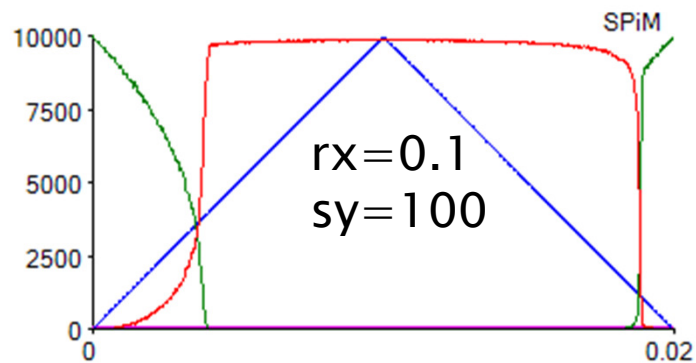
let clock(p:proc(int), t:float) =
(* Produce one p(m) every t sec with precision
dt,
with m incremented from 0 *)
(val dt= 100.0 run step(p, 0, t, dt, dt))
and step(p:proc(int), m:int, t:float, n:float,
dt:float) =
if n<=0.0 then (p(m)|step(p,m+1,t,dt,dt))
else delay@dt/t; step(p,m,t,n-1.0,dt)

let schedule(n:int) =
if n < 5000 then sx()
else if n < 10000 then lsxkill:0
else ()

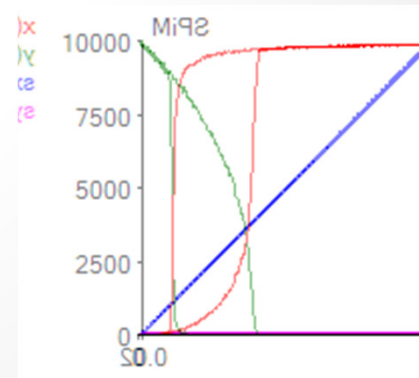
run clock(schedule,0.000001)
    
```



x0
y0
sx0
sy0

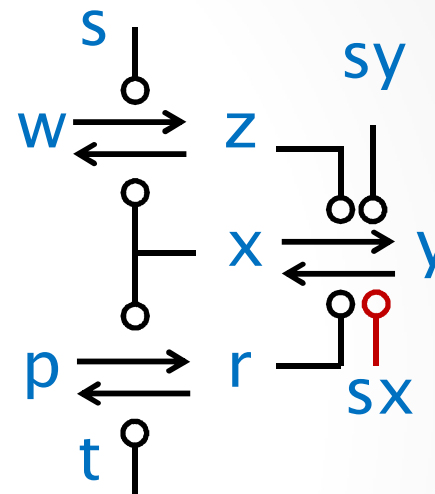
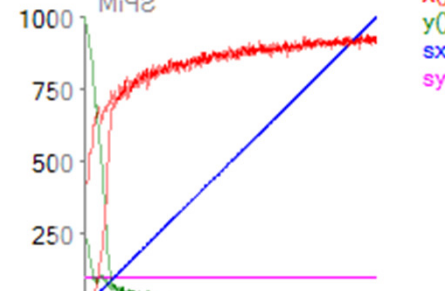
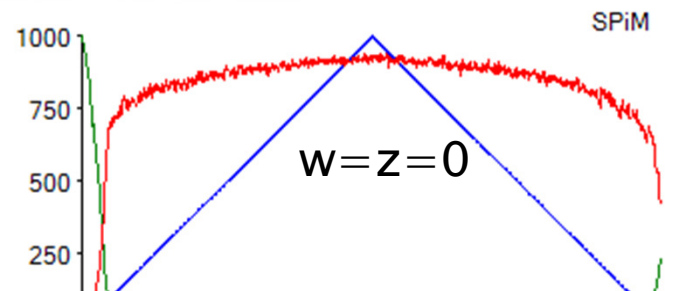
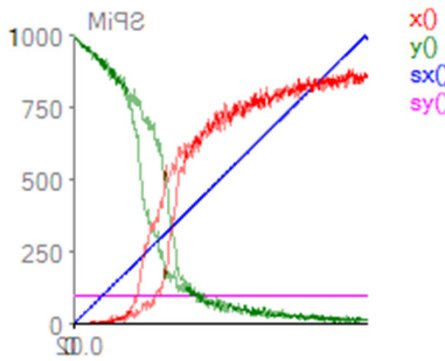
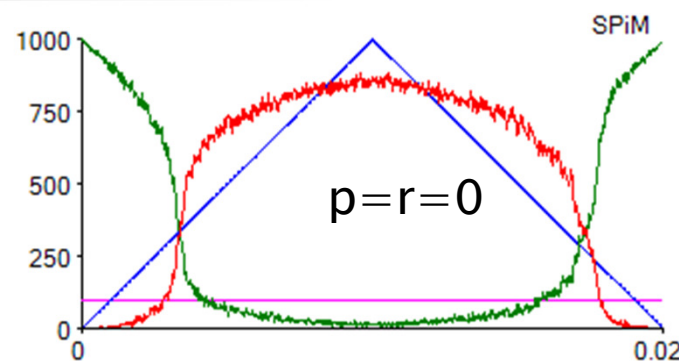
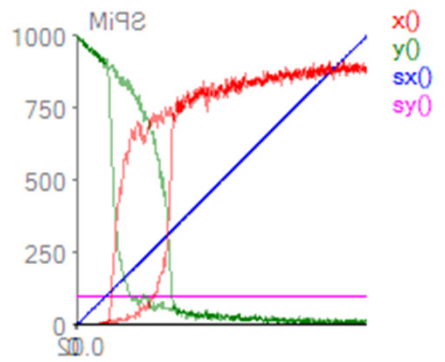
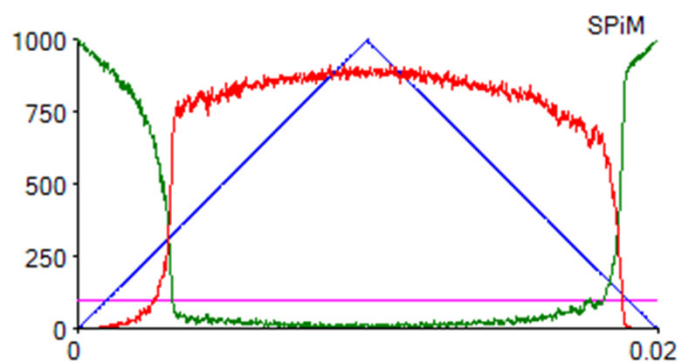


x0
y0
sx0
sy0



One-Input Switches

- Hysteresis in cell cycle switches



```

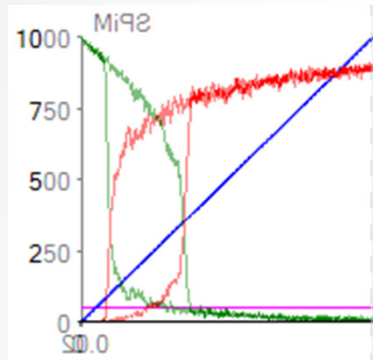
genetic model 5121 1000
species 100 y() 1000
initial 1000 y() 1000
initial 1000 sy() 1000
initial 1000 z() 1000
initial 1000 p() 1000
initial 1000 t() 1000
initial 1000 x() 200
initial 1000 r() 100
initial 1000 s() 100
initial 1000 w() 100

in 1000
in 1000 sy()
in 1000 z()
in 1000 p()
in 1000 t()
in 1000 x()
in 1000 r()
in 1000 s()
in 1000 w()

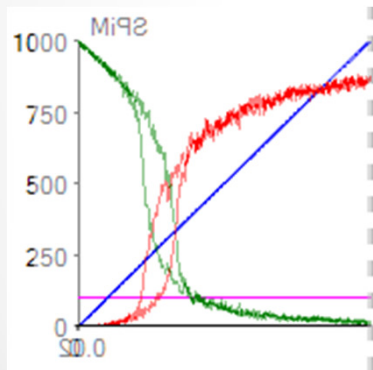
when {
  x() > 1000
  sy() > 1000
  z() > 1000
  p() > 1000
  t() > 1000
  x() > 1000
  r() > 1000
  s() > 1000
  w() > 1000
}
}
    
```

initial conditions:
 1000 of y
 1000 of z
 1000 of p
 1000 of t
 200 of s
 100 of sy

varying sx 0 to 1000



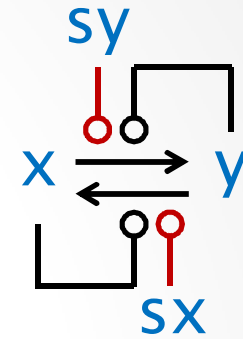
twice s, half t, and half sy



five times t

Two-input Switches

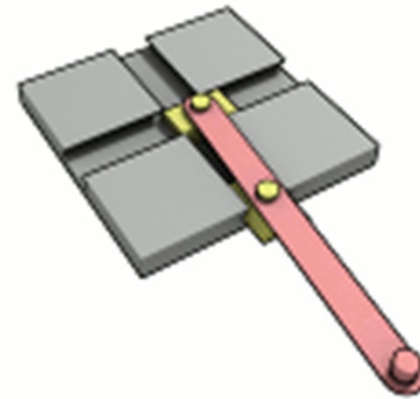
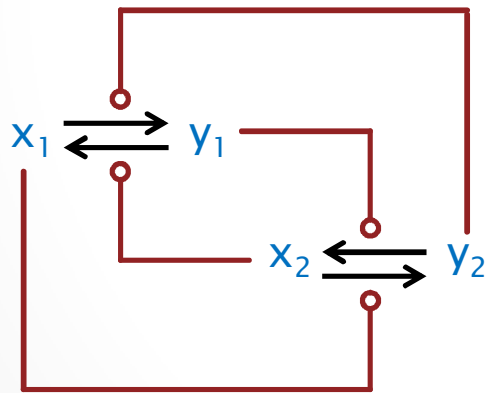
- (not really relevant here)



Oscillators

The Trammel of Archimedes

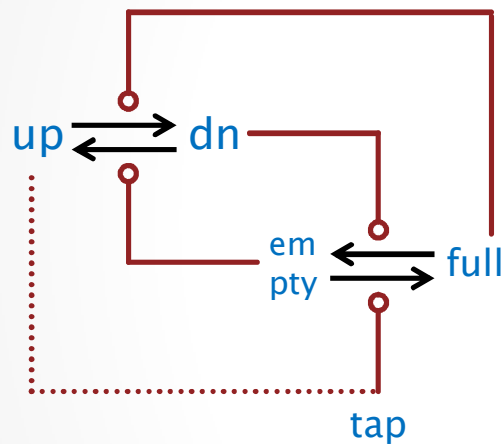
- A device to draw ellipses
 - Two interconnected switches.
 - When one switch is on (off) it flips the other switch on (off). When the other switch is on (off) it flips the first switch off (on).



en.wikipedia.org/wiki/Trammel_of_Archimedes

The Shishi Odoshi

- A Japanese scarecrow (scare-deer)
 - Used by Bela Novak to illustrate the cell cycle switch.



empty + tap \rightarrow tap + full
up + full \rightarrow full + dn
full + dn \rightarrow dn + empty
dn + empty \rightarrow empty + up

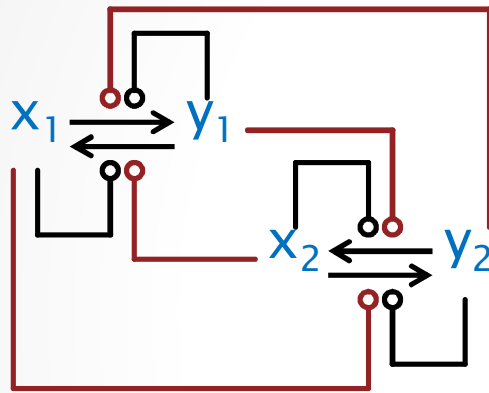


<http://www.youtube.com/watch?v=VbvecTiftcE&NR=1&feature=fwvp>

To make it into a full trammel (dotted line), we could make the up position mechanically open the tap (i.e. take up = tap)

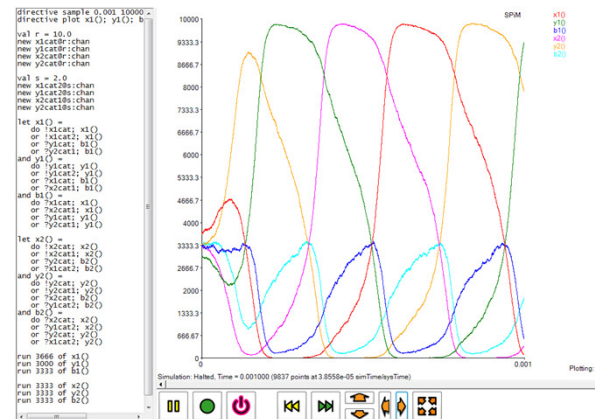
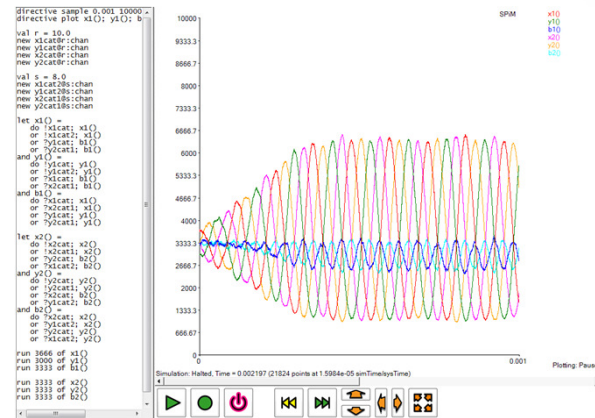
The 2AM Limit-Cycle Oscillator

- Two AM switches in a Trammel pattern



The red reactions need to be slower (even slightly) than the black reactions, but otherwise the oscillation is robust. Oscillation stops at 10 vs. 10 and 1 vs. 10. Here the rates are 8 vs 10.0 top, and 2 vs 10, bottom.

(Simple limit-cycle oscillators in the literature have very critical rate ranges.)



```

directive sample 0.001 10000
directive plot x10; y10; b10; x20;
y20; b20
    
```

```

val r = 10.0
new x1cat@:chan
new y1cat@:chan
new x2cat@:chan
new y2cat@:chan
    
```

```

val s = 8.0
new x1cat2@:chan
new y1cat2@:chan
new x2cat1@:chan
new y2cat1@:chan
    
```

```

let x10 =
do !x1cat: x10
or !x1cat2: x10
or !y1cat: b10
or !y2cat1: b10
and y10 =
do !y1cat: y10
or !y1cat2: y10
or !x1cat: b10
or !x2cat1: b10
and b10 =
do !x1cat: x10
or !x2cat1: x10
or !y1cat: y10
or !y2cat1: y10
    
```

```

let x20 =
do !x2cat: x20
or !x2cat1: x20
or !y2cat: b20
or !y1cat2: b20
and y20 =
do !y2cat: y20
or !y2cat1: y20
or !x2cat: b20
or !y1cat2: b20
and b20 =
do !x2cat: x20
or !y1cat2: x20
or !y2cat1: y20
or !x1cat2: y20
    
```

```

run 3666 of x10
run 3000 of y10
run 3333 of b10
    
```

```

run 3333 of x20
run 3333 of y20
run 3333 of b20
    
```

Influx Oscillators

- Similar but:
 - The two-input switches are replaced by one-input switches which are reset by constant influxes.

```

directive sample 0.002 1000
directive plot x1():y1():x2():y2():b2():c1():c2()

val r = 10.0
new x1cat@r:chan
new y1cat@r:chan
new x2cat@r:chan
new y2cat@r:chan

val s = 10.0
new x1cat2@s:chan
new y1cat2@s:chan
new x2cat2@s:chan
new y2cat2@s:chan

val t = 100.0
new c1ch@t:chan new c2ch@t:chan

let c1gen() = delay@100000.0:(c1gen() | c1())
and c1() = !c1ch:()
let c2gen() = delay@100000.0:(c2gen() | c2())
and c2() = !c2ch:()

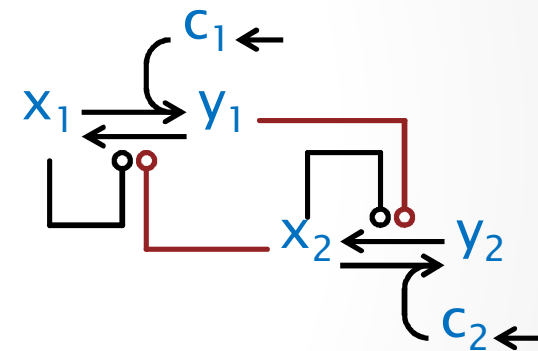
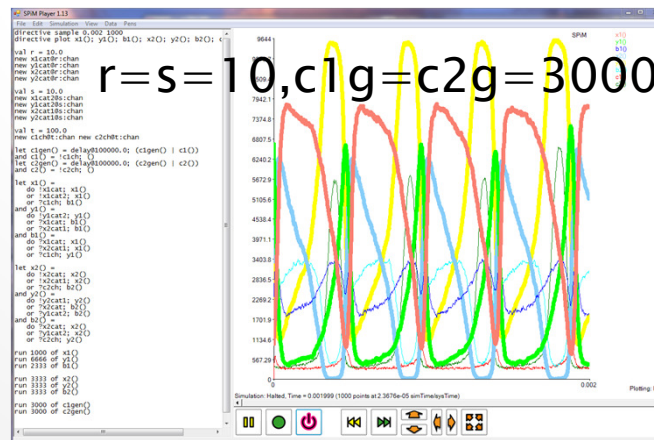
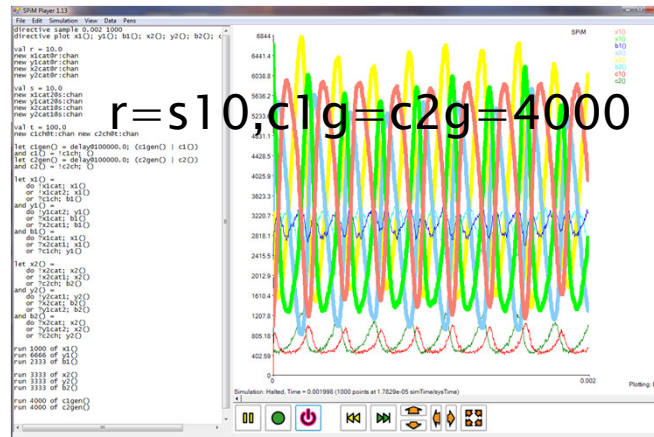
let x1() =
do !x1cat:x1()
or !x1cat2:x1()
or !x1cat1:b1()
and !b1() =
do !x1cat:x1()
or !x2cat1:x1()
or !x1ch:y1()

let x2() =
do !x2cat:x2()
or !x2cat1:x2()
or !x2cat2:b2()
and !b2() =
do !x2cat:x2()
or !y1cat2:x2()
or !x2ch:y2()

run 1000 of x1()
run 6666 of y1()
run 2333 of b1()

run 3333 of x2()
run 3333 of y2()
run 3333 of b2()

run 4000 of c1gen()
run 4000 of c2gen()
    
```

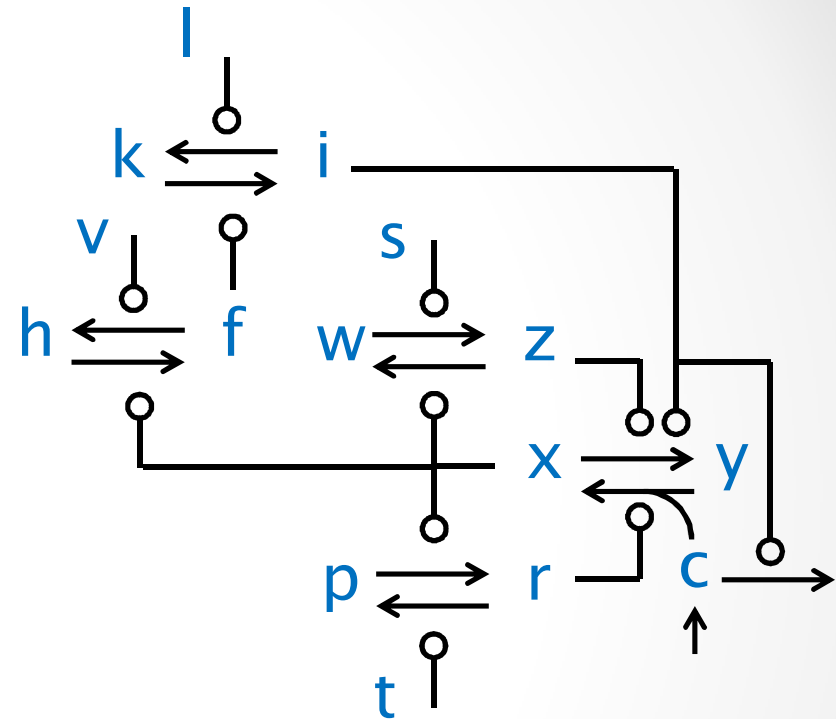


Works best with $s=r$.

Needs constant influx of $c1, c2$

Novak–Tyson Oscillator

- **First switch**
 - Is the ‘transformed’ AM switch in one–input configuration (driven by constant influx of cyclin).
- **Second switch**
 - Is a simple two–stage switch working as a delay (the first switch is so good in terms of hysteresis that the second switch is not very critical for oscillation).
 - It can be replaced by a one–stage switch (Ferrell’s cell cycle oscillator) but oscillation is a bit harder to obtain.
- **Connection**
 - Single links, as in the influx oscillator.



Journal of Cell Science 106, 1153-1168 (1993)
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Numerical analysis of a comprehensive model of M-phase control in *Xenopus* oocyte extracts and intact embryos

Bela Novak* and John J. Tyson†

Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24060-0406, USA

Novak-Tyson Oscillator

```
directive sample 0.02 1000
directive plot x0; y0; b0; z0; w0; r0; s0; t0; p0; q0; f0; g0;
h0; v0; i0; j0; k0; l0; c0
```

```
val rt = 100.0
val rt2 = 1.0
val rt3 = 200.0
val rc = 10000.0
```

```
new c@rt:chan
new xcat@rt:chan new zcat@rt:chan new rcat@rt:chan
new scat@rt:chan new tcat@rt:chan new vcat@rt:chan
new lcat@rt:chan
```

```
new fcat@rt3:chan new icat@rt3:chan
new xcat2@rt2:chan
```

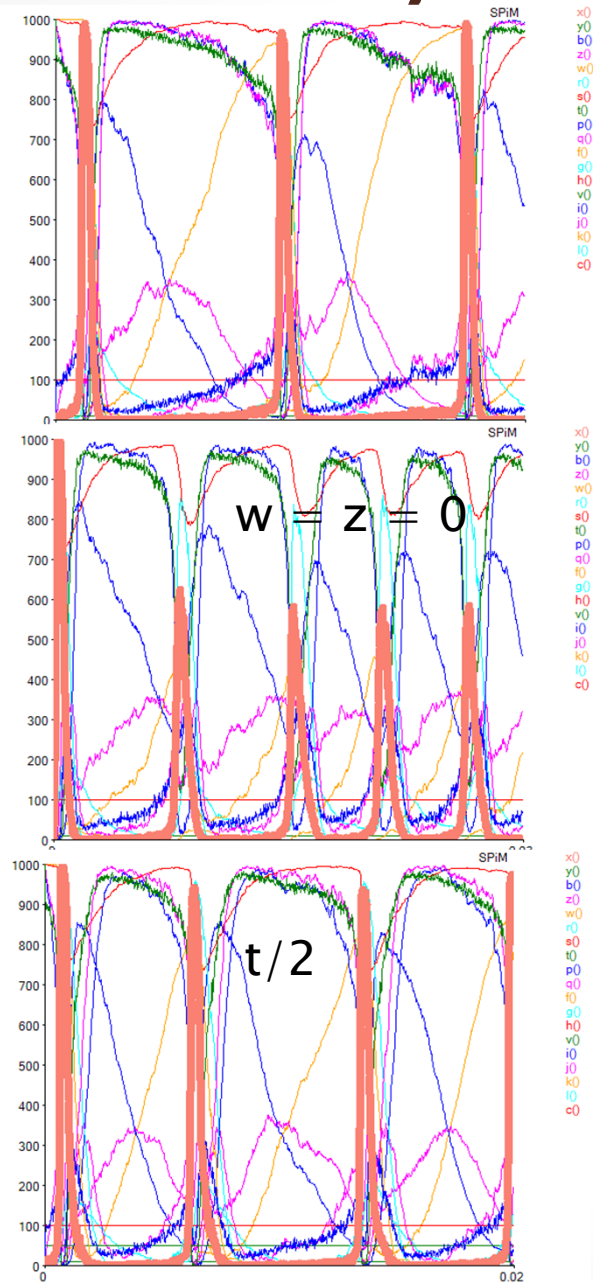
```
let ci0 = delay@rc:(cy0)ci0()
and cy0 = !c; 0
```

```
let x0 = do !xcat: x0 or !xcat2: x0 or ?zcat: b0 or ?icat: b0
and y0 = do ?rcat: b0 or ?c; b0
and b0 = do ?rcat: x0 or ?c; x0 or ?zcat: y0 or ?icat: y0
and z0 = do !zcat: z0 or ?xcat: u0
and r0 = do !rcat: r0 or ?tcat: q0
and s0 = !scat: s0
and w0 = ?scat: u0
and u0 = do ?scat: z0 or ?xcat: w0
and t0 = !tcat: t0
and p0 = ?xcat: q0
and q0 = do ?xcat: r0 or ?tcat: p0
and f0 = do !fcat: f0 or ?vcat: g0
and g0 = do ?vcat: h0 or ?xcat2: f0
and h0 = ?xcat2: g0
and v0 = !vcat: v0
and i0 = do !icat: i0 or ?lcat: j0 or ?c; i0
and j0 = do ?lcat: k0 or ?fcat: i0
and k0 = ?fcat: j0
and l0 = !lcat: l0
```

```
run 100 of s0
run 100 of t0
run 10 of v0
run 10 of l0
```

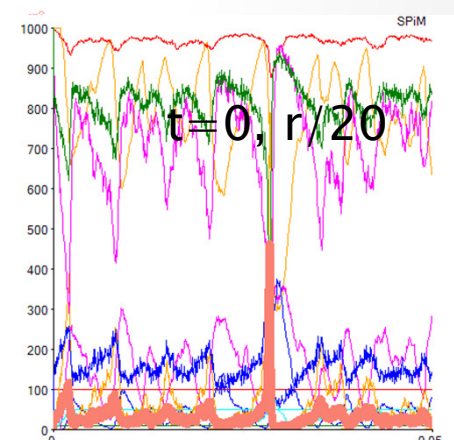
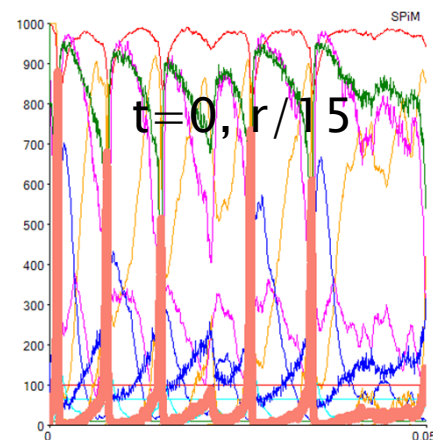
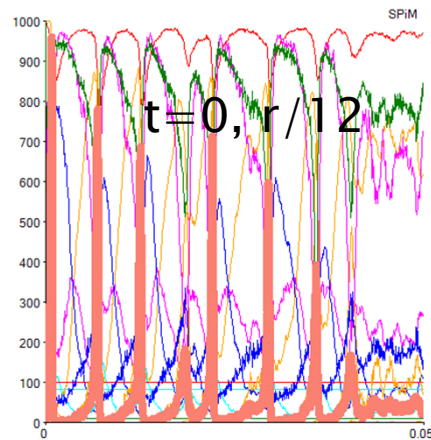
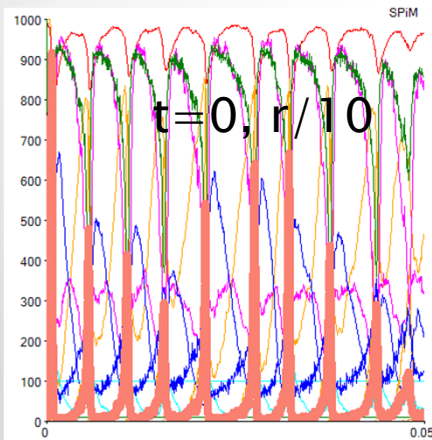
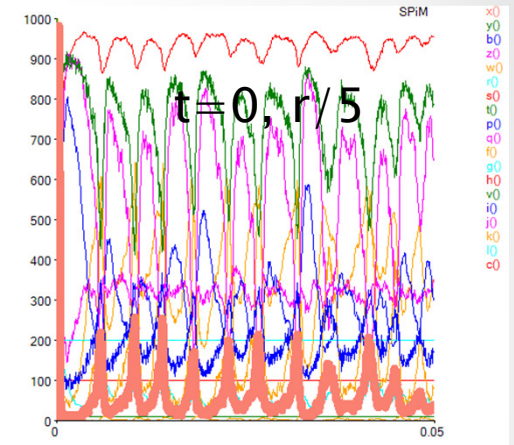
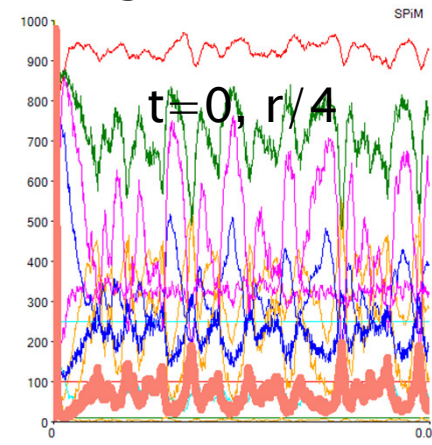
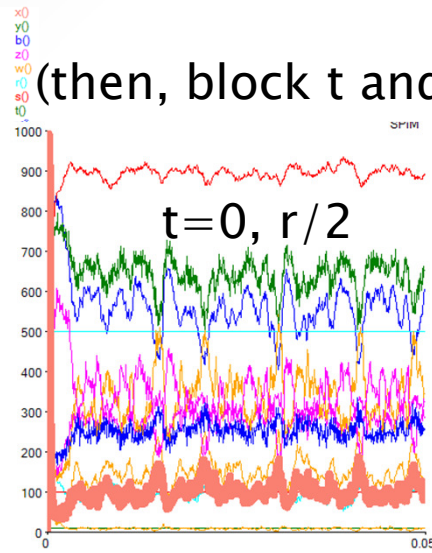
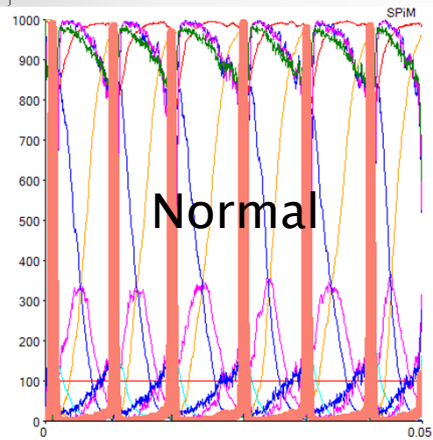
```
run 1000 of y0
run 1000 of z0
run 1000 of p0
run 1000 of h0
run 1000 of k0
```

```
run 1000 of ci0
```

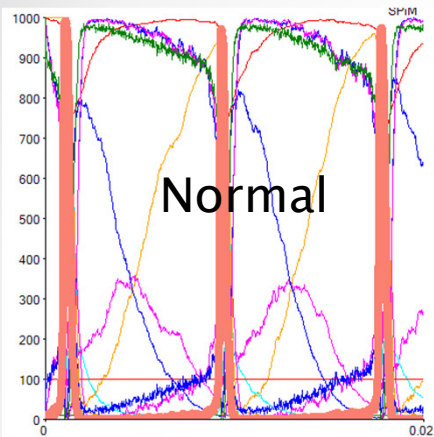


$p=r=0$, or $t/4$, or $t*2$:
no oscillation

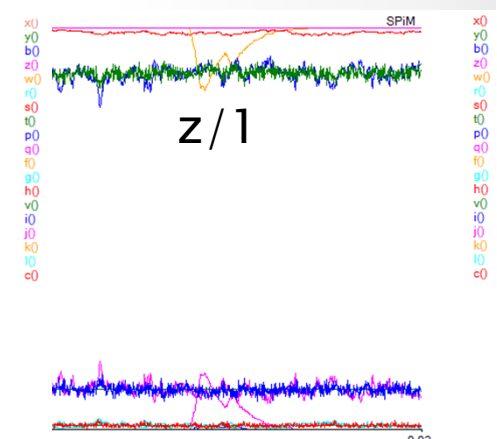
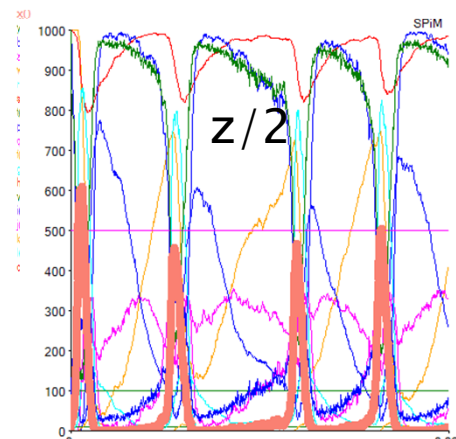
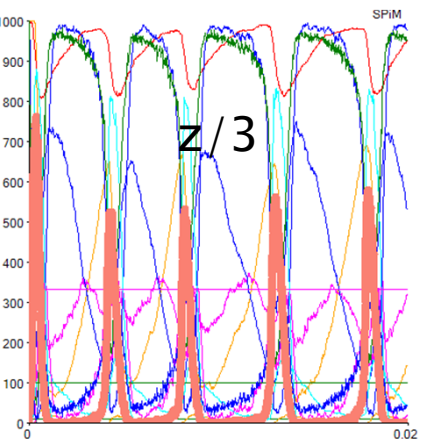
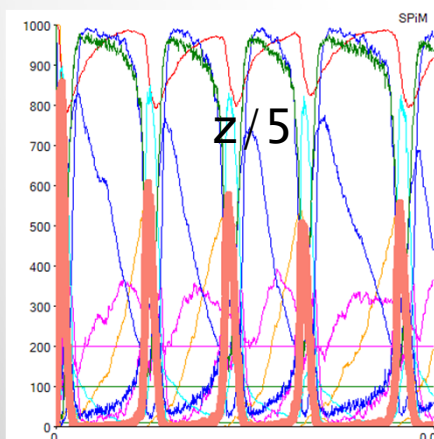
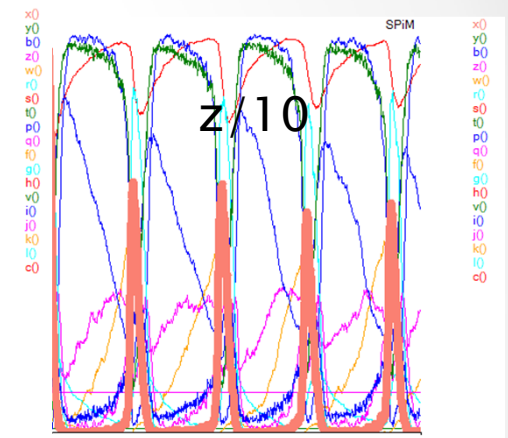
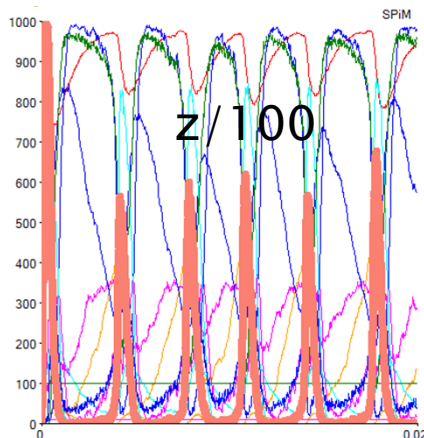
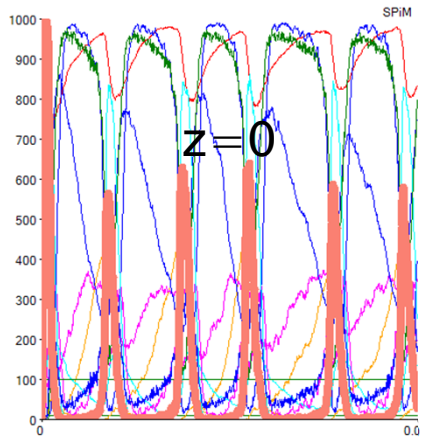
Without double-positive loop

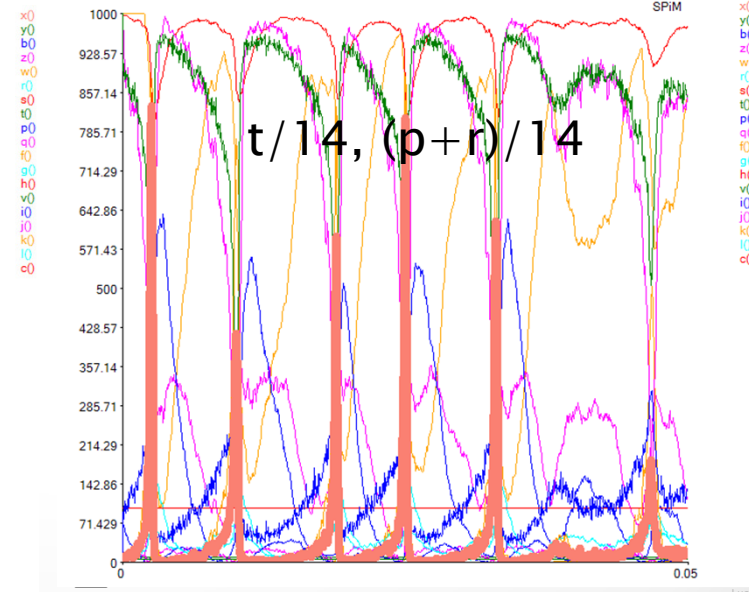
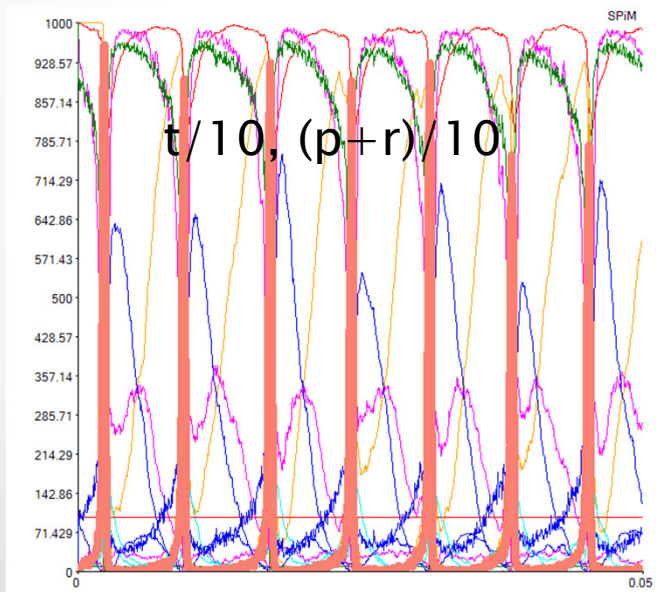
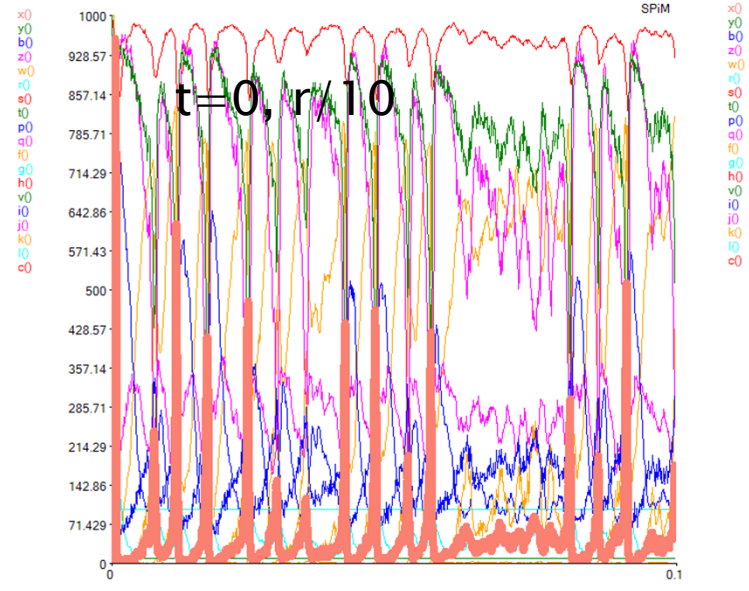
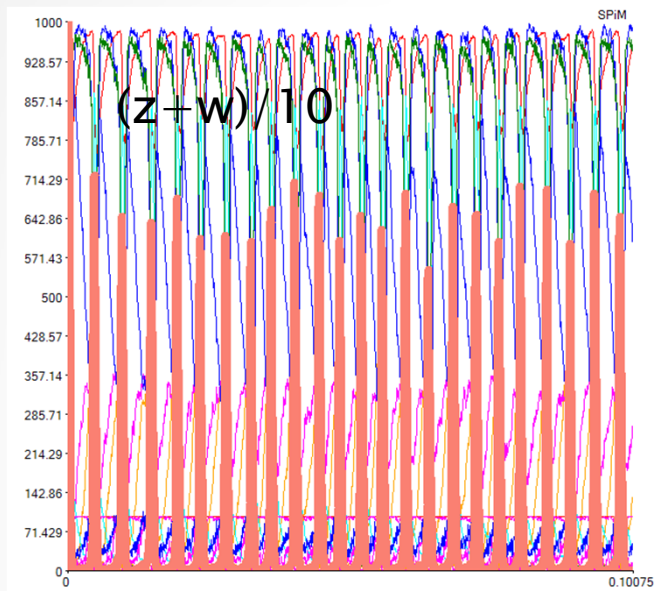


Without double-negative loop



(then, with x no longer acting on z, change amount of z)





Conclusions

Conclusions

- A range of ‘network transformation’
 - Can explain the structure of some natural network
 - From some non-trivial underlying algorithms
 - Discovering the transformation can elucidate the structure and function of the networks
 - But how can we say that these transformations ‘preserve (essential) behavior’?