

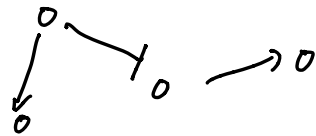
Central dogma 1958 Crick

"Flow of information"

DNA → RNA → Protein

└──────────────────┘
unit

⇒ Notion of gene networks



They process information (in a loose sense)

Classical example: Lac Operon

J. Mol. Biol. 1961

E coli: change of sugar ⇒ glucose from lactose

B galactosidase



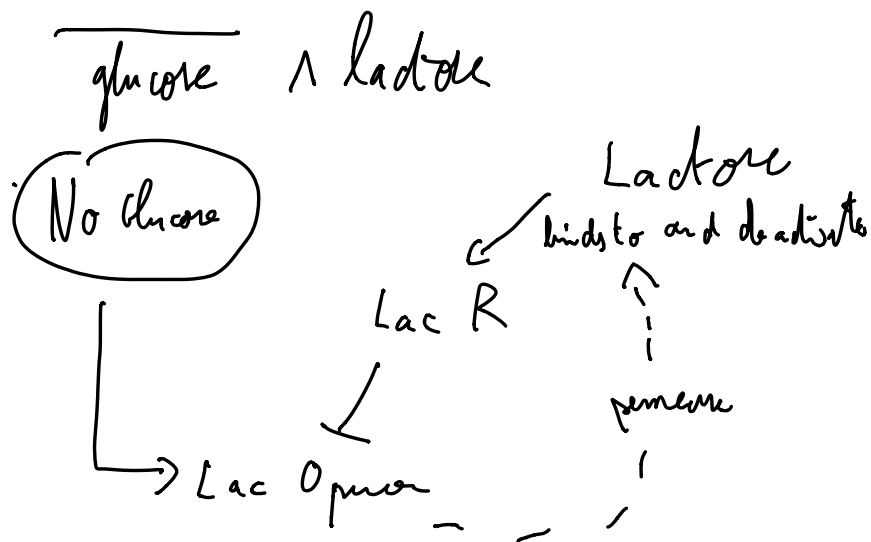
binding sites
performing a logical calculation

coding sequences

A repressor: Lac R. If no lactose, repressor is here \Rightarrow no transcription

An activator: CAMP, here only if glucose is absent.

This is our first example of information processing: this is a logical gate performing the computation



Now there is a catch

Nowick and Wener, 1957:

Enzyme induction as a "all or more phenomenon"

There is a positive feedback

This creates cellular memory: once you induce, even low concentration of lactose ensure that you stay on.

"all the progeny of an induced bacterium are induced as long as maintenance inducer is present"

⇒ information processing over several generations.

Fast Forward until the early 2000s

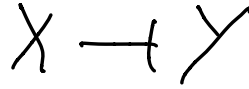
- genome sequencing made easy
- genetic engineering easier

...

one can start:

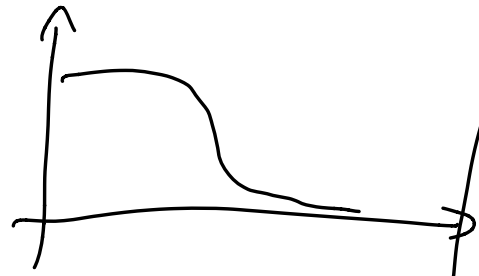
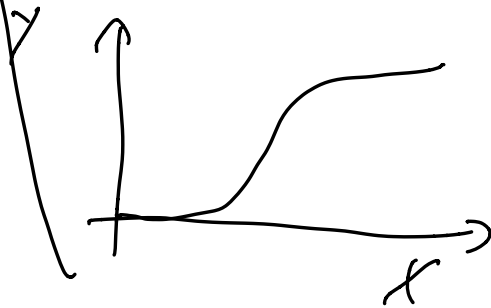
- mapping all these logical interactions
- synthesizing new constructs / dynamics.
based on rational designs
- more theory

Building blocks: activations / repressors



$$\dot{Y} = \frac{\beta X^m}{X^m + X_0^m} - \gamma$$

$$\dot{Y} = \frac{\beta}{1 + \left(\frac{X}{X_0}\right)^m} - \gamma$$



Network motifs Uri Alon

Idea: . take networks

. randomize connections

. look for statistically over-represented networks

A first motif: "autoregulation"

nodes

E. Coli:

400 nodes; 500 edges

Yeast: 700 nodes; ~1000 edges

\cap
 X

10%!
(40 in *E. coli*)

you would
roughly expect
 $400 \times \frac{1}{400} \sim 1$

only the direct ones
there are indirect ones

what could be their dynamical functions?

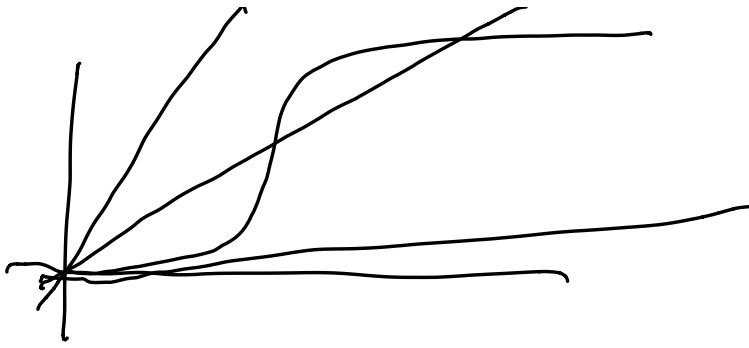
let us start with

\curvearrowright
 X

An interesting feature: multistability

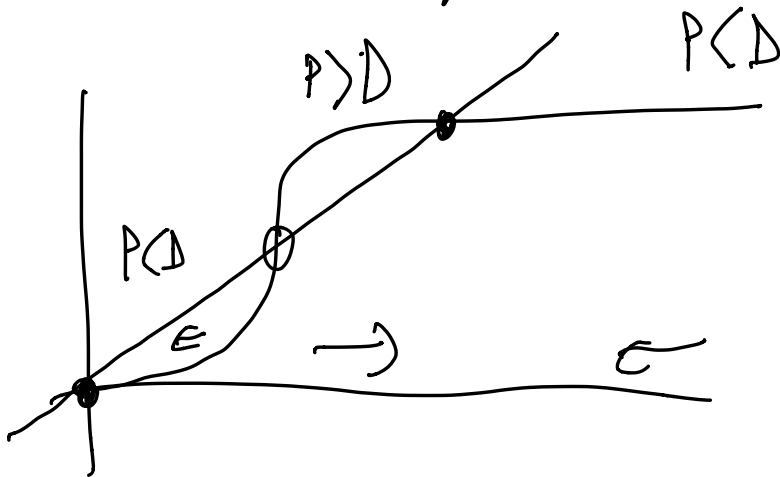
$$\dot{X} = \underbrace{\frac{\beta X^m}{X^m + X_0^m}}_{\text{production}} - \underbrace{\lambda X}_{\text{degradation}} = -\partial_X V(X)$$

Multistability: let us solve $\dot{X} = 0$ (extrema of potential)



1 \rightarrow 3 \rightarrow 1 (2 if tangent)

0 always in a steady state
 a pair a steady state can appear.
 What about their stability?



There is a high steady state.

Depending on the initial conditions, the system can

stabilize in either of these. "Memory"
Epigenetic state.

Motif is very important for differentiation, e.g.

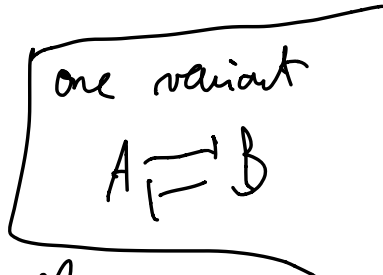
TERMINAL SELECTOR GENE

Oliver Hobert, PNAS 2008

ASE among neurons (HE-1)

A ST-1 dopaminergic neurons

Myo D (\Rightarrow) myogenesis



Of course important for cell reprogramming
Problem. more Thick Prothymine $P(x) \propto e^{-\beta V(x)}$ you will
cis vs trans : check Martin Howard more

You can lock in the long term with

epigenetic markers (e.g. methylation)

Martin Howard & Caroline Dean

Polycomb silencing, Science, 2017

X

$$\dot{X} = \frac{\beta}{1 + \left(\frac{X}{x_0}\right)^n} - \gamma X$$

obviously monostable. More interesting: dynamics

2 interesting effects:

- speed-up of response
- oscillations

Response speed-up (Rosenfeld, Elowitz, Alon, J Mol Biol 2002)

Imagine $\dot{X} = \lambda - \delta X$



$$X(t) = \frac{\lambda}{\delta} (1 - e^{-\delta t}) \quad \text{time-scale: } \frac{1}{\delta}$$

Compare with $\dot{X} = \frac{\beta}{1 + \frac{x}{x_0}} - \delta X$

Approx $\dot{X} \approx \frac{\beta x_0}{x} - \delta X$

$$\frac{1}{2} \frac{d}{dt} x^2 = \beta x_0 - \delta x^2$$

$$x^2(t) \approx \frac{\beta}{\delta} (1 - e^{-2\delta t})$$

$$X(t) \approx \sqrt{\frac{\beta}{\delta} (1 - e^{-2\delta t})}$$

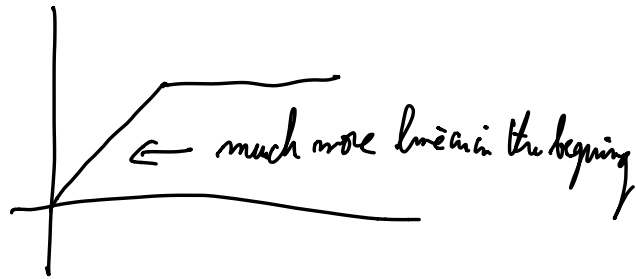
Half s.s. condition: $1 - e^{-2\delta t} = \frac{1}{4}$

$$2\delta t = \ln \frac{4}{3}$$

$$t = \frac{1}{\delta} \frac{1}{2} \ln \frac{4}{3} \approx 0.21 \delta$$

\Rightarrow x5 faster

(Intuitively)

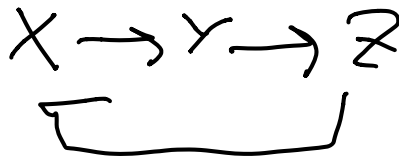


More interesting: oscillators.

For this we need a delay. No lack of this in biology (transcription, translation, etc...)

Ex $\dot{X} = f(X(t-\tau)) - \delta X$
explicit delay (Glass, Mackey, 70'; Julia Lewis, Curr Biol, 2003)

Goodwin model



$$\dot{X} = \frac{k_x}{1+Z^n} - \delta_x X$$

$$\dot{Y} = k_y X - \delta_y Y$$

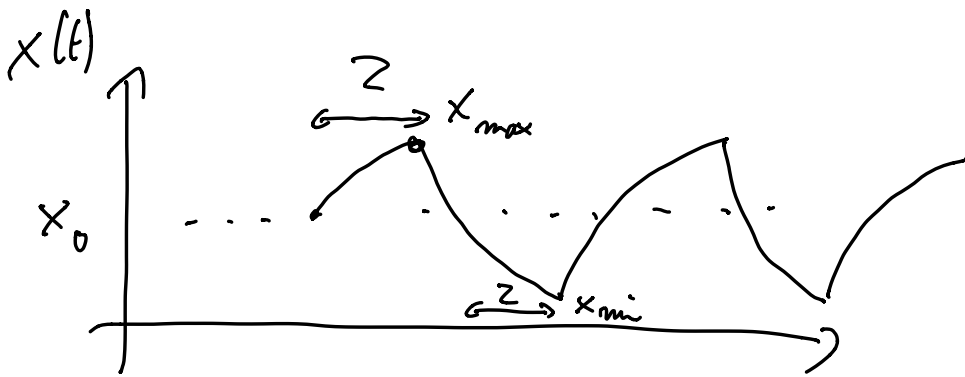
$$\dot{Z} = \dots$$

Skip

$\epsilon = k_1 \gamma - \delta$ \rightarrow "infinite" equation
 Let us start with delayed model

$$f(x(t-z)) = \begin{cases} 0 & \text{if } x(t-z) > x_0 \\ p & \text{if } x(t-z) \leq x_0 \end{cases} \quad \begin{aligned} \dot{x} &= -\delta x \\ \dot{x} &= p - \delta x \end{aligned}$$

(to do this, take $\frac{p}{1 + (\frac{x}{x_0})^n} \xrightarrow{n \rightarrow \infty} f$)



You can compute x_{max} and x_{min} in a self consistent way.
 As well as the period.

If $p/\delta \gg 1$



Period $\approx 2z$. You can then easily compute first order correction

$$T \sim 2Z + \frac{K}{\delta} + \dots \quad \delta \gg 1$$

$$K = \ln \frac{r^2}{r-1} \quad r = \frac{\rho}{X_0 \delta} > 1$$

(PF, Hahn, PRE 2005)

More complicated networks

Feed Forward Loop



All arrows can be positive and negative.

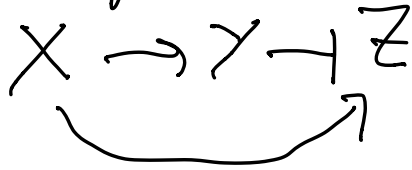
Mangan & Alon, 2003, PNAS

"coherent" same signs



~ 30 = both E. coli and Yeast

Incoherent e.g.

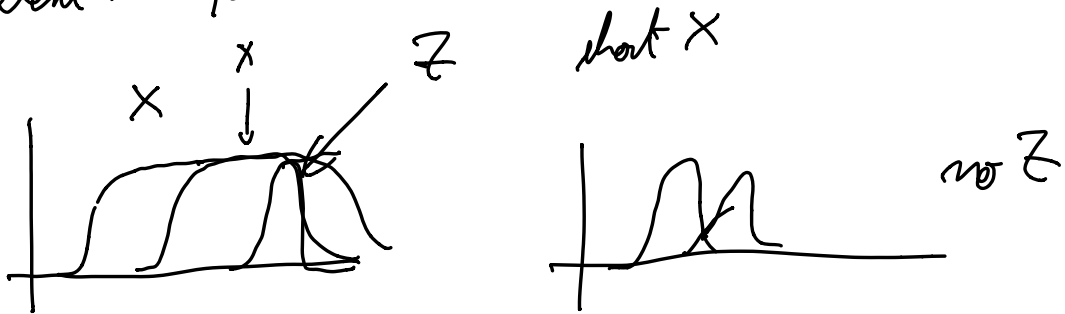


5 in E. Coli

21 in Yeast

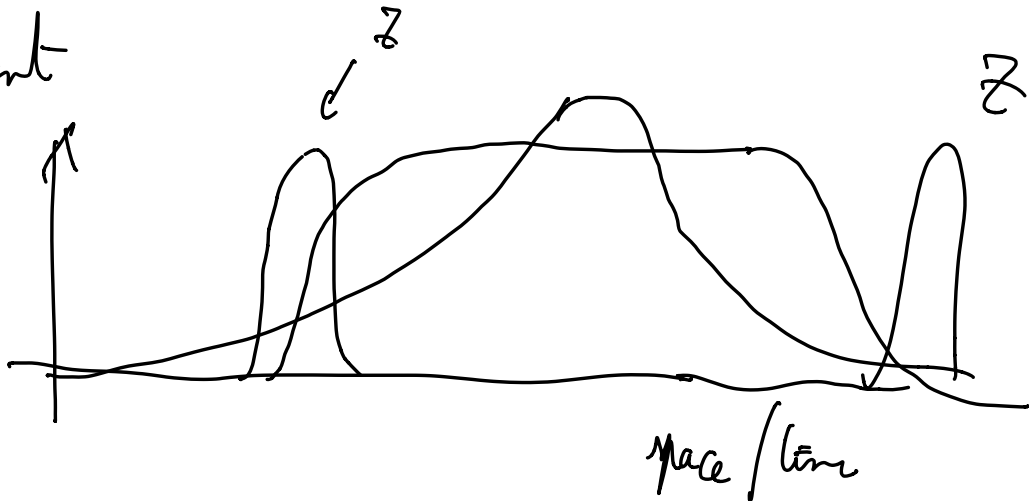
Functional role?

Coherent: "persistence detector"



"Dumb" phones work like this

Incoherent



"stupid" module

Adaptation



$$\dot{z} = f(x) - z$$

steady state

$$\dot{y} = \frac{1}{f(x)} - y$$

$z=1$ adaptation

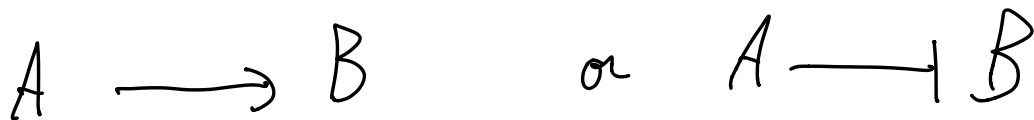
But this induces delay



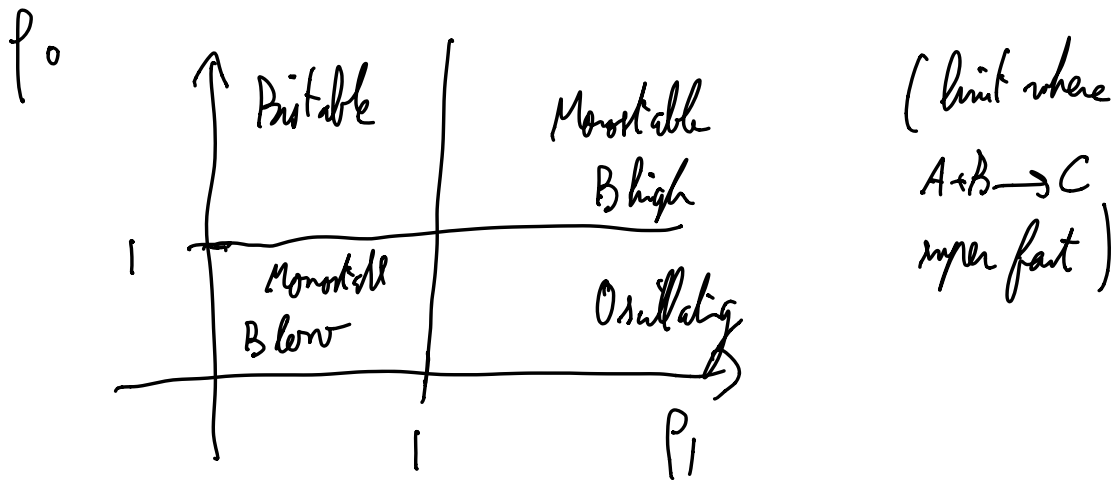
when x increases $\Rightarrow f(x)$ bigger
 but y did not change yet
 $\Rightarrow z \rightarrow$ increases

For instance: if we add Protein-Protein interaction
 or allosteric, one can do different tricks
 Yequ. Mon, PNAS 2002

The Mixed Feedback Loop



Phase diagram (PF & Hahn, PRE, 2005)



p_0 : rescaled production rate of B vs A when A is unbound

p_1 : ----- A bound

You could imagine system where p_1 and p_0 are regulated so that you go from oscillating to bistable.

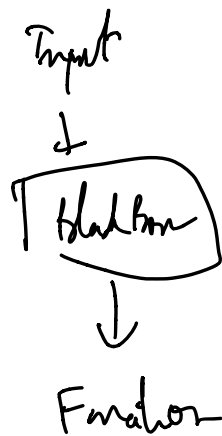
There are \neq ways to do this but \neq pathways would give you \neq interesting dynamics (in particular if you go through the critical point)

Example: lac operon
circadian clocks.

Fly PER:TIM \equiv B
[TC:CLK \equiv A
Mammals PER:CRY
CLK:BMAL

Here I look a very much structure/function approach. A reason is that there are examples of the networks working like this. But it does not mean they are like this for this protein.

Another aspect: modularity



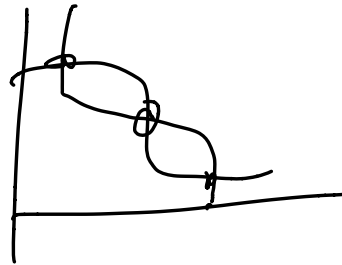
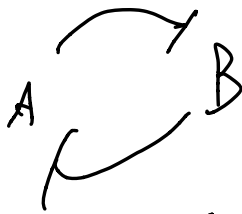
But we can clearly identify modules, and if we believe there are functional, why don't we see more interacting things

Answer: variation of selective pressure

Imagine eq. \Rightarrow a note person \Rightarrow to have f, g , then shift some bits.

How made module

Toggle Switch



$$\dot{B} = \frac{A_0^m}{A_0^m + A^m} - \lambda B$$

$$\dot{A} = \frac{1}{1 + C \left(\frac{A_0^m}{A_0^m + A^m} \right)^m} - \lambda A$$

$$\approx \frac{(A_0^m + A^m)^m}{(A_0^m + A^m)^m + C A_0^m} - \lambda A$$

↳ effective points of demand

Representation

