

A compositional approach to the stochastic dynamics of gene networks

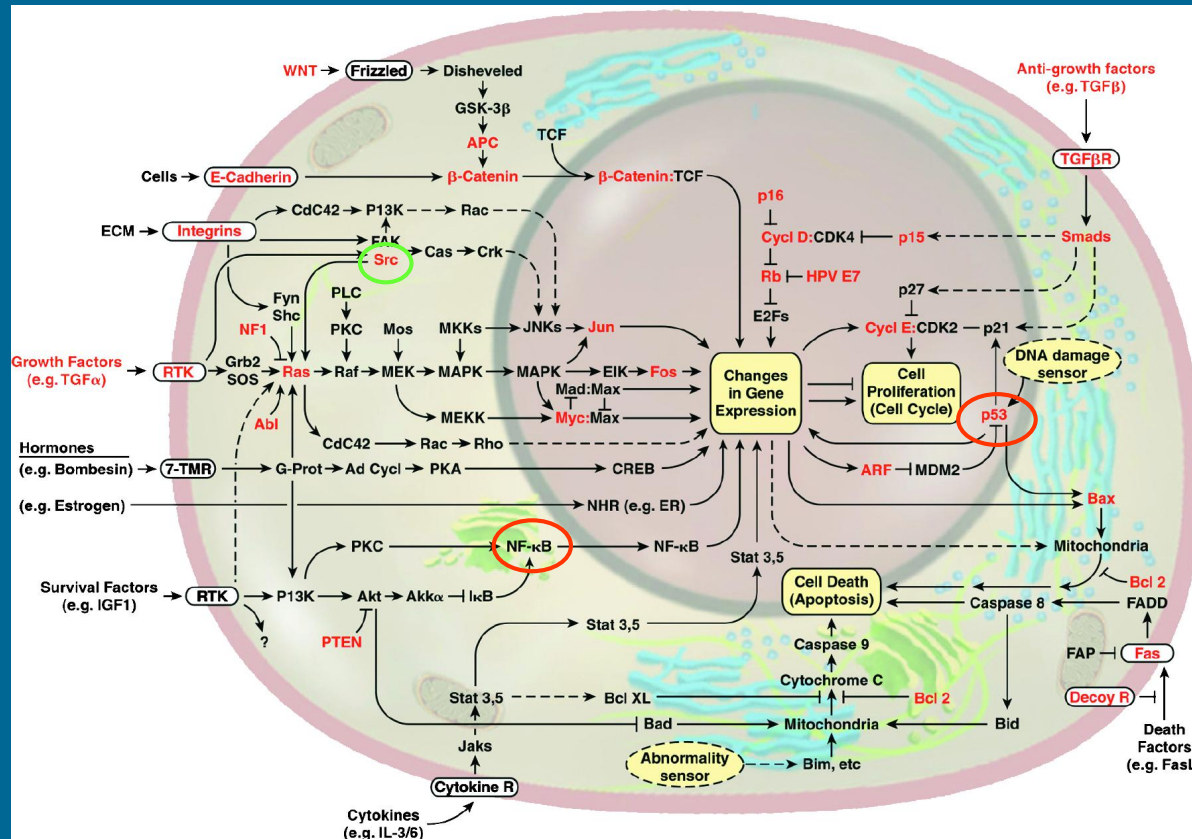
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(Microsoft Research, Cambridge UK)

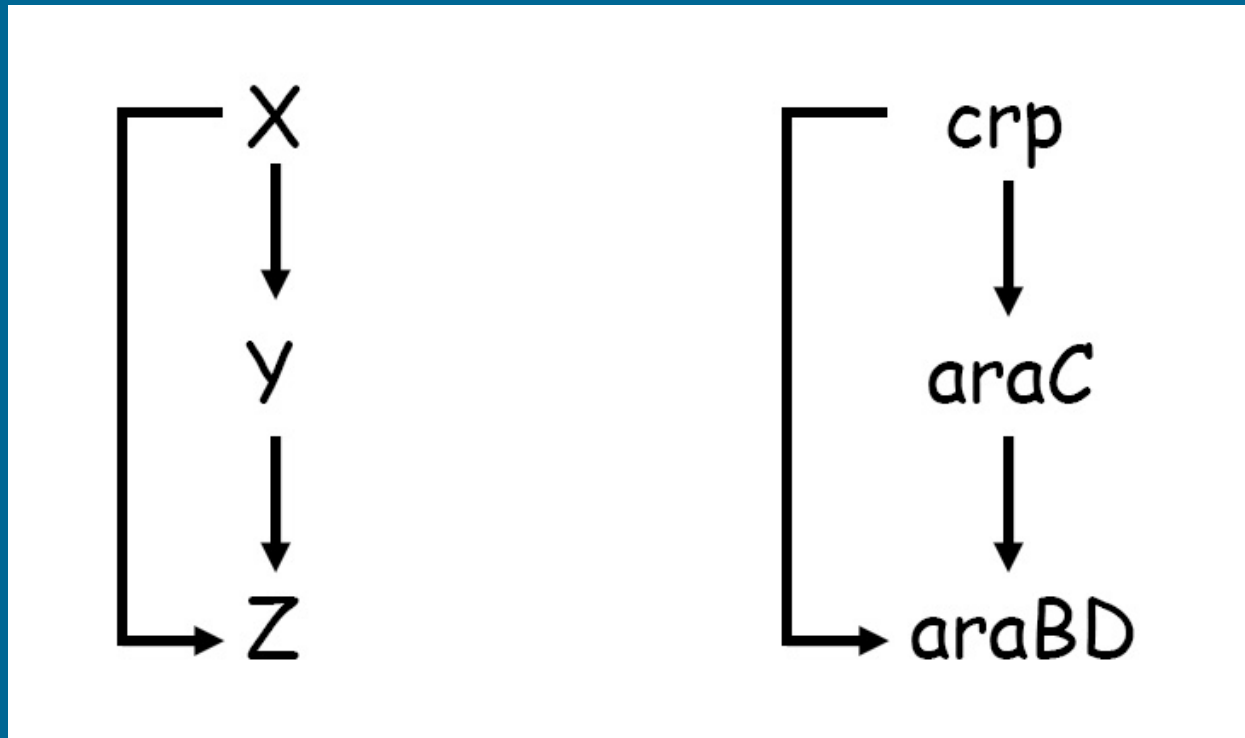
The menu:

- Motivation
- Gene networks as gene circuits in stochastic π -calculus
- Examples, from simple to less simple
- Outlook

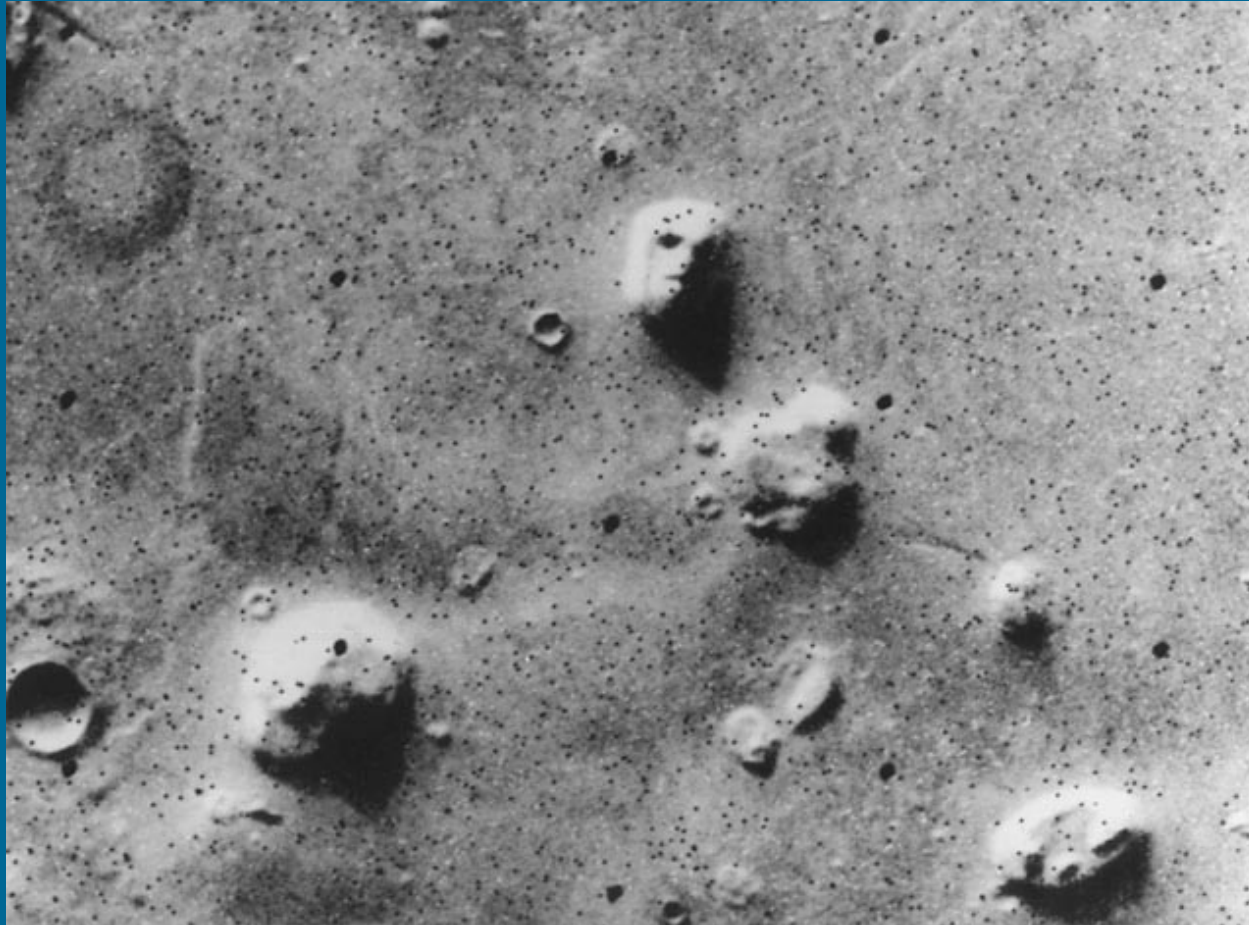
...finding structures in complexity...



...modules and motifs...



...but watch out for anthropomorphisms...

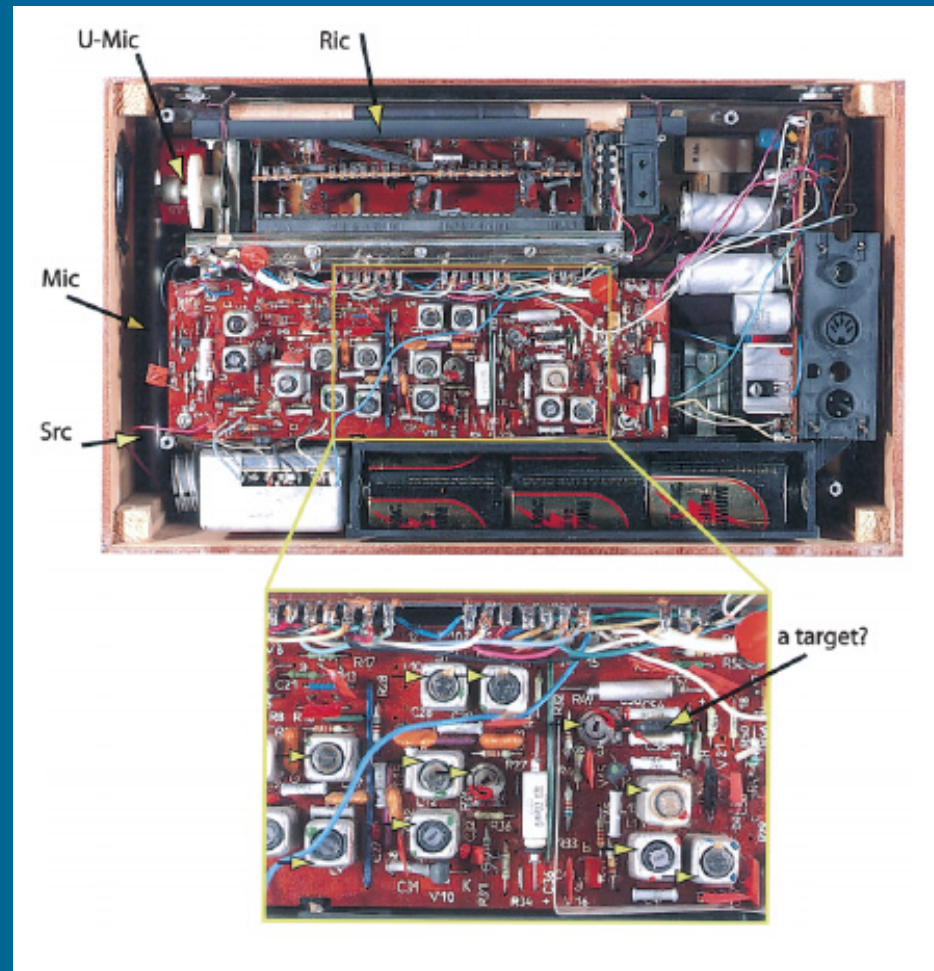


...with better resolution...



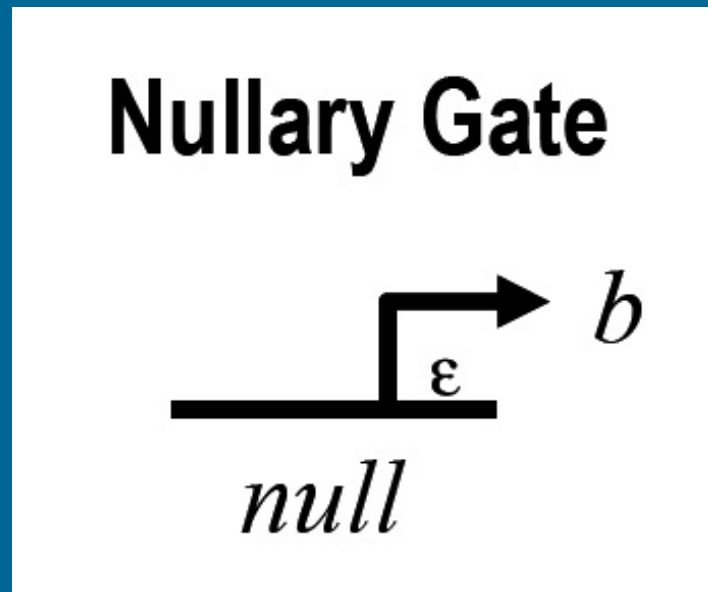
...what you see might not be there!

... engineered modules: a useful paradigm?



...let's try to build gene networks as gene circuits...

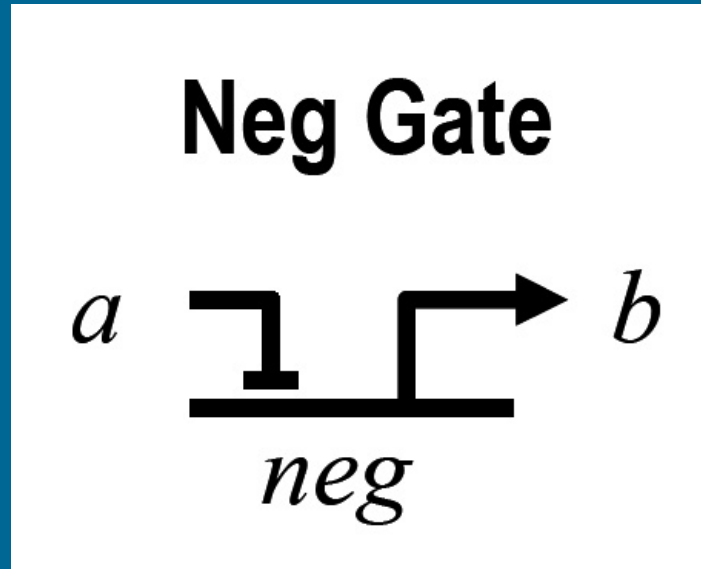
a) A gene gate which transcribes constitutively:



$$null(b) = \tau_{\epsilon} \cdot (tr(b) | null(b))$$

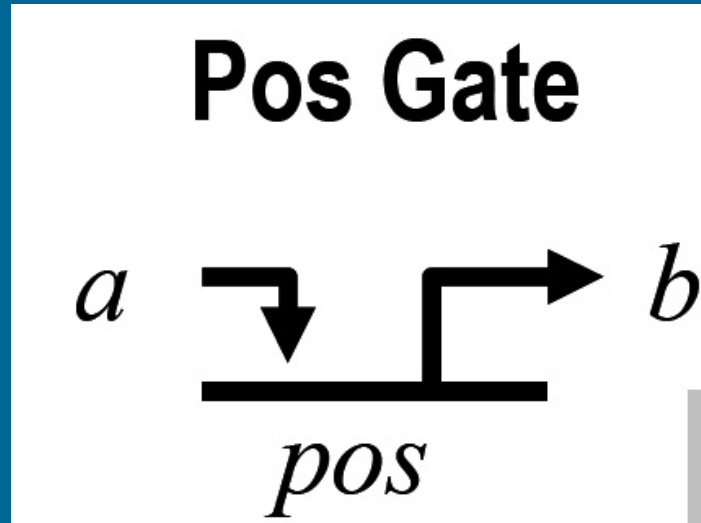
$$tr(b) = !b.tr(b) + \tau_{\delta}.0$$

b) an inhibitory gate:



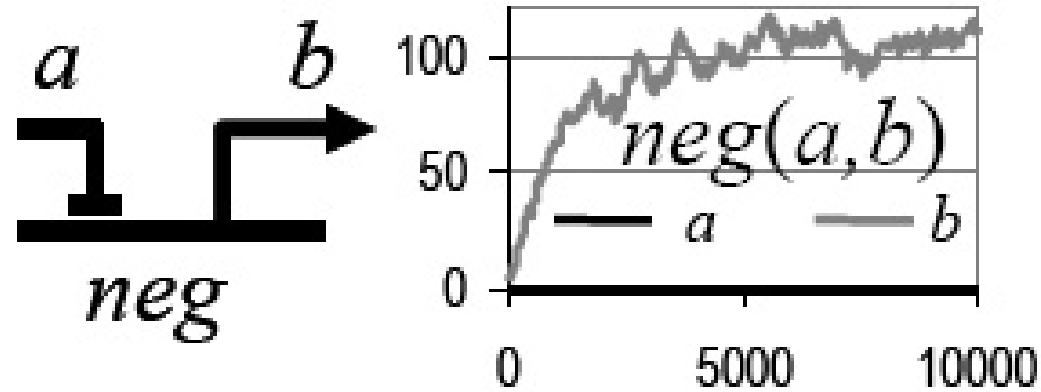
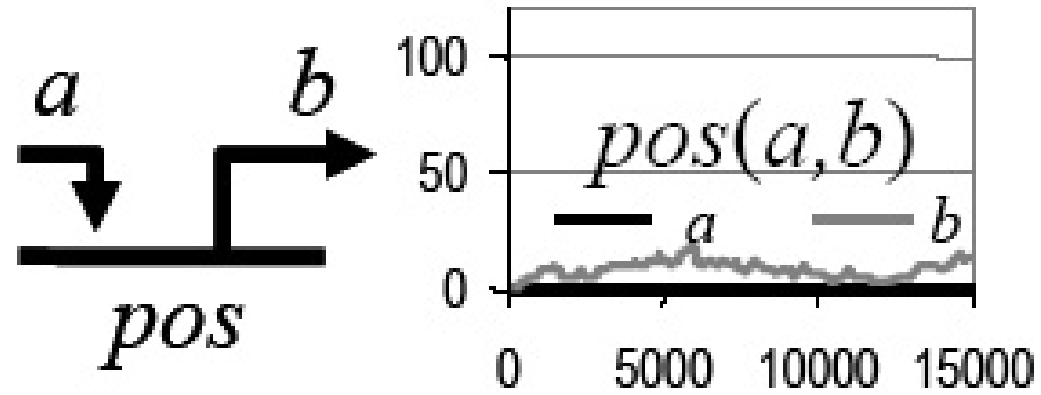
$$neg(a, b) = ? a \cdot \tau_{\eta} \cdot neg(a, b) + \tau_{\epsilon} \cdot (tr(b) | neg(a, b))$$

c) an excitatory gate:

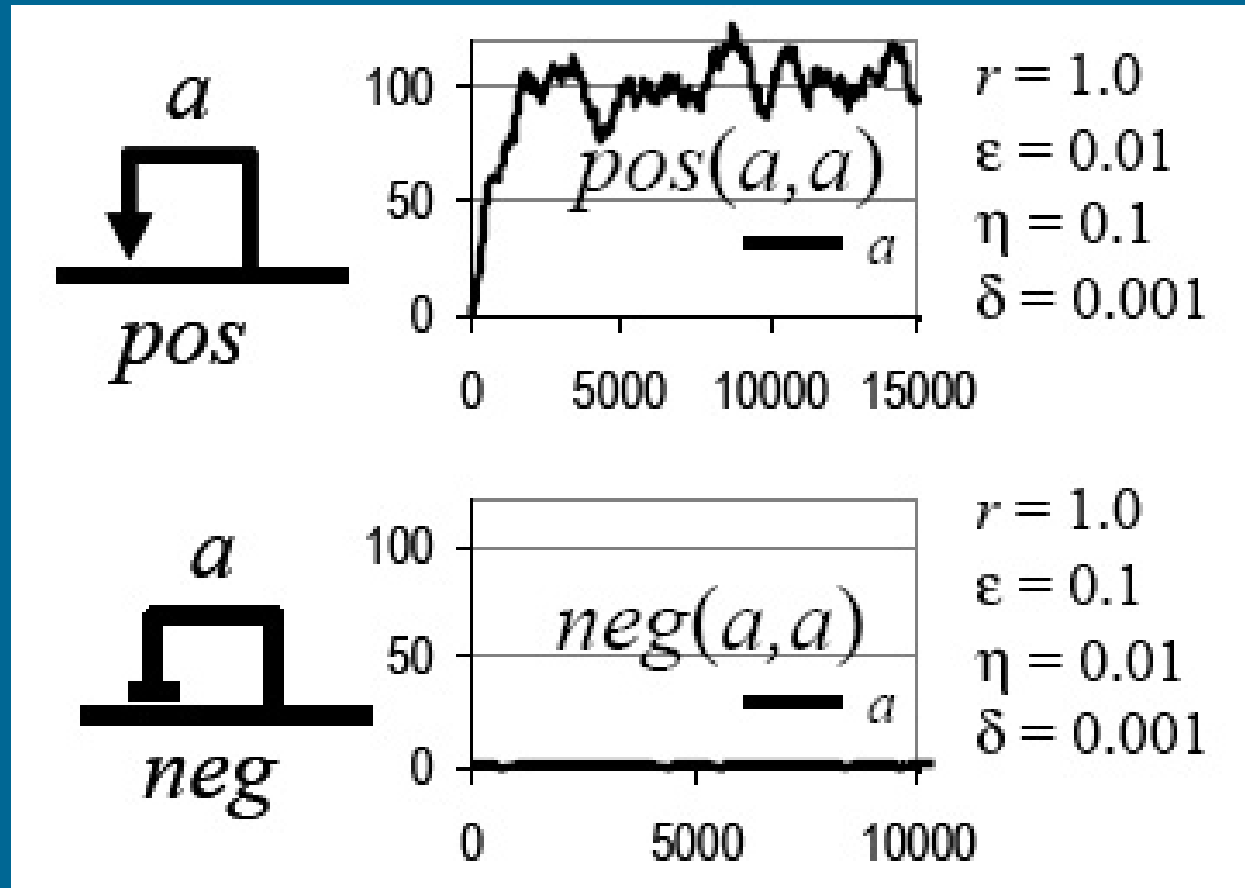


$$pos(a, b) = ? a \cdot \tau_{\eta} \cdot (tr(b) | pos(a, b)) + \tau_{\epsilon} \cdot (tr(b) | pos(a, b))$$

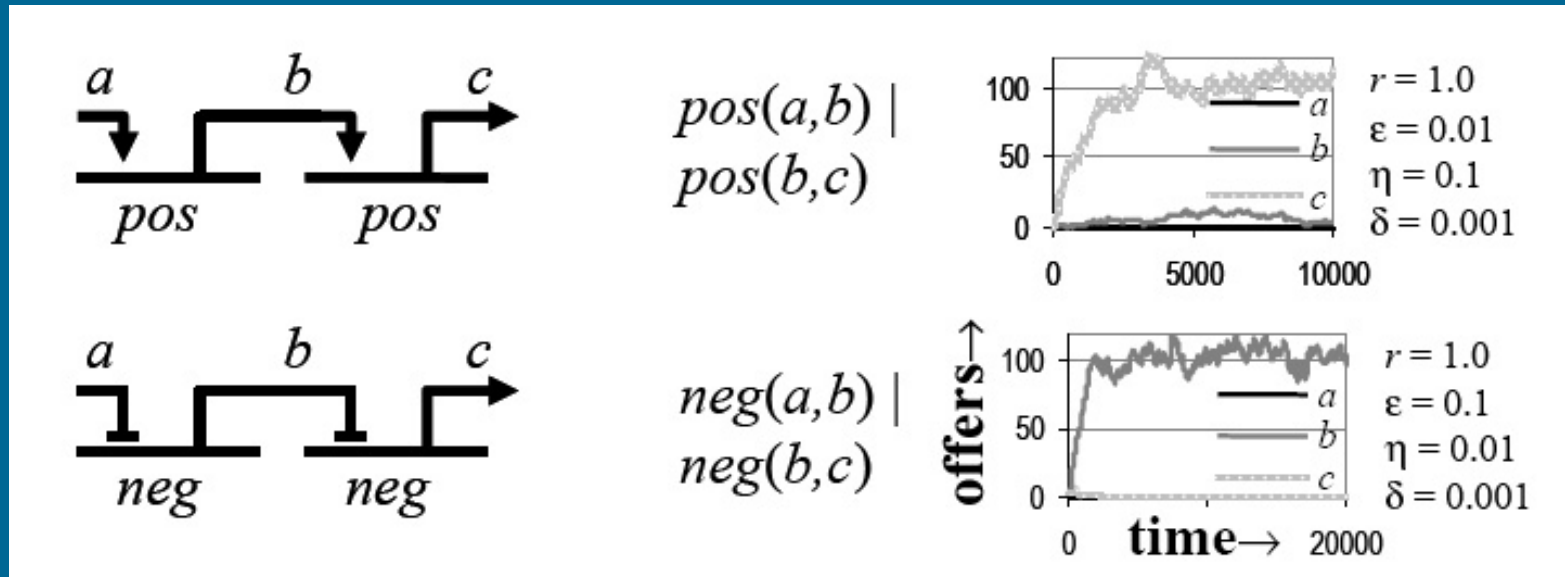
Examples: very simple 1



Examples: very simple 2

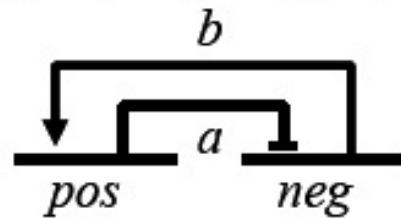


Examples: very simple 3

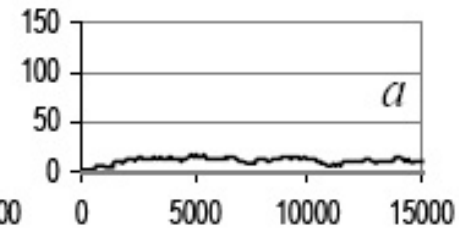
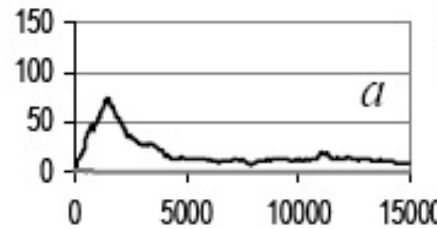


Examples: simple

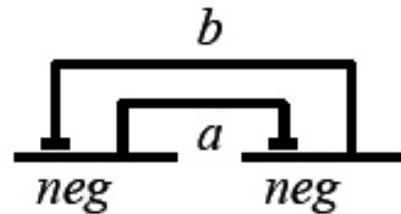
$pos(b,a) \mid neg(a,b)$



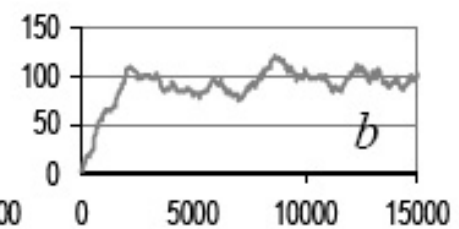
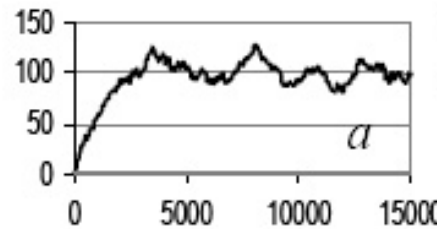
Monostable



$neg(b,a) \mid neg(a,b)$

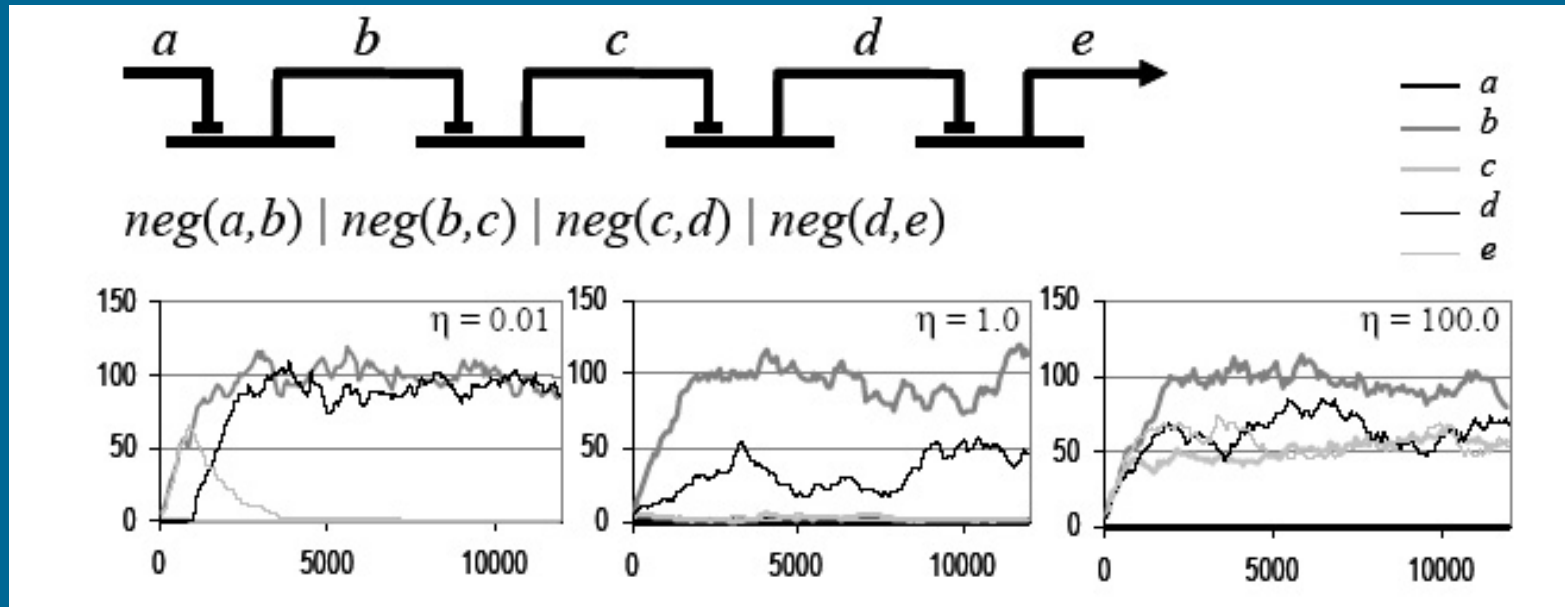


Bistable

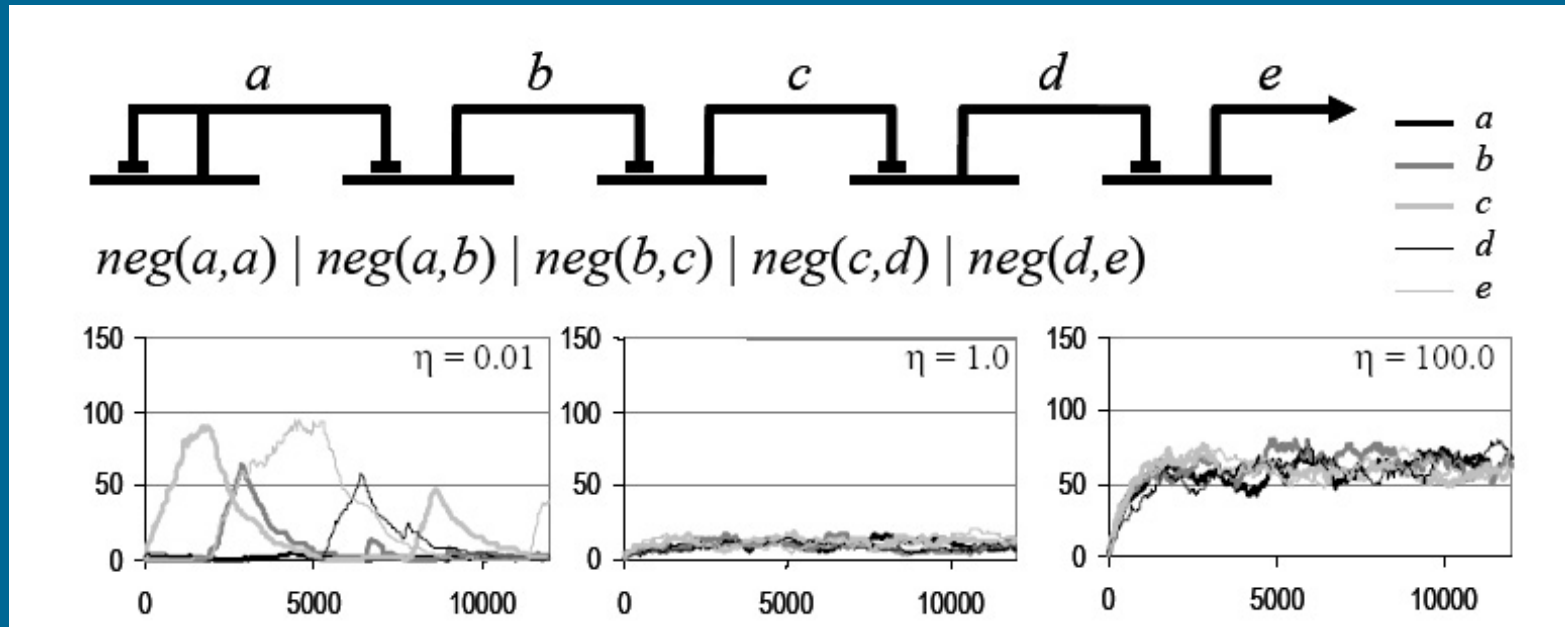


$r = 1.0, \delta = 0.001; pos: \epsilon = 0.01, \eta = 0.1; neg: \epsilon = 0.1, \eta = 0.01$

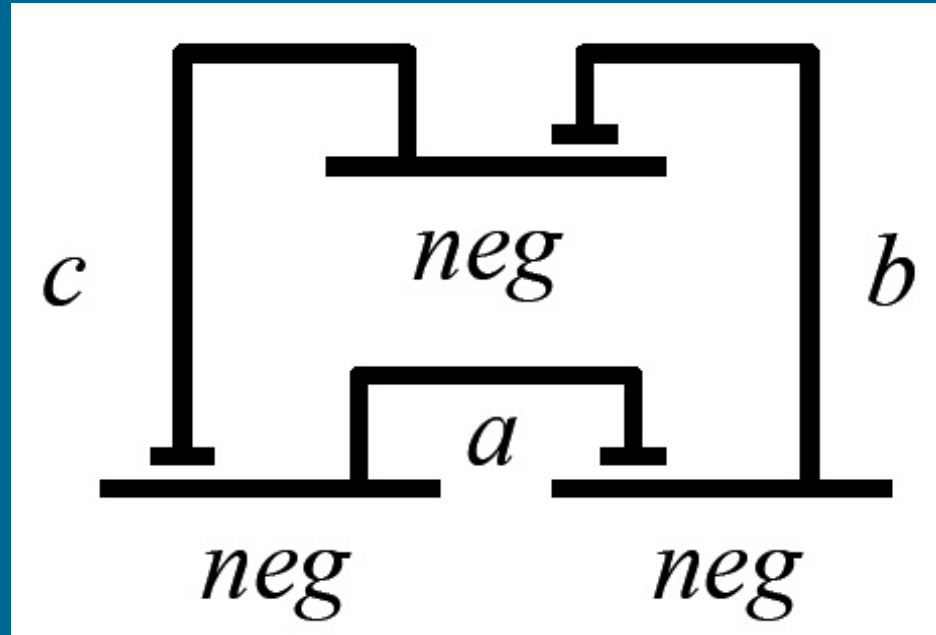
Examples: less simple 1



Examples: less simple 2

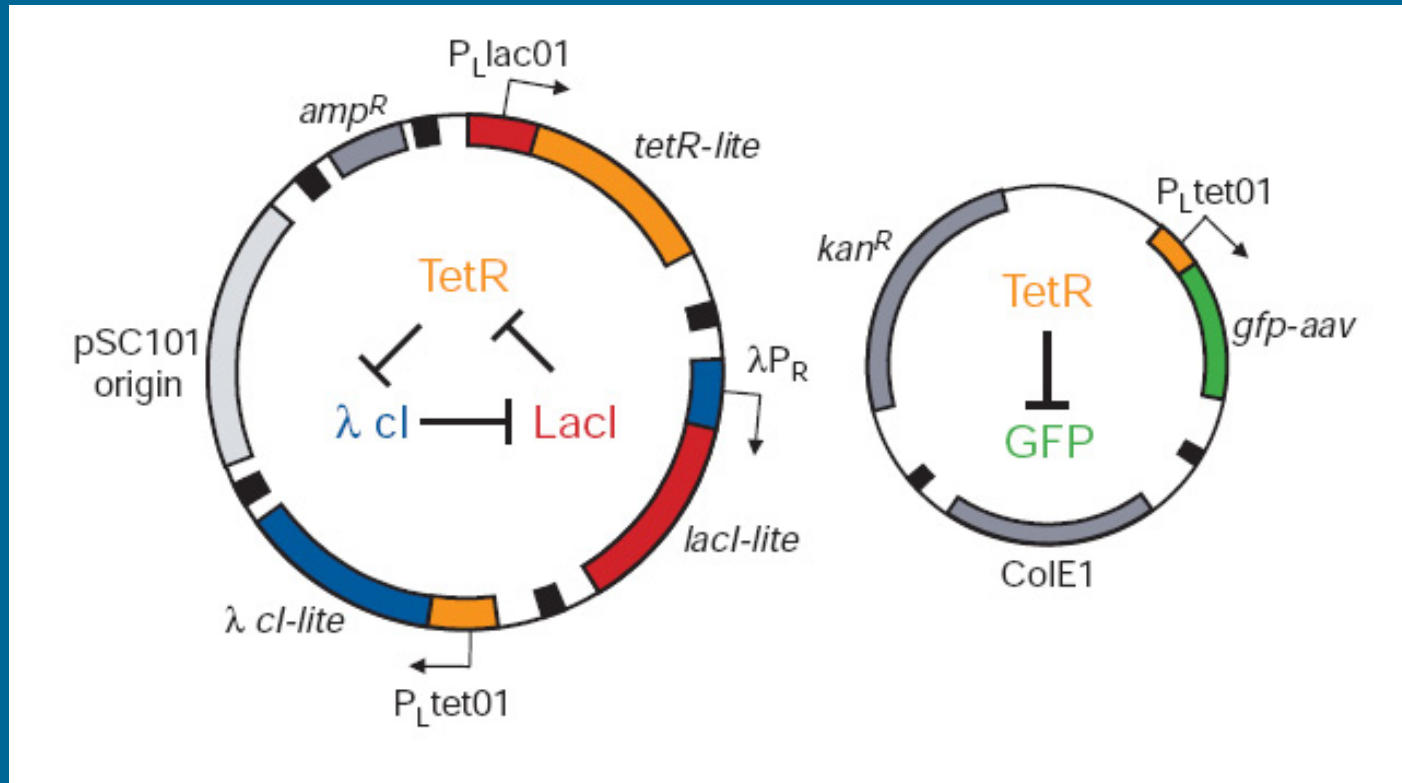


Example: The Repressilator



$$neg(c, a) | neg(a, b) | neg(b, c)$$

...the real system: three bacterial genes (+ GFP)



M. B. Elowitz, S. Leibler, Nature (2000)

...ODE modeling...

$$\frac{dm_i}{dt} = -m_i + \frac{\alpha}{1 + p_j^n} + \alpha_0$$

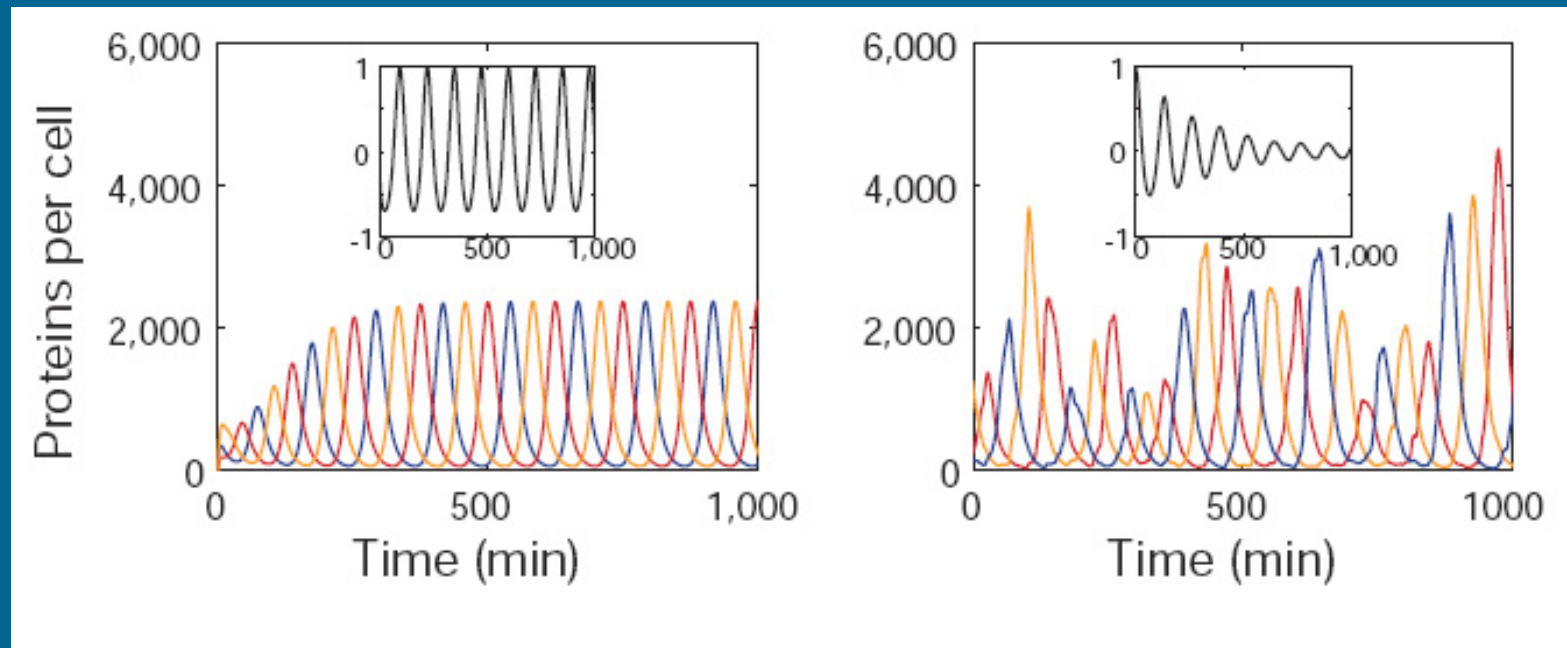
$$\frac{dp_i}{dt} = -\beta(p_i - m_i)$$

$$i = (lacI, tetR, cI), \quad j = (cI, lacI, tetR)$$

... compare with

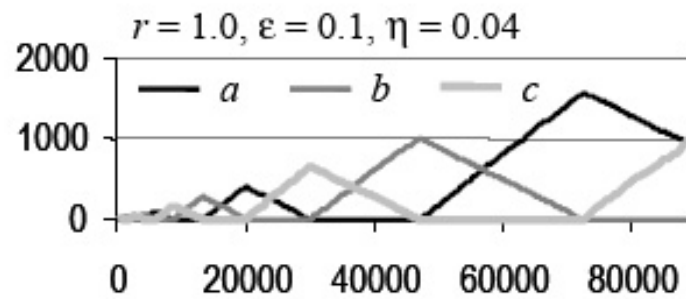
$$neg(c, a) | neg(a, b) | neg(b, c)$$

...the ODE results...and Gillespie...

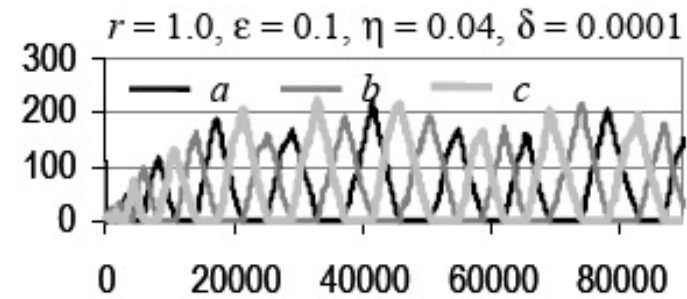


...to be compared with...

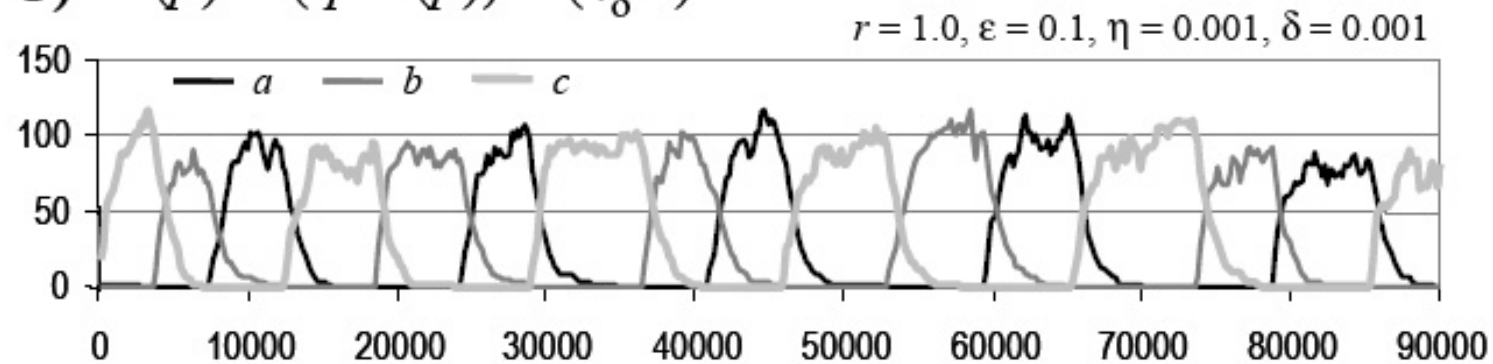
A) $tr(p) = !p.0$



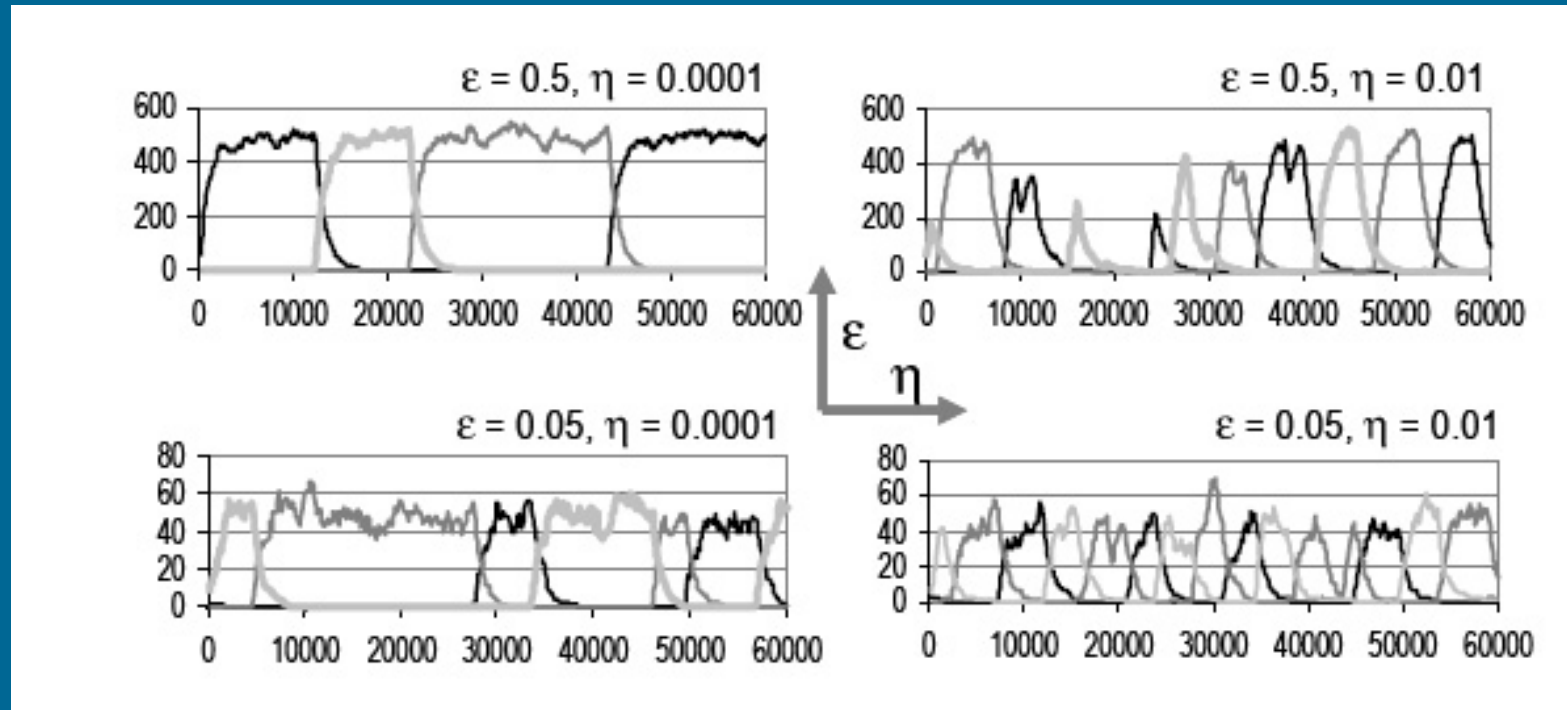
B) $tr(p) = (!p.0) + (\tau_{\delta}.0)$



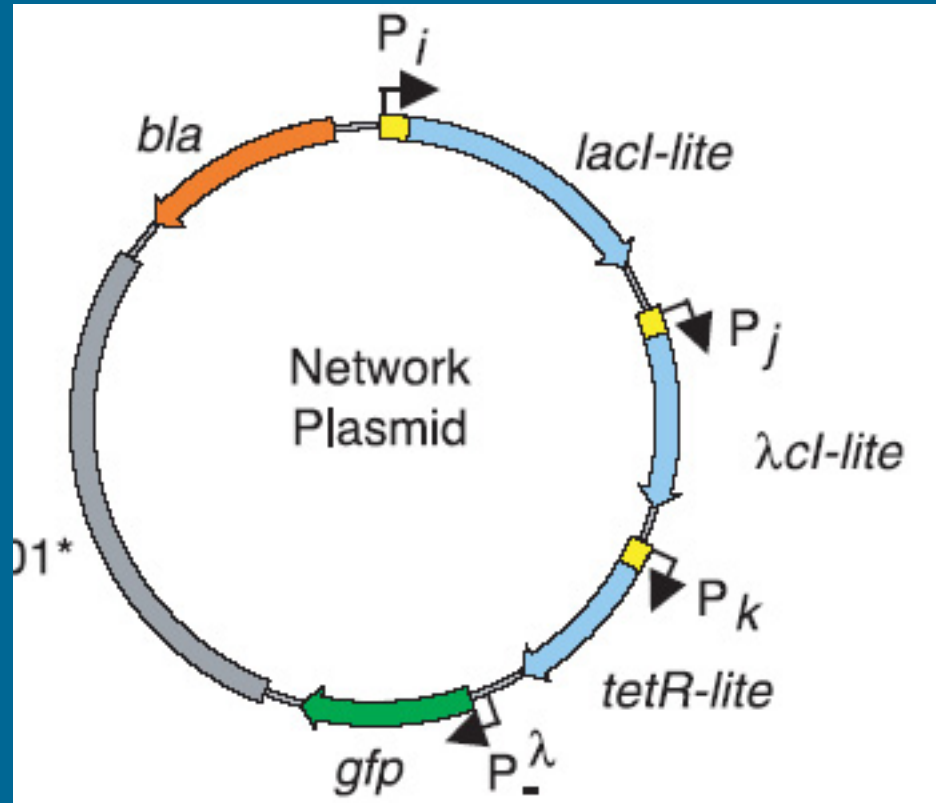
C) $tr(p) = (!p.tr(p)) + (\tau_{\delta}.0)$



... and more parameter play...

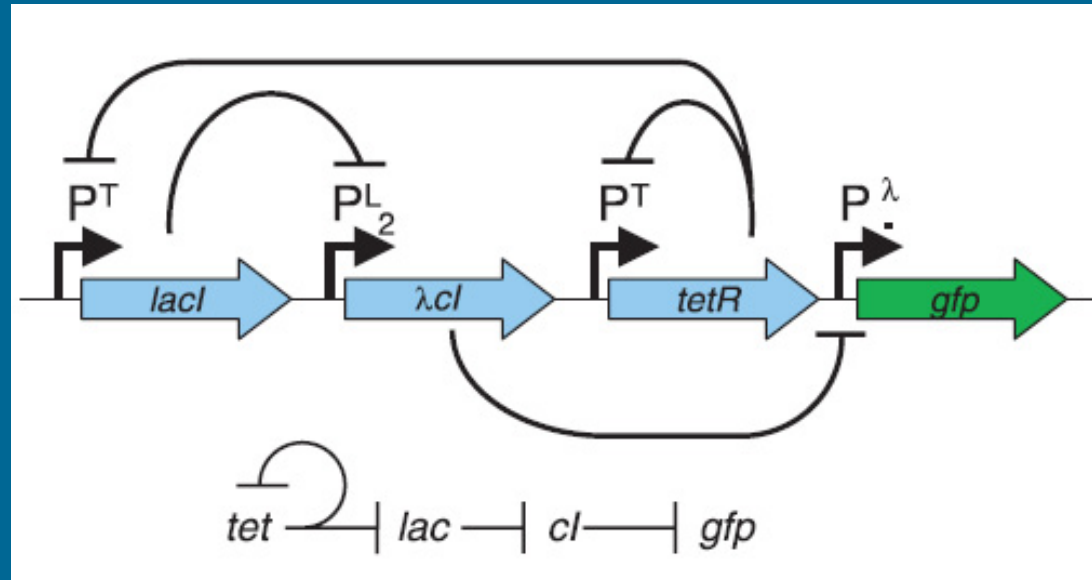


More complex example: combinatorial gene circuits

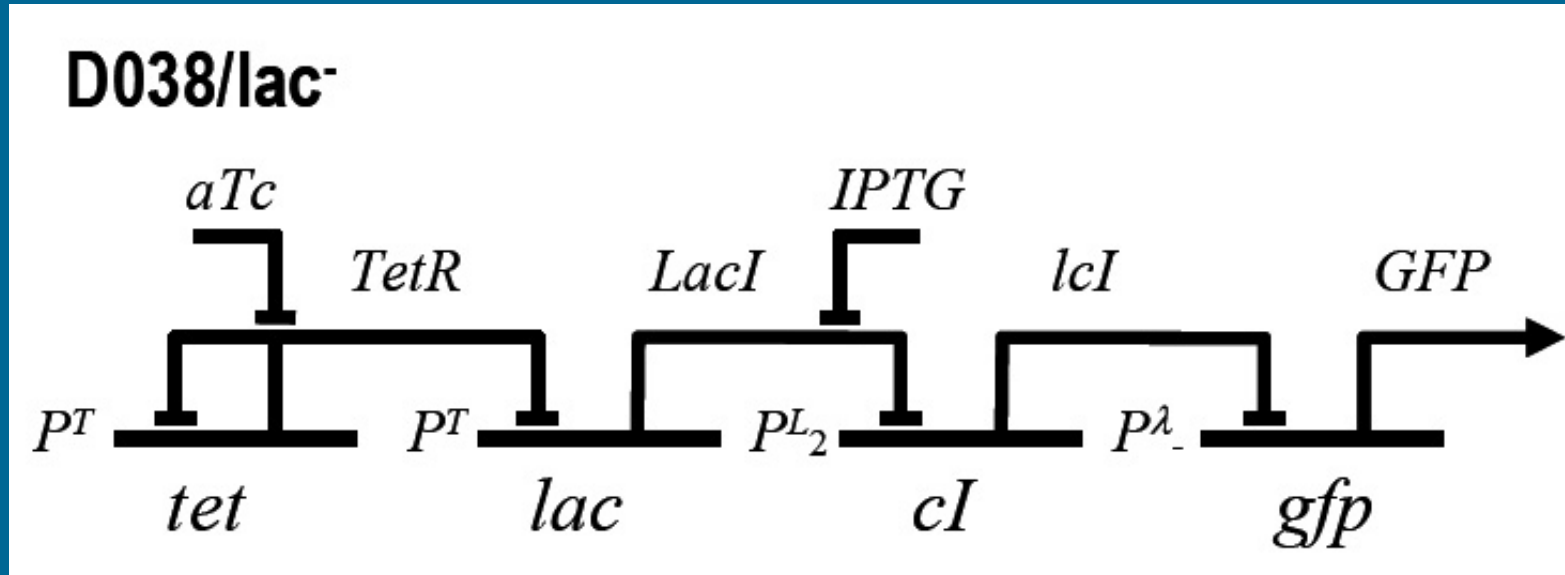


C. C. Guet, M. B. Elowitz, W. Hsing, S. Leibler, Science (2002)

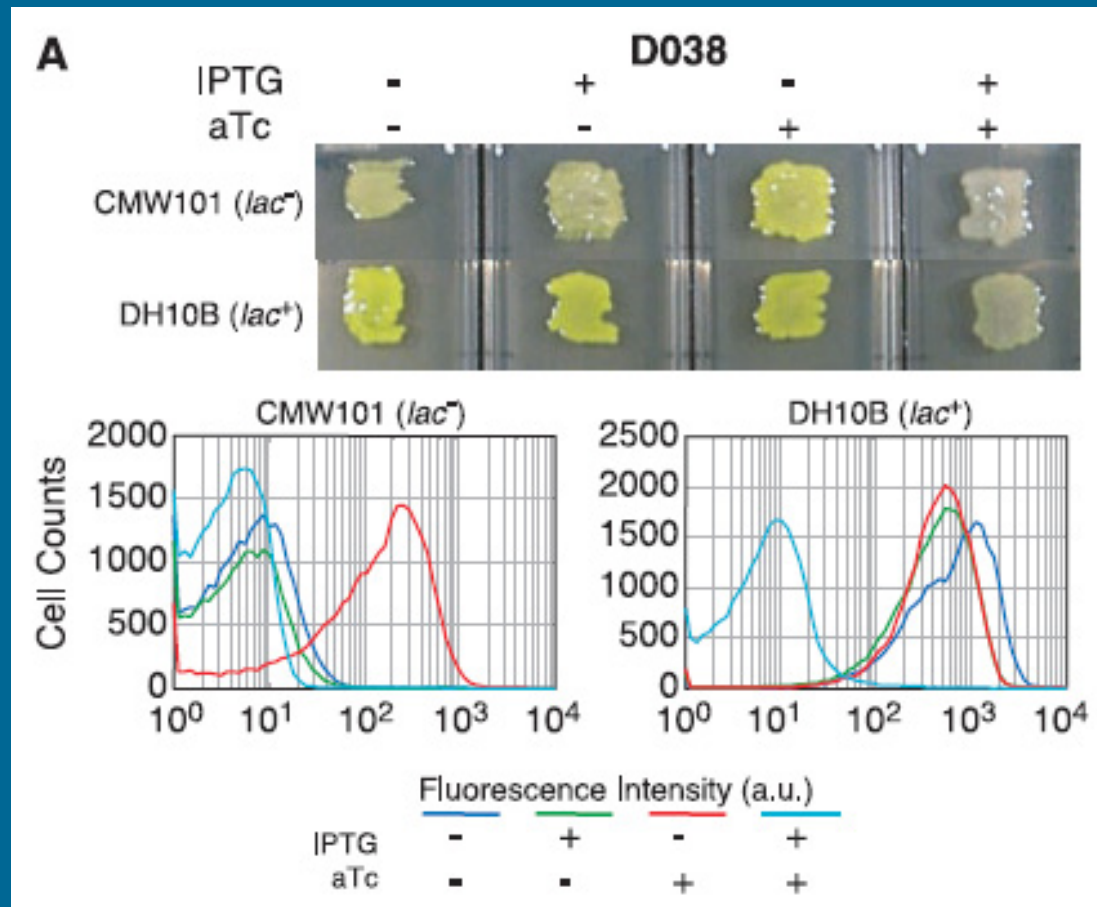
A specific case study: D038



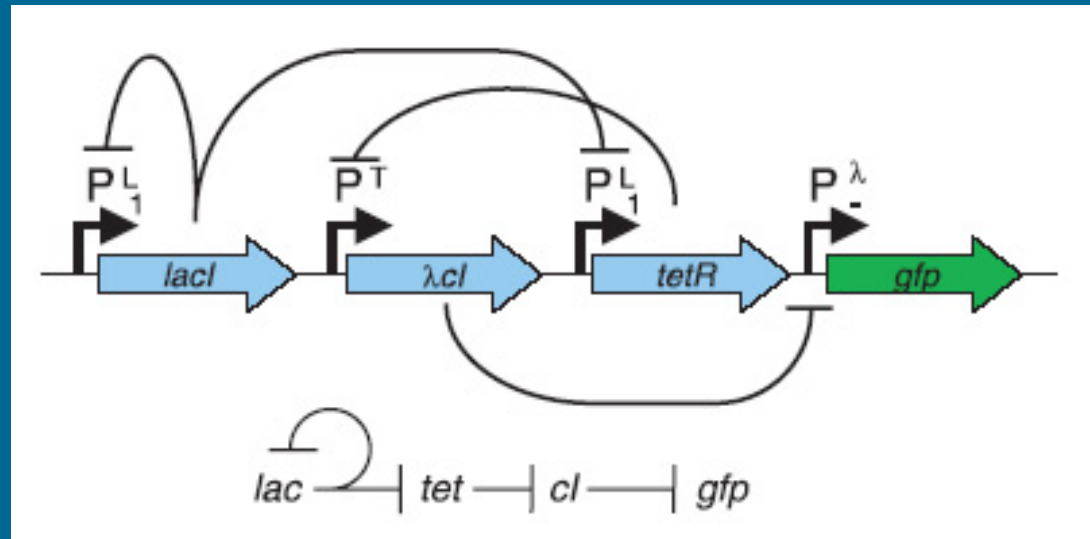
D038 in π -gate modelling



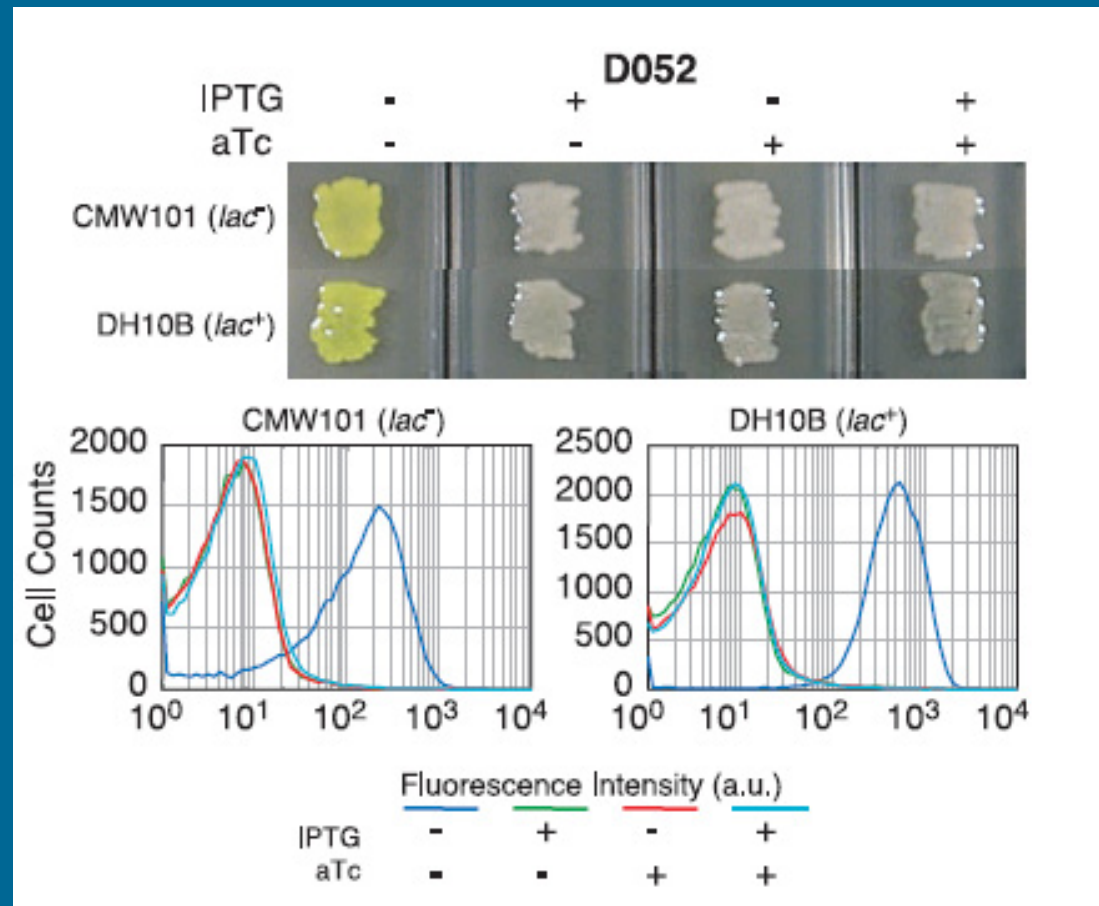
D038: Experimental results



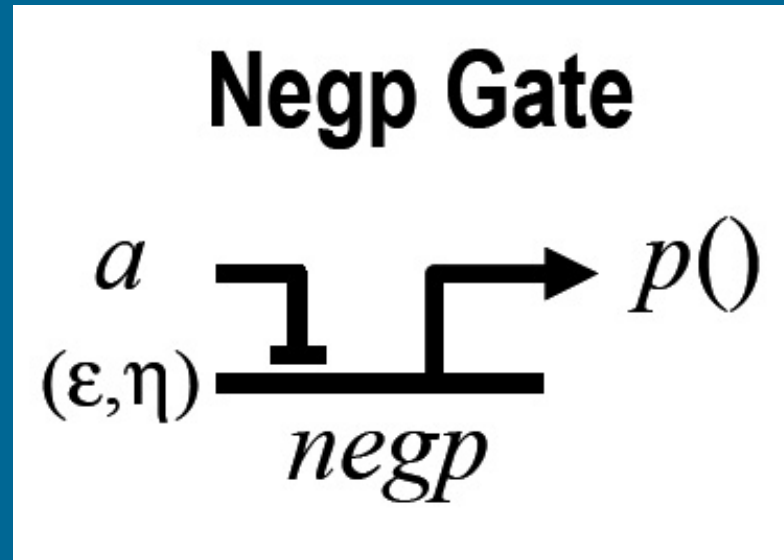
A second example: D052



A second example

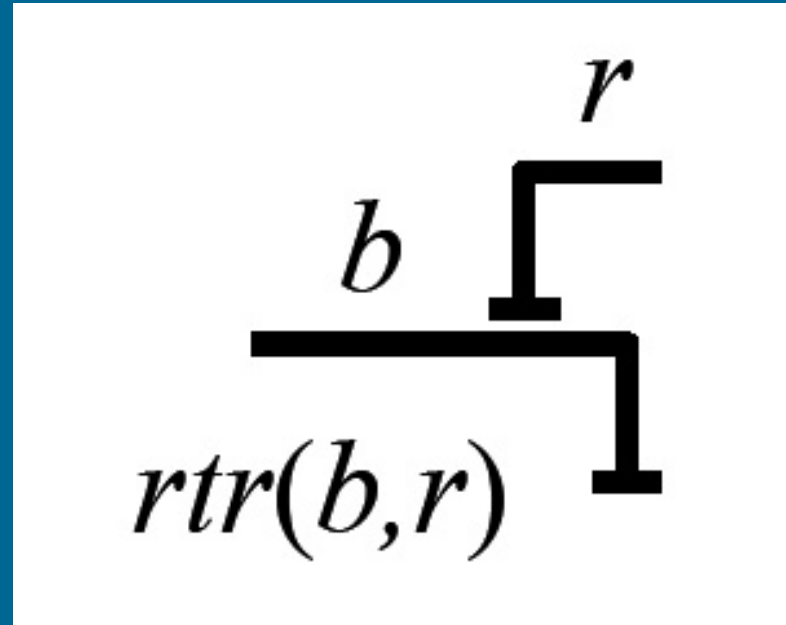


D038 in π -gate modelling: ...more complex gates needed...



$$negp(a, (\epsilon, \eta), p) = ? a \cdot \tau_{\eta} \cdot negp(a, (\epsilon, \eta), p) + \tau_{\epsilon} \cdot (p() | negp(a, (\epsilon, \eta), p))$$

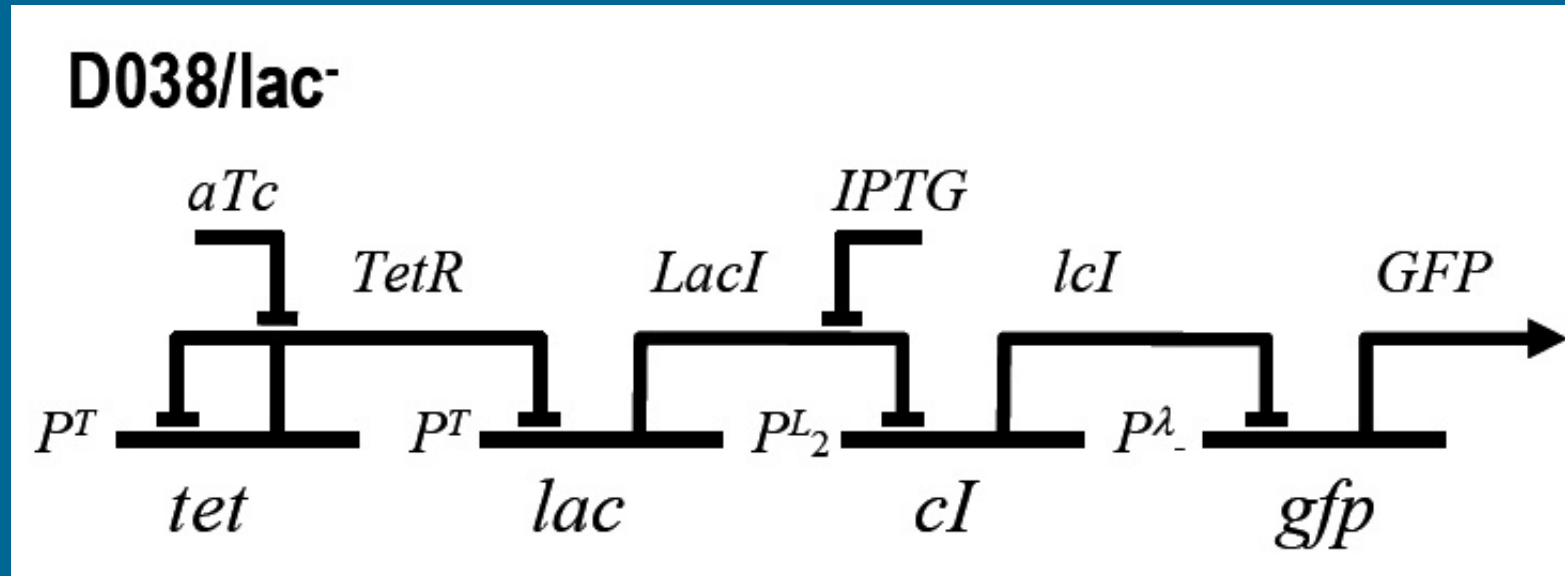
...repressible transcription factors...



$$rtr(b, r) = !b.rtr(b, r) + !r.0 + \tau_{\delta}.0$$

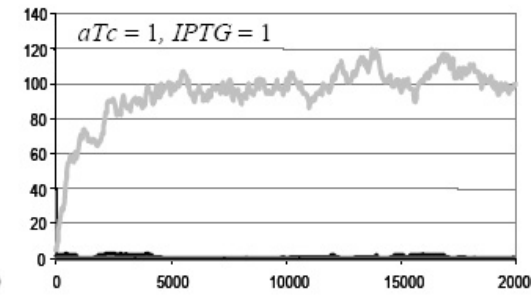
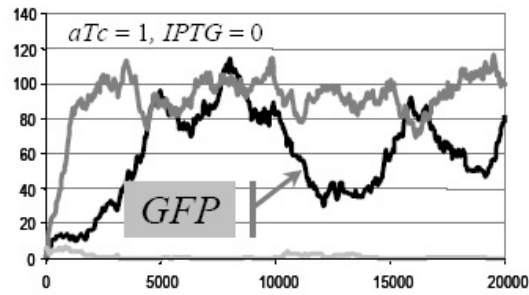
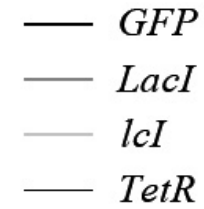
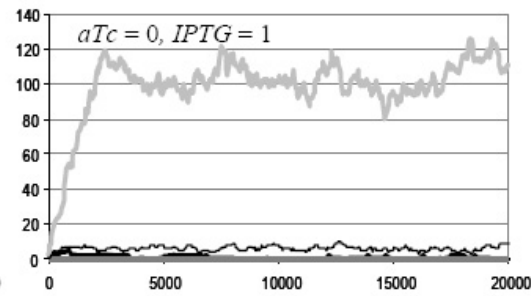
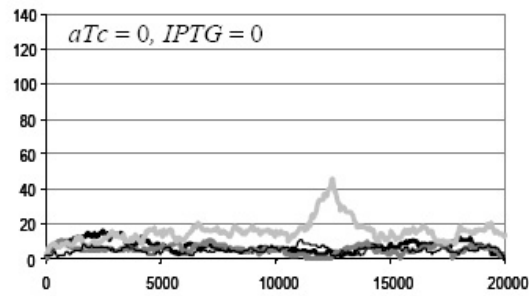
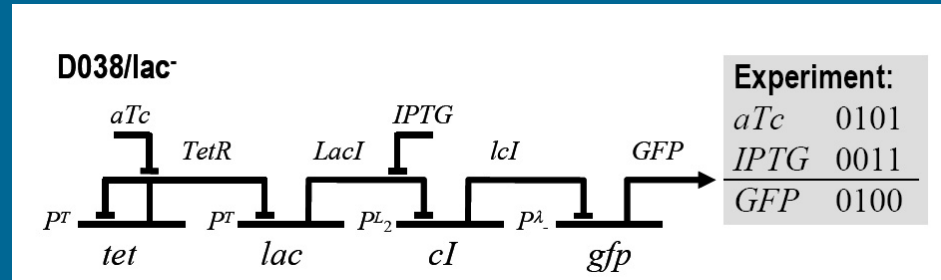
$$rep(r) = ?r.rep(r)$$

D038: Boolean analysis



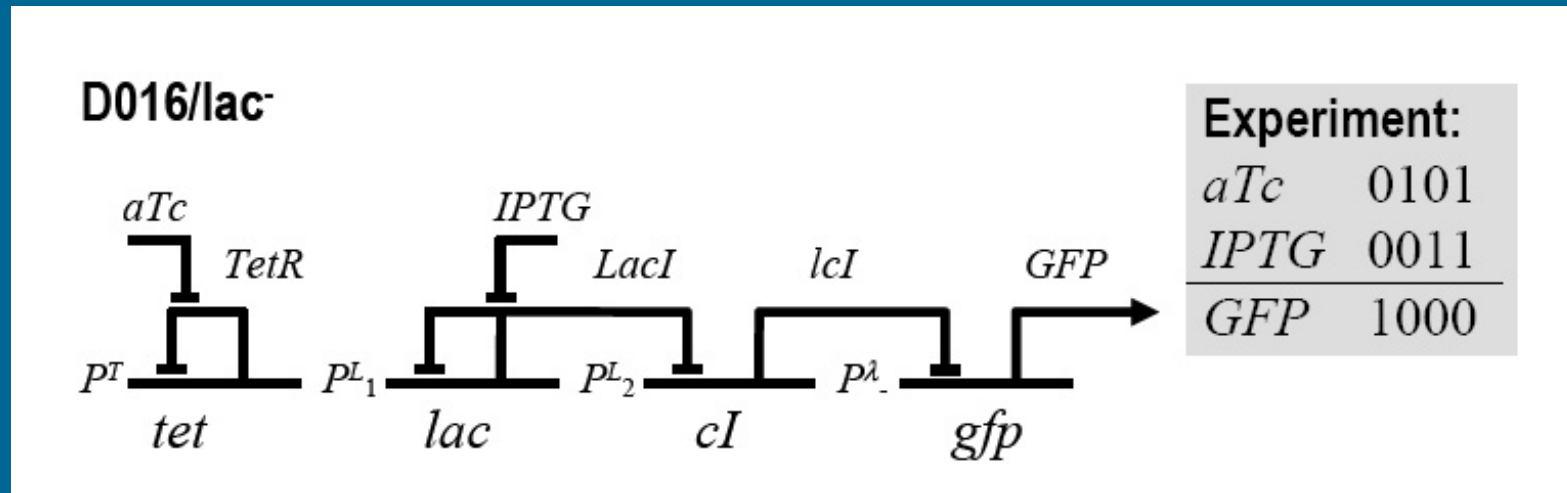
no repressors: $GFP = 0 \rightarrow lacI = 1 \rightarrow LacI = 0 \rightarrow TetR = 1$;
self-loop: $TetR = 1 \rightarrow TetR = 0 \rightarrow GFP = 0.5$.

D038

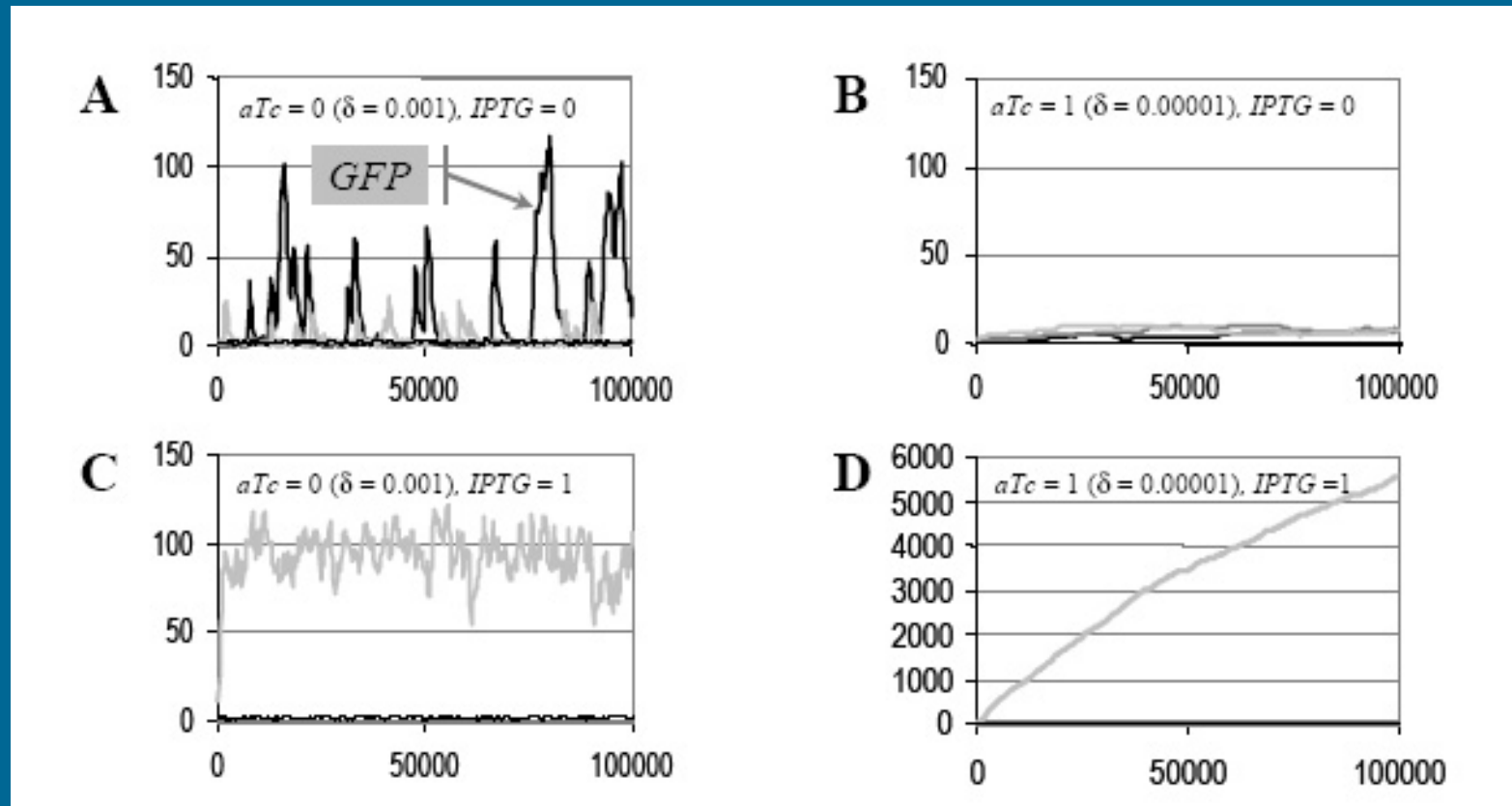


$r = 1.0$, $\epsilon = 0.1$, $\eta = 0.25$ (P^T), $\eta = 1.0$ (P^{L_2} , P^{λ}), $\delta = 0.001$

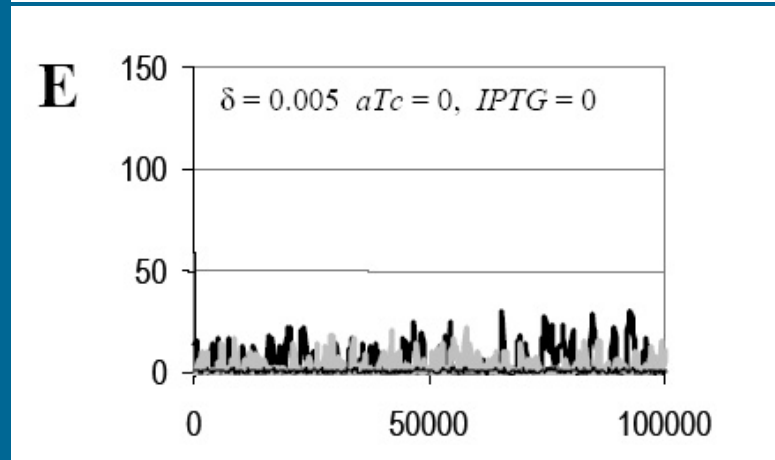
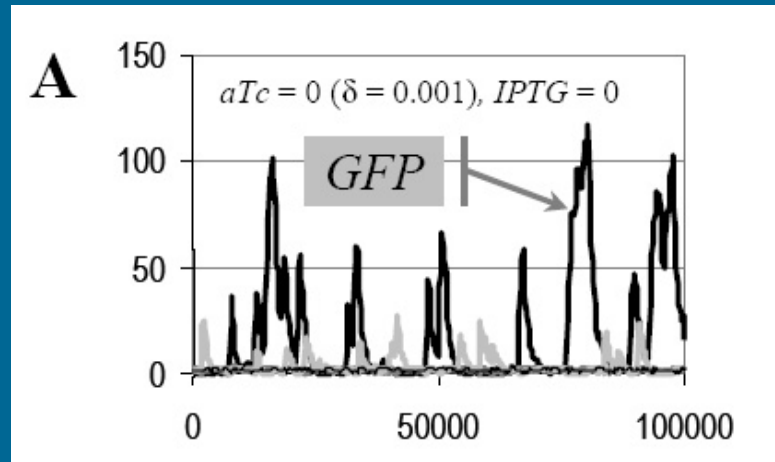
A final example: D016



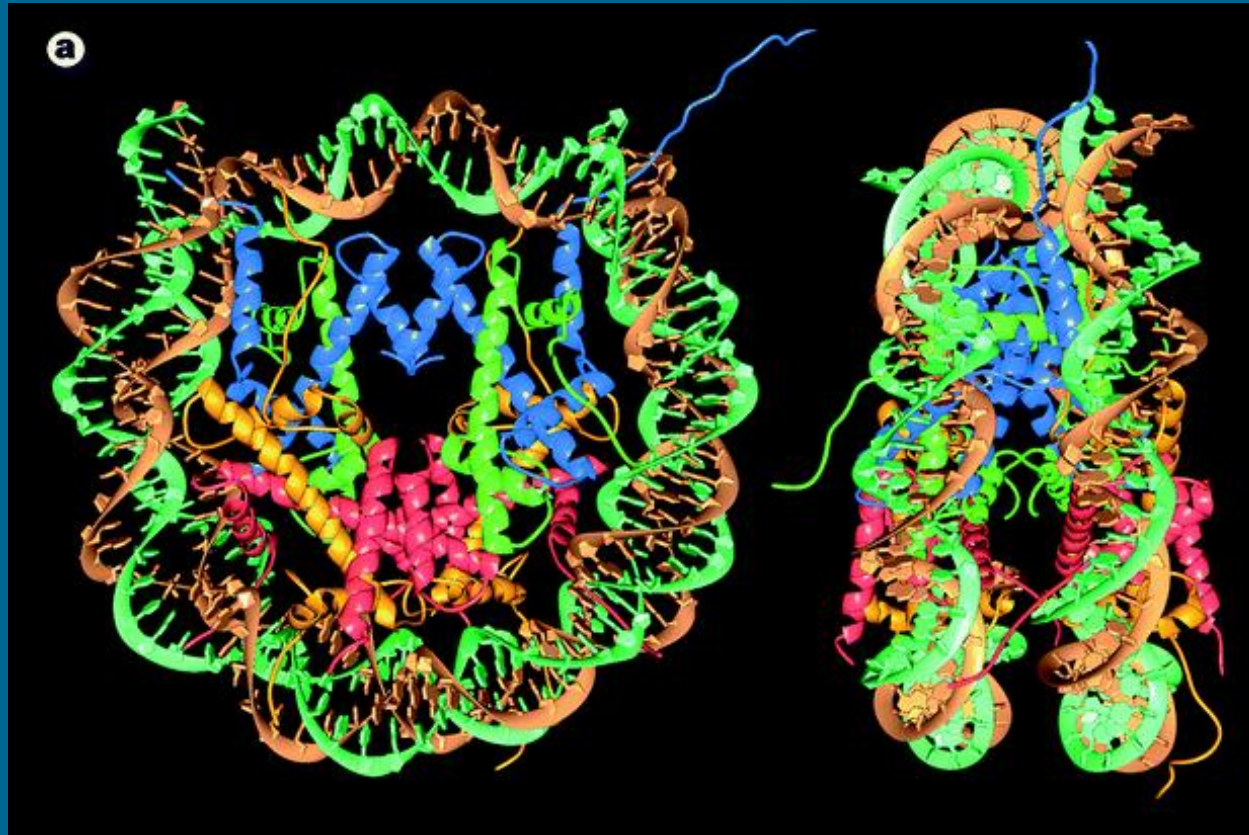
A final example: D016



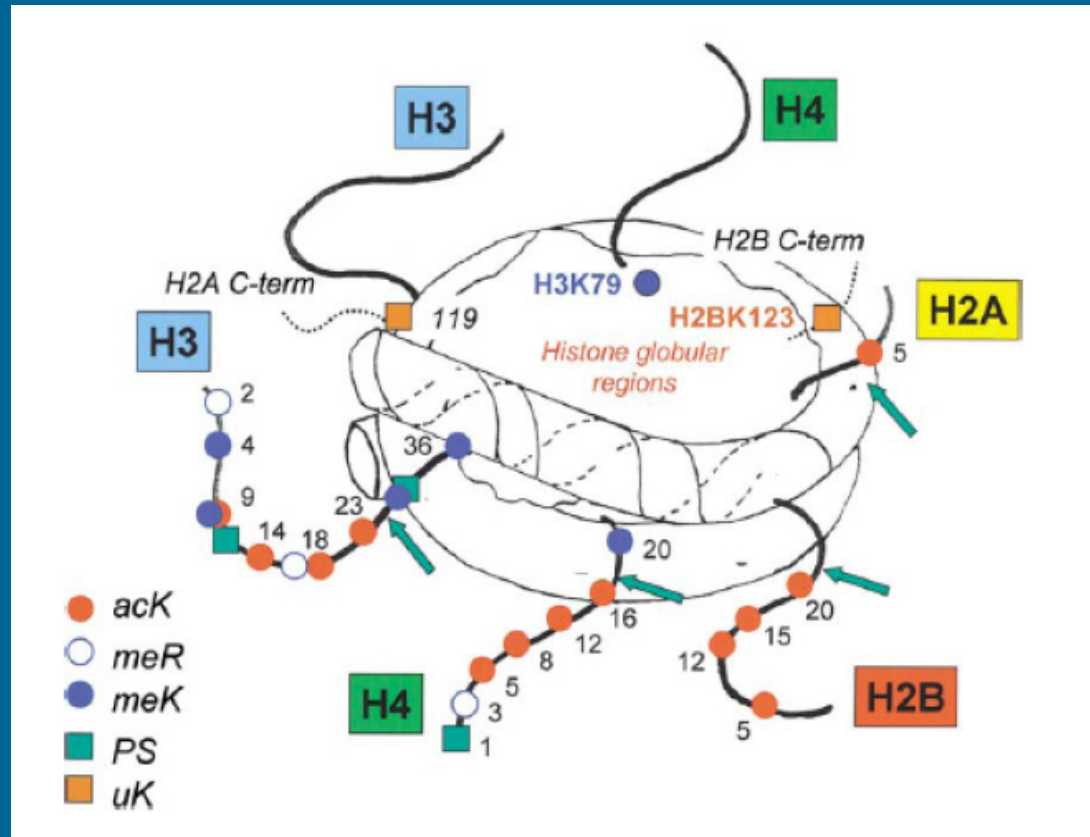
A final example: D016



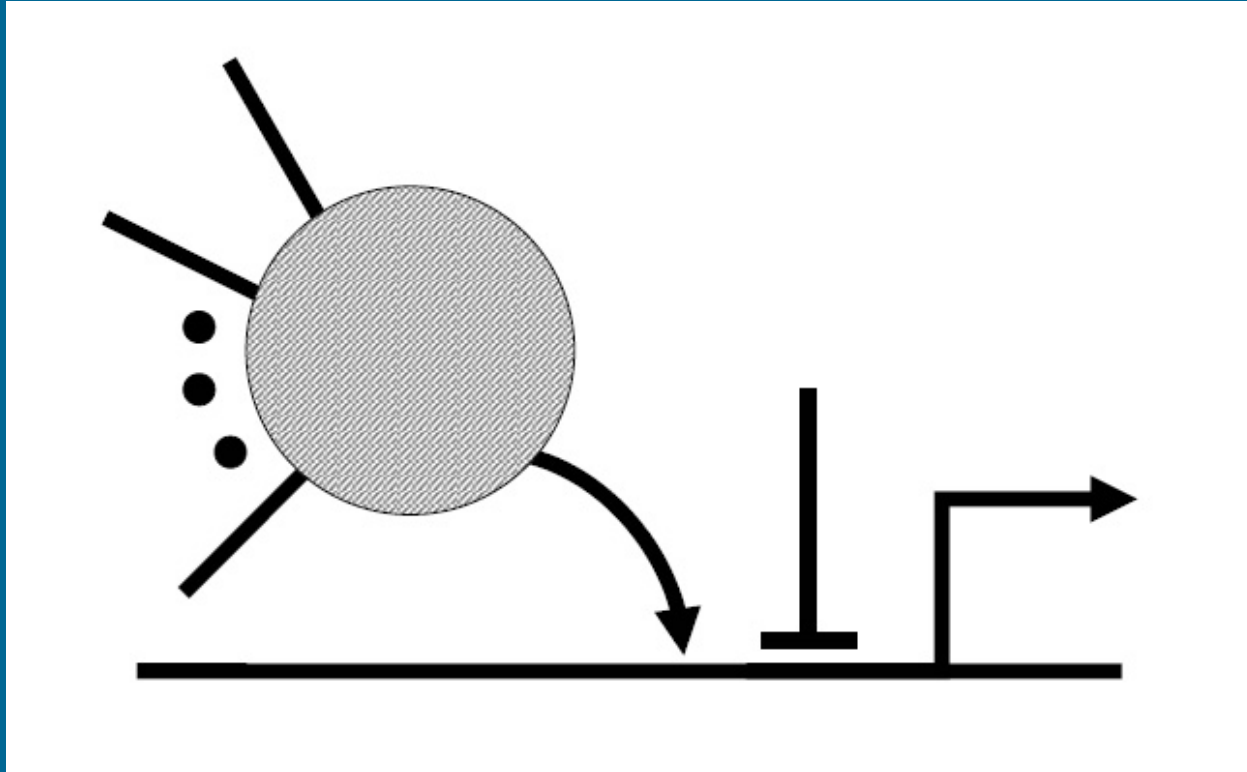
Outlook: chromatin, the nucleosome



Outlook: chromatin, histone tail modifications



Outlook: chromatin, stochastic π -network



Organisational outlook: next meeting Aci VicAnne

Modélisation et Cancer

Institut de Biologie de Lille

17/18 mai 2006