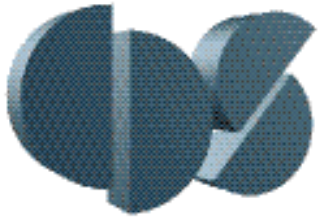
Lecture 1: Biomolecular Modeling



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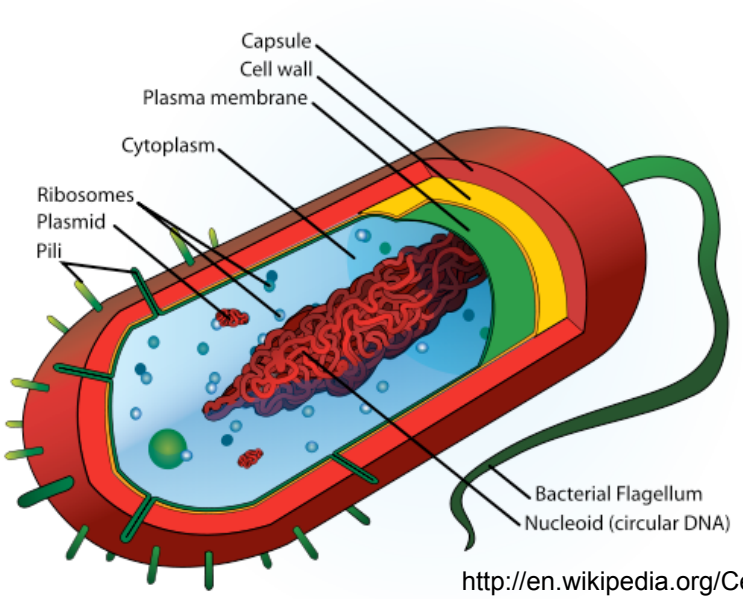
Goals:

- Motivate the role of dynamics and feedback in the the cell
- Provide mathematical tools for analyzing and predicting the dynamics of transcriptional regulation in the cell
- Work through case study for the lac operon (model control system)

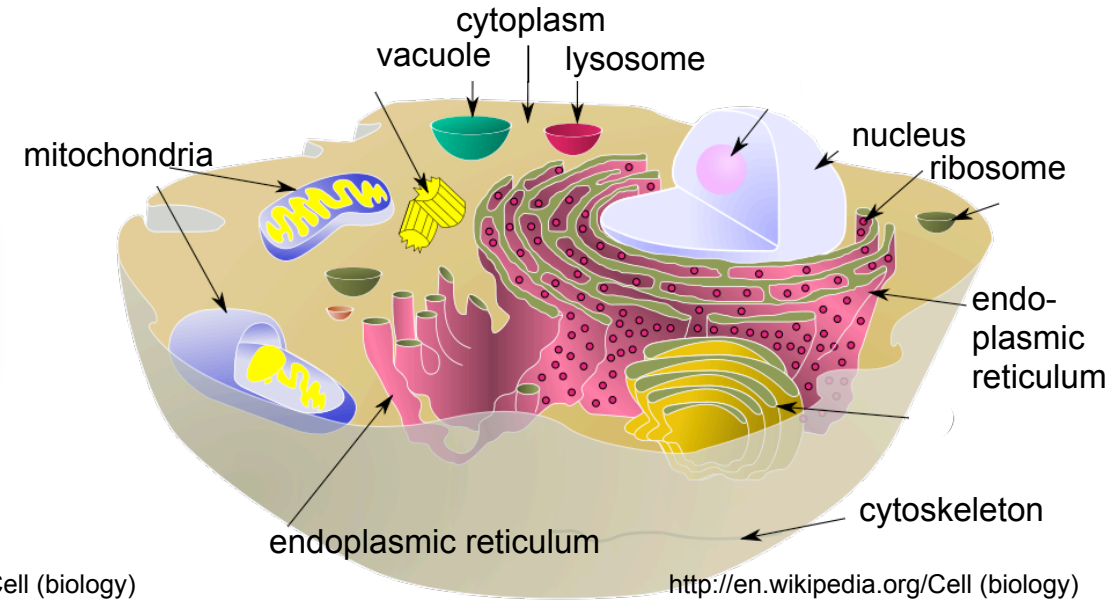
References

- Alberts et al, *Essential Cell Biology*, 3rd edition, 2009.
- R. Phillips, J. Kondev and J. Theriot, *Physical Biology of the Cell*, 2008.
- N. Yildirim, M. Santillan, D. Horiki and M. C. Mackey, “Dynamics and bistability in a reduced model of the lac operon”. Chaos, 14(2):279-292, 2004.
- D. Del Veccho and R. M. Murray, *Biomolecular Feedback Systems*, http://www.cds.caltech.edu/~murray/amwiki/BFS (preprint)

Architecture of the Cell



http://en.wikipedia.org/Cell (biology)



http://en.wikipedia.org/Cell (biology)

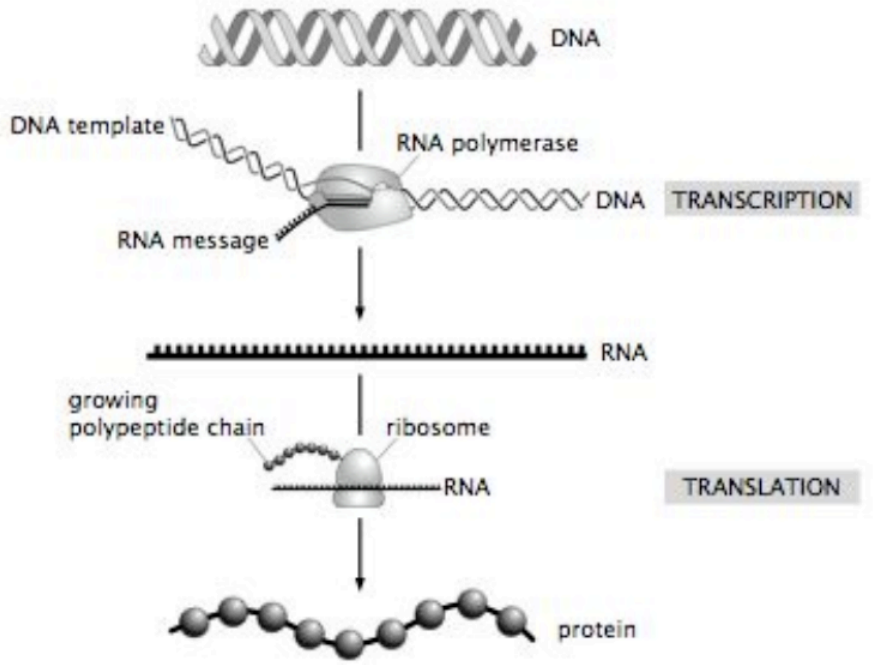
Prokaryote (bacterium)

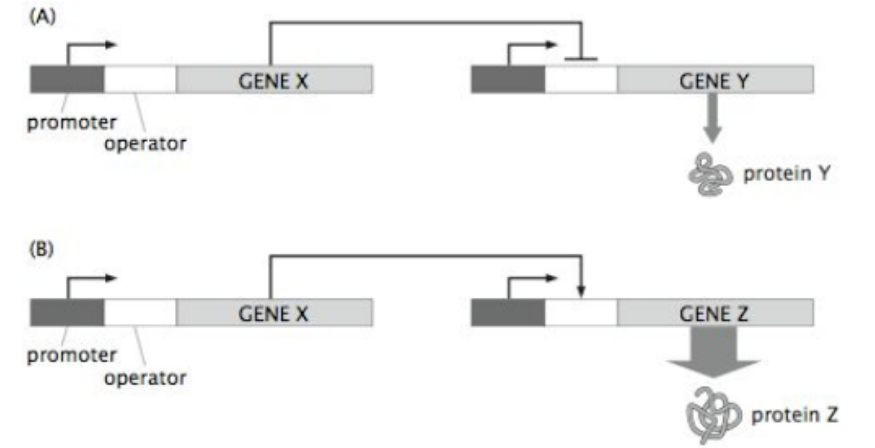
- Simplest type of cell: cell wall, cytoplasm, flagella/pili
- DNA is circular, single copy
- Simple cell division (mitosis): DNA duplicated in each daughter cell
- Examples: *E. coli*, *Bacillus subtilis*
  - *E. coli:* 1 μm long, 20 min cycle

Eukaryote: single and multi-cell

- Much more complicated structure
- DNA resides in nucleus; proteins are formed in the cytoplasm
  - DNA organized in chromosomes
- Organelles implement cell functions
  - Nucleus: contains DNA
  - Mitochondria: energy production

Central Dogma: DNA to Proteins





Transcription: DNA to mRNA

- Double stranded DNA contains nucleotide sequence (A, C, T, G) on a sugar (deoxyribose) backbone
- Watson-Crick pairing: A:T, C:G
- RNA polymerase *transcribes* DNA sequence to RNA sequence (A, C, U, G sequence on a ribose backbond)

Translation: mRNA to protein

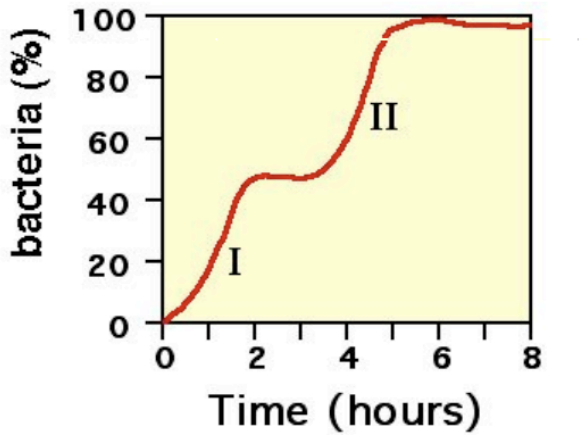
- (Eukaryotes) pre-mRNA is spliced and processed to form mature mRNA
- mRNA is *translated* by ribosomes into a chain of amino acids using the genetic code (3 bp code for 1 aa)
- Amino acid chain (polypeptide chain) folds into a protein

Regulation: control gene expression

- Proteins bind to DNA, RNA and proteins to modulate expression

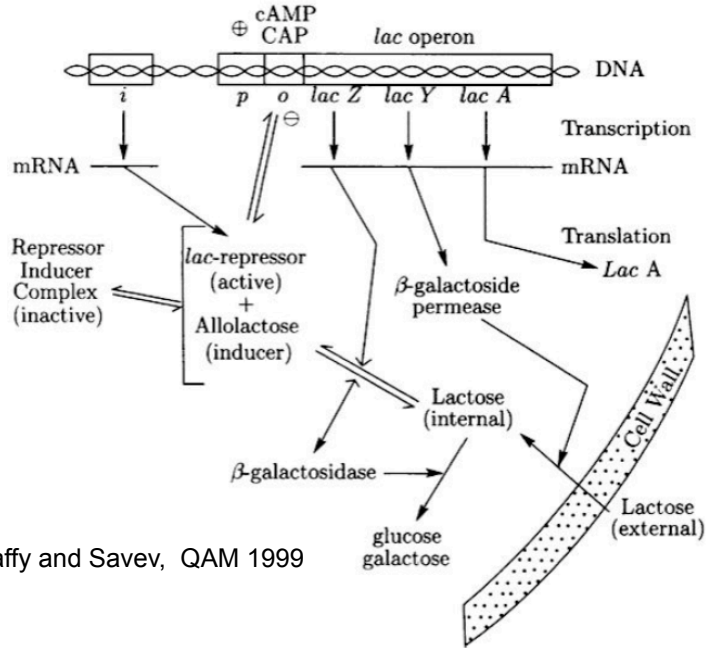
Model Control System: The Lac Operon

http://en.wikipedia.org/wiki/Image:Bacterial_growth_monod.png



Key idea (Jacob & Monod, 1950s): produce proteins when you need them

- Bacterial growth dependent on nutrient environment
- Lactose only consumed if glucose is not present
- Q: How does E. coli decide when to produce proteins?
- A: Lac "operon" (≈ control system)
- KPT07: "Lac operon is the hydrogen atom of regulation"

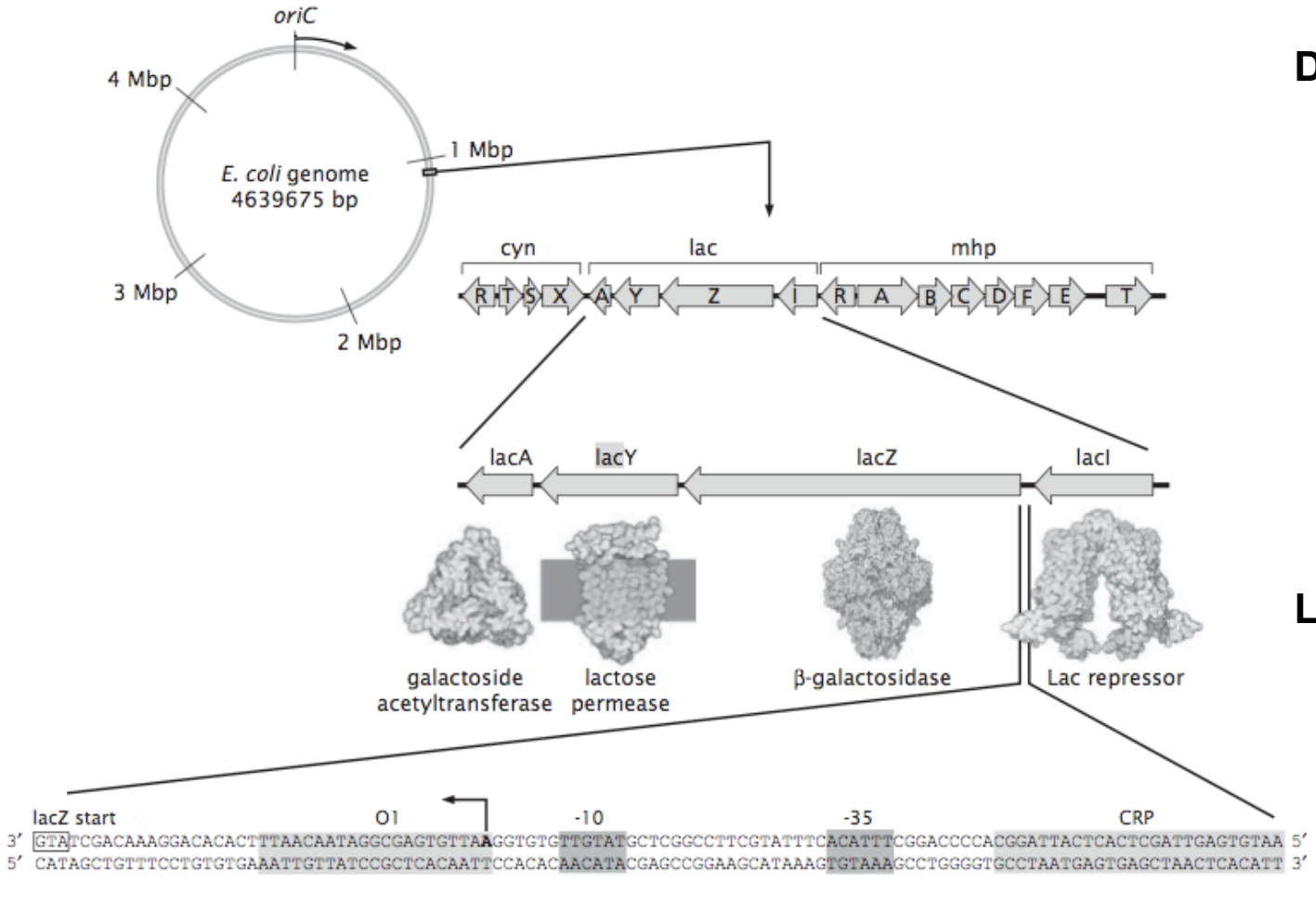


Mahaffy and Savev, QAM 1999

How does it work?

- Proteins for digesting lactose are controlled by binding of repressor and activator
- CAP (activator): recruits RNA polymerase when bound to cAMP, whose concentration is controlled by absence of glucose (+glucose ⇒ no cAMP)
- Repressor: blocks transcription by causing DNA looping unless it is bound to allolactose, a byproduct of lactose metabolism
- Feedback: if lactose present, then create proteins required to turn on lac operon, which creates the proteins required to matabolise lactose

E. Coli Genome



Phillips, Kondev, Theriot (2008)

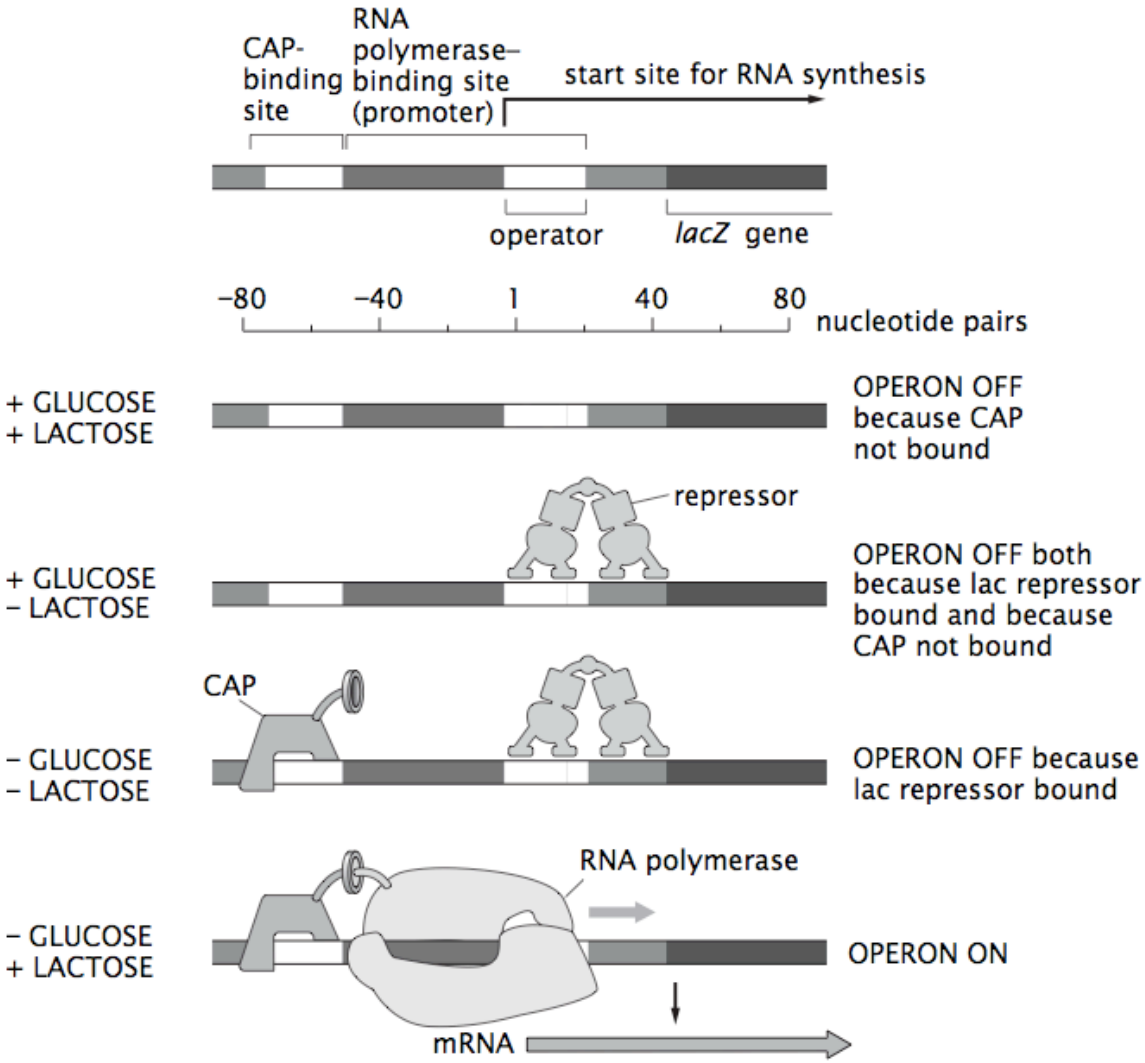
DNA facts

- Typical gene is about 1000 bp (300 aa) long
- E. coli genome is 4.6 Mb, with ~4000 genes
- Human genome is about 4 Gb, with ~25,000 genes

Lac control circuitry

- Main circuitry is about 6000 bp (genes plus regulatory regions)
- Can see structure of the promotor in DNA sequence

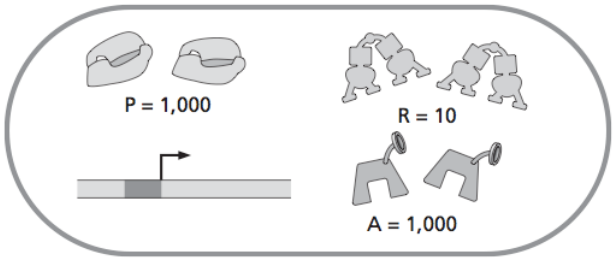
Operon Layout and Molecular Census



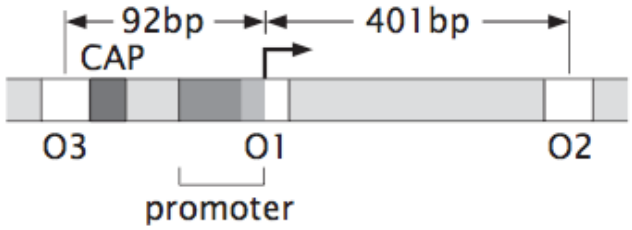
Phillips, Kondev, Theriot (2008)

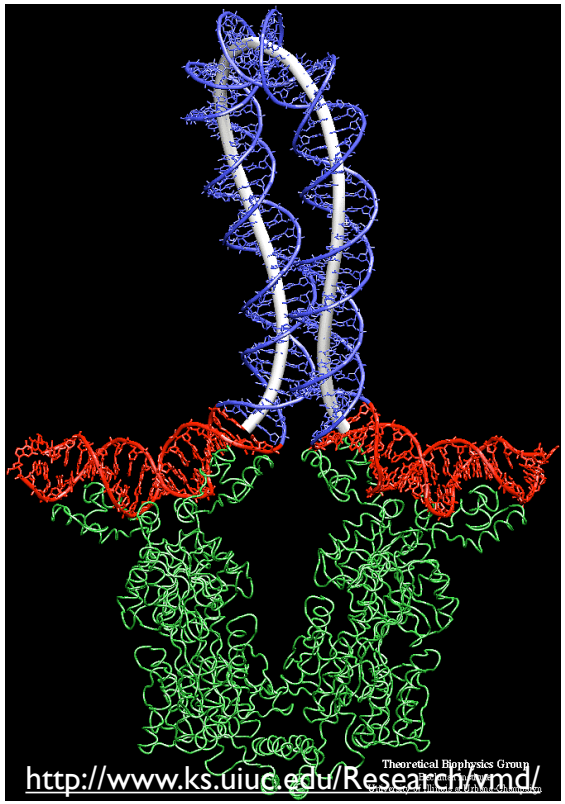
The regulatory landscape

- Repressor binds in a region that blocks the binding of RNAP
- If CAP is present (activated by cAMP, which is present in the absence of glucose), it recruits RNAP
- Can assign energies to each of these events and work out statistical mechanics (see PKT)



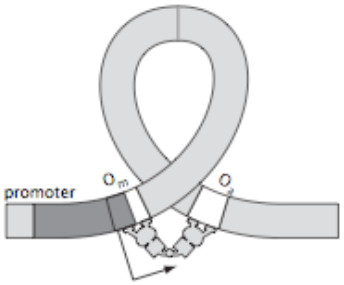
Repressor and DNA looping





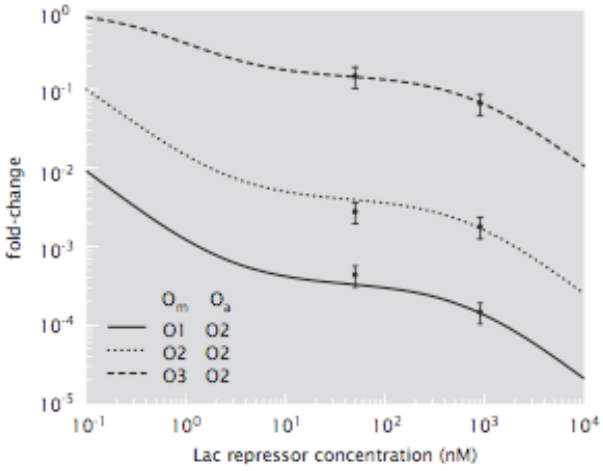
Repressor acts through DNA looping

- Looking can occur between binary binding site (O1) and secondary sites on DNA (O2, O3)



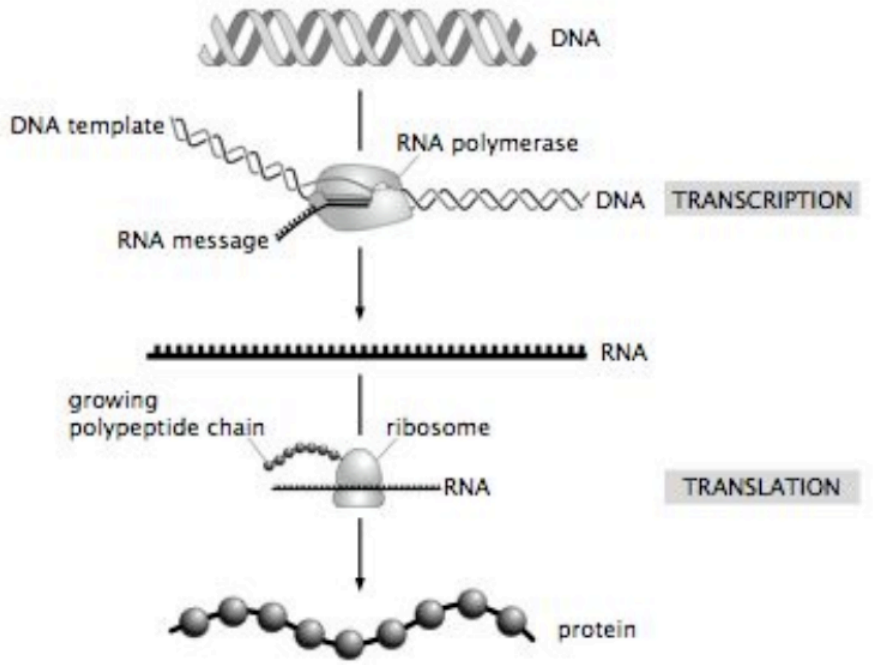
$$\text{Repression} = \frac{p_{\text{bound}}(R=0)}{p_{\text{bound}}(R)}$$

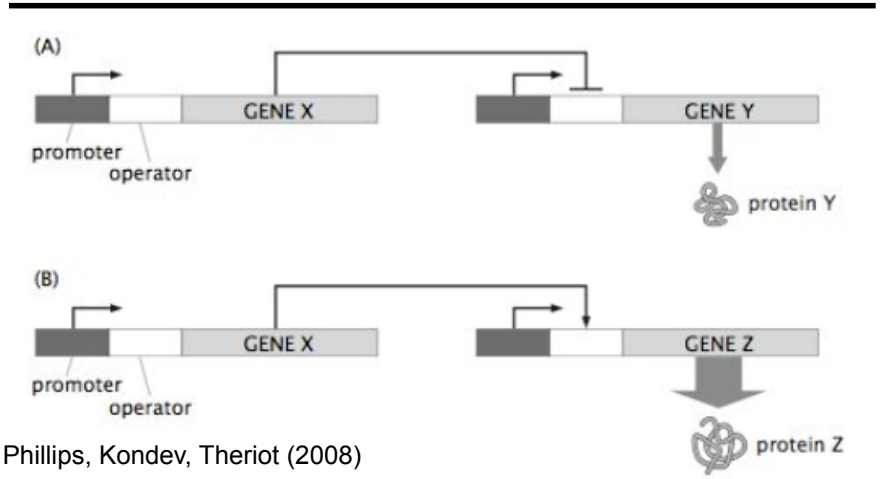
- Modeling via statistical mechanics: compute p_{bound} of RNA binding to DNA for different situations
- Experiments: relocate secondary binding sites and see what happens
- Still get some repression even if there is only one operator site present (no looping?)



Phillips, Kondev, Theriot (2008)

Rates of Transcriptional Regulation





Phillips, Kondev, Theriot (2008)

Primary timescales:

- mRNA production: 10-30 bp/sec
- Protein production: 10-30 aa/sec
- Protein folding: (depends)

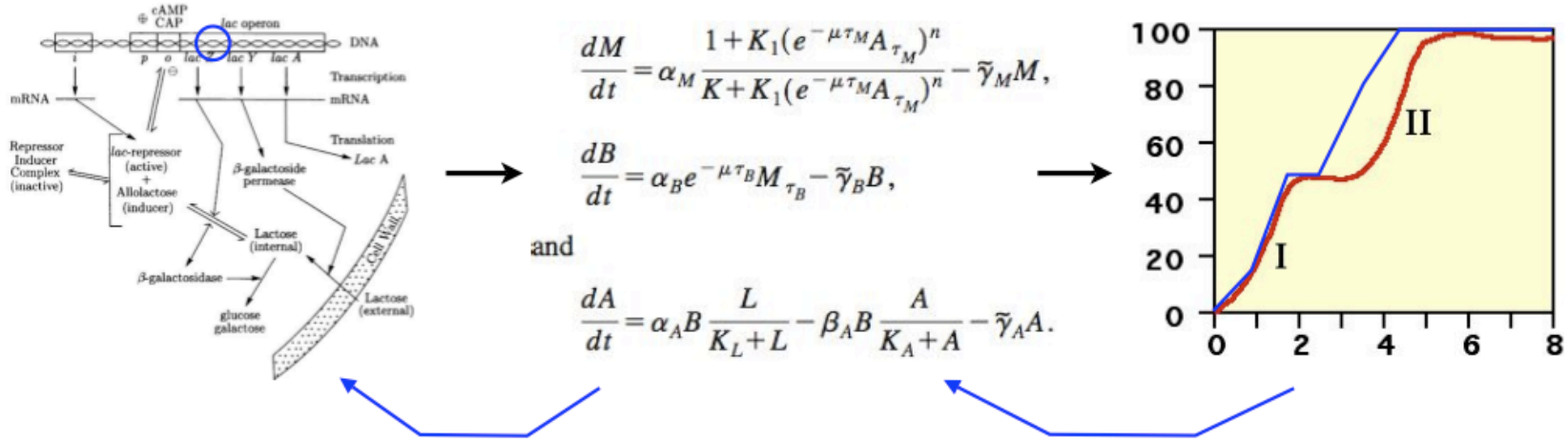
DNA, protein from PKT08, mRNA production from Vogel & Jensen

Other important rates

- mRNA half life : ~100 sec
- Protein half life: ~5 x 10^4 sec
- Protein diffusion (along DNA): up to 10^4 bp/sec
- Typically assume that activators and repressors reach equilibrium state much more quickly than other time scales

Half life times from Yildirim and Mackey, 2003; Protein diffusion from Blainey et al, PNAS 2006.

From Numbers to Equations: Dynamical Modeling



Modeling philosophy: Ask questions first, build model later

- Many different models possible for the same system; no such thing as "the model"
- The model you use depends on the questions you want to answer
- Never build a model without first posing the questions

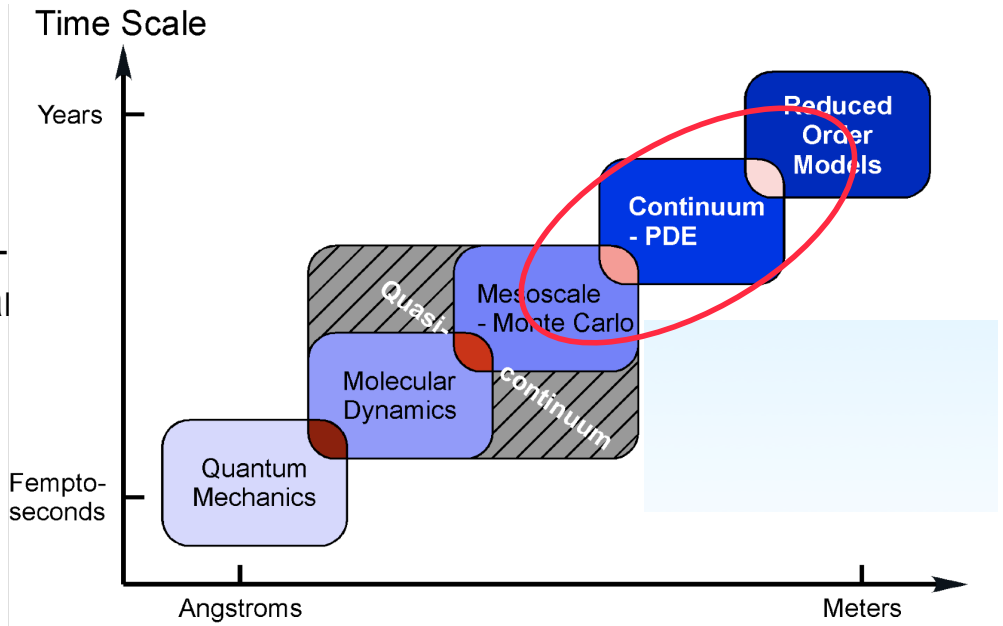
Analysis and design based on models

- A model provides a prediction of how the system will behave
- Feedback can give counter-intuitive behavior; models help sort out what is going on
- Models don't have to be exact to be useful; they just need to help explain (and predict)

Dynamic Modeling Approaches

Possible approaches to modeling

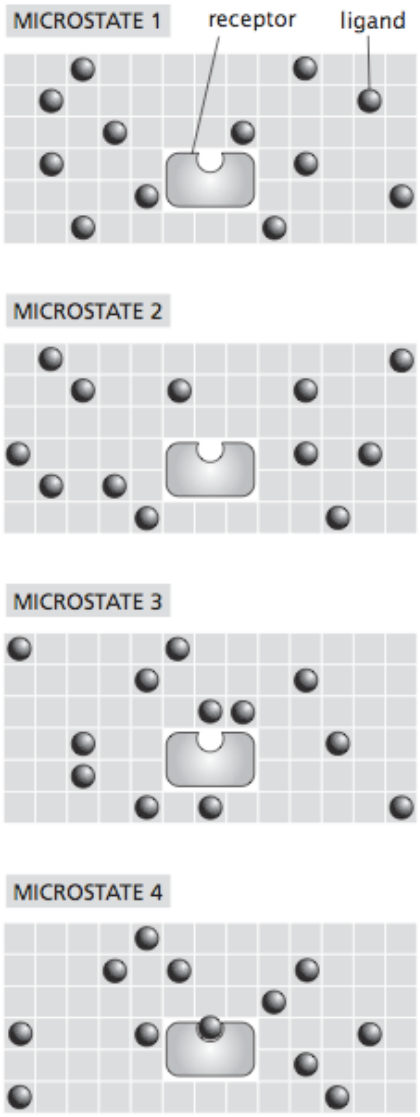
- Molecular dynamics - keep track of vibration of molecules and detailed reaction dynamics
- Monte Carlo/Stochastic simulation - extend ideas from statistical mechanics to include time
- Continuum/partial differential equations - keep track of evolution in space and time
- Reduced order models - ordinary differential equations that capture bulk properties

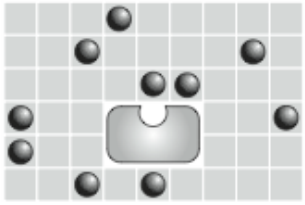
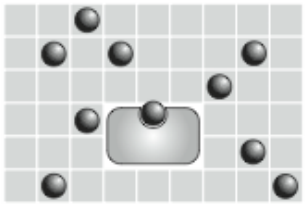


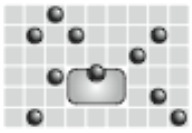
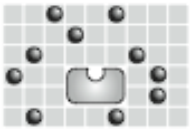
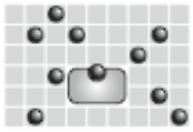
Choice of model depends on the questions you want to answer

- Modeling takes practice, experience and iteration to decide what aspects of the system are important to model at different temporal and spatial scales
- Good analysis models make testable predictions and produce “surprising” results
- Good design models capture enough of the important behavior to give allow good design decisions

Statistical Mechanics Viewpoint



STATE	ENERGY	MULTIPLICITY	WEIGHT
	$L\varepsilon_{sol}$	$\frac{\Omega!}{L!(\Omega-L)!} \approx \frac{\Omega^L}{L!}$	$\frac{\Omega^L}{L!} e^{-\beta L\varepsilon_{sol}}$
	$(L-1)\varepsilon_{sol} + \varepsilon_b$	$\frac{\Omega!}{(L-1)!(\Omega-L+1)!} \approx \frac{\Omega^{L-1}}{(L-1)!}$	$\frac{\Omega^{L-1}}{(L-1)!} e^{-\beta[(L-1)\varepsilon_{sol} + \varepsilon_b]}$

$$p_{bound} = \frac{\sum_{states} \left(\text{  } \right)}{\sum_{states} \left(\text{  } \right) + \sum_{states} \left(\text{  } \right)}$$

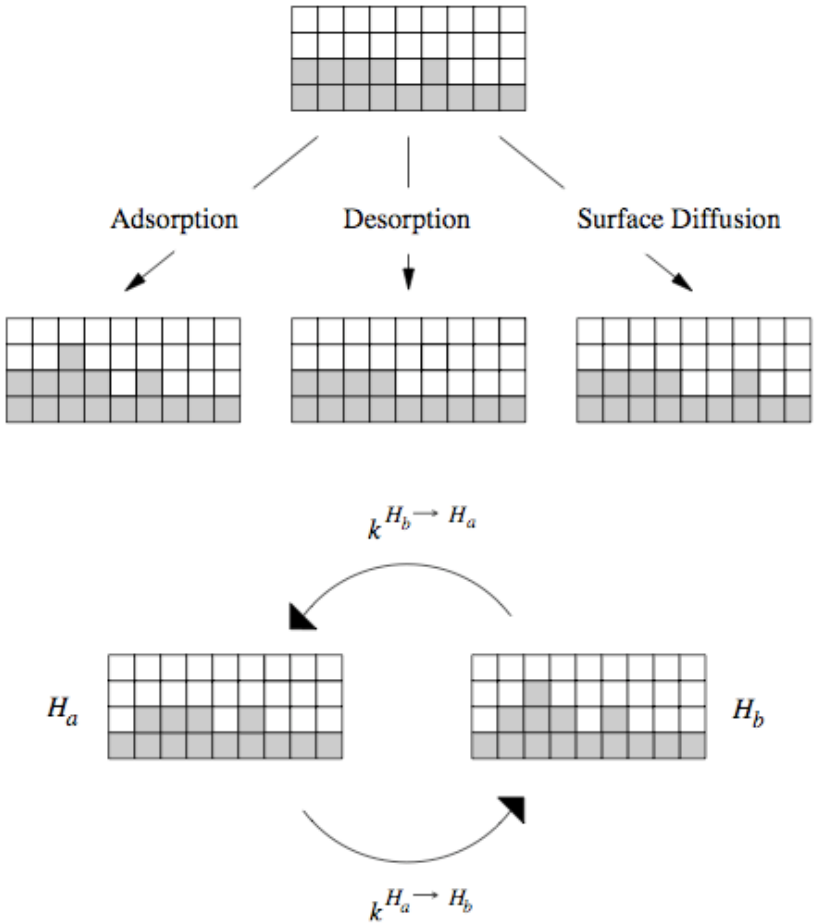
Partition function

- Sum up the weights for desired states (bound) versus all possible states

Provides an *equilibrium* view of the *world*

- Computes the "steady state" probability that a situation occurs
- Based on energy arguments; allows study of complex situations

The Master Equation: Detailed Events and Rates



$$\frac{d}{dt}P_H(t) = \sum_{H'} k^{H' \to H} P_{H'}(t) - \sum_{H'} k^{H \to H'} P_H(t)$$

Key idea: transition rates between microstates

- Enumerate micro-states corresponding to the system of interest
- Define the system "state" in terms of the individual probabilities of each microstate at each instant in time
- Dynamics are given by rate of change of the probability of each individual state

Transition rates depend on detailed model of molecular dynamics

- Example: lattice structure captured by Botzmann model

$$k_{\mathrm{des,i}} = \nu \exp\left(-\frac{E_{\mathrm{des},0} + i\Delta E}{k_b T}\right)$$

(ν = vibrational frequency, 10^{13})

- For DNA, RNA, protein interactions, can look at probability of collision + binding energy to reason about rates; also possible to identify via experiments

Simulating the Master Equation for Chemical Reactions

Stochastic Simulation Algorithm (SSA)

- N states (X_1, X_2, ..., X_N) where X_i is the number of copies of species S_i in the system
- M reaction channels R_i that define changes in the state; $v_{ij}(X)$ = change in X_i for R_j
- Propensity function: $a_i(X)\,dt$ = probability that a reaction R_i will occur in time interval dt
- SSA ("Gillespie algorithm"): determine how many reactions occur in a given time step and execute; then update propensity functions and repeat
- Choose time steps to be small enough that propensity functions are roughly constant

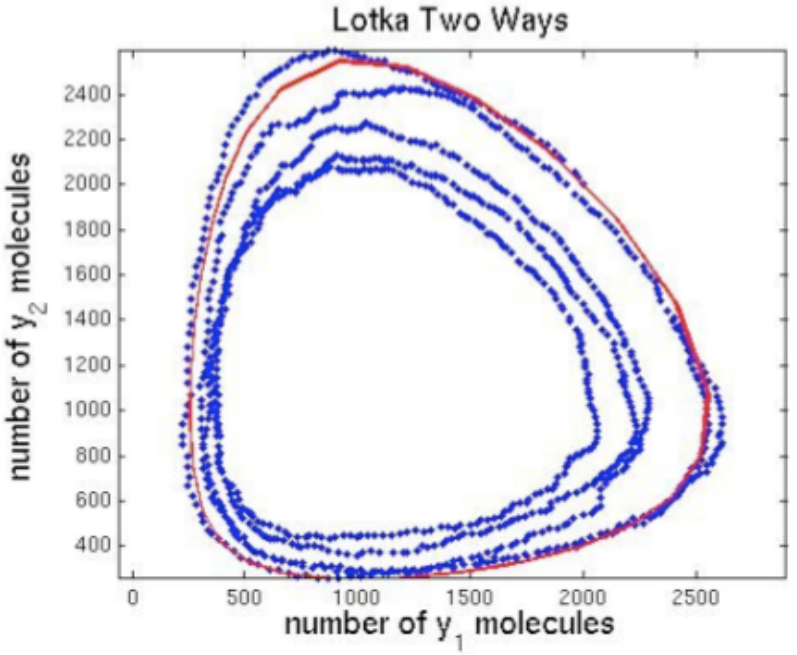
Example

$$\begin{aligned} \mathrm{X}_\infty + \mathrm{Y}_1 &\longrightarrow 2\,\mathrm{Y}_1 && \text{with propensity } a_1 \\ \mathrm{Y}_1 + \mathrm{Y}_2 &\longrightarrow 2\,\mathrm{Y}_2 && \text{with propensity } a_2 \\ \mathrm{Y}_2 &\longrightarrow \mathrm{Z} && \text{with propensity } a_3 \end{aligned}$$

- Propensity function: $a1(X) = c_1\, X_\infty\, Y_1$ to account for multiple copies of each species

Tools

- SBML - modeling language + many tools
- StochKit (Linda Petzold) - C++ libraries
- SimBiology (MATLAB) - includes SSA



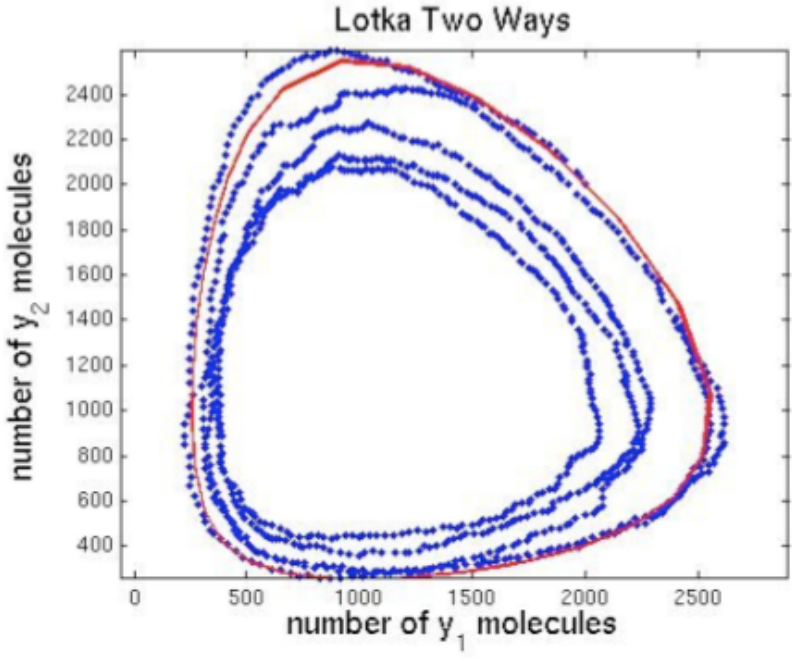
http://www.caam.rice.edu/~caam210/reac/lec.html

Chemical Kinetics: The Law of Mass Action

Alternative approach: keep track of concentrations

- If number of molecules is large, we can keep track of concentration of each species
- No longer track individual events; assume an average rate of events and use ODEs

$$\begin{aligned} \mathrm{X}_\infty + \mathrm{Y}_1 &\longrightarrow 2\,\mathrm{Y}_1 \qquad \text{with rate } k_1 \\ \mathrm{Y}_1 + \mathrm{Y}_2 &\longrightarrow 2\,\mathrm{Y}_2 \qquad \text{with rate } k_2 \\ \mathrm{Y}_2 &\longrightarrow \mathrm{Z} \qquad \text{with rate } k_3 \end{aligned}$$



- Keep track of change due to each reaction

$$\begin{aligned} d[Y_1]/dt &= k_1[X_\infty][Y_1] - k_2[Y_1][Y_2] \\ d[Y_2]/dt &= k_2[Y_1][Y_2] - k_3[Y_2] \end{aligned}$$

More complicated reactions:

$$2\,\mathrm{A} + \mathrm{B} \underset{k_{-1}}{\overset{k_1}{\rightleftharpoons}} \mathrm{A_2B}$$

$$\begin{aligned} d[\mathrm{A}]/dt &= 2k_{-1}[\mathrm{A_2B}] - 2k_1[\mathrm{A}]^2 \cdot [B] \\ d[\mathrm{B}]/dt &= k_{-1}[\mathrm{A_2B}] - k_1[\mathrm{A}]^2 \cdot [B] \\ d[\mathrm{A_2B}]/dt &= k_1[\mathrm{A}]^2 \cdot [B] - k_{-1}[\mathrm{A_2B}] \end{aligned}$$

$$\frac{dx}{dt} = Sv(x)$$

Stochiometry matrix — Reaction rates

- x = concentration vector
- S = stochiometry matrx
- $v(x)$ = Rate vector

Michaelis-Menten Kinetics

Enzymatically controlled reactions

- Enzyme E acts as a catalyst for reaction

$$\mathrm{E} + \mathrm{S} \underset{k_-}{\overset{k_+}{\rightleftharpoons}} \mathrm{ES} \xrightarrow{r} \mathrm{E} + \mathrm{P}$$

- Dynamics follow from mass action kinetics

$$\begin{aligned}
\frac{d[E]}{dt} &= k_-[ES] - k_+[E]\cdot[S] + r[ES] \\
\frac{d[S]}{dt} &= k_-[ES] - k_+[E]\cdot[S] \\
\frac{d[ES]}{dt} &= k_+[E]\cdot[S] - k_-[ES] - r[ES] \\
\frac{d[P]}{dt} &= r[ES]
\end{aligned}$$

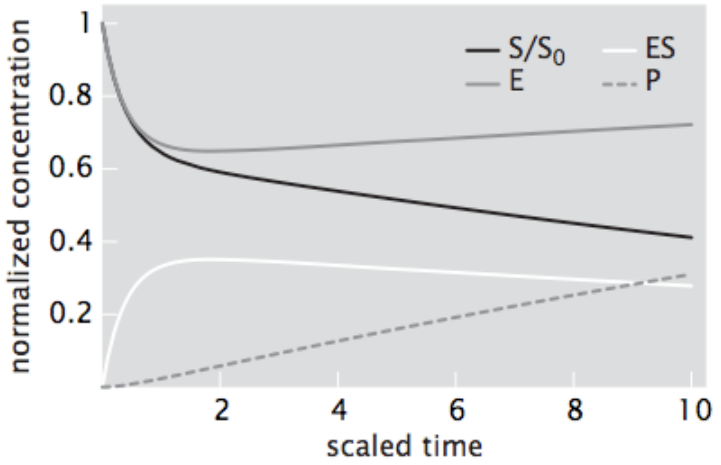
- If we assume enzyme dynamics are fast compared to other species, we can simplify the resulting dynamics:

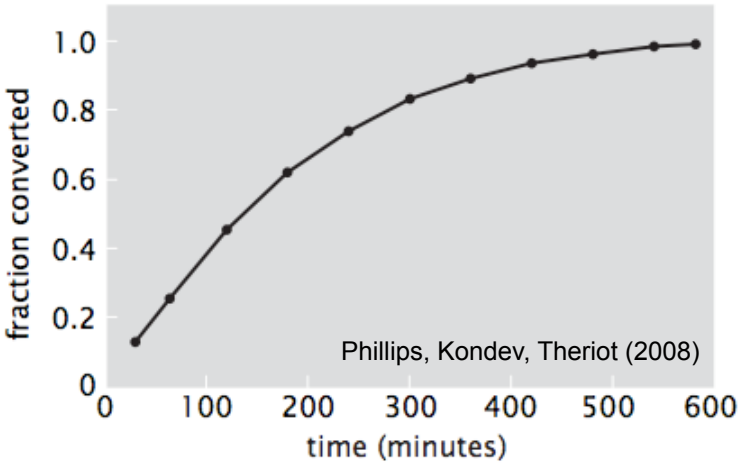
$$[\mathrm{ES}] = [\mathrm{E}]\cdot[\mathrm{S}]/K_m$$

$$K_m = \frac{k_- + r}{k_+}$$

$$\boxed{\frac{d[\mathrm{P}]}{dt} = r[\mathrm{E}]_{\mathrm{tot}}\frac{[\mathrm{ES}]}{[\mathrm{E}]+[\mathrm{ES}]} = V_{\max}\frac{[\mathrm{S}]}{K_m + [\mathrm{S}]}}$$

Michaelis-Menten kinetics

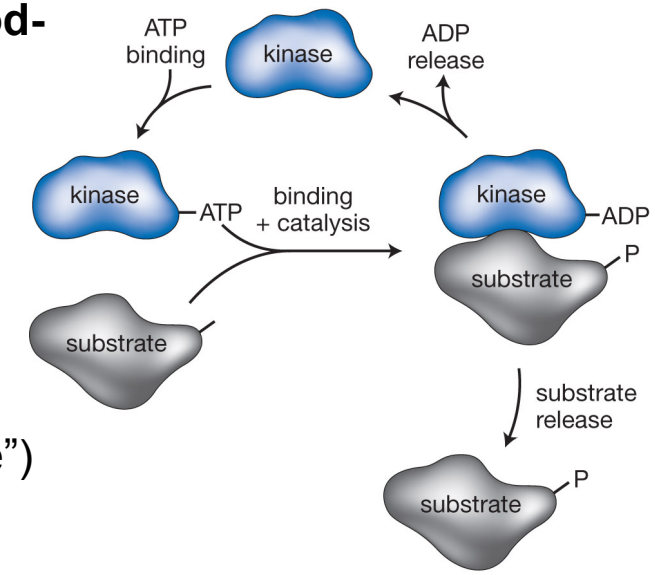


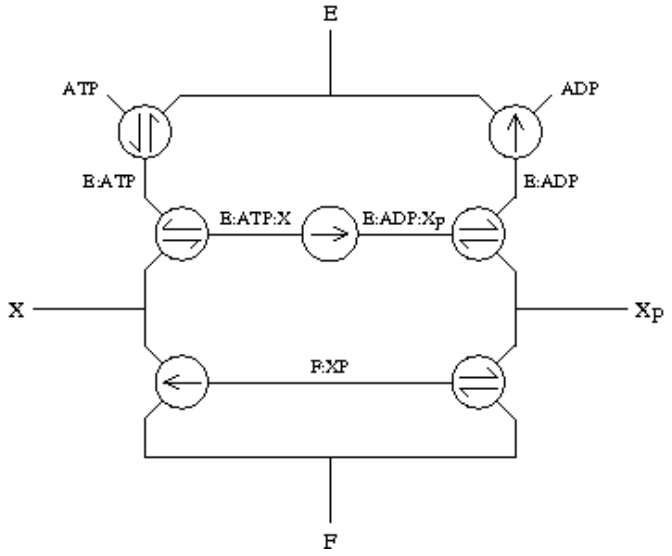


Phosphorylation

Post-translational modification of proteins

- Addition of a phosphase(PO_4) group to a protein
- Modifies shape of protein; affects binding to other proteins (Xp "active")





Kinase

- Binds ATP and catalyzes a transfer of phosphate group to protein
- Enzymatic reaction (kinase is available again after reaction)

Phosphatase

- Removes phosphate group
- Non-specific enzyme

Phosphorylation

$$\mathrm{E} + \mathrm{ATP} \rightleftharpoons \mathrm{E{:}ATP}$$

$$\mathrm{E{:}ATP} + \mathrm{X} \rightleftharpoons \mathrm{E{:}ATP{:}X}$$

$$\mathrm{E{:}ATP{:}X} \longrightarrow \mathrm{E{:}ADP{:}Xp}$$

$$\mathrm{E{:}ADP{:}Xp} \rightleftharpoons \mathrm{E{:}ADP} + \mathrm{X}$$

$$\mathrm{E{:}ADP} \longrightarrow \mathrm{E} + \mathrm{ADP}$$

Dephosphorylation

$$\mathrm{Xp} + \mathrm{F} \rightleftharpoons \mathrm{Xp{:}F}$$

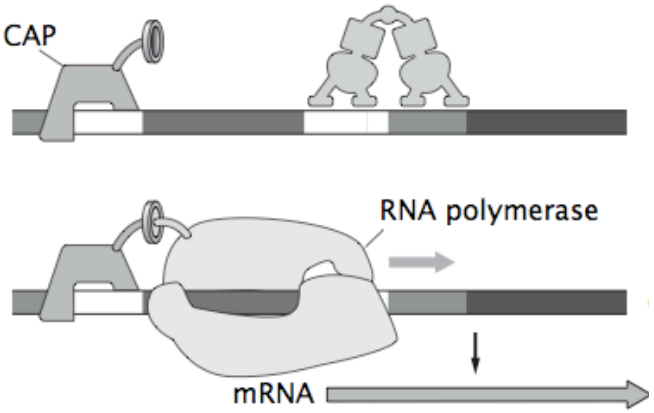
$$\mathrm{Xp{:}F} \longrightarrow \mathrm{X} + \mathrm{F}$$

Consider adding hydrolysis more explicitly in dephosphorylation

Transcriptional Regulation

Prokaryotic regulation occurs via binding of transcription factors (proteins) to DNA

- Activator: recruits RNA polymerase
- Repressor: blocks binding of RNAP
- Model dynamics by tracking binding events



Reduced order model: Hill functions

- Assume that binding dynamics are fast compared to transcription

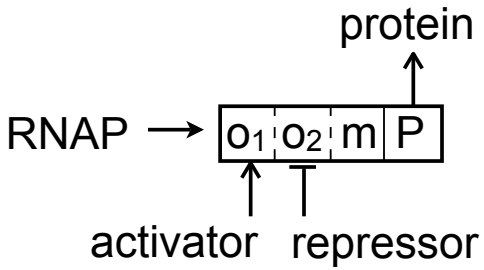
Hill function

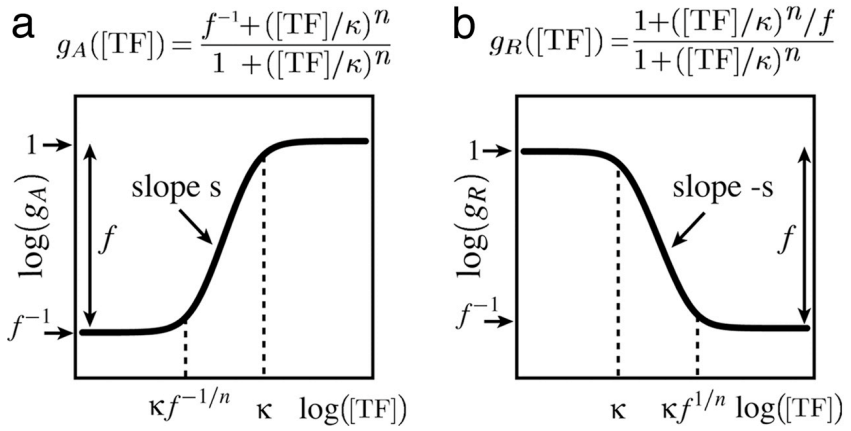
degradation

mRNA $\frac{dmY}{dt} = f(X) - \gamma \quad mY$

protein $\frac{dY}{dt} = \beta \quad mY - \delta \quad Y$

translation

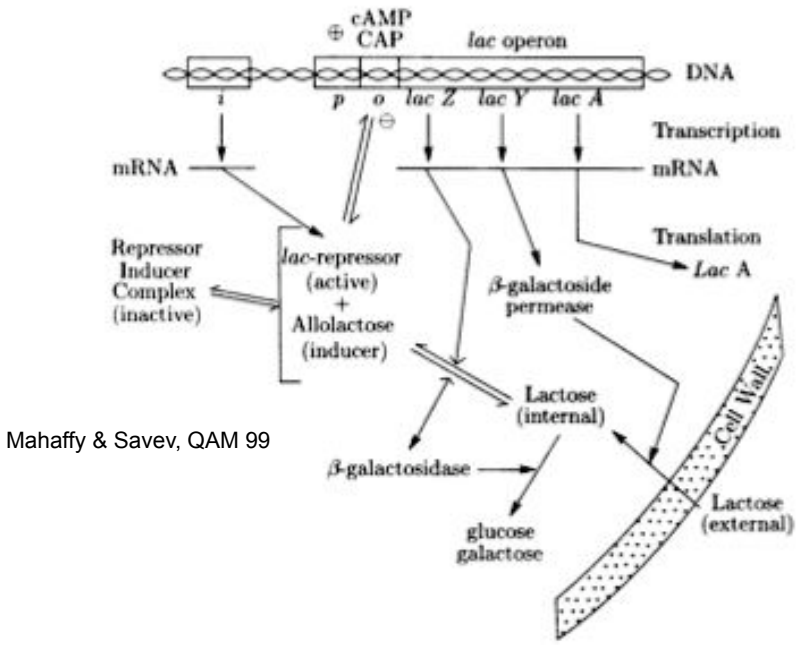




Activation Repression

Buchler, Gerland and Hwa (PNAS, 2005)

Yildirim-Mackey Model for the Lac Operon



Mahaffy & Savev, QAM 99

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n}{K + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n} - \bar{\gamma}_M M$$

$$\frac{dB}{dt} = \alpha_B e^{\mu\tau_B} M(t-\tau_B) - \tilde{\gamma}_B B$$

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{a}{K_A + A} - \tilde{\gamma}_A A$$

Questions:

- In the absence of glucose, what concentration of lactose is required for the *lac* operon to become "active"?
- Focuses on "bistability": *lac* operon has two stable equlibrium points:
  - low lactose: machinery off
  - high lactose: machinery on

Model

- Ordinary differential equation for rates of transcription, translation and degradation of β-galactosidase (β-gal) and allolactose
- Assume levels of lactose outside the cell is constant and level of permease (from *lacY*) is constant to simplify the model
- Takes into account time delays in producing proteins (RBS transcription + protein translation)

Model Derivation: β-Gal Production

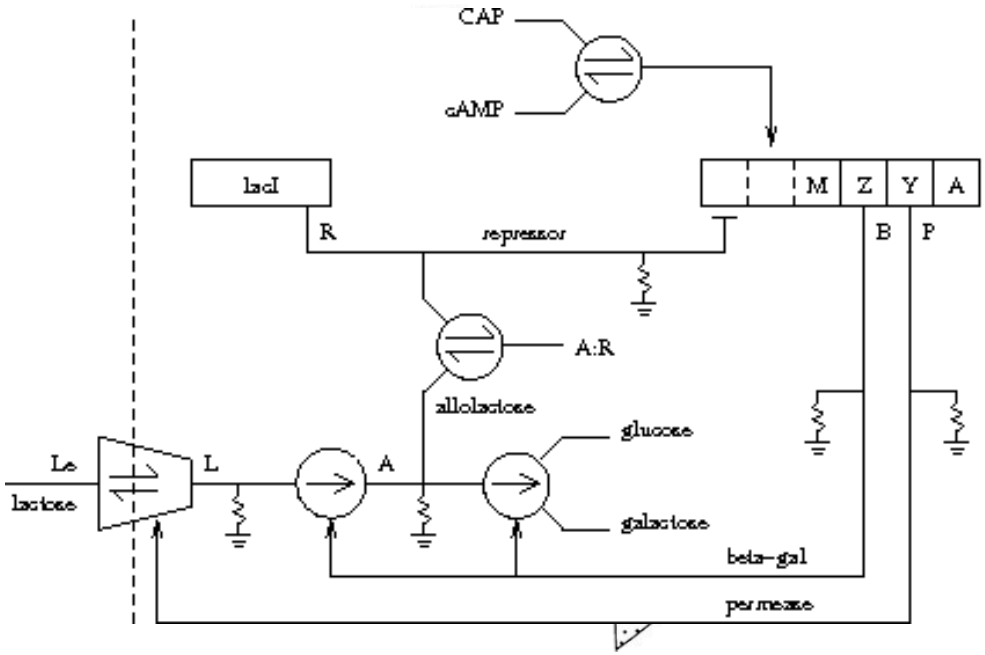
$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n}{K + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n} - \bar{\gamma}_M M$$

$$\frac{dB}{dt} = \alpha_B e^{-\mu\tau_B} M(t-\tau_B) - \tilde{\gamma}_B B$$

M = lacZ mRNA concentration

B = β-gal concentration

A = allolactose concentration



mRNA production

- Production rate related p_{bound} via a modified Hill function, ala

$$\frac{dM}{dt} = \alpha\big([1 - p_{\text{bound}}(A)] + \epsilon\big) - \gamma M$$

- RNA degradation via exponential decay
- Account for time delay in translation of RBS via τ_M :
  - Use allolactose concentration, *A*, at time t - τ_M
  - Exponential factor to account for dilution due to cell division

Protein production

- Assume rate of production is proportional to amount of mRNA
- Include protein degradation via exponential decay
- Add time delay to account for time to produce functional protein, τ_B

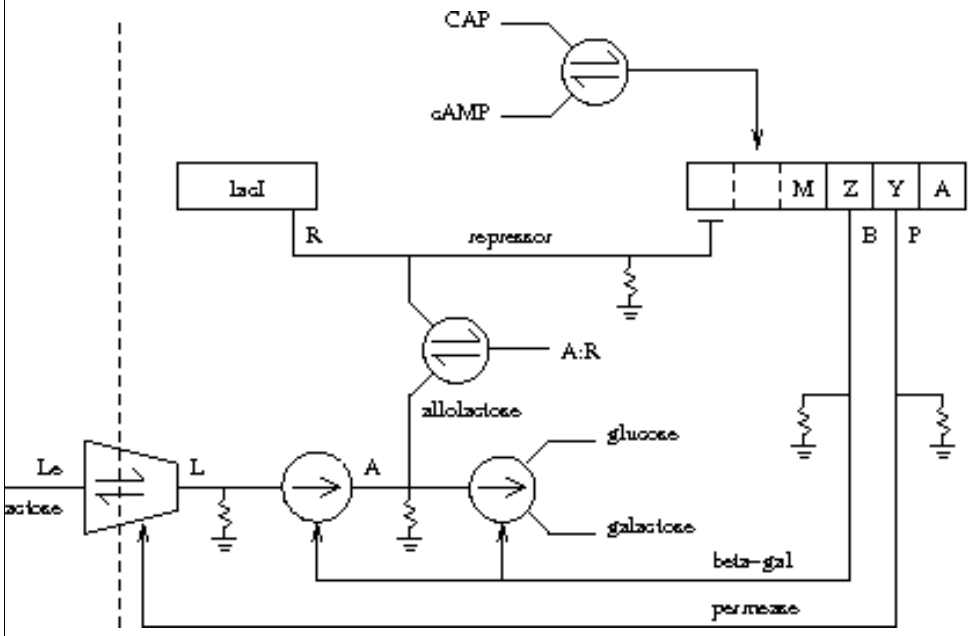
Model Derivation: Allolactase Dynamics

$$\frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L}^{①} - \beta_A B \frac{A}{K_A + A}^{②} - \tilde{\gamma}_A A^{③}$$

$$\frac{dL}{dt} = \alpha_L P \frac{L_e}{K_{L_e} + L_e}^{①} - \beta_{L_1} P \frac{L}{K_{L_1} + L}^{②}$$

$$- \beta_{L_2} B \frac{L}{K_{L_2} + L}^{③} - \tilde{\gamma}_L L^{④}$$

$$\frac{dP}{dt} = \alpha_P e^{-\mu \tau_P} M(t - \tau_P)^{①} - \tilde{\gamma}_P P^{②}$$



A = allolactose concentration

L = internal lactose concentration

P = permease concentration

B = β-gal concentration

Allolactose

1. Converted from lactose with Michaelis Menten-like kinetics (Huber et al)
2. Converted back to glucose and galactose
3. Degradation

Lactose (internal)

1. Transported to interior of cell by permease
2. Loss back to external environment
3. Converted to allolactose by β-gal
4. Degradation

Permease

1. Produced by *lacY* gene (after delay)
2. Degradation

Determining the Constants

Parameter	Value
$\mu_{\max}$	3.47×10^{-2} min^{-1}
$\bar{\mu}$	3.03×10^{-2} min^{-1}
α_M	997 nM-min^{-1}
α_B	1.66×10^{-2} min^{-1}
α_A	1.76×10^{4} min^{-1}
γ_M	0.411 min^{-1}
γ_B	8.33×10^{-4} min^{-1}
γ_A	1.35×10^{-2} min^{-1}
n	2
K	7200
K_1	$2.52\times10^{-2}(\mu\,\mathrm{M})^{-2}$
K_L	0.97 mM
K_A	1.95 mM
β_A	2.15×10^{4} min^{-1}
τ_M	0.10 min
τ_B	2.00 min

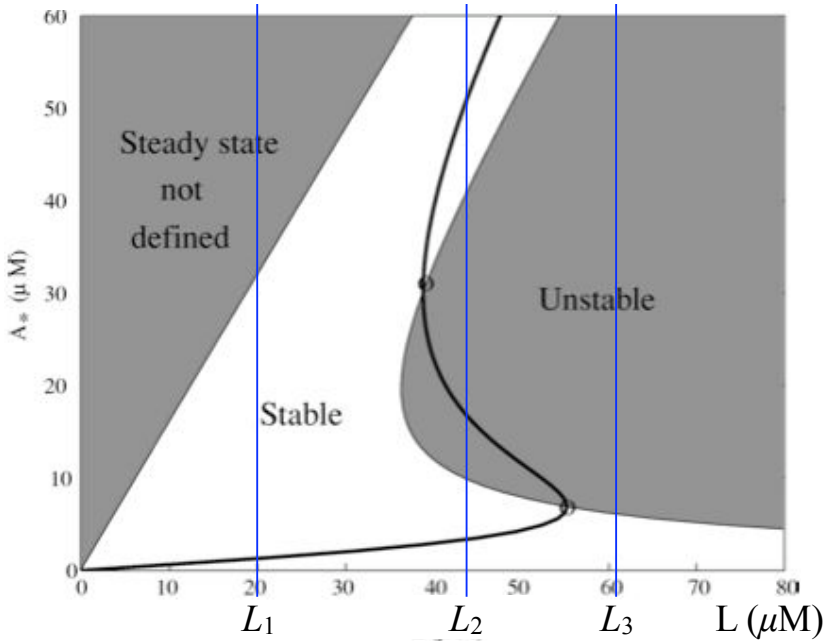
Yildirim, Santillan, Horike and Mackey:

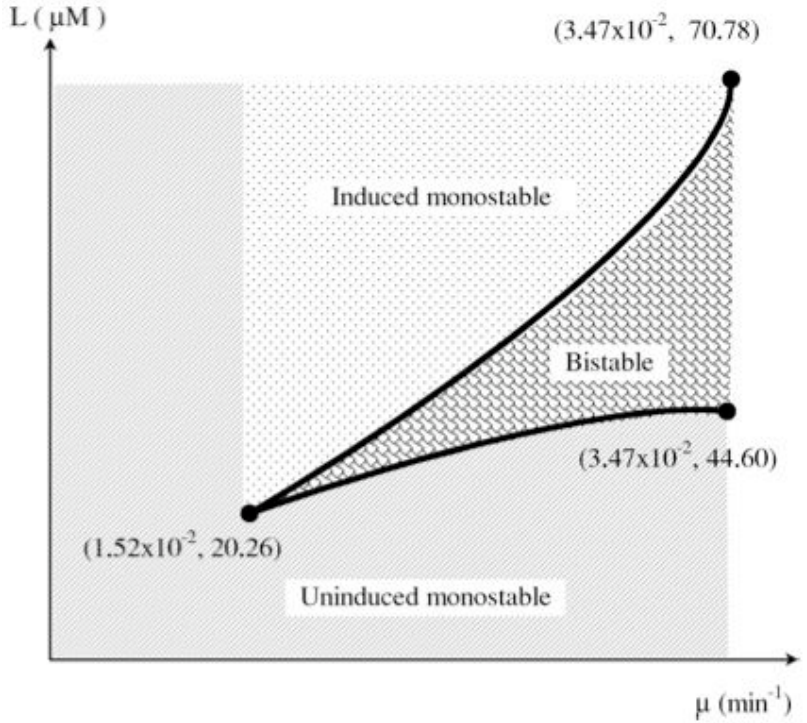
- μ - dilution rate, based on 20 minute cell division time
- α_x - production rate, based on steady state values
- γ_x - decay rate, based on half life experiments
- τ_M - time delay to produce RBS, based on RNA elongation rates
- τ_B - time delay to translate protein, based on protein length and translation speed
- n - Hill coefficient (no justification!)
- K - based on basal rate of production (Yagil & Yagil)
- K_1 - based on dissociation constant (Yagil & Yagil)
- K_x - measured by Wong, Gladney and Keasling (97)
- β_A - loss of allolactase, through conversion to glucose and galactose. Measured by Hubert et al (75)

Note: repressor binding model is pretty ad hoc...

$$\frac{dM}{dt} = \alpha_M \frac{1 + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n}{K + K_1(e^{-\mu\tau_M} A(t-\tau_m))^n} - \bar{\gamma}_M M \qquad \frac{dA}{dt} = \alpha_A B \frac{L}{K_L + L} - \beta_A B \frac{a}{K_A + A} - \tilde{\gamma}_A A$$

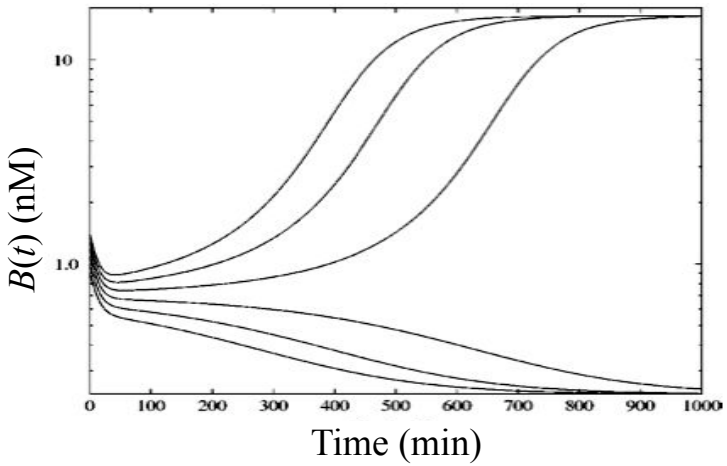
Some Predictions



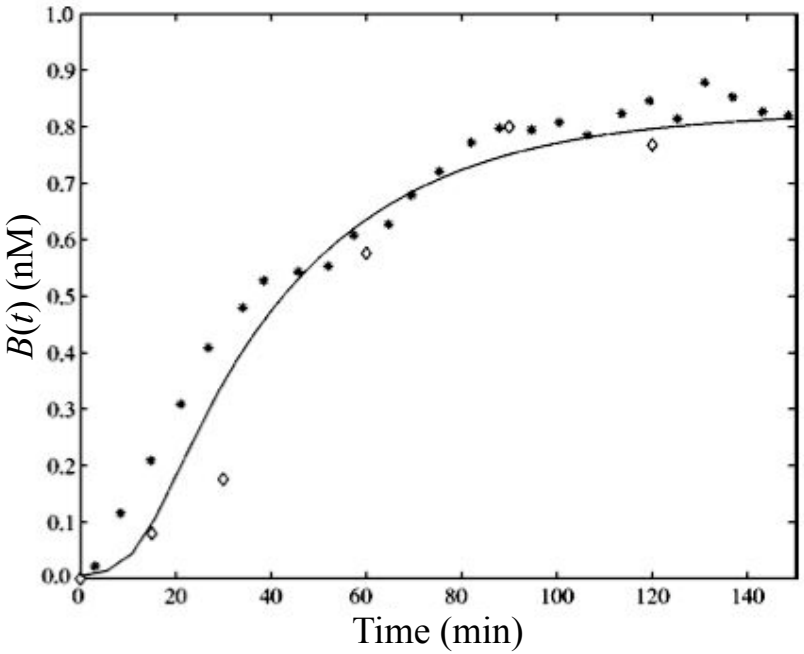


Bistable behavior (saddle node bifurcations)

- Can have single or multiple equilibrium points depending on parameters
- Bifurcation plot: change in stability versus params
  - Note: ossible hysteresis from saddle node
- Parametric stability plot: stability regions
- Simulations: nearby initial conditions can lead to different steady state solutions
- Use to predict behavior (for future experiments)

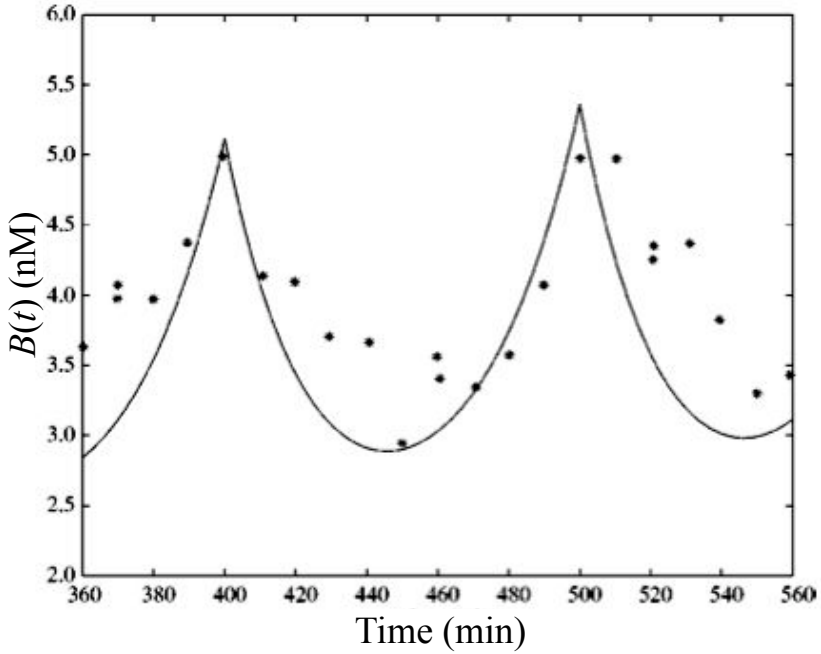


Comparison to Experiment



β-gal activity for L_e = 8 x 10^{-2} mM

- Experimental data from Knorre (1968) for *E. coli* ML30 (◊) and Pestka et al. (1984) for *E. coli* 294 (●)
- Model simulation using constants from Table 1 (slide 16) with μ = 2.26 x 10^{-2} min^{-1} and γ_x (= ??) fit to data



Oscillation in β-gal w/ phosphate feeding

- Periodic phosphate feeding from Goodwin (1969)
- Simulation used μ = 2.26 x 10^{-2} min^{-1} and γ_x (= ??). Other parameters unchanged.
- Q: how should we assess these data?

Modeling Noise in Chemical Reactions

Fundamental assumption (Gillespie, 1992)

- Treat species concentrations as a random variable $X(t)$

  $a_j(x)\,dt$ = the probability, given $X(t) = x$, that one R_j reaction will occur in the next infinitesimal time interval $[t, t + dt)$

Chemical Master equation (exact)

- Describes the evolution of the probability distribution for the microstate X(t)

$$\frac{\partial P(\mathbf{x}, t \,|\, \mathbf{x}_0, t_0)}{\partial t} = \sum_{j=1}^{M} [a_j(\mathbf{x} - \boldsymbol{\nu}_j) P(\mathbf{x} - \boldsymbol{\nu}_j, t \,|\, \mathbf{x}_0, t_0) - a_j(\mathbf{x}) P(\mathbf{x}, t \,|\, \mathbf{x}_0, t_0)]$$

Chemical Langevin equation (CLE)

- Assume that time steps are small enough but not too small
  - (i) Time increment *dt* small enough that propensity functions are approx constant
  - (ii) Time increment *dt* large enough that number of events is much larger than 1
- Under these assumptions, can derive stochastic ODE (Gillespie, 2000):

$$X_i(t + dt) = X_i(t) + \sum_{j=1}^{M} v_{ji} a_j(X(t))dt + \sum_{j=1}^{M} v_{ji} a_j^{1/2}\big(X(t)\big) N_j(t)(dt)^{1/2}$$

White noise w/ unit variance

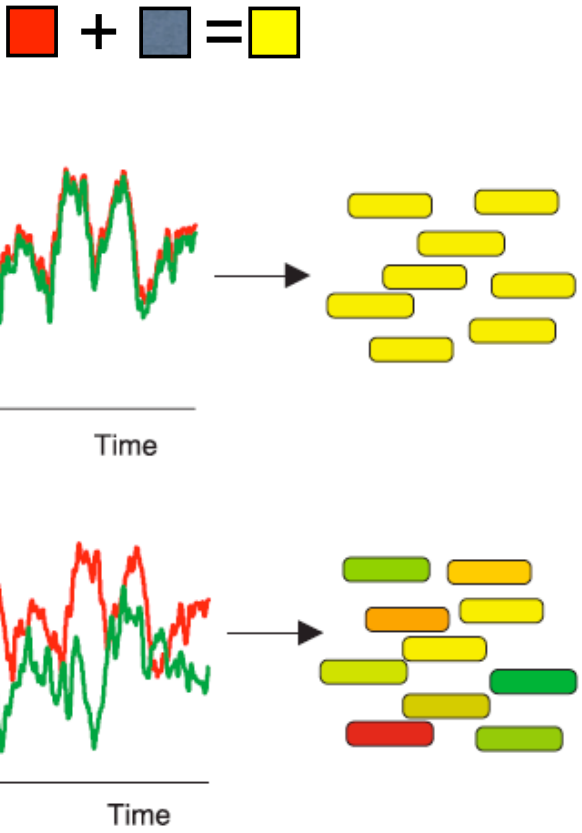
Remarks

- Mass action kinetics are deterministic version of mean of the CLE

Cell Noise (Elowitz et al, 2002)

Noise in cells

- Experiments by Elowitz, Levine, Siggia, Swain. *Science* 2002
- Put RFP and GFP under identical promoters; *should* get yellow
- Results: get range of colors



Extrinsic Noise:

- global to a single cell, but varies from one cell to the next (e.g. cell volume, plasmid copy number)

Intrinsic Noise:

- inherent stochasticity in gene expression (e.g. what order reactions occur in)

$$\dot{x}_i = E(t) \cdot f_i(x_i, I_i(t))$$

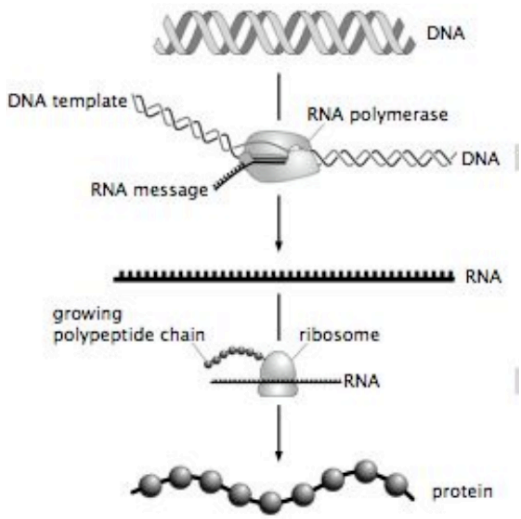
Coefficient of variation: $\mathrm{CV}(X) = \dfrac{\mathrm{std}(X)}{\mathrm{mean}(X)}$

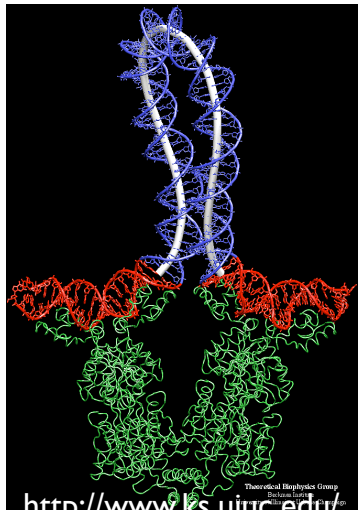
- Normalized measure of noise, commonly used in biology

Modeling Summary

Core processes in biological circuits

- Transcription, translation, binding
- Activation and repression
- Enzymatic reactions, (phosphorylation)



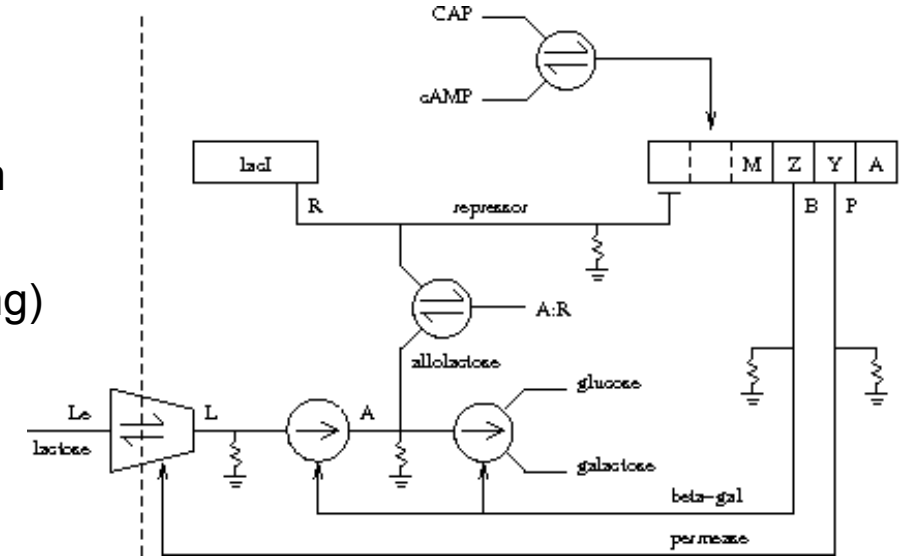


Quantitative modeling approaches

- Statistical thermodynamics
- Chemical master equation, SSA
- Chemical Langevin equation
- Mass action, Michaelis-Menten, Hill functions and ODEs

Lac operon

- Model system for transcriptional regulation
- Activation via CAP:cAMP
- Repression via Lac Repressor (DNA folding)



Next

- Control analysis techniques
- More complex biological circuits