

# Lecture 6: Proteins; entropy rules

Goal: Introduce Boltzmann distribution, probability of microstate

- Ligand-receptor binding
- Gene regulation
- Cooperativity

PBOC Chapter 6.1.1, 6.1.2, 6.4  
(except 6.4.4)

# Statistical mechanics for biophysics

(implies "large system")

Numbers:

RNA polymerase molecules in the nucleus

3-5,000 (E. coli)  
~80,000 (mammalian)

Ligands near cell surface

0.3-300 mM acetylcholine neurotransmitter

What can we answer with these models?

Determine the probability of finding the system in a particular (energy) state.

Calculate the average values of observables.

# Statistical mechanics for biophysics

Previously (Lecture 3):

## Microstates

Definition: a **microstate** is a microscopic arrangement of the constituents of a system

Example: Ligand binding to a receptor protein

### Lattice model

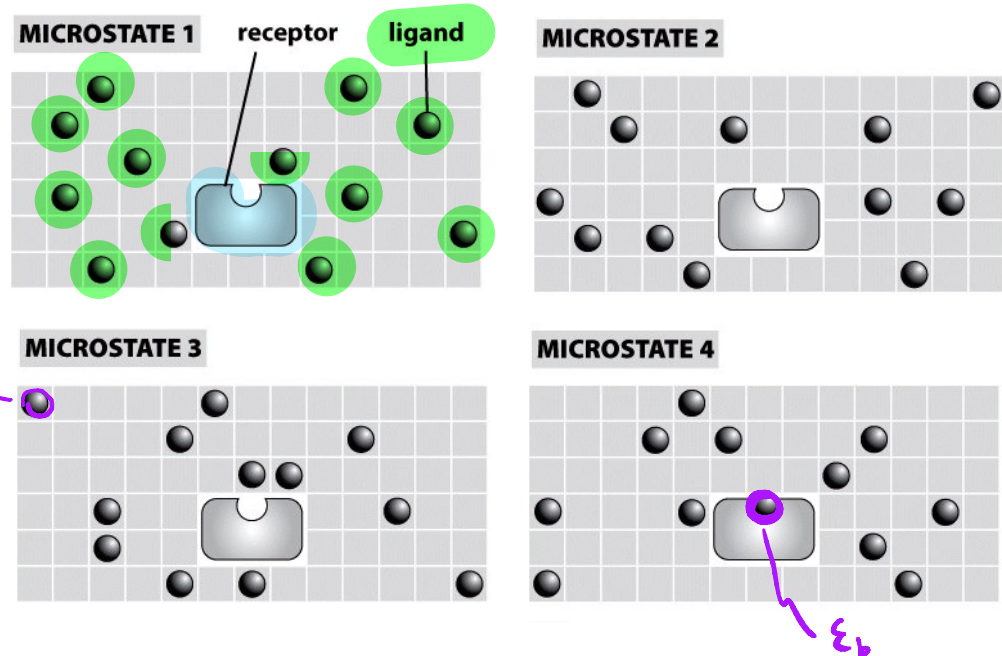
$L$  ligands

$\Omega$  boxes

max. one ligand per box

energy  $\varepsilon_b$  of a bound ligand

energy  $\varepsilon_{sol}$  of a ligand in solution



# Statistical mechanics for biophysics

## *Microstates*

Suppose a system can exist in states with energies  $E_i$ .  
What is the probability of finding the system in a given state?

Boltzmann distribution, probability of finding the system in a microstate with energy  $E_i$  (*derivation, Section 6.1.3*)

$$p(E_i) = \frac{1}{Z} e^{-E_i/k_B T}$$

Partition function, normalization factor so that  $\sum_{i=1}^N p(E_i) = 1$

$$Z = \sum_{i=1}^N e^{-E_i/k_B T}$$



# Statistical mechanics for biophysics

## Microstates

Suppose a system can exist in states with energies  $E_i$ .  
What is the average energy of the system?

$$\beta = \frac{1}{k_B T}$$

The average energy is the  
(probability) weighted mean of the  
energies of the states:

$$\langle E \rangle = \sum_{i=1}^N E_i p(E_i) = \frac{1}{Z} \sum_{i=1}^N E_i e^{-\beta E_i}$$

Note:  $\frac{\partial Z}{\partial \beta} = \sum_{i=1}^N \frac{\partial}{\partial \beta} (e^{-\beta E_i})$

$$= -\frac{1}{Z} \frac{\partial Z}{\partial \beta} = -\frac{\partial}{\partial \beta} (\ln Z)$$

chain rule

chain rule  
 $(f(g(x)))' = g'(x) f'(g(x))$

$$= \sum_{i=1}^N -E_i e^{-\beta E_i}$$

# Statistical mechanics for biophysics

Example: Ligand binding

**Lattice model**

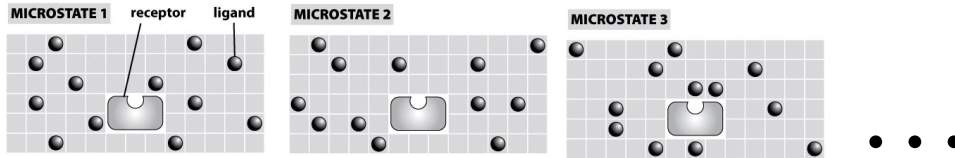
$L$  ligands

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max. one ligand per box

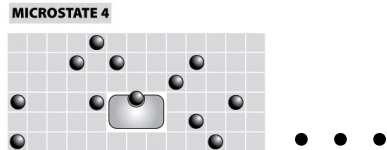
*Microstates: multiplicity* (Lecture 3)

Microstates with receptor unoccupied



$$\text{number of microstates} = \frac{\Omega!}{L!(\Omega-L)!}$$

Microstates with receptor occupied



$L \rightarrow L-1$

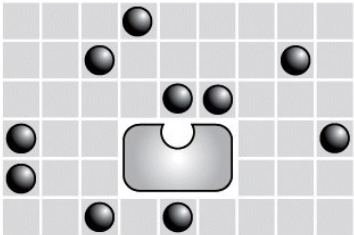
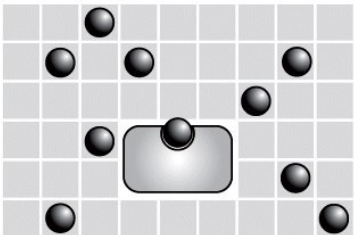
number of microstates?

$$\frac{\Omega!}{(L-1)!(\Omega-(L-1))!}$$

# Statistical mechanics for biophysics

Example: Ligand binding to receptor protein

*Microstates: energy, weight*

	STATE	ENERGY	MULTIPLICITY	WEIGHT
receptor unbound		$L\varepsilon_{sol}$ <i>(total energy of system)</i>	$\frac{\Omega!}{L!(\Omega-L)!} \approx \frac{\Omega^L}{L!}$ <i>for <math>\Omega \gg L</math></i>	multiplicity x Boltzmann weight "partial" partition function $\frac{\Omega^L}{L!} e^{-\beta L\varepsilon_{sol}}$ <i>multiplicity Boltzmann weight</i>
receptor bound		$(L-1)\varepsilon_{sol} + \varepsilon_b$	$\frac{\Omega!}{(L-1)!(\Omega-L+1)!} \approx \frac{\Omega^{L-1}}{(L-1)!}$ <i>M terms <math>\approx N</math> in value</i>	$\frac{\Omega^{L-1}}{(L-1)!} e^{-\beta[(L-1)\varepsilon_{sol} + \varepsilon_b]}$

Note: approximation of  $\frac{N!}{(N-M)!}$  for  $N \gg M$

$$= \underbrace{N \cdot (N-1) \cdot \dots \cdot (N-(M+1))}_{M \text{ terms } \approx N \text{ in value}} = N^M$$

# Statistical mechanics for biophysics

Example: Ligand binding to receptor protein

*Microstates: probability*

$$p_{\text{bound}} = \frac{\sum_{\text{states}} \left( \begin{array}{c} \text{diagram: 1 ligand bound} \end{array} \right)}{\sum_{\text{states}} \left( \begin{array}{c} \text{diagram: 1 ligand bound} \end{array} \right) + \sum_{\text{states}} \left( \begin{array}{c} \text{diagram: 0 ligands bound} \end{array} \right)}$$

$$= \frac{\frac{\Omega^{L-1}}{(L-1)!} e^{-\beta[(L-1)\varepsilon_{\text{sol}} + \varepsilon_b]}}{\frac{\Omega^L}{L!} e^{-\beta L \varepsilon_{\text{sol}}} + \frac{\Omega^{L-1}}{(L-1)!} e^{-\beta[(L-1)\varepsilon_{\text{sol}} + \varepsilon_b]}}$$

$$= \frac{\frac{L}{\Omega} e^{-\beta[\varepsilon_b - \varepsilon_{\text{sol}}]}}{1 + \frac{L}{\Omega} e^{-\beta[\varepsilon_b - \varepsilon_{\text{sol}}]}}$$

Define:  $\Delta\varepsilon = \varepsilon_{\text{sol}} - \varepsilon_b$

$$c(L) = L/V_{\text{box}}$$

# ligands  
system size

saturation:

$$c(L = \Omega) = c_0 = \Omega/V_{\text{box}}$$

$$p_{\text{bound}} = \frac{\frac{c}{c_0} e^{-\beta\Delta\varepsilon}}{1 + \frac{c}{c_0} e^{-\beta\Delta\varepsilon}}$$

Langmuir isotherm

Hill function of coefficient 1

# Statistical mechanics for biophysics

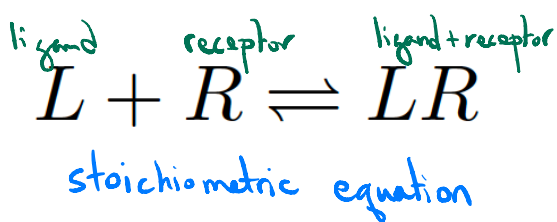
Example: Ligand binding to receptor protein

Microstates: probability

(PB.0.C 6.4.1)

$$p_{\text{bound}} = \frac{\sum_{\text{states}} \left( \begin{array}{|c|} \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \end{array} \right)}{\sum_{\text{states}} \left( \begin{array}{|c|} \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \end{array} \right) + \sum_{\text{states}} \left( \begin{array}{|c|} \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \bullet \bullet \bullet \bullet \bullet \\ \hline \end{array} \right)} = \frac{\frac{c}{c_0} e^{-\beta \Delta \epsilon}}{1 + \frac{c}{c_0} e^{-\beta \Delta \epsilon}}$$

[L] ligand concentration  
:



$$K_d = \frac{[L][R]}{[LR]}$$

dissociation constant

$$p_{\text{bound}} = \frac{[LR]}{[R] + [LR]}$$

substitute:  $[LR] = \frac{[L][R]}{K_d}$

★

$$p_{\text{bound}} = \frac{\frac{[L]}{K_d} \rightarrow 1}{1 + \frac{[L]}{K_d} \rightarrow 1}$$

0.5

⇒  $K_d = c_0 e^{\beta \Delta \epsilon}$

chemistry      stat mech

$p_{\text{bound}} = 0.5$ ,  $c = K_d$

entropy loss = energy gain

# Statistical mechanics for biophysics

Example: Ligand binding to receptor protein

Estimate:  $V_{\text{box}} = 1 \text{ nm}^3$ ;  $c_0 = \frac{1 \text{ molecule}}{\text{nm}^3}$

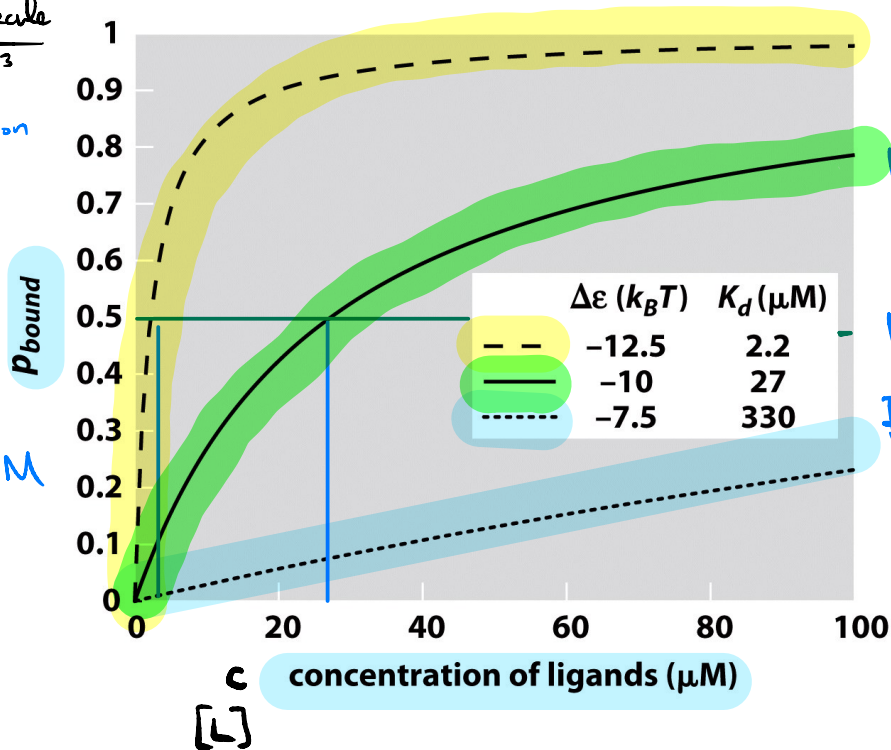
then  $c_0 = \frac{\Omega}{V_{\text{box}}} = \left( \frac{6 \times 10^{23}}{10^{24}} \right)$  *conversion to M*

$= 0.6 \text{ M}$

(Note:  $1 \text{ M} = \frac{6 \times 10^{23} \text{ molecules}}{1000 \text{ cm}^3}$   $\otimes$ )

"saturation" in biochemistry texts:  $\sim 1 \text{ M}$

Receptor occupancy



As  $\Delta\epsilon$  increases, exponential dependence leads to strong selection of binding partners.

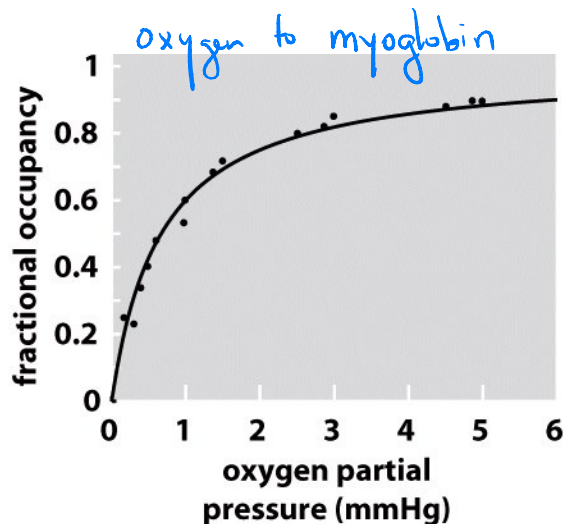
Point mutations can lead to major changes in cell behaviors.

# Statistical mechanics for biophysics

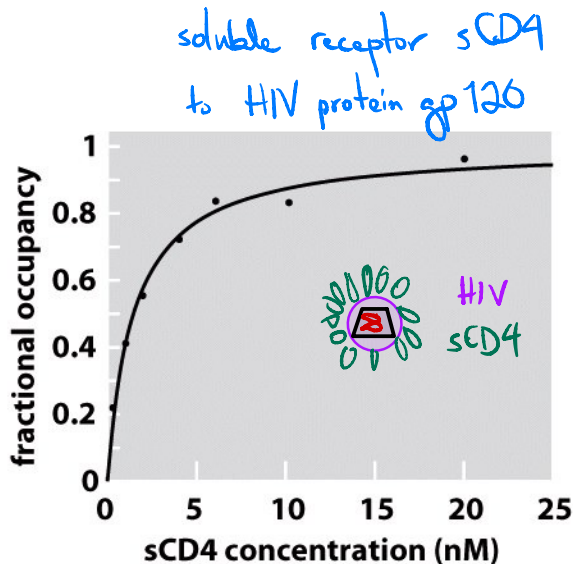
Example: Ligand binding to receptor protein

## Receptor occupancy

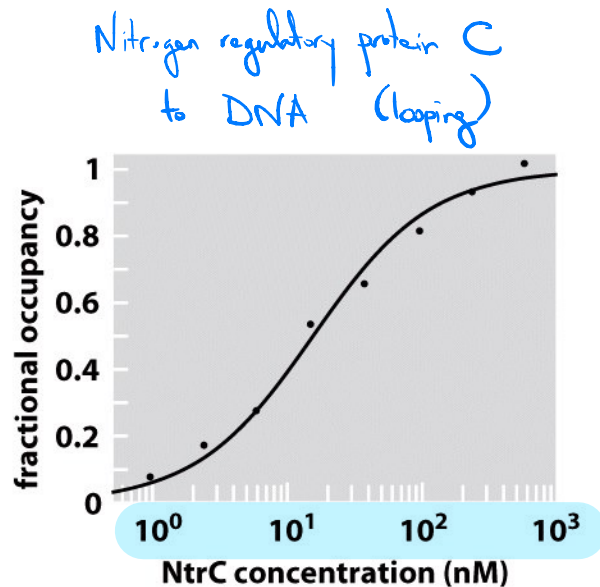
Experimental data



$$c_0 = 1 \text{ atm} = 760 \text{ mmHg}$$
$$\Rightarrow \epsilon \approx -7.04 k_B T$$



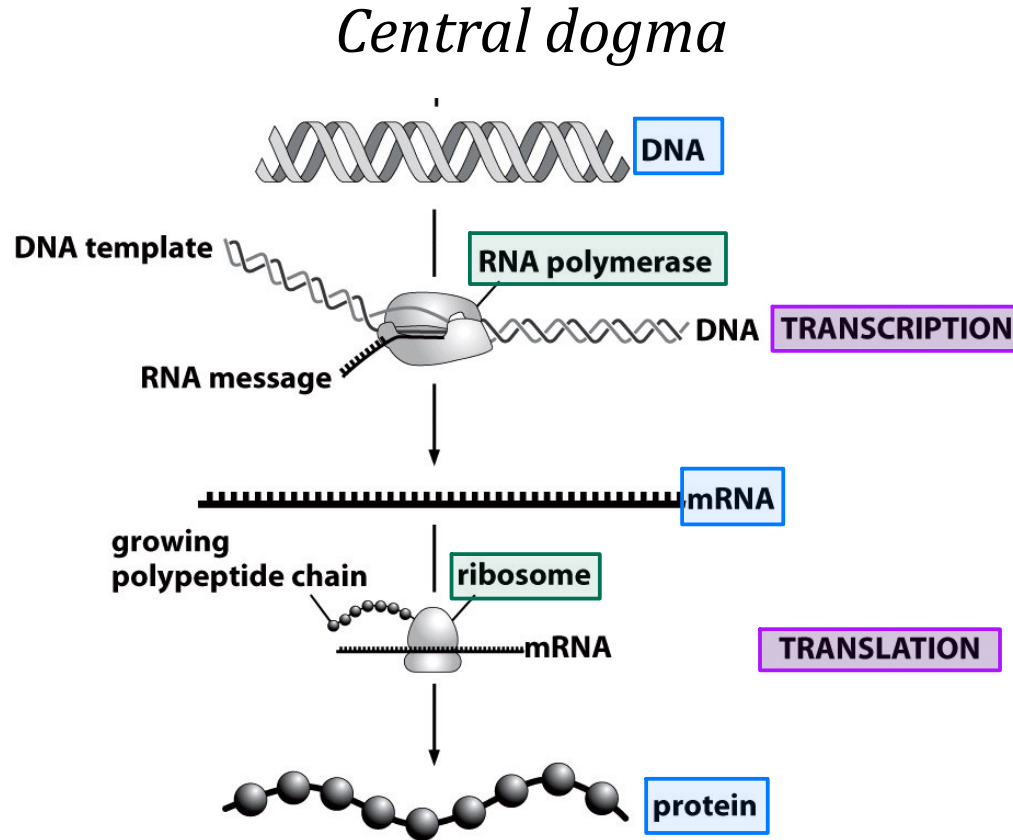
$$c_0 = 0.6 \text{ M}$$
$$\Rightarrow \epsilon \approx -19.84 k_B T$$



$$c_0 = 0.6 \text{ M}$$
$$\epsilon \approx -17.47 k_B T$$

# Statistical mechanics for biophysics

Previously :



polymer languages

processes

molecular machines



# Statistical mechanics for biophysics

*How do cells make decisions?*

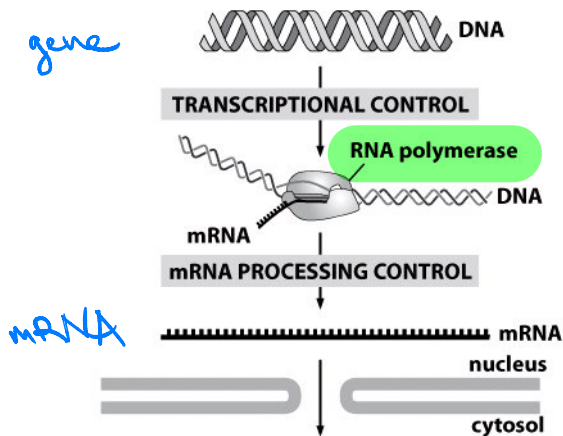
*How can different cells in an organism  
maintain different protein concentrations?*

Example: Soil-dwelling amoeba, *Dictyostelium discoideum*

Vegetative, aggregation, migration, culmination

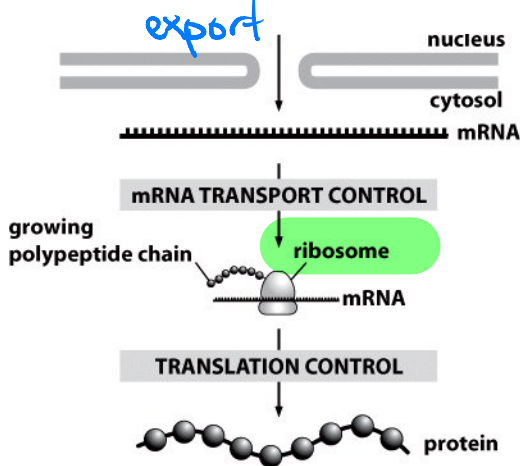
# Statistical mechanics for biophysics

Will the cell make a particular mRNA?



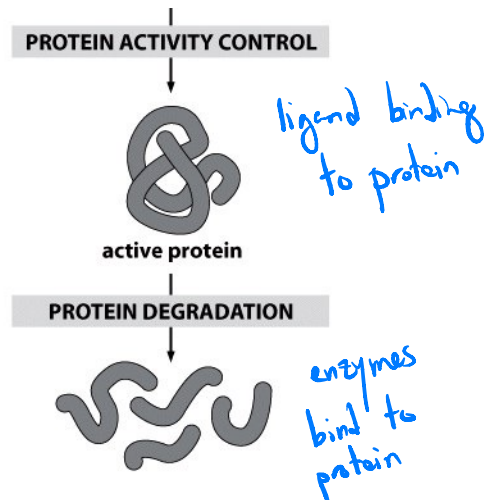
Will an mRNA be processed to become mature?

Will an mRNA be transported to the cytoplasm?



Will an mRNA be translated by the ribosome?

Will a protein exist in an active conformation?



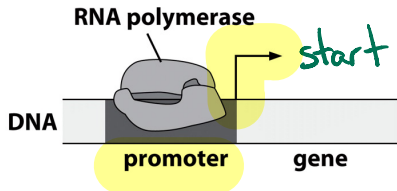
How long will a protein last before being degraded?

# Statistical mechanics for biophysics

Will the cell make a particular mRNA?

Example: Transcriptional control

*Simple case, direct binding*



## Lattice model

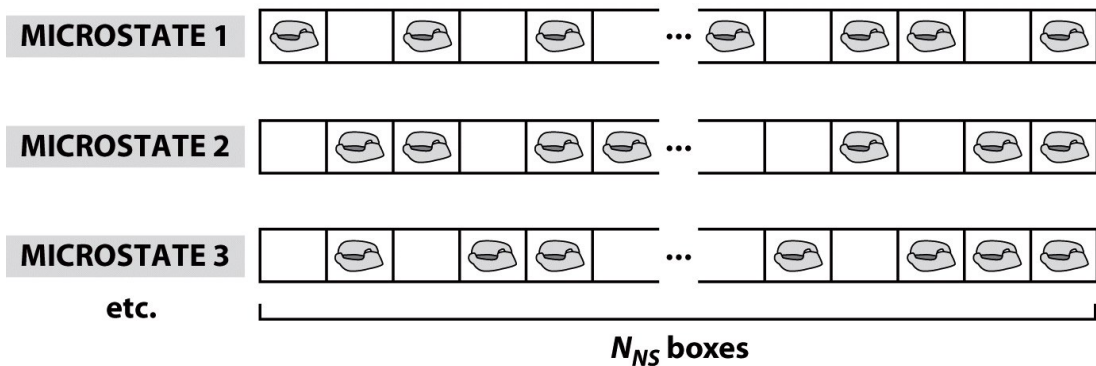
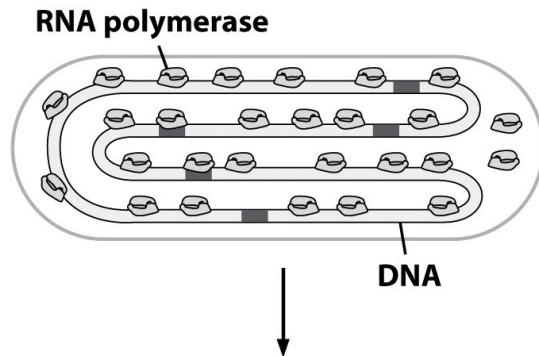
$P$  RNA polymerases

$N_{NS}$  boxes

max. one RNAP per box

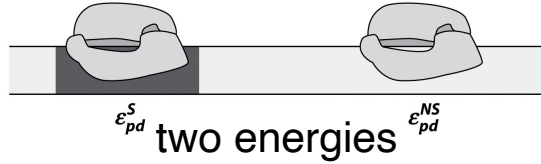
assume all are bound

## Microstates



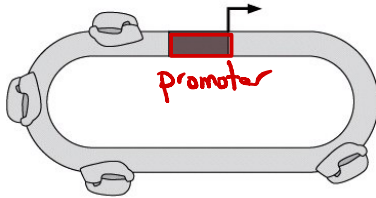
# Statistical mechanics for biophysics

## Example: Transcriptional control



## Microstates

promoter  
not bound

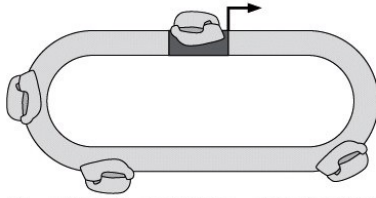


$$P \epsilon_{pd}^{NS}$$

$$\frac{N_{NS}!}{P! (N_{NS} - P)!} \approx \frac{(N_{NS})^P}{P!}$$

$$\frac{(N_{NS})^P}{P!} e^{-P \epsilon_{pd}^{NS} / k_B T}$$

promoter  
bound



$$(P-1) \epsilon_{pd}^{NS} + \epsilon_{pd}^S$$

$$\frac{N_{NS}!}{(P-1)! [N_{NS} - (P-1)]!} \approx \frac{(N_{NS})^{P-1}}{(P-1)!}$$

$$\frac{(N_{NS})^{P-1}}{(P-1)!} e^{-(P-1) \epsilon_{pd}^{NS} / k_B T} e^{-\epsilon_{pd}^S / k_B T}$$

# Statistical mechanics for biophysics

Example: Transcriptional control

*Microstates: probability*

$$p_{\text{bound}} = \frac{\sum_{\text{states}} \left( \text{Diagram of DNA with } P \text{ proteins bound to a promoter} \right)}{\sum_{\text{states}} \left( \text{Diagram of DNA with } P \text{ proteins bound to a promoter} \right) + \sum_{\text{states}} \left( \text{Diagram of DNA with } P \text{ proteins bound to a non-specific site} \right)}$$

$$= \frac{\frac{N_{NS}^{P-1}}{(P-1)!} e^{-\beta[(P-1)\epsilon_{NS} + \epsilon_S]}}{\frac{N_{NS}^P}{P!} e^{-\beta P \epsilon_{NS}} + \frac{N_{NS}^{P-1}}{(P-1)!} e^{-\beta[(P-1)\epsilon_{NS} + \epsilon_S]}}$$

$$= \frac{\frac{P}{N_{NS}} e^{-\beta \Delta \epsilon}}{1 + \frac{P}{N_{NS}} e^{-\beta \Delta \epsilon}}$$

Define:  $\Delta \epsilon = \epsilon_{NS} - \epsilon_S$

$$= \frac{1}{\frac{N_{NS}}{P} e^{\beta \Delta \epsilon} + 1}$$

Langmuir isotherm

Hill function of coefficient 1

# Statistical mechanics for biophysics

## Example: Transcriptional control

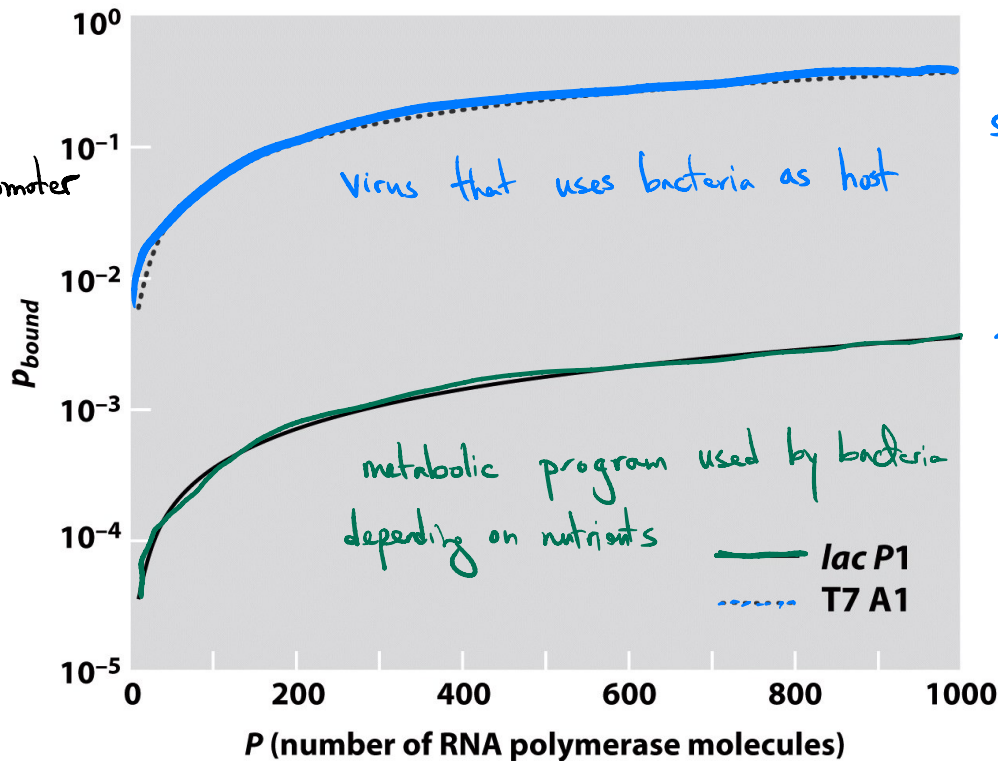
Estimate:

$\Delta\epsilon = -2.9 k_B T$  E. coli *lac P1* promoter

$\Delta\epsilon = -8.1 k_B T$  bacteriophage T7 promoter

~5000 RNA polymerase in E. coli

## RNA polymerase occupancy



robust,  
strong  
response

flexible  
response

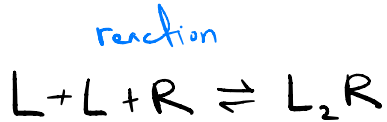
"hijacking" resources of host  
make it much more likely  
to transcribe pathogen genes  
than own genes.

# Statistical mechanics for biophysics

## Cooperativity

(P.B.C 6.4.3)

concentration  
Analog signal  $\rightarrow$  on/off  
digital output



equilibrium  
dissociation constant

$$K_d = \frac{[L]^2 [R]}{[L_2R]}$$

$$\Rightarrow [L_2R] = \frac{[L]^2 [R]}{K_d}$$

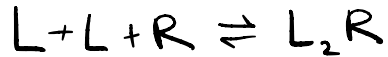
# Statistical mechanics for biophysics

## Cooperativity

(PB.C 6.4.3)

concentration  
Analog signal → on/off  
digital output

reaction



equilibrium  
dissociation constant

$$K_d = \frac{[L]^2[R]}{[L_2R]}$$

$$\Rightarrow [L_2R] = \frac{[L]^2[R]}{K_d} \quad \text{⊗}$$

probability of binding

$$P_{\text{bound}} = \frac{[L_2R]}{[R] + [L_2R]} \quad \text{⊗} = \frac{[L]^2}{K_d^2 + [L]^2}$$

$$= \frac{\left(\frac{[L]}{K_d}\right)^2}{1 + \left(\frac{[L]}{K_d}\right)^2} \quad \text{Hill function with coefficient } n=2$$



# Statistical mechanics for biophysics

## Cooperativity

(PB.C 6.4.3)

concentration  
Analog signal → on/off  
digital output

probability of binding

$$P_{\text{bound}} = \frac{[L_2 R]}{[R] + [L_2 R]} = \frac{[L]^2}{K_d^2 + [L]^2}$$
$$= \frac{([L]/K_d)^2}{1 + ([L]/K_d)^2}$$

Hill function  
with coefficient  
 $n=2$

In general, for  $n^{\text{th}}$  degree cooperativity

$$P_{\text{bound}} = \frac{([L]/K_d)^n}{1 + ([L]/K_d)^n} = \frac{\left(\frac{c}{c_0} e^{-\beta \Delta \varepsilon}\right)^n}{1 + \left(\frac{c}{c_0} e^{-\beta \Delta \varepsilon}\right)^n}$$

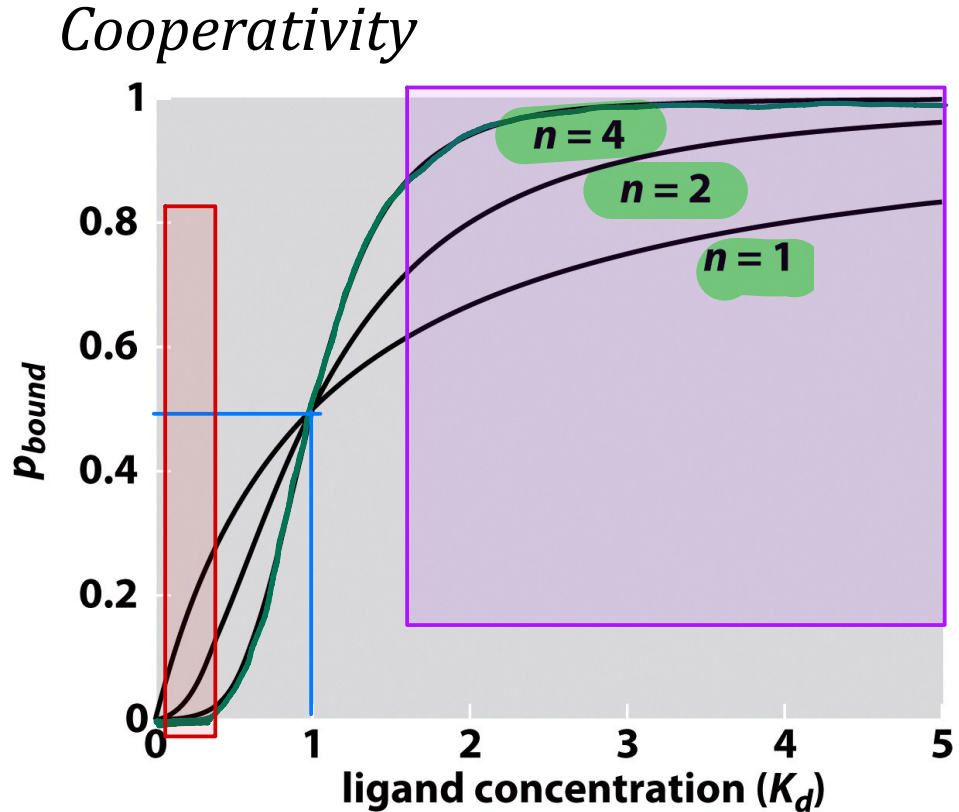
Hill function  
with coefficient  $n$

# Statistical mechanics for biophysics

Binding curves  
with different Hill  
coefficients

higher  $n \rightarrow$  more switch-like  
binding response

"on" state and "off" state  
very narrow in-between range






(Chapter 7)

Case study in cooperativity: toy model for hemoglobin, "dimoglobin"

$N$  oxygen molecules,  $\Omega$  boxes,  $\epsilon_{sol}$ ,  $\epsilon_b$ ,  $J$  cooperativity energy

two  
oxygen  
binding  
sites




<u>State</u>	<u>Energy</u>	<u>Multiplicity</u>	<u>Weight</u>
			$P_0$
			$P_1$
			$P_2$

Write down  $P_2$ , probability that both sites are bound.

What is the average occupancy  $\langle N \rangle$ ?

(Chapter 7)




Case study in cooperativity: toy model for hemoglobin, "dimoglobin"

	<u>State</u>	<u>Energy</u>	<u>Multiplicity</u>	<u>Weight</u>
two oxygen binding sites		$N \epsilon_{sol}$	$\Omega^N / N!$	$\frac{\Omega^N}{N!} e^{-\beta N \epsilon_{sol}}$
		$(N-1) \epsilon_{sol} + \epsilon_b$	$\Omega^{N-1} / (N-1)!$	$\frac{\Omega^{N-1}}{(N-1)!} e^{-\beta [(N-1) \epsilon_{sol} + \epsilon_b]}$
		$(N-2) \epsilon_{sol} + J + 2 \epsilon_b$	$\Omega^{N-2} / (N-2)!$	$\frac{\Omega^{N-2}}{(N-2)!} e^{-\beta [(N-2) \epsilon_{sol} + J + 2 \epsilon_b]}$

Write down  $P_2$ , probability that both sites are bound.

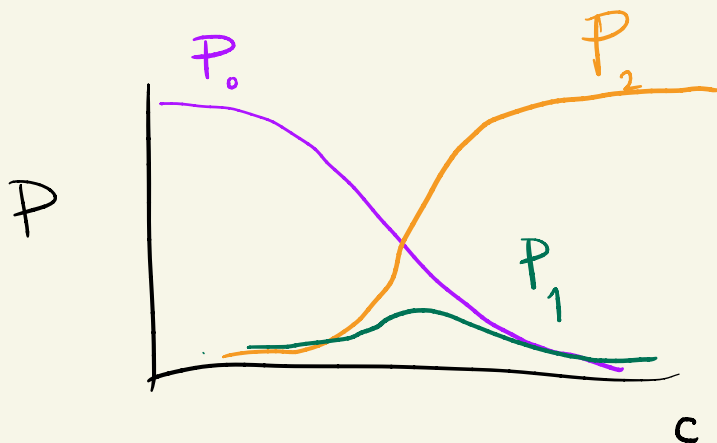
What is the average occupancy  $\langle N \rangle$ ?

Case study in cooperativity: toy model for hemoglobin, "dimoglobin"

- State
- 
  - 
  - 

$$P_2 = \frac{\frac{N(N-1)}{2} e^{-\beta(J + 2\varepsilon_b - 2\varepsilon_{sol})}}{1 + 2 \frac{N}{2} e^{-\beta(\varepsilon_b - \varepsilon_{sol})} + \frac{N(N-1)}{2} e^{-\beta(J + 2\varepsilon_b - 2\varepsilon_{sol})}}$$

$$\approx \frac{\left(\frac{c}{c_0}\right)^2 e^{-\beta(J + 2\Delta\varepsilon)}}{1 + 2 \frac{c}{c_0} e^{-\beta\Delta\varepsilon} + \left(\frac{c}{c_0}\right)^2 e^{-\beta(J + 2\Delta\varepsilon)}}$$



$$\langle N \rangle = P_1 + 2P_2$$

# Lecture 6: Entropy rules

## Summary

### Models

- Lattice model with microcanonical ensemble requires states, energies, Boltzmann weights
- Lattice model can be used to calculate

Probability of energy states, Average values

- Cooperativity can be described by a Hill function, with  $n$  the degree of cooperativity.

### Interpretation

$> 10 \times$

- Strong binding ( $|\epsilon| \gg k_B T$ ) means higher occupancy at low concentration, long-lived
- Weak binding ( $|\epsilon| > k_B T$ ) makes for low occupancy, short-lived states
- Cooperativity doesn't change  $K_d$ , but changes shape of curve.
- Receptor proteins binding to ligands can start a chain of events (signaling), or block
- Each part of the central dogma relies on binding

# Lecture 7: Two-state system, ion channels

Goal: Statistical mechanics modeling. Compute the probability of microstates, including applied forces.

- Two-state system
- Mechanosensitive ion channels

PBOC Chapter 7.1.2, 11.5