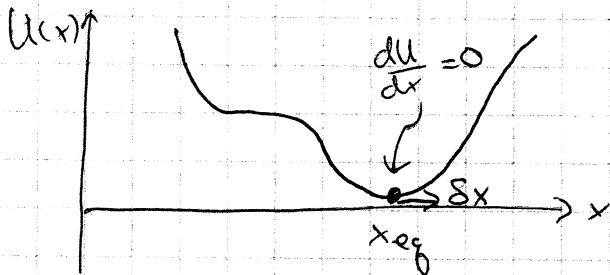


Mechanical Energy Revisited:

- Recall that we said that a structure would come to mechanical equilibrium when $\Sigma \vec{F} = 0$ or conversely $\frac{dU(x)}{dx} = 0$



Q: What is the energy of the structure near ~~eq~~ x_{eq} ?

- For small deformations from equilibrium, δx , we can expand $U(x)$ in a Taylor series

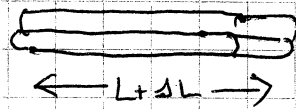
$$\begin{aligned}
 U(x_{eq} + \delta x) &\approx U(x_{eq}) + \underbrace{\frac{dU}{dx}}_{=0} \Big|_{x_{eq}} \delta x + \frac{1}{2} \frac{d^2U}{dx^2} \Big|_{x_{eq}} \delta x^2 \\
 &= U(x_{eq}) + \frac{1}{2} \frac{d^2U}{dx^2} \Big|_{x_{eq}} \delta x^2
 \end{aligned}$$

- This has the form $U(x) = \frac{1}{2} k x^2$ where the spring constant $k = \frac{d^2U}{dx^2}$
- Thus, near the equilibrium position, the structure behaves like a simple spring \equiv elastic media
e.g.: lipid membrane, DNA elasticity, actin filaments

Stress & Strain:

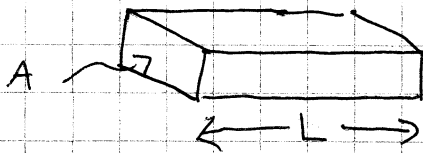


→
stretch

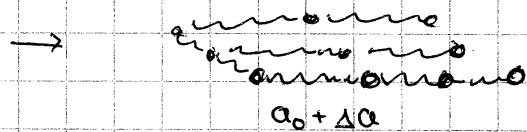
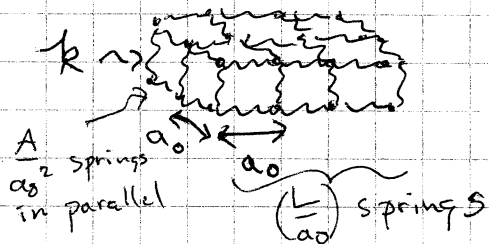
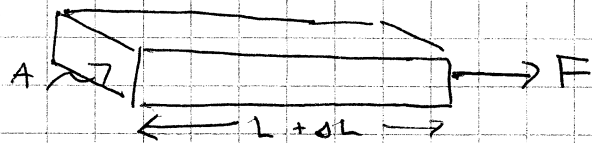


e.g. DNA

- Near equilibrium (i.e. for "smallish" ΔL) behaves like a bunch of springs



→
stretch



- Strain: $\epsilon = \frac{\Delta L}{L}$ stress: $\sigma = \frac{F}{A}$

- Hook's law for elastic materials:

$$\sigma = E \epsilon$$

where

$E \equiv$ young's modulus

- Derivation from microscopic view:

- The force F is balanced by the N springs of the face in parallel, so

$$N k \Delta a = F \quad \text{and} \quad N = \frac{A}{a_0^2}$$

so
$$\Delta a = \frac{F}{k} \frac{a_0^2}{A}$$

• All springs stretch the same extension, Δa along the beam, so the total extension ΔL is:

$$\Delta L = \left(\frac{L}{a_0} \right) \Delta a = \left(\frac{L}{a_0} \right) \frac{F}{k} \frac{a_0^2}{A}$$

• Rewriting into Hook's law:
$$\frac{F}{A} = \left(\frac{k}{a_0} \right) \frac{\Delta L}{L}$$

$$\underbrace{\hspace{1.5cm}}_E \quad \quad \quad \underbrace{\hspace{1.5cm}}_E$$

• so microscopically: $E = \frac{k}{a_0}$ ← bond spring
 ← bond length

Elastic Energy (used later in course):

$$E_{\text{strain}} = \frac{EA}{2} \int_0^L \left(\frac{\Delta L}{L} \right)^2 dx = \frac{EA}{2} \int_0^L \left(\frac{d\delta(x)}{dx} \right)^2 dx$$

non-uniform stretch
↓

≡ quadratic cost in displacement.

~~Energy of a spring is $\frac{1}{2} k x^2$ and the energy of a beam is $\frac{EA}{2} \int_0^L \left(\frac{d\delta(x)}{dx} \right)^2 dx$~~

An Intro To Entropy:

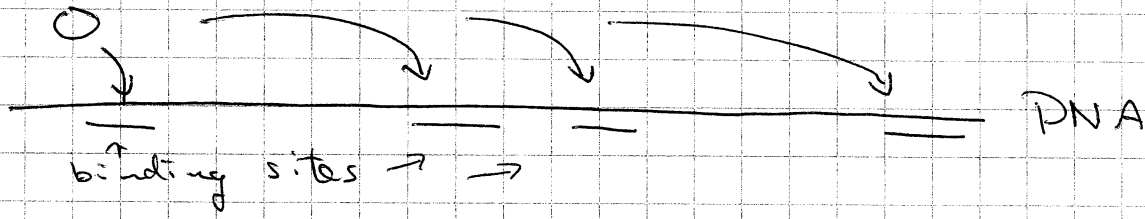
• Disorder $\equiv S \propto$ # of states available

• Boltzmann: $S = k_B \ln W$

where

$W =$ # of states (degeneracy) for a system with energy E

e.g. Entropy of Protein binding to DNA

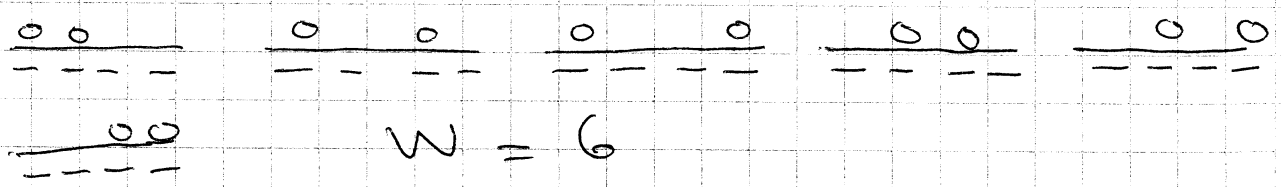


• Protein binding to DNA on a binding site gains energy E

Ⓐ 1 site bound: $E_{tot} = -E$; $S = k_B \ln 4$



Ⓑ 2 sites bound: $E_{tot} = -2E$ $S = k_B \ln 6$



etc.

5

General Result for N_p occupied sites out of N sites:

- Combinations - N sites choose N_p
- Talk it through

- 1) N choices for first protein
- 2) $(N-1)$ " " 2nd protein
- ⋮
- N_p) $(N - N_p + 1)$ " " N_p protein

$$= N \cdot (N-1) \cdot (N-2) \cdots (N - N_p + 1) \text{ arrangements}$$

- However we have double counted - arrangements are not distinguishable, need to divide by the # of arrangements of the N_p sites
- Talk it through:

- 1) N_p positions for 1st occupied site
- 2) $N_p - 1$ " " 2nd " "
- ⋮
- N_p) 1 " " last " "

$$= N_p \cdot (N_p - 1) \cdot (N_p - 2) \cdots 1$$

So

$$W = \frac{N(N-1) \cdots (N - N_p + 1)}{N_p(N_p - 1) \cdots 1}$$

$$W = \frac{N!}{N_p!(N - N_p)!}$$

- this is the # of combinations of N_p objects selected out of N objects with no ordering (May have seen this in a Stats course)

Aside: Hat full of letters A, B, C, D, E, F (N=6)

- Select $N_p = 3$ letters

\Rightarrow ADC, CAD, ACD, ...

we don't care about the ordering

\Downarrow
ACD

Entropy is found via $S = k_B \ln W$

so

$$S = k_B \ln \frac{N!}{N_p!(N-N_p)!}$$

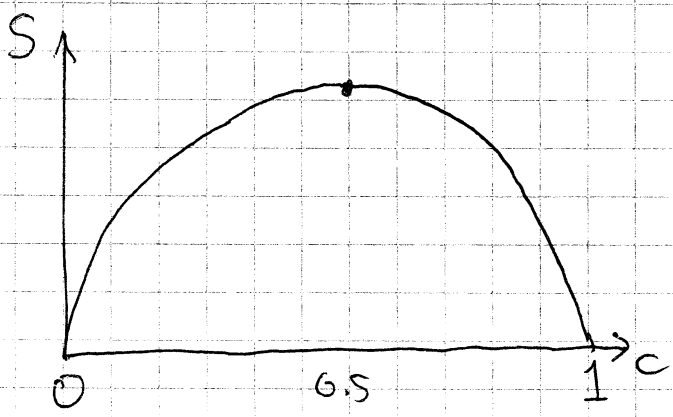
• Now N is large $\sim 5 \times 10^6$ for E. coli (# of bp)
so we can make an approximation

Stirling $\Rightarrow \ln N! \approx N \ln N - N$

• So (work the following out):

$$S = -k_B N [c \ln c + (1-c) \ln(1-c)]$$

where $c = \frac{N_p}{N}$



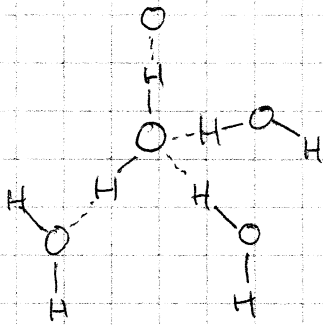
• For this system the entropy is at a maximum when $\frac{1}{2}$ the sites are occupied

\Rightarrow this corresponds to the most configurations

• Entropy and Hydrophobicity:

IDEA: when a hydrophobic molecule is placed in water, the water molecules lose some of their configurations \rightarrow lose entropy

- water consists of a network of hydrogen bonded H_2O molecules



- A single H_2O molecule can form ≈ 4 hydrogen bonds \rightarrow tetrahedron

- H_2O molecules ~~is~~ ^{is} continually forming and breaking H-bonds with their 4 neighbours

- 6 Configurations for H_2O in tetrahedron (see Fig)
- If one of the sites of the tetrahedron is replaced by a non-polar molecule, the # of available configurations drops to 3!
- Entropy change due to addition of non-polar molecule

$$\Delta S_{\text{hydro}} = \underbrace{k_B \ln 3}_{\text{constrained } H_2O} - \underbrace{k_B \ln 6}_{\text{unconstrained } H_2O} = -k_B \ln 2$$

- Thus there is an entropy loss which costs free energy

$$\Delta F_{\text{hydro}} = n k_B T \ln 2$$

where n is the # of displaced H_2O molecules

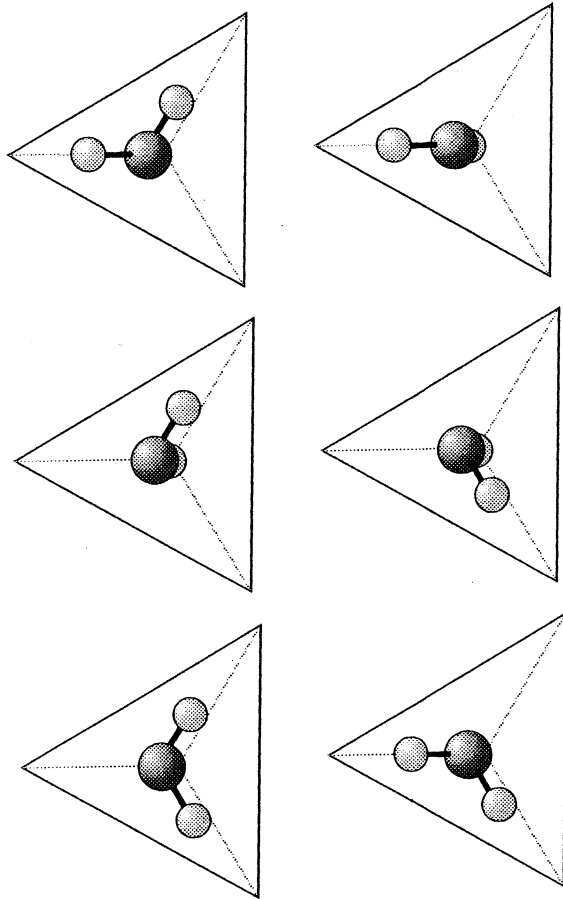
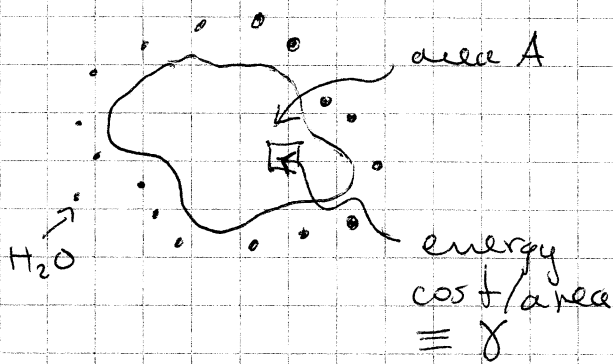


Figure 5.26: Orientations of water molecules in a tetrahedral network. Each image shows a different arrangement of the water molecule that permits the formation of hydrogen bonds with neighboring water molecules. The hydrogen bonds are in the directions of the vertices that are *not* occupied by hydrogens in the figure. (Adapted from K. Dill and S. Bromberg, *Molecular Driving Forces*, New York, Garland Press, 2003.)

that the free energy cost to embed a given hydrophobic molecule in water is

• Can recast in terms of area of hydrophobic molecule



• # of H_2O molecules affected \propto Area, A

• hydrophobic energy cost per area = γ

• so $\Delta F_{hydro} = \gamma A$

• Some #'s: for $1 \text{ nm}^2 \rightarrow 10 \text{ H}_2\text{O}$ molecules

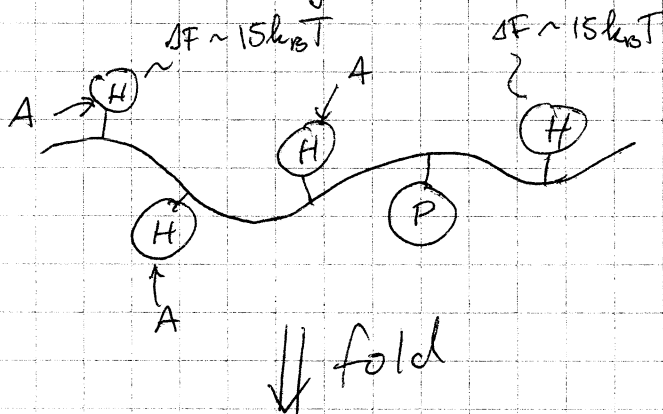
so $\gamma = 10 \frac{k_B T \ln 2}{\text{nm}^2} \approx 7 \frac{k_B T}{\text{nm}^2}$

• for an O_2 molecule in H_2O , $A \approx 0.15 \text{ nm}^2$

so $\Delta F \approx 1 k_B T$

Thus dissolving O_2 in H_2O is easy

Hydrophobicity drives Protein Folding:



• when unfolded, each "H" hydrophobic amino acid costs $\sim 15 k_B T$ of energy

• So, hydrophobic parts condense such that their exposed area is less

