



General tutorial session #5:

SPACE, TIME, AND ENERGY
LANDSCAPE IN MECHANOBIOLOGY



08 / 11 / 2006

Molecular forces

Wonnuk Hwang

but first ☺

Funding opportunities at National Science Foundation

Jimmy Hsia

jhsia @ nst. gov

- new opportunities . nano- and bio- mechanics and materials submission windows 09/01 - 10/01/2006 and 02/15 - 03/15/07
- newer opportunities . partnerships for international research & education due 10/30/2006 to support 14-17 projects, \$ 2.5 M each.
- newest opportunities . East Asia and Pacific summer institutes for U.S. citizens for students in Australia, China, Japan, Korea, Taiwan .
 . emerging frontiers in research and innovation (EFRI) crosscutting & disciplinary areas.
 2006 was the program's first year : 16 proposals
 topics for 2007 solicitation : (1) autonomously reconfigurable engineered systems enabled by Cyberinfrastructure, (2) cellular and biomolecular engineering

- Basic considerations

Generalized force as free energy gradient $f = - \frac{\partial E}{\partial x}$ or, in vector form $\vec{F} = - \vec{\nabla} E$

1. what is the radial dependence of \vec{F} , U ?

2. what is the interaction range of \vec{F} ?

3. " " " energy implied by \vec{F} ?

and use U as potential energy (for E)

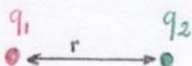
Types of intermolecular interactions : ① electrostatic (ES), ② Van der Waals / steric
 ③ hydrogen bonding, ④ hydrophobic

① electrostatic

$$U_{ES}(r) = \frac{1}{4\pi\epsilon_0 E} \cdot \frac{q_1 q_2}{r}$$

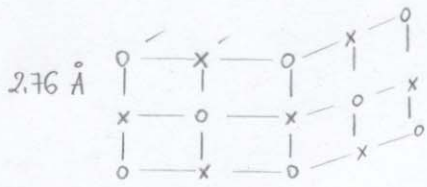
with $\epsilon_0 = 8.89 \times 10^{-12} \text{ C}^2/\text{J}\cdot\text{m}$

$\epsilon = \begin{cases} 1 & \text{(air)} \\ 80 & \text{(water)} \end{cases}$ dielectric constant



Space, time and energy scales in mechanobiology - 2.

ex: sodium chloride NaCl



$$q_{Na} = -q_{Cl} = e = 1.6 \times 10^{-19} \text{ C}$$

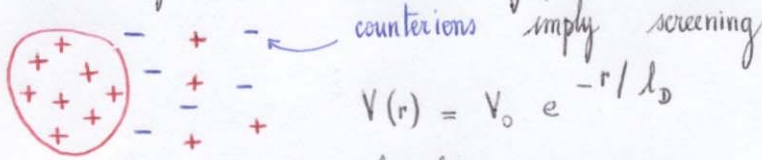
$$U_{NaCl} = 120 \text{ kcal/mol}$$

thermal energy as energy ruler
 $P(E) \propto \exp\left(\frac{-E}{k_B T}\right)$

a salt NaCl crystal is stable at room temperature
 but in water $U_{NaCl} = \frac{120}{80} = 1.5 \text{ kcal/mol} > k_B T \Rightarrow$ salt dissolves

at $T = 300 \text{ K}$, $k_B T \approx 0.59 \text{ kcal/mol}$
 $E \gg k_B T$ is unlikely while $E \ll$ is probable

electrostatic screening: in an electrolyte solution where a charged group is buried



$$V(r) = V_0 e^{-r/l_D}$$

electrolyte $i = 1, 2, 3, \dots$

of bulk concentration $\rho_{\infty i}$
 of valency z_i (with $z_{Na} = +1$)

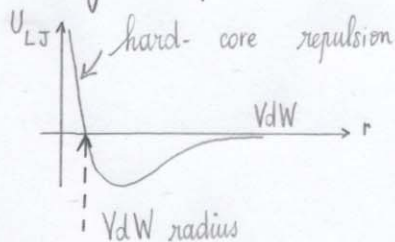
the Debye length is $l_D = \frac{1}{\sqrt{\sum_i \rho_{\infty i} \frac{z_i^2 e^2}{\epsilon_0 \epsilon k_B T}}}$

(no screening at high T from agitation!)

ex: $[NaCl] = 1 \text{ mM}$ $l_D = 9.6 \text{ nm}$ and in pure water at $pH = 7$ (10^{-7} M)
 1 M $l_D = 3 \text{ \AA}$ $l_D = 960 \text{ nm} \sim 1 \mu\text{m}$

② Van der Waals / steric interactions

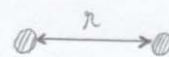
Lennard Jones potential $U_{LJ}(r) = A \left[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^6 \right]$



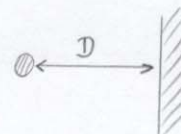
* steric: strong, short-ranged.
 • VdW

VdW with surfaces

$$VdW \sim \frac{1}{r^6}$$



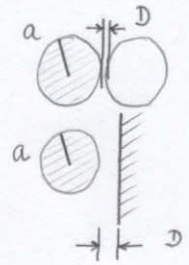
$$VdW \sim \frac{1}{D^3}$$



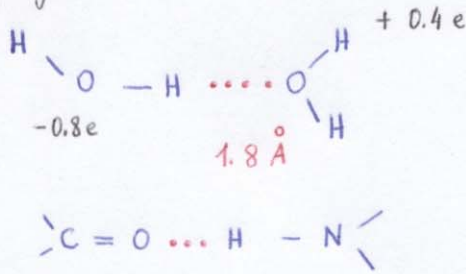
Space, time, and energy scales in mechanobiology - 3.

VdW with spheres $VdW \sim \frac{1}{D^3}$ if $a \gg D$

VdW can matter at macroscopic scales, by walls.



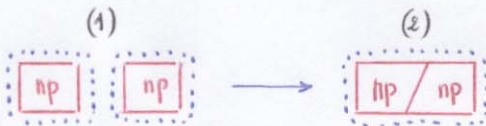
③ Hydrogen bonds



{ short - ranged
 directional
 accounts for specificity of protein structure

Compare energies { $U_{H-bond} \sim 3-9$ kcal/mol
 $U_{VdW} \sim 0.24$
 $U_{ATP \text{ hydrolysis}} \sim 14$
 $U_{covalent \ bond} > 100$

④ hydrophobicity : water around nonpolar molecules forms a network of hydrogen bonds = "clathrate"



(2) entropically preferable because less order

hydrophobic interaction is attractive entropic

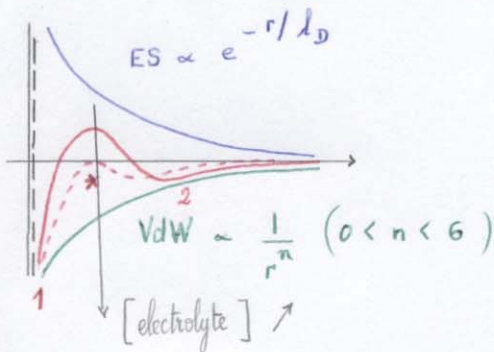
long - ranged (~ 10 nm)

it is also { proportional to solvent-accessible surface area of nonpolar groups
 = surface-tension driven γ

$\gamma \sim 72$ mJ/m² (air) or 50 mJ/m² (H-carbons), relative to water
 ~ 80 cal/mol. Å² geometry-dependent

DLVO

most interactions above are attractive, insensitive to electrolytes : VdW, H-bonds
 but ES interaction is repulsive, and sensitive to electrolytes.



* critical coagulation concentration \rightarrow aggregation
 1, 2 primary & secondary minima

Thermal forces and Brownian motion

Ju Li

- add random variables:

$$Y = X_1 + X_2 + \dots + X_N$$

$$\bar{y} = \langle Y \rangle \equiv E[Y] = E[X_1] + E[X_2] + \dots + E[X_N]$$

$$\text{var}[Y] \equiv \langle (Y - \langle Y \rangle)^2 \rangle = \text{var}[X_1] + \dots + \text{var}[X_N]$$

$$E[(Y - E[Y])^2] = N \text{var}[X]$$

from linearity of operator: $y = \frac{Y}{N}$, $E[y] = \frac{E[Y]}{N} = E[X]$
 average becomes more deterministic $\text{var}[y] = \frac{\text{var}[Y]}{N^2} = \frac{N \text{var}[X]}{N^2} \xrightarrow{N \rightarrow \infty} 0$
 as more samples

- X may be sampled by probability density

the central limit theorem states that, irrespective of the shape of X, Y is Gaussian

$$\rho(y) \rightarrow \frac{1}{\sqrt{2\pi N \sigma_x^2}} \exp\left(-\frac{(y - N E[Y])^2}{2 N \sigma_x^2}\right)$$

if you convolute 2 Gaussians, you get Gaussian \Rightarrow attractor shape

- diffusion equation (1D): $\partial_t \rho = -\partial_x (-D \partial_x \rho) = D \partial_x^2 \rho$
 random walk motion of step $\pm a$

at $t=0$ initial conditions known \Rightarrow position = delta function δ

$$x(t) = 0 + \Delta x_1 + \dots + \Delta x_{t/\Delta t}$$

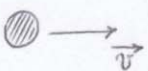
$$E[x(t)] = 0 \text{ on average}$$

but spread now $\text{var}[x(t)] = \frac{t}{\Delta t} \text{var}[\Delta x^2] = \nu t a^2$ with $\frac{1}{\Delta t} = \nu$

$$\rho(x(t)) = \frac{1}{\sqrt{2\pi 2Dt}} \exp\left(-\frac{x^2}{2 2Dt}\right) \text{ by identifying } D \equiv \frac{\nu a^2}{2}$$

parabolic kinetics

Green's function solution to diffusion equation.

- Brownian motion:  $F_{\text{drag}} = -6\pi \eta r v = -\lambda v = m \dot{v}$

if $v(0) = v_0$, $v(t) = v_0 e^{-\frac{\lambda t}{m}} \xrightarrow{t \rightarrow +\infty} 0$

contradicts equipartition theorem $\langle \frac{mv^2}{2} \rangle = \frac{k_B T}{2}$

problematic!

Space, time, and energy scales in mechanobiology - 5.

Einstein: there is not only a dissipative force (drag) but also stimulative force (at microscopic scale).

$$m \dot{v} = F_{\text{diss}} + F_{\text{stim.}} = \text{fluctuation} = -\lambda v + F_{\text{fluct.}}(t)$$

$$\langle F_{\text{fluct.}}(t) \rangle = 0$$

$$\langle F_{\text{fluct.}}(t) F_{\text{fluct.}}(t') \rangle = b(t-t') = B \delta(t-t') \quad \text{white noise}$$

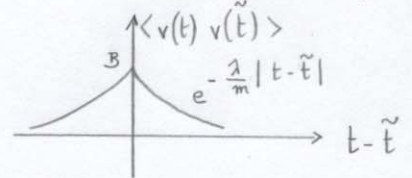
$$v(t) = \frac{1}{m} \int_{-\infty}^t dt' F_{\text{fluct.}}(t') \exp\left[\frac{-\lambda}{m}(t-t')\right] \quad \text{uncorrelated fluct.}$$

convolution = solution of Langevin equation with noise
 velocity correlation even if white noise: $\langle v(t) \tilde{v}(\tilde{t}) \rangle = (B/2m\lambda) e^{-\lambda/m(t-\tilde{t})}$

$$[B] = \text{force}^2$$

the ratio between square of stimulative force and dissipative force is fixed ($\propto T$)

$$\frac{B}{2\lambda} = k_B T = \text{Einstein's relation}$$



- How do diffusion and Langevin equations match?

$$\langle x^2(t) \rangle = 2Dt$$

$$\frac{d}{dt} \langle x(t)x(t) \rangle = 2D = 2 \langle x(t)v(t) \rangle$$

or

$$D = \langle x(t)v(t) \rangle = \left\langle \int_0^t v(t') dt' \cdot v(t) \right\rangle$$

$$\text{or } D = \int_0^t g(t') dt' : \text{fluctuation-dissipation theorem}$$

$$= \int_0^t \langle v(t)v(t') \rangle dt'$$

$$= \int_0^t \underbrace{\langle v(t')v(0) \rangle}_{\equiv g(t')} dt'$$

valid as $t \rightarrow +\infty$

observation time

$$t \gg \frac{m}{\lambda}$$

larger than molecular time scale

(or macroscopic times)

This fluctuation-dissipation theorem (Green-Kubo formula) has many implications:

- thermal conductivity
- semiconductor's electrical conductivity
- shear viscosity

transport properties equilibrium fluct

$$- D = \lambda k_B T \quad \text{Einstein's relation (no mass)}$$

"Reactions", energy landscapes and kinetics

Pat Doyle

see Pat Doyle's handwritten notes.

Cellular sensing of force and geometry in rigidity responses:
protein unfolding by force

Michael Sheetz

- reverse system engineering approach: what components are responsible for cellular responses?
capability to sense form, rigidity and respond is critical to biology
rapid neuronal sensing is through ion channels, but longer-term responses are cytoskeleton-based
transformation is described as the ability to respond to rigidity and grow

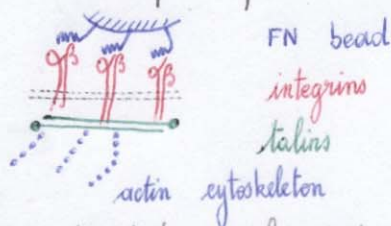
- sensing (geometry & rigidity / force) \rightarrow transduction \rightarrow response (Sheetz - Vogel)
(ms - s) (s) (min, cycles) (Nat. Rev '06)

force causes GFP-paxillin accumulation in RPTP $\alpha +/+$ with fibronectin
reinforcement response mediated by integrins

intracellular / extracellular communication \Rightarrow feedback and integrated response after a few cycles

- early response? and its role?

• spatial distribution of integrins is important for talin binding
timers of integrins \Rightarrow fibronectin strong attachment
2pN slip bond between integrins and cytoskeleton (through talins)



slip bonds \neq catch bonds

• force-dependent reinforcement, where are involved C-Src, vinculin, RPTP α et al.
GFP-paxillin stretch-dependent binding to identify molecules necessary for reinforcement.
can the plasma membrane be removed and the cytoskeleton (CSK) alone show same? yes!

CSK-bound proteins after stretch: { FAK, p130 Cas, PKB / Akt, paxillin
not vinculin (some in vivo & in vitro)

reversible, ATP-independent, mechanical

Space, time and energy scales in mechanobiology - 7.

- measure signaling downstream : $\left\{ \begin{array}{l} \text{G protein activation by csk} \\ \text{Rap1, not Ras, is activated by stretch} \\ \text{Src family kinase phosphorylation of p130 Cas if stretch} \end{array} \right.$

Cas : force transducer since P-Cas correlates with stretch application
protein unfolding or protein distortion responsible for this transduction?

- stretch Cas SD itself? pull a latex surface to uniformly stretch the molecule
- Cas SD phosphorylation requires stretch for c-Src, Fyn, and c-Abl (not Csk) ph.
- unfolding of Cas SD appears to be sufficient and necessary for its phosphorylation
(SD = substrate domain of Cas)

unfolded & phosphorylated Cas is at the periphery of cells (as assessed by Ab stain)

- titin domains unfold as expected for a force sensor (~ 200 pN per unf. event)
hydrogen bonds critically important to dictate unfolding forces & properties
- graded force sensor in one single molecule: domains structure is key concept
(same with FN - Viola Vogel's work)

"Reactions", Energy Landscapes & Kinetics

Pat Doyle
pdoyle@mit.edu
Chemical Engineering Dept.
MIT



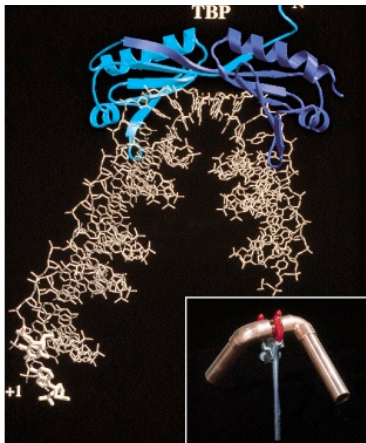
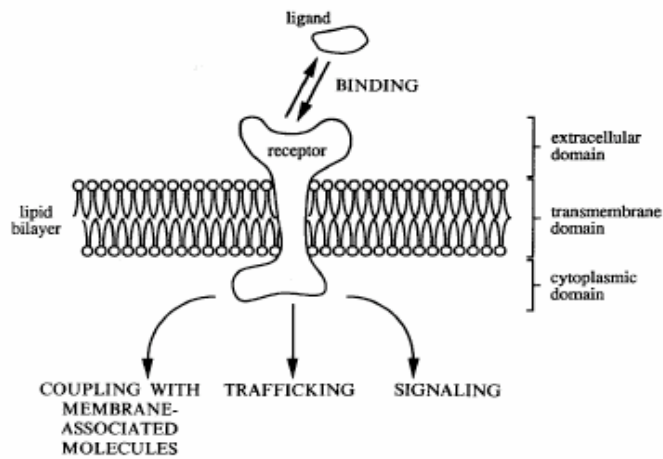
GEM4 Summer School 2006
Cell and Molecular Mechanics in BioMedicine
August 7–18, 2006, MIT, Cambridge, MA, USA

Key References

- *Mechanics of Motor Proteins & the Cytoskeleton*, J. Howard
- *Biophysical Chemistry*, C. Cantor and P. Schimmel
- *Mechanical Processes in Biochemistry*, Bustamante *et al.*, *Ann. Rev. Biochem.*, **73**, 705-748, 2004
- *Brownian Motion in a Field of Force and the Diffusion Model of Chemical Reactions*, H.A. Kramers, *Physica*, **4**, 284-304, 1940

"Reactions"

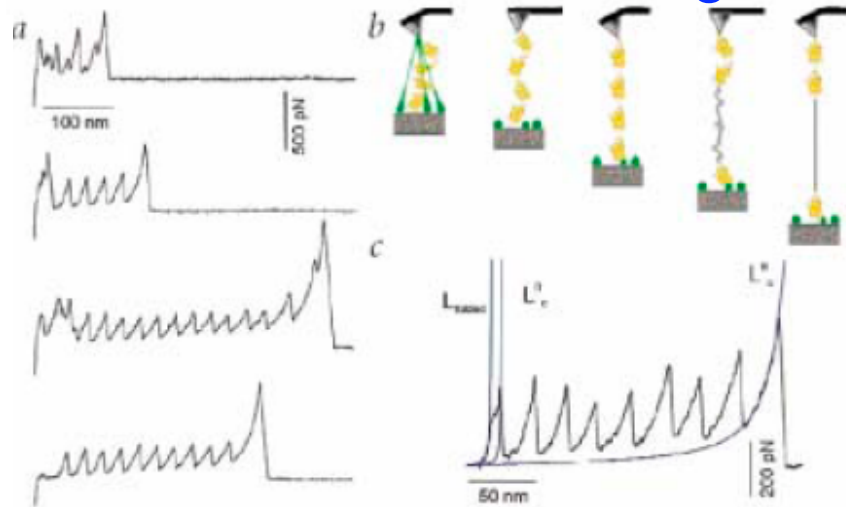
Receptor-ligand



Binding of TAT box-binding protein

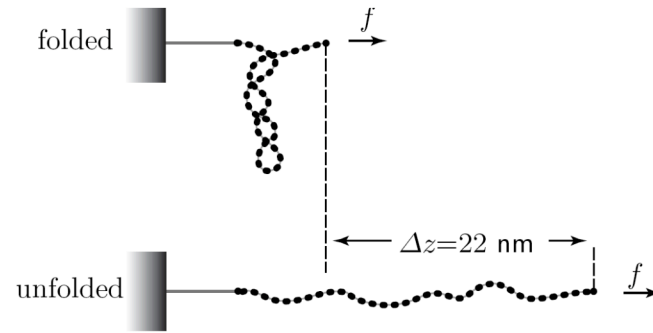
DNA-protein

Titin unfolding



Fisher, Marszalek & Fernandez, *Nature* 2000

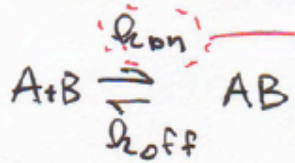
RNA unfolding



Bustamante et al. 1997

Diffusion Limited Reactions

e.g.



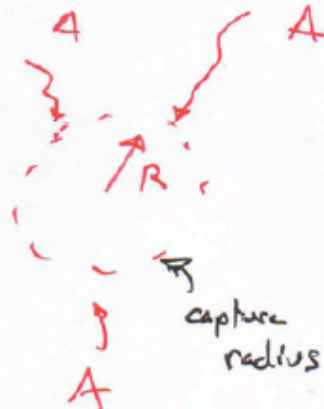
maybe limited by A "finding" B in solution?
how: diffusion!

$$\frac{d[B]}{dt} = -k_{on}[A][B] + k_{off}[AB]$$

$\frac{1}{s} \frac{\text{mol}}{l}$
↓
 $\frac{1}{s} \frac{l}{\text{mol}}$



reformulate
=> B "fixed"



assume:

- steady-state
- $C_A^\infty = C_A(r \rightarrow \infty)$
- $C_A(R) = 0$ ("fast rxn")

$$\nabla^2 C = 0$$

$$C_A = C_A^\infty \left(1 - \frac{R}{r}\right)$$

$$J_A = -D_A \frac{\partial C_A}{\partial r} \quad [=] \frac{\text{molecules}}{\text{area time}}$$

Some details...

$$\frac{\# \text{ collisions at surface}}{\text{time}} = 4\pi R^2 \frac{dC_A}{dt} \bigg|_R$$

$$\sim \frac{D_A R C_A^\infty}{D_A + D_B} \left[\frac{R}{R + R_B} \right] \frac{L^2}{t} \frac{\text{molecules}}{L^3}$$

- ① account for all B capture sites
- ② reformulate to look like mol/l s

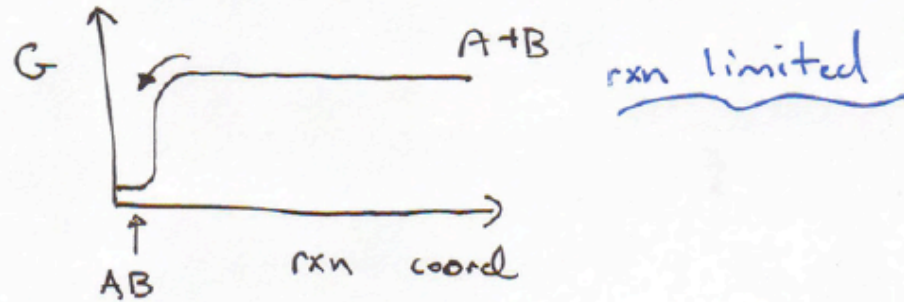
$$k_{\text{on}} [A][B] \sim \frac{D R N_A}{L^3} [A][B]$$

typical #'s , proteins in water $D \sim 10^{-6} \text{ cm}^2/\text{s}$
 $R \sim 3 \text{ nm}$ } $\rightarrow 10^9 - 10^{10} \text{ M}^{-1} \text{ s}^{-1}$

inside a cell $\eta \gg \eta_{\text{water}}$ (100x) $\rightarrow 10^7 - 10^8 \text{ M}^{-1} \text{ s}^{-1}$

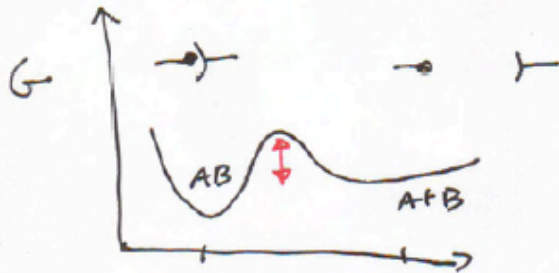
Geometry matters...

Energy Landscapes (1-D)

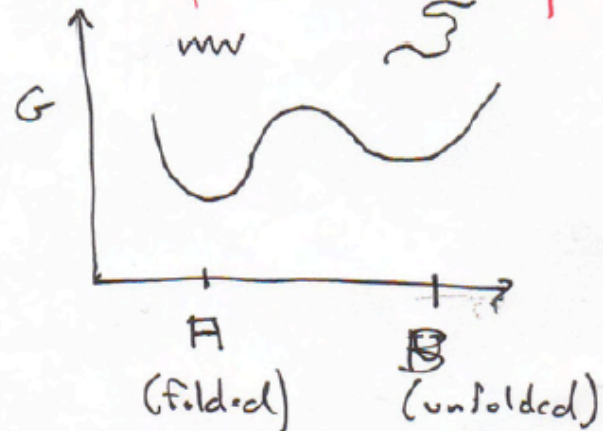


Often barriers (several $k_B T$) exist

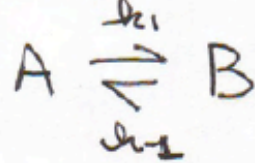
protein-ligand



protein-unfolding



Consider:



$$\frac{d[A]}{dt} = -k_1[A] + k_{-1}[B]$$

equilibrium: detailed balance

Boltzmann \rightarrow

$$\left. \frac{[B]}{[A]} \right|_{\text{equl}} = \frac{k_1}{k_{-1}} \equiv K_{\text{eq}}$$

eq. const.

$$\frac{P_B}{P_A} = \frac{\exp(-G_B / k_B T)}{\exp(-G_A / k_B T)} = \exp\left(\frac{-\Delta G}{k_B T}\right)$$

(note G versus U \rightarrow ensemble of states)

NOTE: equilibrium doesn't care about the barriers!

Kinetics \rightarrow very sensitive to barriers.

example:

suppose

$$P_A(t=0) = 1$$

$$P_A = \frac{1}{1+K_{eq}} \left[1 - \exp \left[- (k_1 + k_{-1}) t \right] \right]$$

temporal dependence!

$$P_B = \frac{1}{1+K_{eq}} \left[K_{eq} + \exp \left[- (k_1 + k_{-1}) t \right] \right]$$

$$t \rightarrow \infty \quad \frac{P_B}{P_A} = K_{eq}$$

Transition State Theory (Eyring ~ 1930)

... result, TS \Rightarrow unstable, short-lived state

$$\alpha_0 = k_1 = \frac{1}{\tau} \exp\left(-\Delta G_u^* / k_B T\right)$$

$$\beta_0 = k_{-1} = \frac{1}{\tau} \exp\left(-\Delta G_f / k_B T\right)$$

τ [F] time, $\frac{\alpha_0}{\beta_0} = \exp\left(-\frac{\Delta G}{k_B T}\right) \checkmark$

- ① Δ rates depend exponentially on barrier heights
- ② role of T
- ③ prefactor $\left(\frac{1}{\tau}\right) \rightarrow$ Eyring \sim cov. bonds \Rightarrow Q.Mech. \Rightarrow vib. freq \rightarrow Arrhenius $\rightarrow \frac{k_B T}{h} \sim 6 \times 10^{12} \text{ s}^{-1}$
 \rightarrow Kramers \sim "diffusion" in damped environment

- ④ any thing that affects energy landscape can change kinetics (possibly equil. too)



Fokker - Planck eqn (1-D)

probability
flux

$$j(x,t) = -D \frac{dP(x,t)}{dx} + \frac{F(x)}{\zeta} P(x,t) \quad (1)$$

diffusion
(Fick's law)

force
drag coeff.

F.-P. eqn

$$\frac{\partial P}{\partial t} = D \frac{\partial^2 P}{\partial x^2} - \frac{\partial}{\partial x} \left[\frac{F(x)}{\zeta} P(x) \right] \quad (2)$$

First Passage Time (simple approach)



Absorbing wall

$$D = \frac{\Delta T}{\xi}$$

$$F = -\frac{dU}{dx}$$

• assume steady state flux
(not equilibrium!)

$$j_0 \equiv \frac{1}{\text{time}}$$

$$t_0 \equiv \frac{1}{j_0} = \text{mean 1st passage time}$$

1) $\frac{\partial P}{\partial t} = 0$ (s.s.)

2) $P(x_0) = 0$ (absorbing wall)

3) $\int_0^{x_0} P(x) dx = 1$ cons. probability

$$k_1 \approx \frac{1}{t_0} = j_0 \quad \text{rate const.}$$

General Solution to Problem Posed

• if $j = \text{const.} \equiv j_0$, can rewrite (1) as:

$$\frac{d}{dx} \left\{ P(x) \exp \left[\frac{U(x)}{\frac{D}{aT}} \right] \right\} = -\frac{j_0}{D} \exp \left[\frac{U(x)}{\frac{D}{aT}} \right]$$

• integrate from x to x_0

$$P(x_0) \exp \left[\frac{U(x_0)}{\frac{D}{aT}} \right] - P(x) \exp \left[\frac{U(x)}{\frac{D}{aT}} \right] = -\frac{j_0}{D} \int_x^{x_0} \exp \left[\frac{U(y)}{\frac{D}{aT}} \right] dy$$

• multiply by $-\exp \left[-\frac{U(x)}{\frac{D}{aT}} \right]$, integrate from $0 \rightarrow x_0$

$$\int_0^{x_0} P(x) dx = \frac{j_0}{D} \int_0^{x_0} \exp \left[-\frac{U(x)}{\frac{D}{aT}} \right] \left\{ \int_x^{x_0} \exp \left[\frac{U(y)}{\frac{D}{aT}} \right] dy \right\} dx$$

First Passage Time

• re arrange

$$\frac{1}{j_0} = \frac{1}{D} \int_0^{x_0} \exp\left[-\frac{U(x)}{aT}\right] \left\{ \int_x^{x_0} \exp\left[\frac{U(y)}{aT}\right] dy \right\} dx$$

Need to input $U(x)$ to solve.....

* Case 1 : suppose $U(x) = 0$

$$t_0 = \frac{x_0^2}{2D} \quad \left(1-D \text{ simple diffusion!}\right)$$

Exponential Effect of Barrier Height

* Case 2: harmonic well: $U = \frac{1}{2} k x^2$

$$U_0 = U(x_0) \gg kT$$

(Kramers 1940)

$$t_0 \approx \frac{1}{D} \sqrt{\frac{\pi a T}{2k}} \frac{kT}{kx_0} \exp\left[\frac{U_0}{k_B T}\right]$$

↑
general

details of
shape of
well

↑
general

$$t \approx \tau \sqrt{\frac{\pi}{4}} \sqrt{\frac{aT}{U_0}} \exp\left[\frac{U_0}{k_B T}\right]$$

where $\tau = \xi/k$

Relaxation time of a damped spring

Details of Derivation...

Solution for Case #2

$$U = \frac{1}{2} k x^2$$

$$t_0 = \frac{1}{D} \int_0^{x_0} \exp\left[-\frac{U(x)}{\Delta T}\right] \left\{ \int_x^{x_0} \exp\left[\frac{U(y)}{\Delta T}\right] dy \right\} dx$$

$$\int_0^{x_0} \exp\left[\frac{U(y)}{\Delta T}\right] dy - \int_0^x \exp\left[\frac{U(y)}{\Delta T}\right] dy$$

dominant since $U_0 \gg \Delta T$

$$t_0 \approx \frac{1}{D} \int_0^{x_0} \exp\left[-\frac{kx^2}{2\Delta T}\right] \left\{ \int_0^{x_0} \exp\left[\frac{ky^2}{2\Delta T}\right] dy \right\} dx$$

$$t_0 \approx \frac{1}{D} \left\{ \int_0^{\infty} \exp\left[-\frac{kx^2}{2\Delta T}\right] dx \right\} \left\{ \int_0^{x_0} \exp\left[\frac{ky^2}{2\Delta T}\right] dy \right\}$$

$$t_0 \approx \frac{1}{D} \left\{ \sqrt{\frac{\pi \Delta T}{2k}} \right\} \left\{ \frac{\Delta T}{k x_0} \exp\left[\frac{k x_0^2}{2\Delta T}\right] \right\}$$

Things that Affect Energy Landscapes

- Force (pulling/pushing, rate)
- Enzymes (catalysts)
- Salt, pH
- "additives" (protein drug stabilization)
-

Two State Example: Protein Unfolding

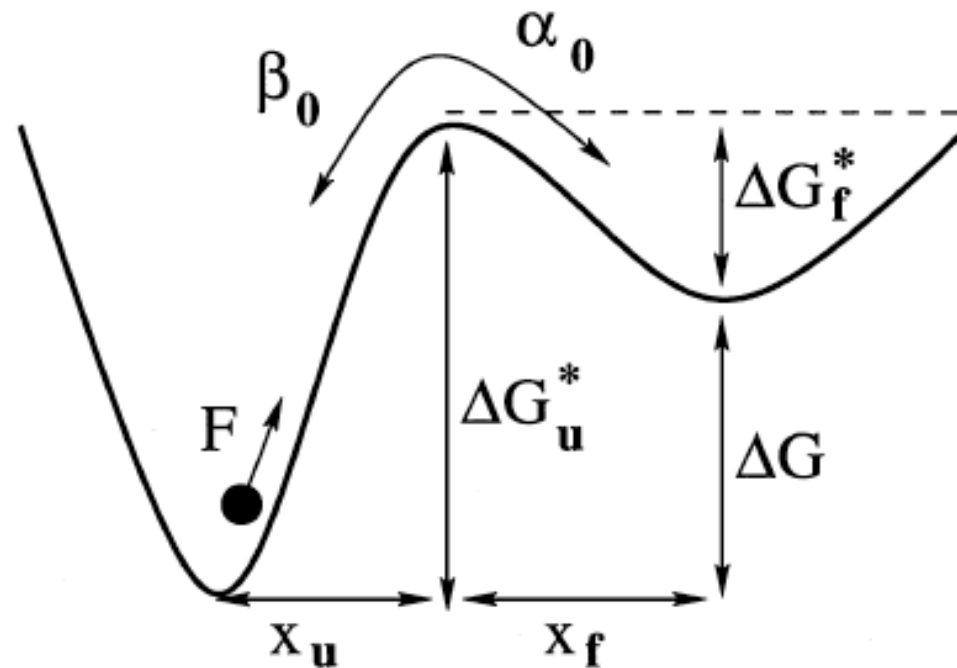


Figure 11 Two-level model for the unfolding of a protein domain (53). The domain in its native state (on the left) unfolds at a rate α_0 by hopping over the barrier (of energy difference ΔG_u^*) to unfolding. In the denatured state (on the right) the refolding rate β_0 is controlled by the energy difference with the transition state ΔG_f^* . When a force F is applied to the system, the free-energy difference ΔG between native and unfolded state is skewed toward unfolding by the work performed by the force: $F(x_u + x_f)$. (Courtesy of H. Gaub)

Force Changes the Energy Landscape

b.

