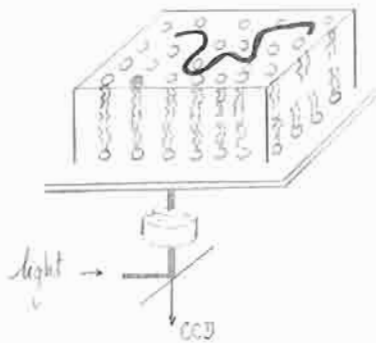
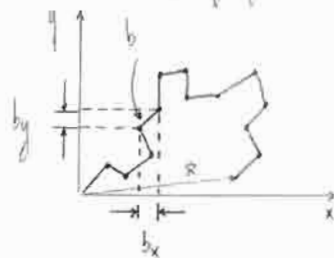


Problem 1



From Mayer & Radler, Phys Rev Lett. 82: 1911 (1999)

a) We model the DNA adsorbed into a lipid bilayer as a 2D freely-jointed chain (N steps of length b)



$$b^2 = \langle b_x^2 \rangle + \langle b_y^2 \rangle$$

random orientation  $\Rightarrow \begin{cases} \langle b_x^2 \rangle = \langle b_y^2 \rangle \\ \langle b_x^2 \rangle = \frac{b^2}{2} \end{cases}$

Gaussian distribution in 1D of the end-to-end distance  $R_x$ .

$$p(R_x) = \left( \frac{2\pi N b^2}{2} \right)^{-1/2} \exp\left( -\frac{R_x^2}{2N \frac{b^2}{2}} \right)$$

Independence of x & y directions  $\Rightarrow p(\underline{R}) = p(R_x) p(R_y)$

$$p(\underline{R}) = \frac{1}{\pi N b^2} \cdot \exp\left( -\frac{R^2}{N b^2} \right)$$

Helmholtz free energy  $dA = -PdV + \underline{f} \cdot d\underline{R} - SdT$

$\langle \underline{f} \rangle = \left( \frac{\partial A}{\partial \underline{R}} \right)_{V,T}$  and for an ideal chain  $A = U - TS = -TS$ , hence  $\langle \underline{f} \rangle = -T \left( \frac{\partial S}{\partial \underline{R}} \right)_{V,T}$

Using  $S = k_B \ln \Omega(\underline{R})$

$= k_B \ln \Omega_{\text{total}} + k_B \ln p(\underline{R})$  see solutions of Lecture 5 (Feb. 24, 2003)

we get  $\langle \underline{f} \rangle = -k_B T \frac{\partial}{\partial \underline{R}} (\ln p(\underline{R})) = \boxed{\frac{2 k_B T}{N b^2} \underline{R} = \langle \underline{f} \rangle_{\text{Gaussian 2D}}}$

b) In class (Lecture 5) we saw that  $\langle \underline{f} \rangle_{\text{Gaussian 3D}} = \frac{3 k_B T}{N b^2} \underline{R}$  hence  $\frac{\text{force 2D}}{\text{force 3D}} = \frac{2}{3}$

It is harder to pull on a chain of end-to-end vector  $\underline{R}$  in 3D than in 2D. The 3D chain appears stiffer because of the larger number of configurations, available to the system in 3D (more degrees of freedom), that we eliminate by pulling on the chain.

c) Limits of validity of the FJC model see Lecture 5:  $N \gg 1$

$R \ll N b$  small extensions.

A corrected expression for  $p(\underline{R})$  would be:

$$p(\underline{R}) = P_{\text{Gaussian}}(\underline{R}) \left[ 1 - \frac{3}{20N} \left( 5 - \frac{10R^2}{N b^2} + \frac{3R^4}{N^2 b^4} \right) \right]$$

d) Temperature dependence

The DNA configuration is driven mostly by entropy and so will be invariant to changes in temperature, while the configuration of proteins (like titin) depends on both entropy & internal energy (weak interactions) - hence FJC model not applicable to proteins.

e) Single-stranded DNA is more flexible (has a shorter Kuhn length, or persistence length) than double-stranded DNA. Therefore, using our result of question a),  $\langle \underline{f} \rangle = \frac{2 k_B T}{N} \underline{R} \cdot \frac{1}{b^2}$ , for a given extension  $\underline{R}$ , a higher force  $\langle \underline{f} \rangle$  will need to be applied to single-stranded DNA.

## Problem 2

a) Free energy changes by stretching a folded RNA: From the graph, assuming that the small hairpin will open first (less stabilization by base pairing)

- extension of "completely folded"  $\approx 110$  nm
- extension of "small hairpin unfolded"  $\approx 140$  nm
- extension of "completely unfolded"  $\approx 180$  nm

$$\Delta A_{\text{①}} = F_{\text{①}} \cdot \Delta x_{\text{①}} \cdot \alpha_A^p = 10 \cdot 10^{-12} \cdot (180 - 110) \cdot 10^{-9} \cdot 6.022 \cdot 10^{23} = 421.5 \text{ kJ} \cdot \text{mol}^{-1} \approx \Delta A_{\text{①}}$$

$$\Delta A_{\text{②}} = F_{\text{②}} \cdot \Delta x_{\text{②}} \cdot \alpha_A^p = 10 \cdot 10^{-12} \cdot (140 - 110) \cdot 10^{-9} \cdot 6.022 \cdot 10^{23} = 180.7 \text{ kJ} \cdot \text{mol}^{-1} \approx \Delta A_{\text{②}}$$

$$\Delta A_{\text{③}} = F_{\text{③}} \cdot \Delta x_{\text{③}} \cdot \alpha_A^p = 10 \cdot 10^{-12} \cdot (180 - 140) \cdot 10^{-9} \cdot 6.022 \cdot 10^{23} = 240.9 \text{ kJ} \cdot \text{mol}^{-1} \approx \Delta A_{\text{③}}$$

b) Ratio of probabilities at equilibrium: using  $A = -k_B T \ln Q$  (notations of Lecture 4) and  $k_B T \approx 2.5 \text{ kJ} \cdot \text{mol}^{-1}$

$$\frac{P_{\text{small unfolded}}}{P_{\text{folded}}} = \exp\left(\frac{-\Delta A_{\text{②}}}{k_B T}\right) = 4 \cdot 10^{-32}$$

Without any force applied onto the RNA molecule, the latter is extremely likely to be completely folded.

c) Force tilts energy profiles & changes distributions

Now, using the same reasoning as in Lecture 4, we can write

$$\frac{P_{\text{small unfolded}}}{P_{\text{folded}}} = \exp\left(\frac{-\Delta A_{\text{②}}}{k_B T}\right) \exp\left(\frac{f \cdot \Delta x_{\text{②}}}{k_B T}\right) = \exp\left(\frac{-180.7}{2.5}\right) \exp\left(\frac{5 \cdot 10^{-12} \cdot (140 - 110) \cdot 10^{-9}}{4 \cdot 10^{-21}}\right) \approx 8 \cdot 10^{-16}$$

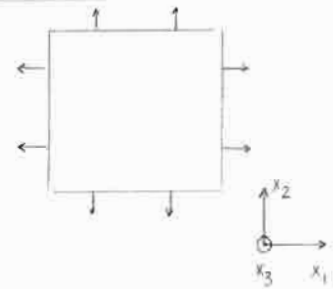
By applying  $f = 5 \text{ pN}$  to the ends of the RNA, we increase the probability of observing the "small hairpin unfolded" state by  $2 \cdot 10^{16}$ ! Force changes the molecule configurations by tilting its energy profile

Problem 3

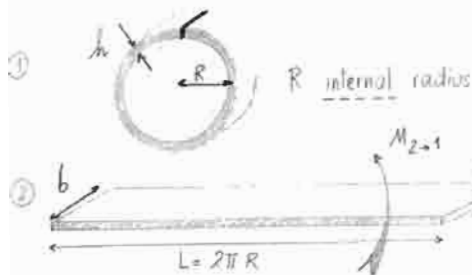
a) Biaxial extension

Hooke's law  $\epsilon_{ij} = \frac{1+\nu}{E} \sigma_{ij} - \frac{\nu}{E} \sigma_{kk} \delta_{ij}$ , with  $\sigma_{11} = \sigma_{22} = \sigma$  and  $\sigma_{33} = 0$ , gives

$$\begin{aligned} \epsilon_{11} &= \frac{1+\nu}{E} \sigma - \frac{\nu}{E} 2\sigma = \frac{1-\nu}{E} \sigma \\ \epsilon_{22} &= \frac{1+\nu}{E} \sigma - \frac{\nu}{E} 2\sigma = \frac{1-\nu}{E} \sigma \\ \epsilon_{33} &= -\frac{2\nu}{E} \sigma \end{aligned}$$



b) Using a cylindrical specimen flat



From L # 12 (03/17/2003), the strain energy  $U$  necessary to bend rod ② by applying a moment  $M_{2-1}$  to it is  $U = \frac{M_{2-1}^2 L}{2EI}$ , with

$$\begin{cases} L = 2\pi R & \text{length of the rod} \\ E = \text{material's Young modulus} \\ I = \int y^2 dA = \int_{y=0}^h \int_{x=0}^b y^2 dx dy = \frac{b h^3}{3} & \text{moment of inertia} \end{cases}$$

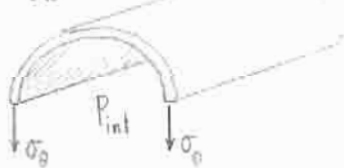
Since moment  $M_{2-1}$  to be applied to ② to get ① = - moment  $M$  to be applied to ① to get ② and  $\frac{1}{2} M_{2-1} \theta = \frac{M^2 L}{2EI}$  with  $\theta = \frac{L}{R_c} = \frac{2\pi R}{R} = 2\pi$  so that  $\frac{1}{2} M_{2-1} \theta = M_{2-1} \pi$

Eventually  $M = -M_{2-1} = -\frac{EI}{R_c} = -\frac{E 2\pi R h^3 b}{3 R L}$

$$M = -\frac{2\pi}{3} E h^3 \frac{b}{L}$$

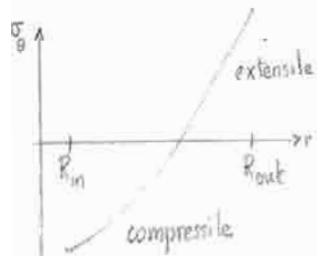
c) Circumferential stress

$$P_{ext} = P_{int}$$



Along the same force balance reasoning as in Homework # 3 Problem 2 question a), one can assert that, averaged over the total thickness of the material wall, the circumferential stress  $\sigma_\theta$  is null.  $\int_{r=R_{in}}^{R_{out}} \sigma_\theta dr = 0$ . However, if we don't assume  $\sigma_\theta$  uniform throughout the wall, physical considerations lead us to guess that:

As the vessel is allowed to relax to a smaller diameter, the inner wall undergoes a larger reduction in strain than the outer wall, since the wall thickness has to increase. Given that the entire wall began at the same circumferential stress (and nearly the same strain), the greater reduction at the inner wall leads us to conclude that is there negative, and that the strain is positive on the outer wall.



d) Slicing of a vessel

Since the inner regions are under compression and the outer regions under tension, a positive moment acts within the wall before this one is cut. After the cut is made, these moments are removed and the vessel will open up more.