

Problem 1

- (a) Show that the average value of the projection of a dipole \mathbf{p} in the direction of an electric field \mathbf{E} , and under the influence of the randomizing effect of temperature, is given by the Langevin function $\mathcal{L}(\alpha)$

$$\langle p_z \rangle = p \langle \cos(\theta) \rangle = p \left[\coth(\alpha) - \frac{1}{\alpha} \right] = p \mathcal{L}(\alpha)$$

where $\alpha (= pE/k_B T)$ is a dimensionless parameter that describes the relative strengths of the interaction energy between the dipole and the electric field (pE) and the thermal energy $k_B T$.

- (b) Show that for $\alpha \ll 1$, the Langevin function becomes

$$\mathcal{L}(\alpha) = \left[\coth(\alpha) - \frac{1}{\alpha} \right] \approx \frac{\alpha}{3}$$

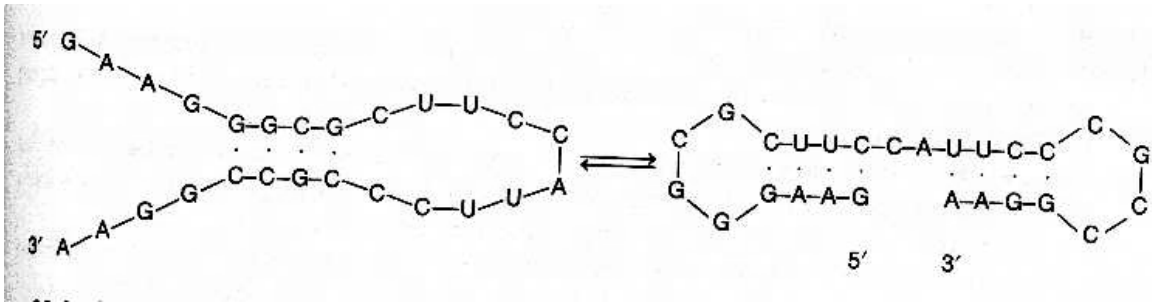
- (c) Is $\alpha \ll 1$ a reasonable approximation for a water molecule at a distance of ~ 1 nm from a unit charge in aqueous solution?

Problem 2

- (a) A sodium ion has an approximate radius of 0.95 \AA in a crystal. The Stokes radius derived from diffusion measurements in aqueous solution is 3.3 \AA . Can you explain this difference in radii?
- (b) Calculate the Debye screening length in 1mM MgCl_2 solution.
- (c) The Svedberg constant for the ribosome (the large complex in the cell responsible for protein synthesis) is 70S . Estimate the size of the ribosome. You may assume that the density of the ribosome is about 20% larger than the density of water.

Problem 3

- (a) Use the RNA folding server on <http://bioinfo.math.rpi.edu/~mfold/> to estimate the difference in free energies for the two possible conformations shown below in 1M NaCl , and at 37°C . (The temperature and ionic conditions are fixed in the program).



(b) Please note that the energy unit used in the program is kcal/mol. What is the conversion between this unit of energy, popular among biochemists, and what we have been using in class ($k_B T$)?

(c) Calculate the relative populations of the two conformations at 37°C

Problem 4

(a) Design a single-stranded RNA sequence that will form a “hairpin” with a “stem” region with Watson-Crick base-pairing and a “loop” region with unpaired bases. Pick a sequence with 10 base pairs in the stem and n bases in the loop. Your sequence will have $20+n$ bases. You may pick the bases in the loop to be all identical (e.g. poly(rU)).

(b) Use the RNA folding server, as in Problem 3, to calculate the free energy of your hairpin with n varying from 2 to 30, and plot a graph of free energy (in units of $k_B T$) versus $\log_e(n)$.

(c) Estimate the slope of the graph for large n and compare it with the theoretical value of 1.5 expected for an ideal chain.