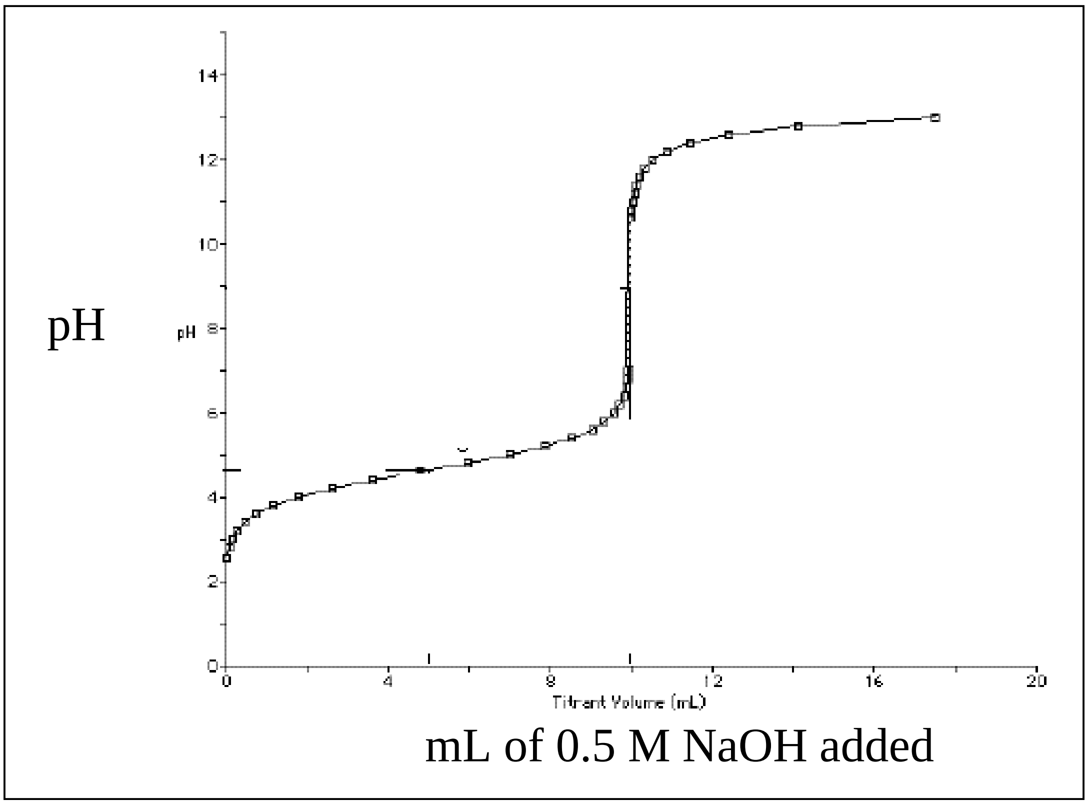
20.110/2.772

Homework Set #10

Due Friday Dec 9, 2005 by 3 pm

1. Small charged polymer beads are suspended in an aqueous salt solution. Estimate the distance two beads can approach each other (i.e. 2X the Debye length κ) if the beads are suspended in: 0.01 M NaCl, 0.1M Nacl, 0.1M $MgCl_2$.

2. A weak acid is dissolved in water to give a concentration of 0.5M. It is titrated with NaOH at 25C to yield curve shown. What is the pK of this acid?



3.)A peptide has the following sequence:

Gly-Ile-His-Ile-Lys-Ala-His-Gly

Estimate the net charge on the peptide at pH 5, pH 7.5, and pH 10 at 25C and at 40C. Sketch a titration curve showing the net charge on the peptide as a function of pH.

The dissociation constants for the side chains and termini are:

Amino acid	pK (25°C)	ΔH^0 (KJ/mol at 25C)
Histidine (RH+ → R + H+)	6.00	29.9
Lysine (RH+ → R + H+)	10.5	11.6
Carboxy terminus	~2.0	~3
Amino terminus	~9.5	~40

You may find structures of the 20 amino acids in a biology or biochemistry text or at the following website: http://web.mit.edu/esgbio/www/lm/proteins/aa/aminoacids.html

4. Consider the 8-mer oligonucleotide sequence 5'-CGAACATG-3' mixed with its complement sequence 5'-CATGTTCG-3'. Each oligomer is initially present at a concentration of 1×10^{-6} M. A table of relevant data is attached as the last page of the exam.
   a. Estimate the melting temperature, T_m, for the annealed oligomers. <u>Hint:</u> These are relatively short oligomers, so the temperatures are likely lower than you may expect for normal DNA melting temperatures.

   b. At what temperature is the concentration of dimers 90% of the maximum possible?

   c. In fact, half of the initial complementary sequence is degraded to the following two shorter oligomers: 5'-CATG-3' and 5'-TTCG-3'. This creates a solution where the primary sequence is present at 1×10^{-6} M, each of the degraded species is present at 0.5×10^{-6} M, and the full length complementary sequence is present at 0.5×10^{-6} M. For the degraded sequence show that the T_m for hybridization (with the original sequence) would not be observed under standard laboratory conditions.

   d. Estimate the fraction of the 5'-CATG-3' that is hybridized at 10°C in a solution containing only this oligomer and the full-length sequence 5'-CGAACATG-3' both at 1×10^{-6} M.

   e. Explain why adding 0.5×10^{-6} M of the full length complement to the solution in (d) would effectively reduce the concentration of free 5'-CGAACATG-3' by half.

f. Using the information you learned in parts c-e, estimate the observed T_m of the hybridized oligomer with the full-length complementary strand in the solution of part c, which contains the degraded species.

TABLE 4.4 Thermodynamic parameters* for calculating double strand stability in DNA (pH 7, 1 *M* NaCl)

	ΔG^0 (kJ mol^{-1}) at 37°C	ΔH^0 (kJ mol^{-1})	ΔS^0 (J K^{-1} mol^{-1})
5'-A, 3'-T + A-, T- → -A-A, -T-T	−4.2	−33.1	−93.0
5'-A, 3'-T + T-, A- → -A-T, -T-A	−3.7	−30.2	−85.4
5'-T, 3'-A + A-, T- → -T-A, -A-T	−2.4	−30.2	−89.2
5'-A, 3'-T + C-, G- → -A-C, -T-G	−6.0	−35.2	−93.8
5'-C, 3'-G + A-, T- → -C-A, -G-T	−6.0	−35.6	−95.0
5'-A, 3'-T + G-, C- → -A-G, -T-C	−5.4	−32.7	−87.9
5'-G, 3'-C + A-, T- → -G-A, -C-T	−5.4	−34.3	−93.0
5'-C, 3'-G + G-, C- → -C-G, -G-C	−9.1	−44.4	−113.9
5'-G, 3'-C + C-, G- → -G-C, -C-G	−9.3	−41.0	−102.2
5'-C, 3'-G + C-, G- → -C-C, -G-G	−7.7	−33.5	−83.3

Initiation: The bringing together of two strands to form a duplex involves a loss of entropy and an unfavorable free energy: ΔG^0(initiation) = +8.1 kJ mol^{-1}, ΔS^0(initiation) = −23.4 J K^{-1} mol^{-1}, ΔH^0(initiation) = +0.8 kJ mol^{-1}.

*Data are from H. T. Allawai and J. SantaLucia Jr., 1997, *Biochemistry* 36, 10581–10594.

5.) Dill 26.8 Zimm-Bragg helix-coil theory for N =4 chain units.

(a)Write the Zimm –Bragg partition function Q_4 in terms of σ and s for a four-unit chain,where *HHHH* is the helical state.

(b)Write an expression for $f_H(s)$for this transition.

6.) Dill 26.9 The Schellman helix-coil model.
A helix-coil model developed by J.A. Schellman is simpler than the Zimm-Bragg model,and works well for short chains. Consider a chain having N units.

(a)Write an expression for Ω_k, the number of configurations of a chain that has all its H units in a single helix k units long, as a function of N and k.

(b)If σ is the parameter for nucleating a helix, and s is the propagation parameter, write an expression for the partition function Q_N over all possible helix lengths k .

(c)Write an expression for $pk(N)$, the probability of finding a k -unit helix in the N -mer.

7.) Dill 28.2 Saturation of myglobin.
Suppose that O_2 molecules bind to myoglobin with association constant K =2 torr^{-1} at 25°C and pH 7.4.

(a)Show a table of the fractional saturation of myoglobin for pressures of 1,2,4,8,and 16 torr O_2.

(b)Does the fractional saturation double for each doubling of the pressure?

8.)Dill 28.4 Three-site binding.
A ligand X can bind to a macromolecule P at three different binding sites with the binding constants K_1,K_2, and K_3:

$$X + P \xrightarrow{K_1} PX$$

$$X + PX \xrightarrow{K_2} PX_2$$

$$X + PX_2 \xrightarrow{K_{31}} PX_3$$

a)Write the binding polynomial, Q.

b)Write an expression for the number of ligands ν bound per P molecule.

c)Compute ν for x = [X] = 0 .05, assuming K_1=1, K_2 = 1, and K_3 = 1000.

d)Assume the same K values as in (c). Below ligand concentration x =x 0 most of the macromolecular P molecules have 0 ligands bound. Above x =x_0 most of the P molecules have three ligands bound. Compute x_0.

e)For x = x_0 in part (d),show the relative populations of the ligation states with 0,1,2, and 3 ligands bound.