

# BB 101: Physical Biology

## TUTORIAL 4: Solutions

1. A freely-jointed chain tends to coil itself because it is trying to maximize entropy. The entropy of a macromolecular chain is dependent upon the number of different conformations that the chain can have in space (configurational entropy:  $S(r) = k_B \ln(\Omega)$ ). If the chain were totally stretched out, it would only have one possible conformation. By coiling itself, it increases the number of conformations it can have, and therefore, its entropy.

2. The expected RMS end-to-end distance for an ideal freely jointed chain of this length is  $b\sqrt{N} = 30 \text{ \AA}$ . The “real” RMS ( $=100 \text{ \AA}$ ) of this chain is greater than this number, Therefore, it does not behave as an ideal chain.

3. Bending stiffness  $k_b = N \xi_p k_B T = \xi_p RT = 300 \text{ \AA kcal mol}^{-1}$

4. Given

$$\begin{aligned} G &= \langle U \rangle - TS \\ &= \sum_i u_i p_i + k_B T \sum_i p_i \ln p_i \\ &= \sum_i p_i \{u_i + k_B T \ln p_i\} \end{aligned}$$

Now, use expression for  $p_i$

$$\begin{aligned} &= \sum_i \frac{1}{Z} e^{-\beta u_i} \left\{ u_i + k_B T \ln \left( \frac{1}{Z} e^{-\beta u_i} \right) \right\} \\ &= \frac{1}{Z} \sum_i e^{-\beta u_i} \{ u_i - k_B T \ln Z - u_i \} \\ &= \frac{1}{Z} \sum_i e^{-\beta u_i} \{ -k_B T \ln Z \} \\ &= \frac{Z}{Z} \{ -k_B T \ln Z \} \end{aligned}$$

Therefore,

$$G = -k_B T \ln Z$$

**5. Given**

$$\begin{aligned}
 U_i &= \sum_{l=1}^2 \sum_{m=l+1}^3 \frac{A}{r_{lm}} \\
 &= \sum_2^3 \frac{A}{r_{1m}} + \sum_3^3 \frac{A}{r_{2m}} \\
 &= \frac{A}{r_{12}} + \frac{A}{r_{13}} + \frac{A}{r_{23}}
 \end{aligned}$$

**(a)** Energy of any straight conformation/microstate

$$\begin{aligned}
 U_s &= \frac{A}{r_{12}} + \frac{A}{r_{13}} + \frac{A}{r_{23}} \\
 &= \frac{1 \text{ } k_B T \text{ } nm}{1 \text{ } nm} + \frac{1 \text{ } k_B T \text{ } nm}{2nm} + \frac{1 \text{ } k_B T \text{ } nm}{1nm} \\
 &= 2.500 \text{ } k_B T
 \end{aligned}$$

**(b)** Energy of any bent conformation/microstate

$$\begin{aligned}
 U_b &= \frac{A}{r_{12}} + \frac{A}{r_{13}} + \frac{A}{r_{23}} \\
 &= \frac{1 \text{ } k_B T \text{ } nm}{1 \text{ } nm} + \frac{1 \text{ } k_B T \text{ } nm}{\sqrt{2} \text{ } nm} + \frac{1 \text{ } k_B T \text{ } nm}{1nm} \\
 &= 2.707 \text{ } k_B T
 \end{aligned}$$

**(c)** There are total 6 straight conformations/microstates possible i.e.  $W_s = 6$

**(d)** There are total 16 bent conformations/microstates i.e.  $W_b = 16$

The probability  $P_s$  that you will find the protein in a straight structural state or straight macrostate is given by

$$P_s = \frac{e^{-\frac{G_s}{k_B T}}}{Z}$$

Where  $G_s = \langle U_s \rangle - TS = \langle U_s \rangle - T k_B \ln W_s$

And,  $\langle U_s \rangle$  is average energy of straight microstates is,  $W_s$  is the number of straight microstates and  $Z$  is the partition function

Similarly, probability  $P_b$  that you will find the protein in a bent structural state or bent macrostate is given by

$$P_b = \frac{e^{-\frac{G_b}{k_B T}}}{Z}$$

$$G_b = \langle U_b \rangle - TS = \langle U_b \rangle - T k_B \ln W_b$$

Where  $\langle U_b \rangle$  is average energy of bent microstates

$$Z = e^{-\frac{G_s}{k_B T}} + e^{-\frac{G_b}{k_B T}}$$

$$\text{Now, } G_s = 2.500 k_B T - k_B T \ln 6 = 2.500 k_B T - 1.792 k_B T = 0.708 k_B T$$

$$\text{And, } G_b = 2.707 k_B T - k_B T \ln 16 = 2.707 k_B T - 2.773 k_B T = -0.066 k_B T$$

**(e)** The probability that you will find the protein in a straight structural state or straight macrostate is given by

$$P_s = \frac{e^{-0.708}}{e^{-0.708} + e^{0.066}} = \frac{e^{-0.708}}{e^{-0.708} + e^{0.066}}$$

$$\approx 0.316$$

**(f)** The probability that you will find the protein in a bent structural state or bent macrostate is given by

$$P_b = \frac{e^{0.066}}{e^{-0.708} + e^{0.066}} = \frac{e^{0.066}}{e^{-0.708} + e^{0.066}}$$

$$\approx 0.684$$

**6. (a)** Let's calculate entropy/disorder  $S_1$  for first column

For this column  $M=1$ , Since nothing is changing in first column

Here  $p_1$  is the probability of finding letter A

$$p_1 = 1$$

$$\text{Therefore, } S_1 = -k_B p_1 \ln p_1 = -k_B \ln 1 = 0$$

Now, let's calculate entropy  $S_2$  for second column

For this column M=4, since there are four different letters in this position.

Let  $p_1, p_2, p_3$  and  $p_4$  denote the probabilities of finding letters A, T, C and G respectively

$$p_1 = \frac{2}{10} = 0.2$$

$$p_2 = \frac{3}{10} = 0.3$$

$$p_3 = \frac{2}{10} = 0.2$$

$$p_4 = \frac{3}{10} = 0.3$$

Therefore,  $S_2 = -k_B(p_1 \ln p_1 + p_2 \ln p_2 + p_3 \ln p_3 + p_4 \ln p_4)$

$$S_2 = -k_B(-1.366)$$

Or,  $S_2 = 1.366k_B$

Now, Let's calculate entropy  $S_3$  for third column

For this column M=4, Since there are four different letters in this position

Let  $p_1, p_2, p_3$  and  $p_4$  denote the probabilities of finding letters A, T, C and G respectively

$$p_1 = \frac{1}{10} = 0.1$$

$$p_2 = \frac{7}{10} = 0.7$$

$$p_3 = \frac{1}{10} = 0.1$$

$$p_4 = \frac{1}{10} = 0.1$$

Therefore,  $S_3 = -k_B(p_1 \ln p_1 + p_2 \ln p_2 + p_3 \ln p_3 + p_4 \ln p_4)$

$$S_3 = -k_B(-0.94)$$

Or,  $S_3 = 0.94 k_B$

**(b)** Since Values of entropy is minimum for first column and hence first position is most conserved. Second position is least conserved as entropy is maximum for this position.