Problem Solving Exercise 1: Protein helix to coil transition

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January 13, 2020

This exercise involves the modeling of cooperative protein unfolding using statistical thermodynamics. You should use the information in the provided handout to carry out the folliwng tasks.

Table 1: Transition energies for each of the steps in a n=4 amino acid system. Transition | Symbol | Energy/J

Transition	Symbol	Energy/J
$0 \rightarrow 1$	q_1	1.1×10^{-19}
$0 \rightarrow 2$	q_2	2.0×10^{-19}
$0 \rightarrow 3$	q_3	2.9×10^{-19}
$0 \rightarrow 4$	q_4	3.7×10^{-19}

- 1. Write a function, that given an arbitrary number of amino acids in a randomly coiled conformation, i, and total amino acids, n, can determine the number of possible permutations C(n, i).
 - Note, that the function factorial from the scipy.special module is capbale of returning an array of factorials from a NumPy array.
- 2. Table 1 gives the energy for the transitions of a fully helical protein chain, of length 4, to having 1, 2, 3, and 4 randomly coiled amino acids. The partition coefficient associated with the fully helical structure is $q_0 = 1.21$.
 - (a) Using Equations 3 and 4 from the handout, determine the value of the total paritition function, q, for this system at a temperature of 273.15 K.
 - (b) Determine the total partition function at 200 K, 400 K, 600 K, 800 K and 1000 K, and plot the variance as a function of temperature.
- 3. The partition function of this process can be generalised, initially by applying a non-cooperative model, create a function to evaluate the non-cooperative model for an arbitrary number of amino acids and plot how the result of this varies in the temperature series mentioned above for proteins with 4, 20, and 100 amino acids, assume a value for γ of 1×10^{-19} J.

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- 4. The zipper model for protein unfolding is a form of cooperative model that is outlined in Equation 10.
 - (a) Write three functions to determine; the partition function for the cooperative model, the fraction of proteins that would be found with i randomly coiled amino acids, and the mean number of randomly coiled amino acids.
 - (b) Plot the variation of p_i as a function of i for a protein consisting of 20 amino acids, where $sigma = 5 \times 10^{-3}$ and s is 1.5, 1, and 0.82.
 - (c) Determine the mean i for each of the above stability parameters.