

J04T.3—DNA as a Polymer Chain

Problem

The statistical mechanics of biological polymers is important for understanding such things as the properties of DNA or protein folding. The simplest “ideal gas”-like description of a polymer treats the dominant free energy terms as coming from the *conformational entropy*: typical polymer configurations can be modeled as a random walk of N steps. The height of each step b represents the lengthscale of a flexible microscopic polymer “link”. This leads to an “ideal polymer” free energy F_0 as a function of the distance between the two free ends $|\vec{R}|$

$$F_0(|\vec{R}|, N) = -TS_{\text{config}} = \text{const} + k_B T \frac{3R^2}{2Nb^2}.$$

- a) Use this expression to find the *mean square* end-to-end distance $\langle R^2 \rangle$. How does it depend on N ?
- b) What is the *most probable* end-to-end distance?

As in the case of the “ideal gas”, the “ideal polymer” picture neglects the interactions between different parts of the polymer. The polymer may be viewed as a ball with radius of order R . The principle “two body” interaction is the excluded volume effect: two links cannot occupy the same point in space. Take v as the “excluded volume” of the region around a link into which a second link of the polymer cannot enter. One can develop a low-density expansion for the interaction energy in powers of vR^3 .

You are asked to investigate the leading (two-link) interaction correction to the free energy in the low-density limit.

$$F(|\vec{R}|, N) = -TS_{\text{config}}(|\vec{R}|, N) + vU(|\vec{R}|, N)$$

- c) Use dimensional analysis and low density arguments to determine U (up to a constant factor) in the limit $v \rightarrow 0$.
- d) Use your answer to (c) to estimate the equilibrium (most probable) end-to-end distance of the non-ideal polymer as a function of N , b , and v . (Your results should reveal a different predicted N -dependence as compared to the “ideal polymer”!)