# Any homework questions on 7.4, Problem J, or 7.7?

### Macromolecule Structure

DNA and to a lesser degree proteins can be modeled as random walks.

Ways in which they are not random walks:

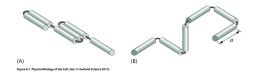
- proteins form  $\alpha$ -helices and  $\beta$ -sheets
- more generally, amino acids interactions hydrophobic, polar, or charged — affect the structure (PDB)
- DNA is typically confined to a smaller volume
- DNA is bound into chromosomes

Nevertheless, a random walk model is a very good starting point, particularly for DNA. Confinement and binding sites can be incorporated into a random walk model.

Also: provides a framework for thinking about entropic forces.

# Freely-Jointed Chain Random Walk

Rigid segments of length a (Kuhn length), with random angles at the connection points.



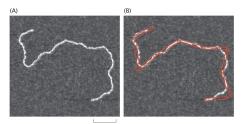


Fig. 8.2: Illustration of how a DNA segment looks like a two-dimensional freely-jointed chain. ←

100 nm Finure 8.2 Physical Biology of the Cell. 2nd. 10 Gardand Science 2013)

## **One Dimensional Random Walk**

- ► N steps of length a, each with a probability 1/2 of moving left or right.
- ► There are 2<sup>N</sup> possible sequences (LRRRLR...) and we assume they are all equally probable.

• The end-to-end distance: 
$$R = \sum_{i=1}^{N} x_i$$
, where  $x_i = \pm a$ 

• Then 
$$\langle R \rangle = \left\langle \sum_{i=1}^N x_i \right\rangle = \sum_{i=1}^N \langle x_i \rangle = 0$$

- So the average position is zero. Note that the angle brackets are averages over all sequences.
- To get a sense of the size, need to measure  $\langle R^2 
  angle \ldots$

### One Dimensional Random Walk, continued

$$\langle R^2 \rangle = \left\langle \left( \sum_{i=1}^N x_i \right) \left( \sum_{j=1}^N x_j \right) \right\rangle = \left\langle \sum_{i=1}^N \sum_{j=1}^N x_i x_j \right\rangle$$

This is just multiplication. Check for N = 2:

$$\underbrace{(x_1 + x_2)(x_1 + x_2)}_{\text{product of sums}} = \underbrace{x_1 x_1 + x_1 x_2 + x_2 x_1 + x_2 x_2}_{\text{sum of products}}$$

Now break up the sum:

$$\langle R^2 \rangle = \left\langle \sum_{i=1}^N x_i^2 \right\rangle + \left\langle \sum_{i \neq j=1}^N x_i x_j \right\rangle = Na^2 + 0$$

So we have learned that the end-to-end distance goes like  $R_{\rm rms}=\sqrt{\langle R^2\rangle}=a\sqrt{N}.$ 

#### Statistical Treatment of One Dimensional Random Walk

Given N steps, with  $n_r$  to the right, then  $N - n_r$  are to the left. For a given N and  $n_r$ , the binomial coefficient tells us how many sequences are possible:

$$W(n_r, N) = \frac{N!}{n_r!(N - n_r)!}$$

Each has a probability  $1/2^N$ , so the probability of  $n_r$  right steps is

$$p(n_r, N) = W(n_r, N) = \frac{N!}{n_r!(N - n_r)!} \frac{1}{2^N}$$

Convert this into R: derive an expression for R in terms of N,  $n_r$ , and  $a \ldots$ 

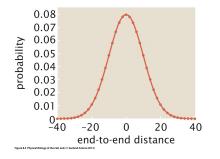
should get  $R = (n_r - n_l)a = (2n_r - N)a$ 

Then we solve for  $n_r$  and  $N - n_r$  and plug in above...

### Statistical Treatment of One Dimensional Random Walk

- ▶ A lot of Stirling approximation math ensues, along with expansions of the logarithm:  $\ln(1+x) \approx x x^2/2 + \dots$
- You will work through this in Problem 8.1 and get to the result that

$$p(R,N) = \frac{2}{\sqrt{2\pi N}} e^{-R^2/2Na^2}$$



#### Convert to a Probability Density P(R, N)

- ▶ p(R, N) is the probability of the end being at exactly some R value that is a multiple of 2a.
- ▶ P(R, N) dR is the probability of the end being between R and R + dR
- Assume dR ≫ 2a, and that p(R, N) is essentially constant in range R to R + dR:

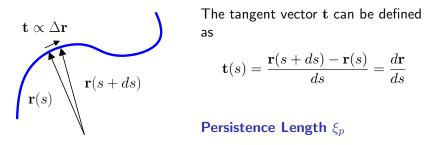
$$P(R,N) dR = \frac{dR}{2a} \times p(R,N) = \frac{1}{\sqrt{2\pi N a^2}} e^{-R^2/2Na^2} dR$$

Generalize to three dimensions:

$$P(\mathbf{R}, N) d^3 R = \left(\frac{3}{2\pi N a^2}\right)^{1/2} e^{-3R^2/2Na^2} d^3 R$$

### **Continuous Polymer Chain**

Let s be a coordinate measured along the polymer, and  $\mathbf{r}(s)$  describe the polymer structure.



 $\blacktriangleright$  generalization of the Kuhn length a in the freely-jointed chain

• Defined via the tangent correlation:  $\langle \mathbf{t}(s) \cdot \mathbf{t}(u) \rangle = e^{-|s-u|/\xi_p}$ .

#### **Relation between Persistence Length and Chain Length**

The end-to-end displacement  ${f R}$  given by

$$\mathbf{R} = \mathbf{r}(L) - \mathbf{r}(0) = \int_0^L \frac{d\mathbf{r}}{ds} \, ds = \int_0^L \mathbf{t}(s) \, ds$$

Since  $\langle \mathbf{R} \rangle = 0$ , look at the square:

$$\langle R^2 \rangle = \left\langle \int_0^L \mathbf{t}(s) \, ds \cdot \int_0^L \mathbf{t}(u) \, du \right\rangle = \underbrace{\int_0^L ds}_{=L} \underbrace{\int_0^L du \, e^{-|s-u|/\xi_p}}_{=2\int_0^\infty e^{-x/\xi_p} dx}$$
$$= 2\xi_p L$$

Continuous polymer:  $R_{\rm rms} = \sqrt{2\xi_p L}$   $\Rightarrow$   $a = 2\xi_p$ Freely-jointed chain:  $R_{\rm rms} = a\sqrt{N} = \sqrt{aL}$ 

# **Radius of Gyration**

End-to-end distance can fluctuate wildly. More robust measure of size:

$$\langle R_G^2 \rangle = \frac{1}{N} \sum_{i=1}^N (\mathbf{r}_i - \mathbf{r}_{\mathsf{CM}})^2$$

where  $\mathbf{r}_{\mathsf{CM}} = (1/N) \sum_i \mathbf{r}_i$ 

HW Problem 8.2: show that  $\sqrt{\langle R_G^2 \rangle} = \sqrt{L\xi_p/3}$ .

Hints:

- work with freely jointed chain, and use  $a = 2\xi_p$  at the end
- squaring sums:  $(\sum_i x_i)^2 = (\sum_i x_i)(\sum_j x_j) = \sum_i \sum_j x_i x_j$

# **Typical sizes**

For DNA,  $\xi_p \simeq 50$  nm:

Bacteriophage T2 genome has  $1.5\times 10^5$  bp, so  $L\sim 5\times 10^4$  nm.

$$\sqrt{\langle R_G^2 \rangle} = \sqrt{L\xi_p/3}$$

$$=\sqrt{\frac{(5\times10^4)(50)}{3}}\simeq900\,\text{nm}.$$

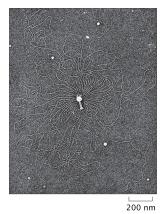


Figure 1.16 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

# **Typical sizes**

For DNA,  $\xi_p \simeq 50$  nm:

Bacteria genome:  $N_{\rm bp} \sim 4.6 \times 10^6$ , so  $L \sim 1.5 \times 10^3 \ \mu{\rm m}.$ 

$$\sqrt{\langle R_G^2 \rangle} = \sqrt{L\xi_p/3}$$

$$= \sqrt{\frac{(1.5 \times 10^3)(0.050)}{3}} \simeq 5\,\mu{\rm m}.$$

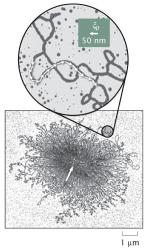


Figure 8.5 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

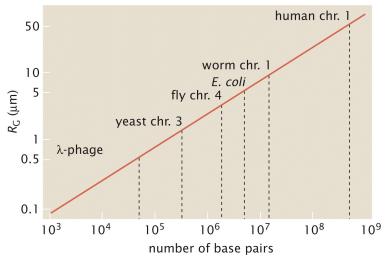


Figure 8.6 Physical Biology of the Cell, 2ed. (© Garland Science 2013)