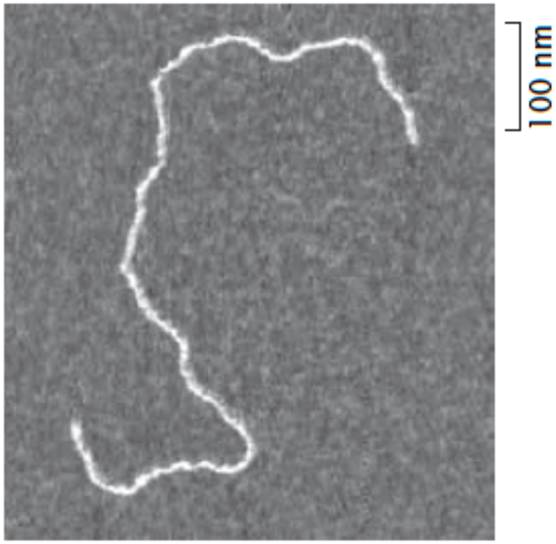
Today’s class:

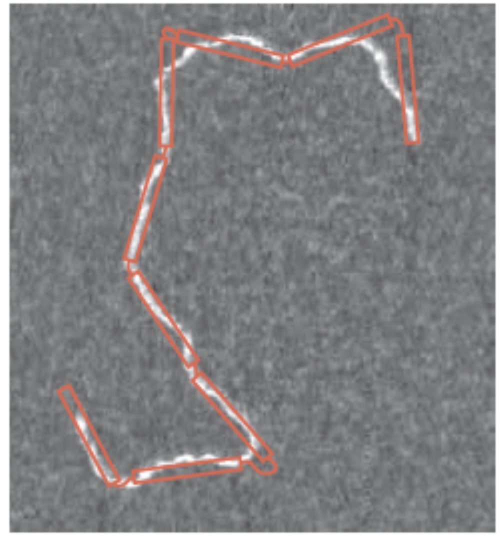
Deformable DNA described as Random Walks

This lecture follows the parts of chapter 8 from the book
‘Physical Biology of the Cell’ by Philips, Kondev, Theriot and Garcia, 2nd Ed

DNA structures can be represented as Random Walks



DNA on a surface captured by AFM
Wiggins et al Nature Nanotech 2006



DNA approximated by an array of randomly oriented segments

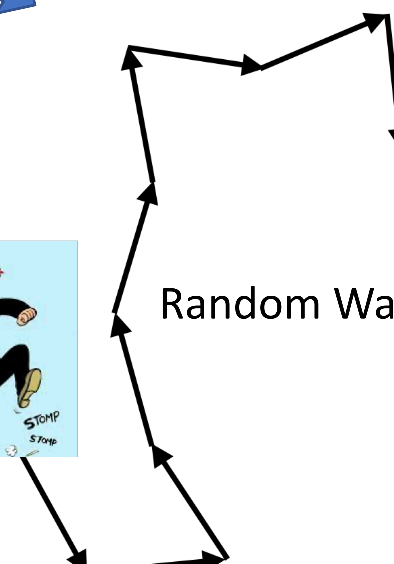
Each macromolecular configuration is a random walk along contour

Each step of random walk = one ‘rigid’ segment

Independent steps, no dependence on history

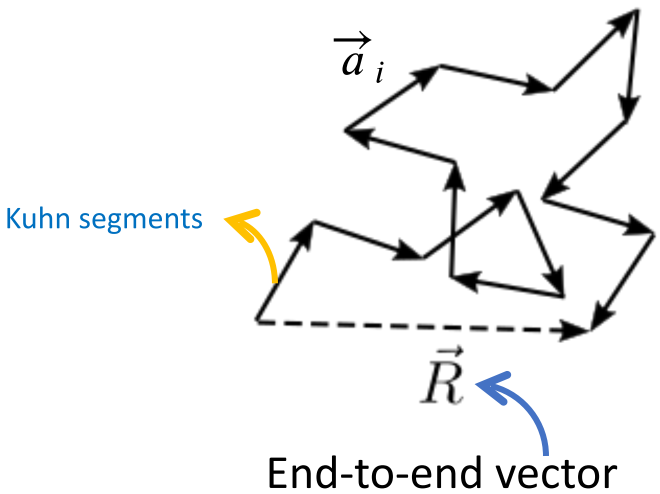
For a 1D random walker, $p_R = p_L = 1/2$

For a chain of N segments, 2^N macromolecular configurations



Random Walk

The Freely Jointed Chain model



Non-interacting polymer of N Kuhn segments of length a

Fully unfolded length, $L = Na$

Some important results:

$$\left\langle \vec{R} \right\rangle = \left\langle \sum_{i=1}^{N} \vec{a}_i \right\rangle = \sum_{i=1}^{N} \left\langle \vec{a}_i \right\rangle = 0$$

$$\left\langle R^2 \right\rangle = \left\langle \vec{R} \bullet \vec{R} \right\rangle$$

$$= \left\langle \sum_{i,j}^{N} \vec{a}_i \bullet \vec{a}_j \right\rangle = \left\langle \sum_{i}^{N} a_i^2 \right\rangle + \overbrace{\left\langle \sum_{i \neq j}^{N} \vec{a}_i \bullet \vec{a}_j \right\rangle}^{= 0}$$

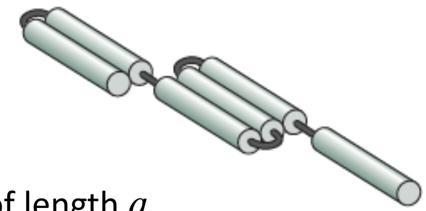
RMS end-to-end distance

$$\boxed{\sqrt{\left\langle R^2 \right\rangle} = a\sqrt{N}}$$

$$\boxed{\left\langle R^2 \right\rangle = Na^2}$$

Volume occupied by the polymer $V_{poly} \propto \left(\sqrt{\left\langle R^2 \right\rangle}\right)^3 = a^3 N^{\frac{3}{2}}$ > total volume of the unjointed monomers

The probabilistic interpretation of the FJC

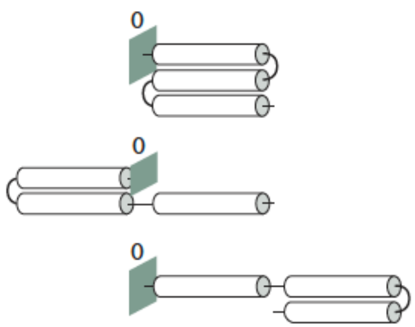


For a 1D chain

N segments of length a

n_r right directed segments

$n_l = N - n_r$ left directed segments



$N = 3,\ n_r = 2$

Degeneracy = 3

At thermodynamic equilibrium, all states are equally probable for the FJC

We can use this to compute the probability distribution function of the end-to-end distance

Each step occurs with probability 1/2

Probability of any sequence of N steps $= \left(\frac{1}{2}\right)^N$

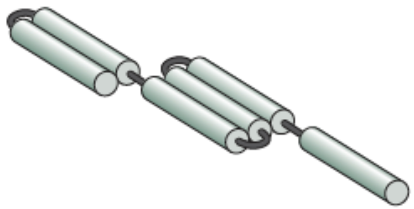
Number of ways to realize n_r → $\dfrac{N!}{n_r!\left(N-n_r\right)!}$ From degeneracy

$$\text{Total probability, } p\left(n_r\right) = \frac{N!}{n_r!\left(N-n_r\right)!}\left(\frac{1}{2}\right)^N$$

Problem: Show $p\left(n_r\right)$ is normalized.

Hint: use binomial theorem

How to get $p(R)$ from $p(n_r)$?



For a 1D chain

N segments of length a

n_r right directed segments

$n_l = N - n_r$ left directed segments

$$R = (n_r - n_l)a$$

$$n_r = \left(\frac{N}{2} + \frac{R}{2a}\right)$$

Making replacements in $p(n_r) = \dfrac{N!}{n_r!(N-n_r)!}\left(\dfrac{1}{2}\right)^N$

$$p(R) = \frac{N!}{\left(\frac{N}{2}+\frac{R}{2a}\right)!\left(\frac{N}{2}-\frac{R}{2a}\right)!}\left(\frac{1}{2}\right)^N$$

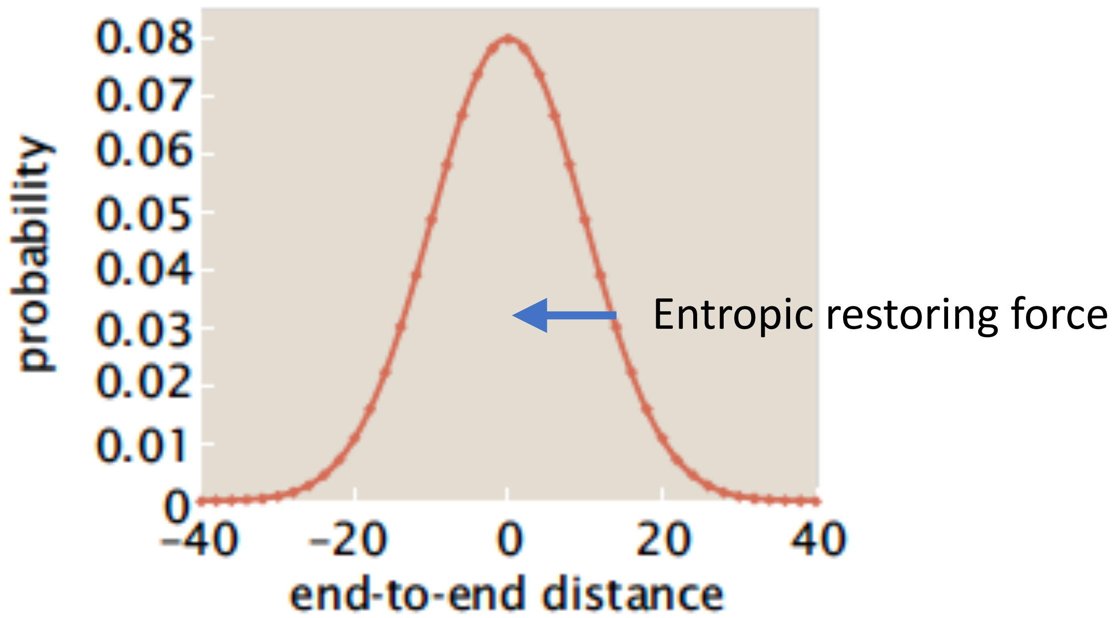
When unfolded length $L = Na \gg R$ $\Rightarrow$ $p(R) = \dfrac{2}{\sqrt{2\pi N}} e^{-R^2/2Na^2}$

Gaussian distribution!

Here $p(R)$ has zero mean and variance Na^2

Analysis of the end-to-end probability

End-to-end probability for a 1D polymer with 100 segments



Most probable state, $R = 0$
If the chain is stretched $(R > 0)$ it
experiences an 'entropic restoring force'
Entropic Elasticity

End-to-end probability for E.coli genome

For E.coli genome → 5×10^6 bp

If this is modeled as an open DNA chain it will have $N \approx 15000$ segments, since estimated Kuhn segment ≈ 300 bp long

Deduce the probabilities of $R = 0,\ 100a,\ \ 1000a$

Hint: probability is given by: $p(R) = \dfrac{2}{\sqrt{2\pi N}} e^{-R^2/2Na^2}$

Probability of $R = 0 \approx 0.007$

Probability of $R = 100a \approx 0.005$

Probability of $R = 1000a \approx 2 \times 10^{-17}$