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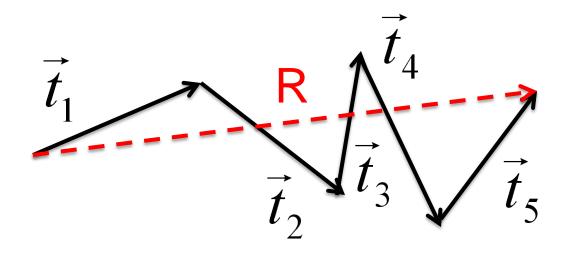
#### Lecture 25

### **Statistics**

# Size of a folded protein: Simplest model

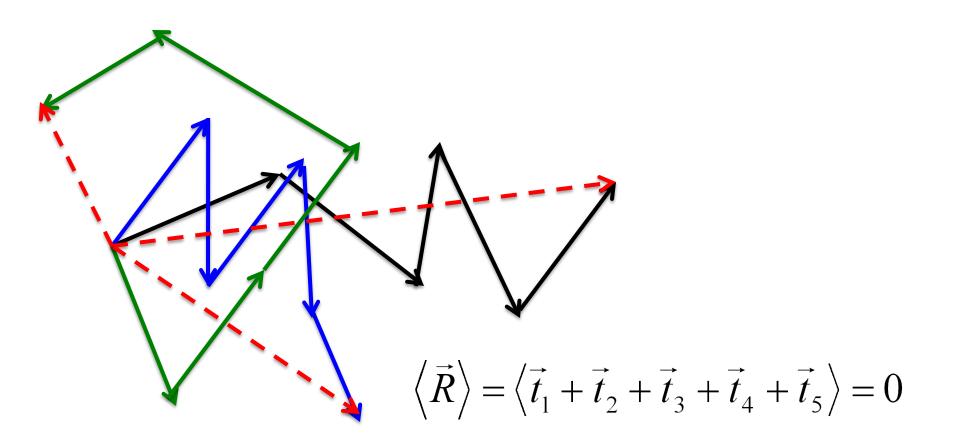
Imagine that a protein of N amino acids has no preferred Orientation (completely flexible)

#### **End-to-end distance**



 $\vec{R} = \vec{t}_1 + \vec{t}_2 + \vec{t}_3 + \vec{t}_4 + \vec{t}_5$ 

### **Random orientation**



### End-to-end distance

$$\left\langle \vec{R}^2 \right\rangle = \left\langle \left( \vec{t}_1 + \vec{t}_2 + \vec{t}_3 + \vec{t}_4 + \vec{t}_5 \right)^2 \right\rangle$$

#### Mean-square average

$$\left\langle \vec{R}^2 \right\rangle = \left\langle \left( \vec{t}_1 + \vec{t}_2 + \vec{t}_3 + \vec{t}_4 + \vec{t}_5 \right)^2 \right\rangle = 5b^2$$

# Where b is the length of each monomer/amino acid

### **Standard deviation**

$$\left\langle \vec{R}^2 \right\rangle = \left\langle \left( \vec{t}_1 + \vec{t}_2 + \vec{t}_3 + \vec{t}_4 + \dots + \vec{t}_N \right)^2 \right\rangle = Nb^2$$

$$\sigma = \sqrt{\left\langle \vec{R}^2 \right\rangle - \left\langle R \right\rangle^2} = b\sqrt{N}$$

# Summary

#### Flexible protein: Average

#### Flexible protein: Standard deviation

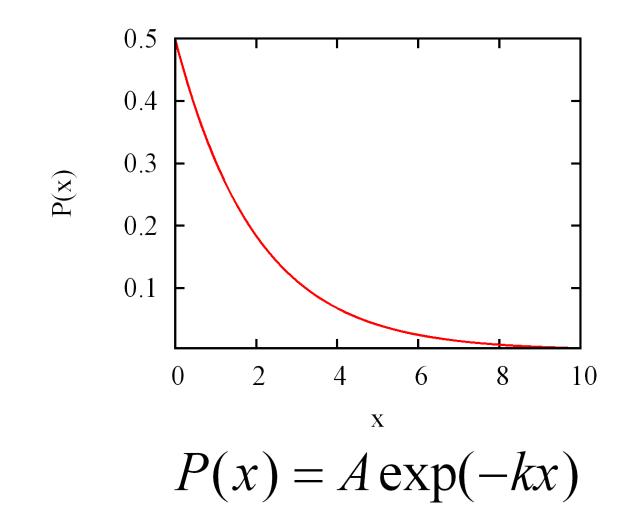


# Do you know ... ?

Microtubules rapidly grow and shrink exhibiting the phenomenon known as dynamic instability. What is the length distribution of microtubules ?

Imagine that proteins bind on to the DNA with a rate k. What is the probability that you have to wait at time 'dt' between consecutive binding events ?

## **Exponential distribution**



$$P(x) = A \exp(-kx)$$

#### How do we find A?

$$\int_0^\infty P(x)dx = \int_0^\infty A\exp(-kx)dx = 1$$

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$$\int_{0}^{\infty} P(x)dx = \int_{0}^{\infty} A \exp(-kx)dx = 1$$
$$\Rightarrow A = k$$

$$\langle x \rangle = \int_0^\infty x P(x) dx$$
  
 $\langle x^2 \rangle = \int_0^\infty x^2 P(x) dx$ 

$$\langle x \rangle = \int_0^\infty xk \exp(-kx) dx = \frac{1}{k}$$
$$\langle x^2 \rangle = \int_0^\infty x^2 k \exp(-kx) dx = \frac{2}{k^2}$$
$$\sigma = \sqrt{\langle x^2 \rangle - \langle x \rangle^2} = \frac{1}{k}$$

# Exponential distribution has standard deviation as big as average