#### **MAE 545: Lecture 21,22 (4/24)** How proteins find Statisti target sites on DNA? ow proteins ting and statistic target site must be recognized with 1 base-pair (1 base-pair 1 bp results) precision and the 1 bp results and 1 bp resul

# **Statistical mechanics of polymers**



#### **Growth dynamics of by** rounds of 3D and 1D diffusion, each with average duration τ3D and τ1D, respectively. (*B*) The antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites. This allows the protein to associate some distance ∼*n*¯ away from the target site and reach it by se increaturely increase the reaction from 1bp to ∼n⊃. The antenna effectively increase the antenna effect is a **microtubules actin filaments and**





# **Dynamics of molecular motors**



## **How proteins find target sites on DNA?**





#### **Translation of mRNA**



## **Protein-DNA interactions**



#### **diffusion limited with the confinent with the confinent with the confinent with the cell nucleoid (in bacteria)**

 $k_{\text{on}}^{\text{S}} \approx k_{\text{on}}^{\text{NS}}$ 

# diffusion limited binding strengths

$$
k_{\rm on}^{\rm S} \approx k_{\rm on}^{\rm NS} \approx 4\pi D_3 b
$$
  $k_{\rm off}^{\rm S} = A_{\rm s} e^{-\Delta G^{\rm S}/k_B T} \ll k_{\rm off}^{\rm NS} = A_{\rm s} e^{-\Delta G^{\rm NS}/k_B T}$   
 $k_{\rm off}^{\rm S} \sim 10^{-6}$ 

## **How long proteins remain bound on DNA?**

 $k_{\mathrm{off}}$ 



**Probability that protein remains bound for time**  *t* and then it unbinds between time  $t$  and  $t + \Delta t$  :

$$
k_{\text{off}}\Delta t \times (1 - k_{\text{off}}\Delta t)^{t/\Delta t}
$$
\n
$$
\boxed{p(t) = k_{\text{off}}e^{-k_{\text{off}}t}}
$$
\n
$$
p(t) = k_{\text{off}}e^{-k_{\text{off}}t}
$$
\n
$$
k_{\text{off}} = \sqrt{\frac{\sum_{t=1}^{k} p(t)dt}{t}}
$$

Average binding time  $\langle t \rangle =$ 0  $t\,p(t)dt =$  $k_{\mathrm{off}}$ 

**Proteins remain bound to specific target sites for minutes to hours, while they unbind from nonspecific sites after milliseconds to seconds.**



 $k_{\rm on}$  $k_{\mathrm{off}}$  $[P] + [T] \stackrel{\text{on}}{\longrightarrow} [P-T]$ 

*d*[P-T] *dt*  $= k_{on}[P][T] - k_{off}[P-T]$ 

6 **[T] concentration of empty target sites [P-T] concentration of proteins bound to target sites [P] concentration of free proteins**

target site must be recognized with 1 base-pair (0*.*34 nm) precision, as displacement by 1 bp results initially empty target sites [P-T]=0

$$
\frac{d[\mathbf{P}\text{-}\mathbf{T}]}{dt} = (k_{\text{on}}[\mathbf{T}])[\mathbf{P}] \equiv \frac{[\mathbf{P}]}{t_s}
$$

#### 1*d* 3*d* (*A*) (*B*) **characteristic search time**

$$
t_s = (k_{\rm on}[\mathrm{T}])^{-1}
$$

## **How quickly proteins find target sites on DNA?**

**Characteristic search time via 3D diffusion**

$$
k_{\rm on} = 4\pi D_3 b \qquad t_s = (k_{\rm on}[{\rm T}])^{-1}
$$

**1917 Smoluchowski theory**

**Example: characteristic search time for lac repressor protein in E. coli**

 $b \approx 0.34$ nm  $D_3 \approx 30 \mu m^2/s$  $[T] \sim 1$  per cell  $\sim 10^{-9} M$  $k_{\rm on} \sim 10^8 M^{-1} s^{-1}$  *t<sub>s</sub>*  $\sim 10 s$ 



**Figure 1.** (*A*) Schematic representation of the protein–DNA search problem. The protein (yellow) **Molar concentration**  $1 M = 6 \times 10^{26} \text{m}^{-3}$ 

1*d* 3*d* (*A*) (*B*) J. Mol. Biol. **53**, 401-417 (1970) **in vitro experiments (1970)**  $k_{\text{on}}^{\text{exp}} \sim 10^{10} M^{-1} s^{-1}$  *t<sub>s</sub>* ~ 0*.*1*s* A.D.Riggs *et al.*,

#### **Why is experimentally observed rate 100 times larger?**

#### Berg - von Hippel theory (1980s) or cell nucleus (in eukaryotes). Compare with figure 9(*A*) which shows confined DNA. (*B*) The target site must be recognized with 1 base-pair (0*.*34 nm) precision, as displacement by 1 bp results

#### **(facilitated diffusion)**

- **1. Proteins diffuse in space and nonspecifically bind to a random location on DNA.**
- **2. Proteins slide (diffuse) along the DNA.**
- **3. Proteins jump (diffuse) to another random location on DNA and continue this sliding/ jumping process until the target site is found.**



**Figure 2.** (*A*) The mechanism of facilitated diffusion. The search process consists of alternating  $D_3$  - diffusion constant in space antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites.  $D_1$ − diffusion constant along the DNA  $b = 0.34$ nm  $L$  **- DNA length** 

#### **How long that is it take to find a target site in this process?** *1.3. History of the problem: theory*

O.G.Berg et al., Biochemistry **20**, 6929-48 (1981) 3D diffusion and effectively 1D diffusion of protein along DNA (*the 1D/3D mechanism*) was suggested. This mechanism was first proposed and dismissed by Riggs *et al* [1] but was soon <u>Dioditumblity</u> 20, 0020 40 (1301)

#### Berg - von Hippel theory (1980s) target site must be recognized with 1 base-pair (0*.*34 nm) precision, as displacement by 1 bp results

#### First assume fixed sliding time  $\tau_{1d}$

**Number of distinct sites visited during each sliding event**

 $n = \sqrt{16D_1\tau_{1d}/(\pi b^2)}$ 

(valid for *n*>>1)

#### **Probability that target site is found during a sliding event**

$$
q=nb/L
$$

**Probability that target site is found exactly after N<sub>R</sub> rounds** 

 $p(N_R) = q(1-q)^{N_R-1}$ 

**Average number of rounds needed to find the target**  $\infty$ 

$$
\overline{N_R} = \sum_{N_R=1} N_R p(N_R) = 1/q
$$



**Figure 2.** (*A*) The mechanism of facilitated diffusion. The search process consists of alternating  $b = 0.34$ nm  $L$  **- DNA length** 

- rounds of 3D and 1D and 1D and 1D and 1D and 1D and 1D, *a*nd time space during the time to the time that the tim antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites.  $D_3$  - diffusion constant in space
- **diffusion constant along the DNA** sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is  $D_1$ - diffusion constant along the DNA
- responsible for the speed-up tend-up the speed-up tend-up to the speed-up tend-up to the speed-up tend-up tend<br>In a characteristic iumning time  $\tau_{3d}$  - characteristic jumping time

#### **Average search time** *1.3. History of the problem: theory*

$$
\boxed{\overline{t}_s = \overline{N_R} \left( \tau_{1d} + \tau_{3d} \right)}
$$

O.G.Berg et al., Biochemistry **20**, 6929-48 (1981)  $\cap$  C Rora ot al by Berg and Blomberg [4] and finally developed by Berg *et al* [5]. The basic idea of the 1D/3D  $proontning$  **</u>** 

suggested. This mechanism was first proposed and dismissed by Riggs *et al* [1] but was soon

#### **Facilitated diffusion** in a different sequence and consequently a different site.

#### **In reality sliding times are exponentially distributed**

$$
p(\tau_{1d}) = k_{\text{off}}^{\text{NS}} e^{-k_{\text{off}}^{\text{NS}} \tau_{1d}}
$$

$$
\langle \tau_{1d} \rangle = \int_0^\infty d\tau_{1d} \,\tau_{1d} \, p(\tau_{1d}) = 1/k_{\text{off}}^{\text{NS}}
$$

#### **Average number of distinct sites visited during each sliding**

$$
\langle n \rangle = \int_0^\infty d\tau_{1d} p(\tau_{1d}) \sqrt{16D_1 \tau_{1d}/(\pi b^2)}
$$

$$
\langle n \rangle = 2\sqrt{D_1 \langle \tau_{1d} \rangle / (b^2)}
$$

**Average probability that target site is found during a sliding event**

 $\langle q \rangle = \langle n \rangle b/L$ 

**Average number of rounds** *NR* **needed to find the target site**

$$
\overline{\langle N_R\rangle}=1/\left\langle q\right\rangle
$$



**Figure 2.** (*A*) The mechanism of facilitated diffusion. The search process consists of alternating rounds of 3D and 1D and 1D and 1D and 1D and 1D, respectively. The state of the time termine the termine termin<br>*F* diffusion constant in space antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites. **- diffusion constant along the DNA** sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is responsible for the speed-up tend-up the speed-up tend-up to the speed-up tend-up to the speed-up tend-up tend<br>in a characteristic iumning time  $b = 0.34$ nm  $L$  **- DNA length**  $D_3$  - diffusion constant in space  $D_1$ - diffusion constant along the DNA  $\tau_{3d}$  - characteristic jumping time

#### **Average search time**

$$
\overline{\langle t_s \rangle} = \overline{\langle N_R \rangle} (\langle \tau_{1d} \rangle + \tau_{3d})
$$

$$
\overline{\langle t_s \rangle} = \frac{L}{2\sqrt{D_1} \langle \tau_{1d} \rangle} (\langle \tau_{1d} \rangle + \tau_{3d})
$$

# **Facilitated diffusion**



(1D) Brownian motion or a random walk. Upon dissociation from the DNA, the protein

## **Example: search time for target site in bacteria on DNA with 106 base pairs**



Simultaneous search for target site by multiple proteins must find its target site  $\mathcal{A}$  and  $\mathcal{A}$  are confined with the cell nucleoid (in backeria) (in backeria) Simultaneous skarch for target site by **Shows** target site must be recognized with 1 base-pair (0,1 bp results) present by 1 bp results, and  $\overline{\mathbf{A}}$  . At  $\mathbf{A}$  and  $\mathbf{A}$  at  $\mathbf{A}$  and  $\mathbf{A}$ **Sinultaneous search for tarchtaneous** <u>emperant sur de a long nucleare</u>

...<br>Anteractions and collisions  $\rightarrow$  interactions and considers  $\rightarrow$ or cell nucleus (*in eucare in nored*). Compare with figure 9(*A*) which shows confined DNA. (*B)*  $\frac{1}{2}$ the must be recognized with 1 base-pair (0,<sup>34</sup> nm) precision, as displacement by 1 bp results and 1 bp results by 1 bp results and 1 bp **Figure 1. (***A***)** Search proteine are ignored. The problem of the problem. The pro must find its target site (red) on a long DNA molecule confined within the cell nucleoid (in bacteria) must find its target site (red) on a long DNA molecule confined with  $\mathcal{L}$  $\Box$ **letoractions and collisions** Figure 1. (*A*) Schematic representation of the protein (yellow) of the protei the *discretions* and opinions **between proteins are ignored Interactions and collisions** 



**Example 18 Set of the Example 2008** Search times for target site by individual

> $p_1(t_s) = \frac{1}{t_s}$  $\langle t_s \rangle$  $e^{-t_s/\langle t_s \rangle}$

What is the typical search time for the fastest *n n* **of** *n* **independently searching proteins?**

rounds of 3D and 1D and 1D and 1D and 1D and 1D and 1D, respectively. The second terminal terminal terminal te<br>Property of the terminal termi **(Extreme value distributions)** 

by Berg and Blomberg [4] and finally developed by Berg *et al* [5]. The basic idea of the 1D/3D

$$
p_n(t_s) = n \times p_1(t_s) \times \left( \int_{t_s}^{\infty} dt' \ p_1(t') \right)^{n-1} = \frac{n}{\langle t_s \rangle} e^{-nt_s/\overline{\langle t_s \rangle}}
$$

**Figure 1.** (*A*) Schematic representation of the protein–DNA search problem. The protein (yellow)

*1.3. History of the problem: theory* probability that one of probabili responsible for the speed-up by facilitated diffusion. responsible for the speed-up by facilitated diffusion. **Figure 2. (***A***)** The meaning of the mechanism of probability that of rounds of 3D and 1D diffusion, each with average duration τ3D and τ1D, respectively. (*B*) The antenna proteins india in diffusion on a proteins take long **namelon** target site at time *t*<sub>s</sub> to find the target sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is This allows the contrains to a<br>This archives the distance in the target some distance in the target site and reach it by a more than the targ sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is *n* **proteins finds the** 

**Figure 2.** (*A*) The mechanism of facilitated diffusion. The search process consists of alternating

sliding, effectively increasing the reaction from 1bp to ∼n⊃. The antenna effectively increasing the antenna effect is  $\mathcal{L} = \mathcal{L} \mathcal{L} = \mathcal{L} \mathcal{L}$ 

 $\mathsf n$  proteins finds the uproteins take longer time 3D diffusion and effectively 1D diffusion of protein along DNA (*the 1D/3D mechanism*) was suggsted. This was first proposed and dismissed by Riggs **proposed and dispite by Riggs and All but was soon Figure 2.** (*A*) The mechanism of facilitated diffusion. The search process consists of alternating rounds of 3D and 1D diffusion, each with average duration τ3D and τ1D, respectively. (*B*) The n proteins finds the proteins take longer time  $\overline{\phantom{a}}$ **target site at time t's a to find the target site and reach it by** sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is sliding, effectively increasing the reaction cross-section from 1bp to ∼*n*¯. The antenna effect is antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites. This appropendium to a target some distance and reach and reach and reach it and reach it and reach it and reach i antenna effect [9]. During 1D diffusion (sliding) along DNA, a protein visits on average *n*¯ sites. This about the protein to a about the control and reach it b probability that one of probability that other n-1

This allows the protein to associate some distance ∞nd reach it and reach it by a protein the target site and reach it by a protein the target site and reach it by a protein the target site and reach it by a protein the t **rounds of 3D and 1D diffusion, each with average duration, each with average duration to 3D and the 1D, respectively. ( rounds and 1D and 1D and 1D average search time is and time is and the search of the is and the search time is and the search tim reduced by factor** *n*

$$
\int_0^\infty dt_s \, t_s \, p_n(t_s) = \frac{\overline{\langle t_s \rangle}}{n}
$$

## **Statistical mechanics of polymers and filaments**



## **Statistical mechanics of polymers and filaments**

**molecular dynamics simulation**



**Note: in equilibrium averaging over time is equivalent to averaging over all possible configurations weighted with Boltzmann weights!**

**partition function (sum over all possible configurations)**

**expected value of**  $\langle \emptyset \rangle = \sum_{c}$ 

$$
Z = \sum_{c} e^{-E_c/k_B T}
$$

$$
\langle \mathcal{O} \rangle = \sum_{c} \mathcal{O}_{c} \frac{e^{-E_{c}/k_{B}T}}{Z}
$$

- $E_c$ **energy of a given configuration**
	- *T* **temperature**
- $k_B$ **Boltzmann constant**

 $k_B = 1.38 \times 10^{-23}$  JK<sup>-1</sup>

# **Persistence length**

#### **correlations between tangents**

$$
\big|\langle \mathbf{t}(s)\cdot \mathbf{t}(s+x)\rangle = e^{-x/\ell_p}\big|
$$

**tangents become uncorrelated beyond persistence length!**



**persistence length**

$$
\ell_p = \frac{B}{k_B T}
$$

- *B* **filament bending rigidity**
- *T* **temperature**
- *kBT <sup>L</sup>* **filament length**

**Short filaments remain straight**

 $L \ll l_p$   $L \gg l_p$ 

**Long filaments perform self-avoiding random walk**



## **Examples: persistence length**

*B*

 $k_B T$ 

 $\ell_p$ 



**Persistence length for polymers is on the order of nm**

**actin**  $\ell_p \approx 17 \,\mu\text{m}$ 

**microtubule**  $\ell_p \approx 1.4 \text{ mm}$ 

 $10<sub>nm</sub>$ 

17

**double stranded DNA**  $\ell_p \approx 50$  nm

#### **single stranded DNA**

 $\ell_p \approx 2$  nm

**uncooked spagetthi**

 $\ell_p \approx 10^{18}$  m

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



## **Ideal chain vs worm-like chain**

*N* **identical unstretchable links (Kuhn segments) of length** *a* **with freely rotating joints**



**Each configuration** *C* **has zero energy cost.**

$$
E_c=0
$$

## **Ideal chain Worm-like chain**

#### **Continuous unstretchable rod**



**Bending energy cost of configuration** *C***:**

$$
E_c=\frac{B}{2}\int_0^L ds \left(\frac{d^2\vec{r}}{ds^2}\right)^2
$$

**Each configuration** *C* **appears with probability**   $p_c \propto e^{-E_c/k_B T}$ 

*L* **=** *Na* **- chain length**

## **Ideal chain vs worm-like chain**

*N* **identical unstretchable links (Kuhn segments) of length** *a* **with freely rotating joints**



**Ideal chain Worm-like chain**

**Continuous unstretchable rod**



$$
\left<\vec{R}_{AB}^2\right>=Na^2=aL
$$

 $\overline{\phantom{a}}$  $\vec{R}_{\angle}^2$  $\binom{2}{AB}$   $\approx 2\ell_p L =$ 2*BL*  $k_{B}T$ 

#### **End-to-end distance fluctuations can be made identical if one choses the segment length to be**

$$
a=2\ell_p
$$

*L* **=** *Na* **- chain length**

# **Stretching of ideal freely jointed chain**



#### **Exact result for end-to-end distance**

 $\hat{x}$ 

 $\hat{y}$ 

*z*ˆ



## **Stretching of worm-like chains**

#### Assume long chains  $L \gg \ell_p$



$$
\frac{F\ell_p}{k_B T} = \frac{1}{4} \left( 1 - \frac{\langle x \rangle}{L} \right)^{-2} - \frac{1}{4} + \frac{\langle x \rangle}{L}
$$

J.F. Marko and E.D. Siggia,

Macromolecules **28**, 8759-8770 (1995)

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#### **Experimental results for stretching of DNA 8760** Marko and Siggia *Macromolecules, Vol. 28, No. 26, 1995*

 $L = 32.8 \mu m$ 



## **Random coil to globule transition in polymers**  $T > \Theta$  *T* <  $\Theta$ **random coil compact globule**

$$
R \sim \sqrt{L\ell_p} \qquad R \sim \big(
$$

#### **at high temperature entropic contributions dominate**



$$
R\sim \left(d^2L\right)^{1/3}
$$

at low temperature strong, first-order-like, coil-to-native transitions. attraction between polymer model show the transition from the transition from the coil to the coil to the coil to the coil to the native state by a state by the nuclear parties of  $\mathbf{S}$ d - diameter of polymer chain interaction parameters single singl of, usually symmetry-related, lowest-energy states). Hence, the nearest-neighbor interaction in the Goj model is similar to *E*p: (9) Doniach, S., Garel, T.; Orland, H. *J. Chem. Phys.* **1996**, *105*, 1605. attraction between polymer chains dominates **Figure 6.** Snapshot showing the molten-globule state of a 512-segment semiflexible lattice polymer at *B*/*E*<sup>p</sup> ) 0.1 and *k*B*T*/*E*<sup>p</sup> ) 3.289 (symbol **at low temperature** 

**A. <u>J. Phys. Chem. B</u> 110**, 3734 (2006)  $\mathsf{B}$ I, <u>J. Phys. Chem. t</u> Figures from: W.B. Hu and D. Frenkel, J. Phys. Chem. B 110, 3734 (2006)

# **Further reading**



# **Dynamics of actin filaments and microtubules**



## **Cytoskeleton in cells**

**Cytoskeleton matrix gives the cell shape and mechanical resistance to deformation.**





#### **Microtubule**

**(wikipedia)**

# **Crawling of cells**



#### **migration of skin cells during wound healing**

**spread of cancer cells during metastasis of tumors**

**amoeba searching for food**  $v \sim 0.1 \mu m/s$ 

## **Immune system: neutrophils chasing bacteria**



**David Rogers, 1950s**

## **Movement of bacteria**

#### *Listeria monocytogenes* **moving in infected cells**



**Julie Theriot (speeded up 150x)**  $v \sim 0.1 - 0.3 \mu m/s$ 



**a b** cap<br>Co  $\overline{a}$ L. A. Cameron *et al.*, Nat. Rev. Mol. Cell Biol. **1**, 110 (2000)

## **Molecular motors**



A*.*B*.* Kolomeisky, J. Phys.: Condens. Matter **25**, 463101 (2013)

**Contraction of muscles**

## **Transport of large molecules around cells (diffusion too slow)**

 $v \sim 1 \mu m/s$ 



#### **Harvard BioVisions**

https://www.youtube.com/watch?v=FzcTgrxMzZk

# **Cell division**

#### **Segregation of chromosomes Contractile ring divides the cell in two**





#### **Microtubules Actin**

# **Swimming of sperm cells**



## **Swimming of Chlamydomonas (green alga)**



#### https://sites.tufts.edu/guastolab/movies/

**Jeff Guasto**

**Jeff Guasto**

 $v \sim 50 \mu \text{m/s}$  *v*  $\sim 60 \mu \text{m/s}$ 

#### **Bending is produced by motors walking on neighboring microtubule-like structures**

## **Actin filaments**





# **Actin filament growing against the barrier**



**work done against the barrier for insertion of new monomer**

$$
W = Fa
$$

**effective monomer free energy potential without barrier**

**effective monomer free energy potential with barrier**





## **Actin filament growing against the barrier**



**Maximal force that can be balanced by growing filament**   $k_{\text{or}}^+$ **(stall force)**

$$
v^{+}(F_{\max}) = 0 \qquad \longrightarrow \qquad F_{\max} = \frac{k_B T}{a} \ln\left(\frac{k_{\text{on}}^{+}[M]}{k_{\text{off}}^{+}}\right)
$$

$$
k_{\text{on}}^{+} \sim 10 \mu \text{M}^{-1} \text{s}^{-1}
$$
  
\n
$$
k_{\text{off}}^{+} \sim 1 \text{s}^{-1}
$$
  
\n
$$
[M] \sim 10 \mu \text{M}
$$
  
\n
$$
a \approx 2.5 \text{nm}
$$
  
\n
$$
F_{\text{max}} \sim 8 \text{pN}
$$

## **Movement of bacteria**



## **Microtubules**



# **Microtubule dynamic instability**



CO GDP-tubulin dimer

shrinkage

CO GTP-tubulin dimer



**Wikipedia**

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**cap disappears**

## **Simple model of microtubule growth**



**Typical values in a tubilin solution** of concentration  $[\mathrm{T}] \approx 10 \mathrm{\mu M}$  :  $v_q \approx 2 \mu m / \text{min}$  $v_s \approx 20 \mu\text{m/min}$   $\sim \text{const}$  $r_{\text{cat}} \approx 0.24 \text{min}^{-1}$  $r_{\rm res} \approx 3 \text{min}^{-1}$  $\propto |\text{T}|$  $\propto$   $\lceil T \rceil$  $\sim$  const

**Let's ignore all molecular details and assume that microtubules switch at fixed rates between growing and shrinking phases**

#### **Master equation:**

 $\partial p_{\rm growth}$  $\partial t$  $=-r_{\rm cat}\,p_{\rm growth}+r_{\rm res}\,p_{\rm shrinking}$  $\partial p_\text{shrinking}$  $\frac{\partial t}{\partial t}$  = + $r_{\text{cat}} p_{\text{growth}} - r_{\text{res}} p_{\text{shrinking}}$ 

 $p_{\text{growth}} + p_{\text{shrinking}} = 1$ 

#### **Steady state (** $\partial p/\partial t \equiv 0$ ):

$$
p_{\text{growth}}^* = \frac{r_{\text{res}}}{r_{\text{res}} + r_{\text{cat}}} \quad p_{\text{shrinking}}^* = \frac{r_{\text{cat}}}{r_{\text{res}} + r_{\text{cat}}}
$$

#### **Average growth speed of microtubules**

$$
\overline{v} = p_{\text{growth}}^* v_g - p_{\text{shrinking}}^* v_s
$$

 $\overline{v} \approx 0.4 \,\mu\text{m/min}$ 

40

## **How cells control the total length of microtubules**



V. Varga *et al.*, Cell 138, 1174-1183 (2009) microtubules (Figure S2). At these low Kip3p concentrations,

## **Density of motors bound to microtubules**



## **Density of motors bound to microtubules**

**[***M***] concentration of unbound motors**

#### **Time evolution for density of bound motors**

$$
\frac{\partial \rho(x,t)}{\partial t} = k_{\text{bind}}[M] - v_{\text{mot}} \frac{\partial \rho(x,t)}{\partial x}
$$

on the Total Kip3p Concentration

tached to the microtubules and moved processively with

#### For initially empty microtubule stabilized, rhodamine-labeled microtubules could be detected burpty microtabard

$$
\rho(x,t) = \begin{cases} \frac{k_{\text{bind}}[M]}{v_{\text{mot}}} x, & 0 < x < v_{\text{mot}} t \\ k_{\text{bind}}[M]t, & x > v_{\text{mot}} t \end{cases}
$$

#### ary density of on the Total Kips Concentration of the Total Street, and the Total Total Total Total Total Total Total Total T<br>3 percentration of the Total Tot  $\frac{1}{\sqrt{2}}$ length. The stationary density of reach the plus end of the microtubule, where they cause depolymerization.  $\frac{1}{2}$ reach the microtubule, who hound motors length. The high processive stationary density of reach the plus end of the microtubule, where they cause depolymerization. The net result is that longer microtubules depolymerize more quickly. Spiking experiments revealed an unusual interaction between **bound motors** The End-Residence Time of Kip3p Depends ialy defisity of **Stationary density of**

$$
\rho^*(x) = \frac{k_{\text{bind}}[M]}{v_{\text{mot}}}x
$$



## **Length dependent depolymerization rate**



**Depolymerization rate is proportional to density of Kip3 motors**

$$
\rho^*(L) = \frac{k_{\text{bind}}[M]}{v_{\text{mot}}}L
$$

**Figure 15.38:** V. Varga *et al.*, <u>Nat. Cell Biol.</u> 8, 957-962 (2006)

## **Controlled length of microtubules**



## **Molecular motors**



A*.*B*.* Kolomeisky, J. Phys.: Condens. Matter **25**, 463101 (2013)

**Contraction of muscles**

## **Transport of large molecules around cells (diffusion too slow)**

 $v \sim 1 \mu m/s$ 



#### **Harvard BioVisions**

https://www.youtube.com/watch?v=FzcTgrxMzZk

# **Movement of molecular motors is powered by ATP molecules**

#### **Myosin motor walking on actin in muscles**

#### **Kinesin motor walking on microtubule**



#### **Graham Johnson**

https://www.youtube.com/watch?v=oHDRIwRZRVI https://www.youtube.com/watch?v=YAva4g3Pk6k

#### **Current was a ratio was generated by flagshing with was generated by flagshing a rate with a periodic signal array repeated by flagshing multiple asymmetric gates with a periodic signal of the amount of the amount of the Current in the fabricated device in the fabricated device in the fabricate increased as the fabricated statement as the fabricated term of the theoretical model. The current algorithm width W decreased, which contradicted** We investigated the structural parameter dependence of the structural parameter dependence of the directed current in GaAs-nanowire-based Brownian ratchet devices. The directed current in GaAs-nanowire-based Brownian ratch depended on the gates N, when N was smaller than 6. We discussed the obtained results in terms of the structural parameters  $\alpha$

#### © 2015 The Japan Society of Applied Physics **Myosin motor**

**ATP driven process drives molecular motors along the filaments**

#### **Brownian ratchet** dependence of carrier transfer efficiency and the effect of electron reservoirs on current generation in flashing ratchet operation.

**net movement of particles is achieved by periodic modulation of asymmetric external potential**





## **ATP concentration dependent speed of motors**



#### **Kinesin motor on microtubules**



**Maximal speed**

 $v_{\text{max}} \approx 0.6 \,\mu\text{m/s}$ 

**ATP concentration at half the maximal speed**  $K_d \approx 50 \,\mu \text{M}$ 

**Figure 16.54:** Figure 16.54: At the Call m. Filmps et al., Fitysical Dividyy of the Gen $q_9$ R. Phillips et al., Physical Biology of the Cell

# **Motors carrying the load**

#### **Force exerted on kinesin motors carrying plastic beads can be controlled with optical tweezers**



$$
F \approx k \Delta x
$$

**Effective spring constant**  *k* **depends on the bead size, refractive indices of the bead and surrounding medium, and the gradient of laser intensity**

# **How motor speed depends on the loading force?**

<u>Na</u> K. Visscher et al., **Nature 400**, 184-189 (1999) K. Visscher et al., Nature **400**, 184-189 (1999)

# **Motor velocity dependence on the load**

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**kinesin walking on microtubules**



K. Visscher et al., Nature **400**, 184-189 (1999)



**How important is viscous drag for motors carrying vesicles?** 

 $-\epsilon \rightarrow 0$  $F_{\rm drag} = 6\pi\eta R v$  $F_{\rm drag} \sim 6\pi 10^{-3} {\rm kgm}^{-1} {\rm s}^{-1} \cdot 1 \mu {\rm m} \cdot 1 \mu {\rm m/s}$  $10<sup>-2</sup>$  and  $\overline{}$  $F_{\rm drag} \sim 10^{-2}\, {\rm pN}$ 

#### **Note: viscous drag is negligible** 54B 5::;7469B F;8 <7:G ;F 6G9 9S=98A<9465C >:56698 O[AK3 DJP3 #;

#### ATP concentration dependent stall force <u>:4:4:55</u>  $\overline{\phantom{a}}$



 $$  $\frac{1}{2}$  nm  $\overline{\text{5 min}}$  $\frac{d}{dx}$ oto **motor step length**

#### $J_{\rm{obs}}$  ; for  $\sim$  54  $\mu$ 85  $\mu$ **Position clamp**



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 $F_{\rm max} = \frac{1}{\sigma_{\rm max}} \approx \frac{1}{\sigma_{\rm max}} \sim 10 {\rm pN}_{1.52}$  K. Visscher et al  $2^{12}$  , and the first state of  $\Delta$ G amp  $\alpha' = \frac{1}{100} \approx 100$  $\mathbb{R}$  and  $\mathbb{R}$   $\mathbb{R}$  ,-./012345363/789 d9 6N54\_ ;78 :;OO95M79P 56 "W\* K;8 P7MM9P6=;4P 54? N9ODK7O ?=P:7PP=;4PC W3 W89298H F3 I;546 54? ]3 I746 K;8 N9OD 2=6N 6N9 545OGP=P ;K 89DO=:56=;4 =4698<9?=569PC "3 "86N78 K;8 9?=6;8=5O  $P_{\text{max}}$  as  $\frac{9}{2}$   $\frac{8}{2}$   $\frac{1}{2}$  $\alpha$  cases  $\alpha$  and  $\alpha$  $F_{\rm max} =$  $\Delta G_{\rm ATP}$ *a*  $\approx$  $20k_BT$ 8nm  $\sim 10 \text{pN}$ 

K. Visscher et al., <u>Nature</u> 400, 184-189 (1999) M. VISSCHEI EL AL., <u>IVALUIE</u> 400, T64-T0

# **Skeletal muscle contraction by myosin motors**



# **Skeletal muscle contraction by myosin motors**



**motors per bundle**

 $\Box$  $\Box$  $\Box$ 60 M line **Estimated force generated by myosin motors** 

**Muscles contract at twice the speed of myosin motors**

 $\sim 0.1$ -1 $\mu$ m/s

#### when a middle represents the middle represents the aligned myosin thick filaments and the aligned myosin thick fil  $\mathbf{v}$  bands show the position of actine. The diagrams below the change in sarcomere length during muscle muscle **Muscles may contract by**

$$
300 \times \frac{2 \text{pN}}{\pi (30 \text{nm})^2} \sim 20 \text{N/cm}^2
$$
 **Muscles m**

# **Skeletal muscle contraction is controlled by nerve cells**



**Electric signal from nerve cells releases Ca2+ from sarcoplasmic reticulum**



#### Low Ca<sup>2+</sup>, muscles are relaxed

myosin binding sites on actin.



#### High Ca<sup>2+</sup>, muscles are contracted

(a) Tropomyosin and troponin work together to block the (b) When a calcium ion binds to troponin, the troponin-<br>tropomyosin complex moves, exposing myosin binding sites.



Calcium ion Troponin-tropomyosin complex, moved

## **How muscles get ATP energy?**



### **How muscles get ATP energy?**



## **How muscles get ATP energy?**



#### **Aerobic respiration**



**Note: Citric acid cycle = Krebs cycle**

# **Electron transport chain**



**NADH products of the Cytric acid cycle are used to pump H+ to the space between outer and inner mitochondrial membrane.**

**Gradient of H+ concentration drives the ATP synthase motor that converts ADP to ATP.**

**Note: ATP synthase can run in reverse and use ATP to pump H+ at low concentrations.**

#### **ATP synthase**



## **Energetics of ATP hydrolysis**

#### **How much energy is released during ATP hydrolysis?**



**Chemical potentials are typically defined**  relative to concentration  $c_0 \sim 1$  M.

 $\mu_s(c_s) = \mu_s(c_0) + k_B T \ln(c_s/c_0)$ 

# **Crawling of cells**



#### **migration of skin cells during wound healing**

**spread of cancer cells during metastasis of tumors**

**amoeba searching for food**  $v \sim 0.1 \mu m/s$ 

## **Immune system: neutrophils chasing bacteria**



**David Rogers, 1950s**

#### **Crawling of cells** 952 Chapter 16: The Cytoskeleton

#### fish skin cell  $\hspace{1mm} v = 0.2 \mu\mathrm{m/s}$



#### **Swimming of sperm cells**  $\epsilon$  singlet  $\epsilon$

#### **Sperm flagellum is constructed from microtubules**



 $(A)$  100 nm inner sheath central singlet microtubule radial spoke outer dynein arm nexin plasma membrane inner dynein arm A microtubule B microtubule outer doublet microtubule (B)  $($  (C)  $)$  $\mathcal{L}$  100  $\mathcal{L}$ plasma de la propiedad de  $\mathcal{N}$  members in the set of  $\mathcal{N}$  is the set of  $\mathcal{N}$  $\sqrt{4}$   $\frac{1}{2}$   $\frac$  $\left| \right|$  of the doublet minimal  $\left| \right|$  $\mathbb{E}[\mathbf{$  $\begin{array}{c|c}\n\hline\n\text{100 nm} & \text{(B)}\n\end{array}$  (B)  $\begin{array}{c|c}\n\hline\n\text{110 mm} & \text{(C)} & \text{(C)} & \text{(D) T} & \text{(E)}\n\end{array}$ microclabate **Charly Dimicrotlabate** 

dynein arm

**Figure 16.4:** Structure of the axoneme. (A) Thin-section electron micrograph of a cross-section of the flagellum of the proteins that make the flagellum beat by substituting the microtubules relative to one another. (C) A side vie neighboring microtubule-like structures **Bending is produced by motors walking on** 



**Jeff Guasto**  $v \sim 50 \mu m/s$ 

## **Further reading**

