

# Bioimage Informatics

Lecture 18, Spring 2012

Bioimage Data Analysis (V)

Single Particle Tracking (part 3)

# Outline

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- Overview of single particle tracking techniques
- Review: linear assignment based single particle tracking
- Multiple hypothesis tracking
  
- Application I: fluorescence speckle microscopy

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- Overview of single particle tracking techniques
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# Overview of Single Particle Tracking Techniques (I)

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- Method 1: simple nearest neighbor tracking
  - Each particle is assigned to its nearest neighbor
  - Often a search radius is adopted
  - Rarely used; applicable only when particles are well separated
- Method 2: global nearest neighbor tracking
  - Association cost between a pair of particles is their distance

$$\min \sum_{i \in G_k} \sum_{j \in G_{k+1}} a^k(i, j) w^k(i, j)$$

$$\text{st. } \sum_i a(i, j) = 1 \quad \sum_j a(i, j) = 1 \quad a(i, j) \in \{0, 1\}$$

$$w^k(i, j) = \left\| x_j^{k+1} - x_i^k \right\|$$

# Overview of Single Particle Tracking Techniques (II)

- Method 3: global smooth motion tracking
  - Association cost between a pair of particles is their motion smoothness

$$\min \sum_{i \in G_k} \sum_{j \in G_{k+1}} a^k(i, j) w^k(i, j)$$

$$\text{st. } \sum_i a(i, j) = 1 \quad \sum_j a(i, j) = 1 \quad a(i, j) \in \{0, 1\}$$

$$c^k(i, j) = w_1 \left[ 1 - \frac{(x_i^k - x_i^{k-1})(x_j^{k+1} - x_i^k)}{\|x_i^k - x_i^{k-1}\| \|x_j^{k+1} - x_i^k\|} \right] + w_2 \left[ 1 - 2 \frac{\sqrt{\|x_i^k - x_i^{k-1}\| \|x_j^{k+1} - x_i^k\|}}{\|x_i^k - x_i^{k-1}\| + \|x_j^{k+1} - x_i^k\|} \right]$$

# Overview of Single Particle Tracking Techniques (III)

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- There are other ways to define the association cost.
  - Example 1: to incorporate particle intensity
- There are a variety of other tracking techniques.
  - Example: joint-probabilistic data-association filter (JPDAF)
  - Many of such techniques come from military applications
  - Many of these techniques are based on assumptions that may not necessarily hold in biological applications

# Overview of Single Particle Tracking Techniques (IV)

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- Distance → Global nearest neighbor

$$w^k(i, j) = \left\| x_j^{k+1} - x_i^k \right\|$$

- Smooth motion → Global smooth motion

$$w^k(i, j) = w_1 \left[ 1 - \frac{(x_i^k - x_l^{k-1})(x_j^{k+1} - x_i^k)}{\|x_i^k - x_l^{k-1}\| \|x_j^{k+1} - x_i^k\|} \right] + w_2 \left[ 1 - 2 \frac{\sqrt{\|x_i^k - x_l^{k-1}\| \|x_j^{k+1} - x_i^k\|}}{\|x_i^k - x_l^{k-1}\| + \|x_j^{k+1} - x_i^k\|} \right]$$

- Mahalanobis distance, where the prediction comes from typically a Kalman filter

$$w^k(i, j) = (x_i^k - \hat{x}_j^k)^T S(x_i^k)^{-1} (x_i^k - \hat{x}_j^k)$$

$$S(x_i^k) = \text{cov}(x_i^k - \hat{x}_j^k)$$

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- Overview of single particle tracking techniques
  - **Review: linear assignment based single particle tracking**
  - Multiple hypothesis tracking
  
  - Application I: fluorescence speckle microscopy



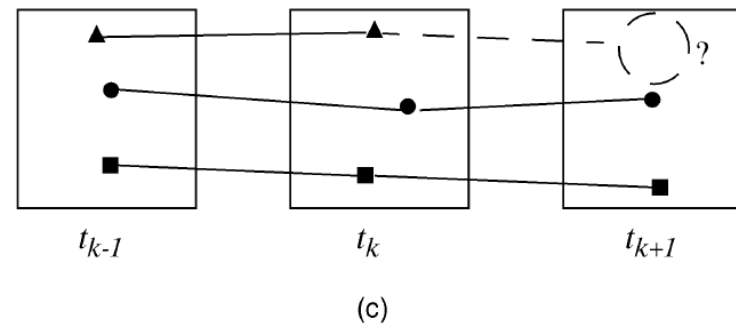
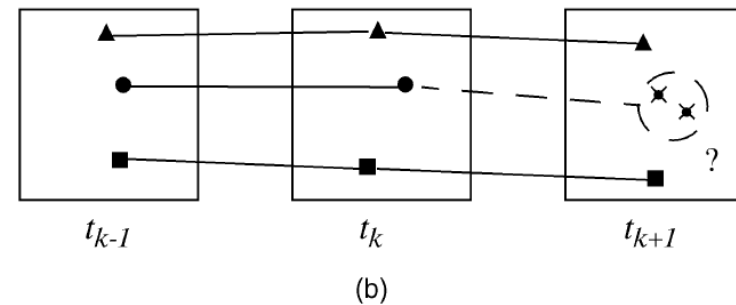
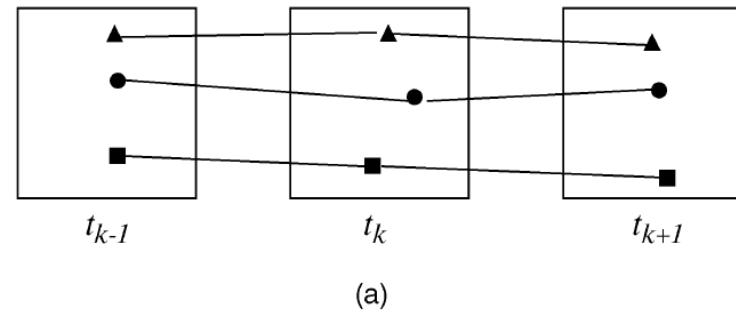
# Definition of Particle Tracking (II)

- Different cases

- Constant number of features
- Feature appearance
- Feature disappearance

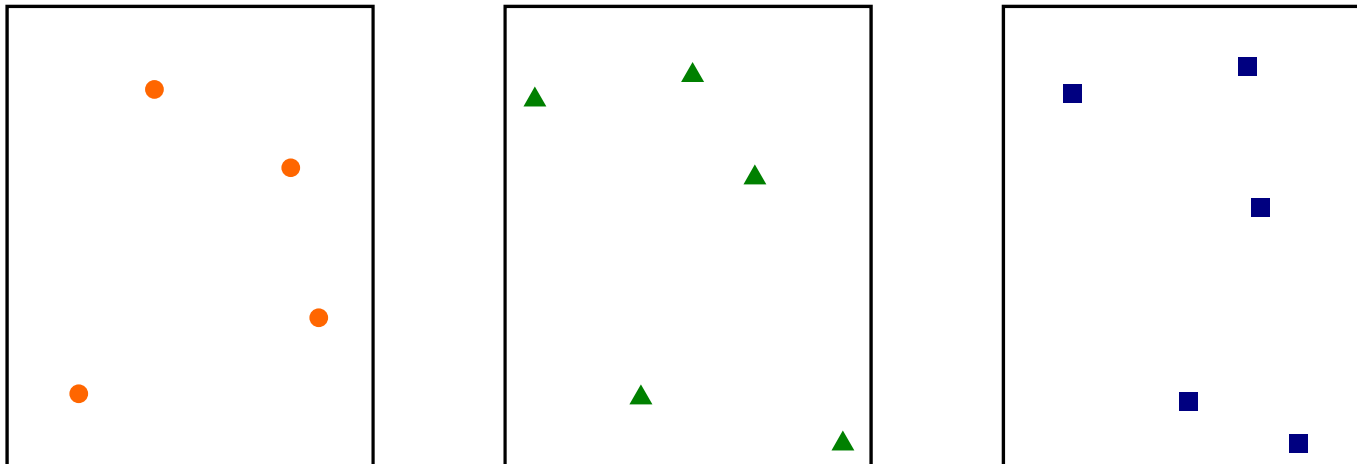
- Cases of feature appearance & disappearance

- Moving in or out of field of view
- Moving in or out of the focal plane
- Assembly/disassembly
- Feature merging/splitting



# Example: Particle Tracking (I)

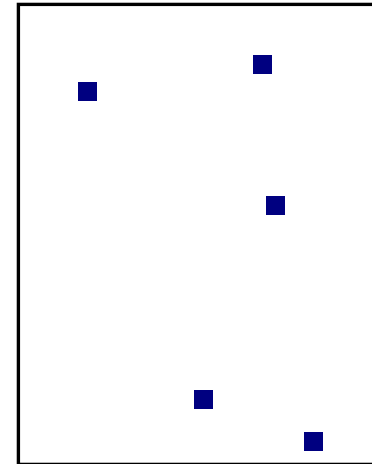
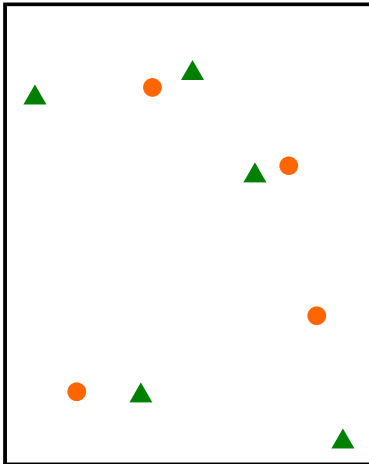
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- Frame  $i-1$
- ▲ Frame  $i$
- Frame  $i+1$

# Example: Particle Tracking (II)

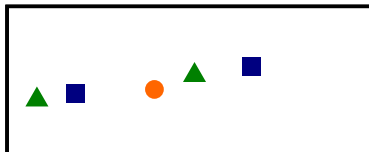
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- Frame  $i-1$
- ▲ Frame  $i$
- Frame  $i+1$

# Example of Particle Tracking (III)

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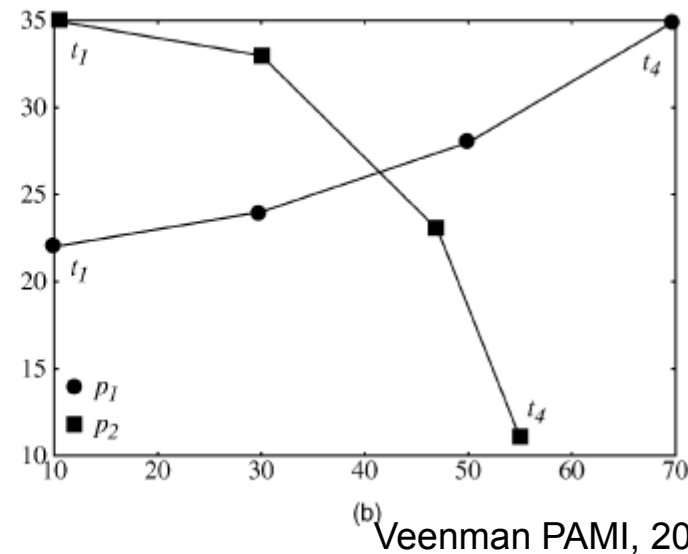
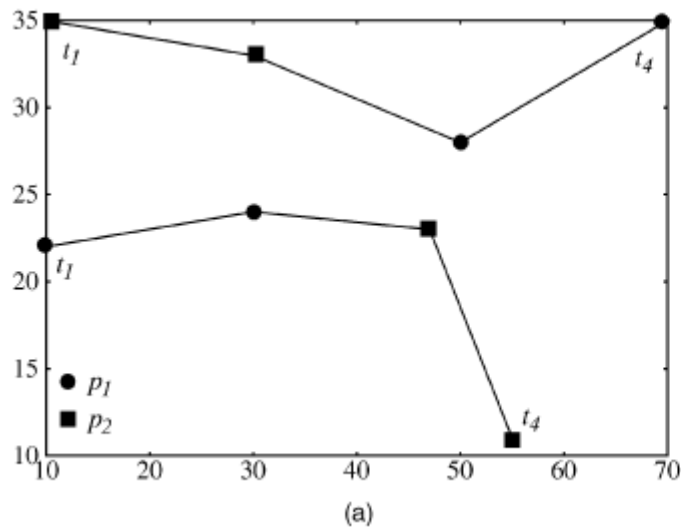
**Accumulated evidence from multiple frames  
makes tracking more reliable.**



- Frame  $i-1$
- ▲ Frame  $i$
- Frame  $i+1$

# Particle Tracking Based on Global Linear Assignment (I)

- An optimization strategy is required to resolve conflicts between competing assignments.
- Selection of assignment weight will critically influence outcomes.



(b) Veenman PAMI, 2001.

# Particle Tracking Based on Global Linear Assignment (II)

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- Formulation of the tracking problem as a bipartite graph assignment

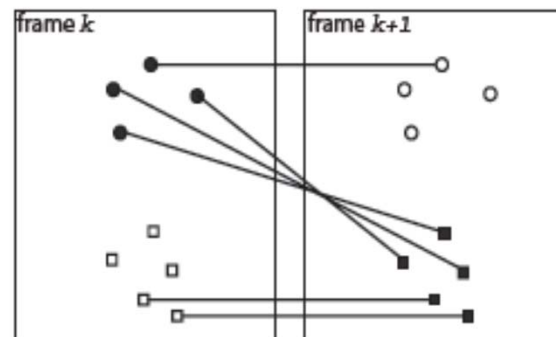
$$\min \sum_{i \in G_k} \sum_{j \in G_{k+1}} a^k(i, j) w^k(i, j)$$

$$\text{st. } \sum_i a(i, j) = 1 \quad \sum_j a(i, j) = 1 \quad a(i, j) \in \{0, 1\}$$

- There are efficient numerical algorithms to solve large scale assignment problems.
- Why not use a tripartite graph?
  - Optimal assignment of tripartite graph is NP-complete.
  - Difficult to resolve conflicts between two tripartite assignments.

# Handling Particle Appearance & Disappearance

- Track appearance and disappearance are handled by introducing virtual points.



**Figure 3. Handling particle appearance and disappearance**

G. Yang, A. Matov, G. Danuser, Reliable tracking of large scale dense antiparallel particle motion for fluorescence live cell imaging, *IEEE CVPR, 2005*

# References on Linear Assignment

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- Burkard R., Cela E., Linear assignment problems and extensions, pp.75-149, in *Handbook of Combinatorial Optimization*, D.-Z. Du & P. M. Pardalos (Eds.), Kluwer Academic Publishers, 1999.

[\(Downloadable from class web page\)](#)



# Assessment of Linear Assignment Based Particle Tracking

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- Disadvantage: The algorithm fundamentally only looks for the best solution over two consecutive frames (greedy).
- Disadvantage: It can not handle feature merging and splitting.
- Advantage: It has low computational complexity and can be used to tracking very large number of particles.

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- Overview of single particle tracking techniques
  - Review: linear assignment based single particle tracking
  - **Multiple hypothesis tracking**
  - Application I: fluorescence speckle microscopy

# MHT-Based Particle Tracking (I)

- “MHT is a deferred decision logic in which alternative data association hypotheses are formed whenever observation-to-track conflict situations occur.”
- Multiple competing hypotheses are represented in a tree structure.

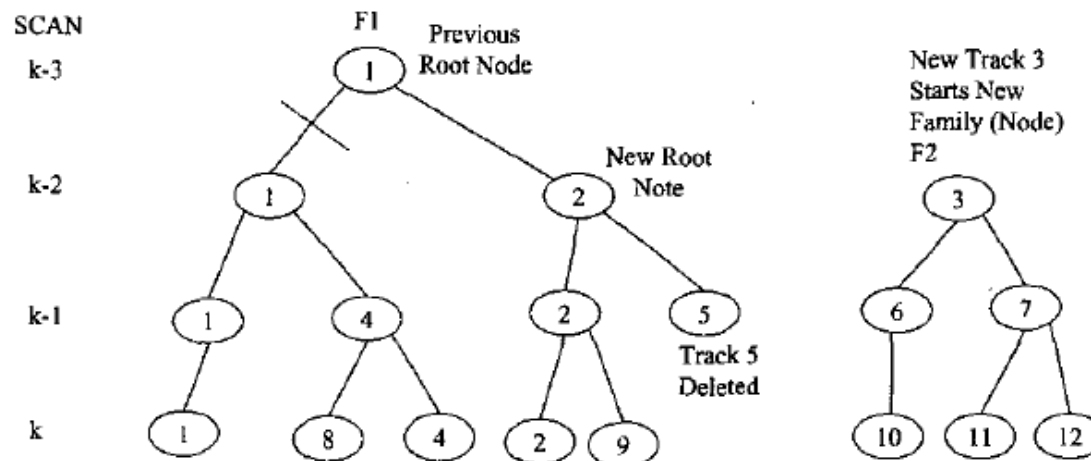


Fig. 4. Family (node) structure with  $N$ -scan pruning.

# MHT-Based Particle Tracking (II)

- The tree structure provides a flexible way to handle feature appearance/disappearance and merging/splitting.

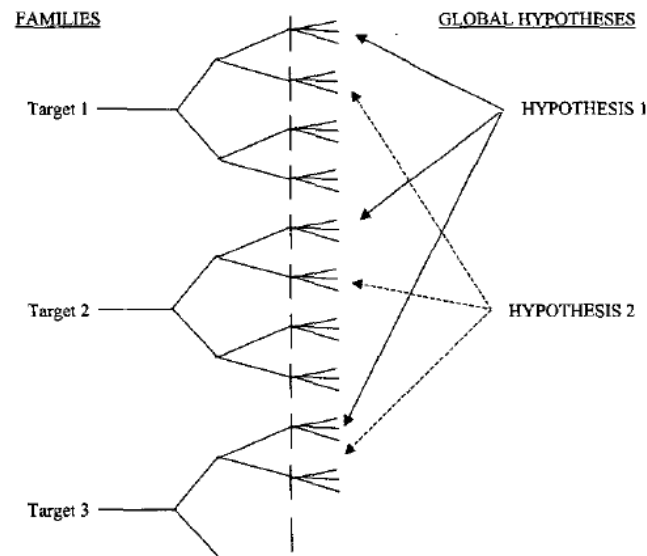


Fig. 5. Formation of hypotheses from tracks in families.

# MHT-Based Particle Tracking (III)

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- Advantages
  - An effective framework to incorporate multi-frame information.
  - A natural way to handle feature appearance and disappearance.
  - A natural way to handle feature merging/splitting.
- Disadvantages
  - Combinatorial explosion if the tree is not pruned.
  - Many variations in implementation.
  - High computation and memory cost.
- Overall a very important approach, especially when the number of features to be tracked is small.

# Methods to Handling Merging & Splitting

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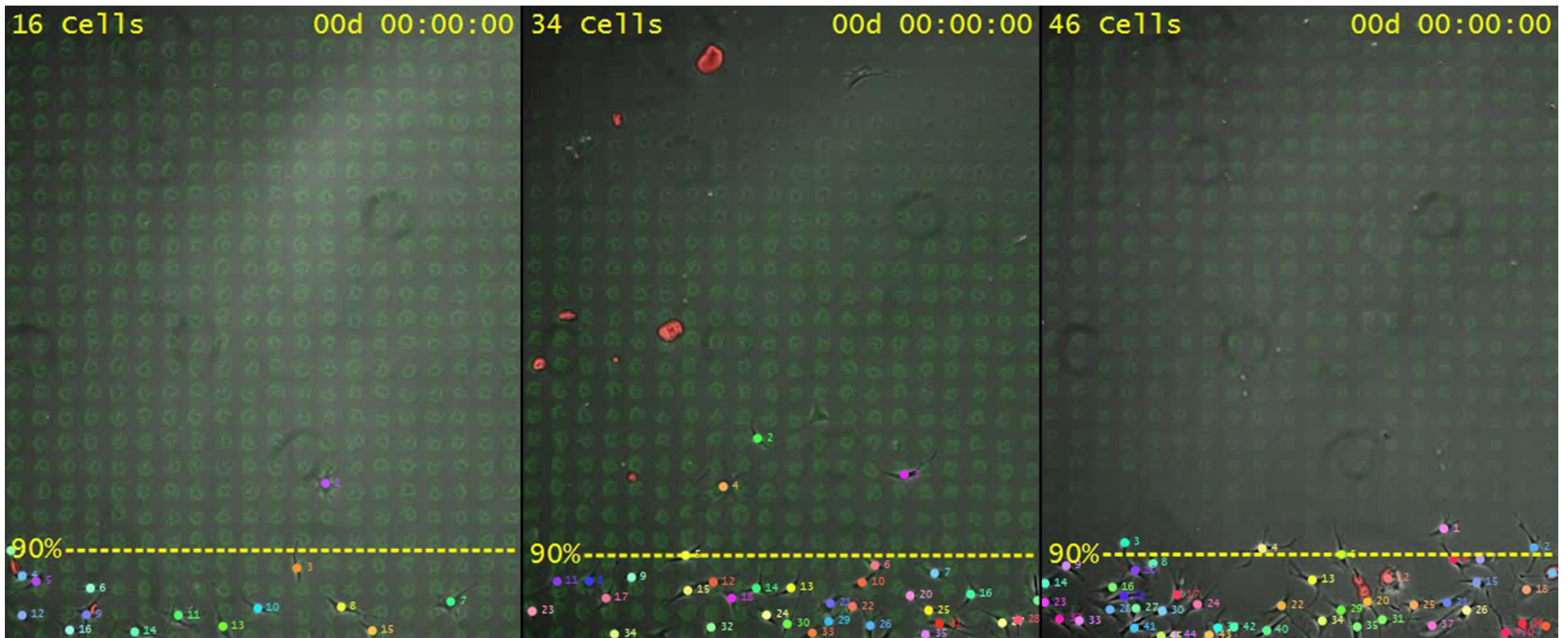
- Tracklet-based approaches

- Kanade T., Yin Z., Bise R., Huh S., Eom S., “Cell Image Analysis: Algorithms, System and Applications,” IEEE Workshop on Applications of Computer Vision (WACV) 2011.
- <http://celltracking.intel-research.net/>

- Graph-based approaches

- Padfield, D, Rittscher, J., Roysam B., “Coupled Minimum-Cost Flow Cell Tracking for High-Throughput Quantitative Analysis,” Medical Image Analysis Journal, 2010.
- [http://www.farsight-toolkit.org/wiki/Main\\_Page](http://www.farsight-toolkit.org/wiki/Main_Page)

# Tracking Migrating Cells

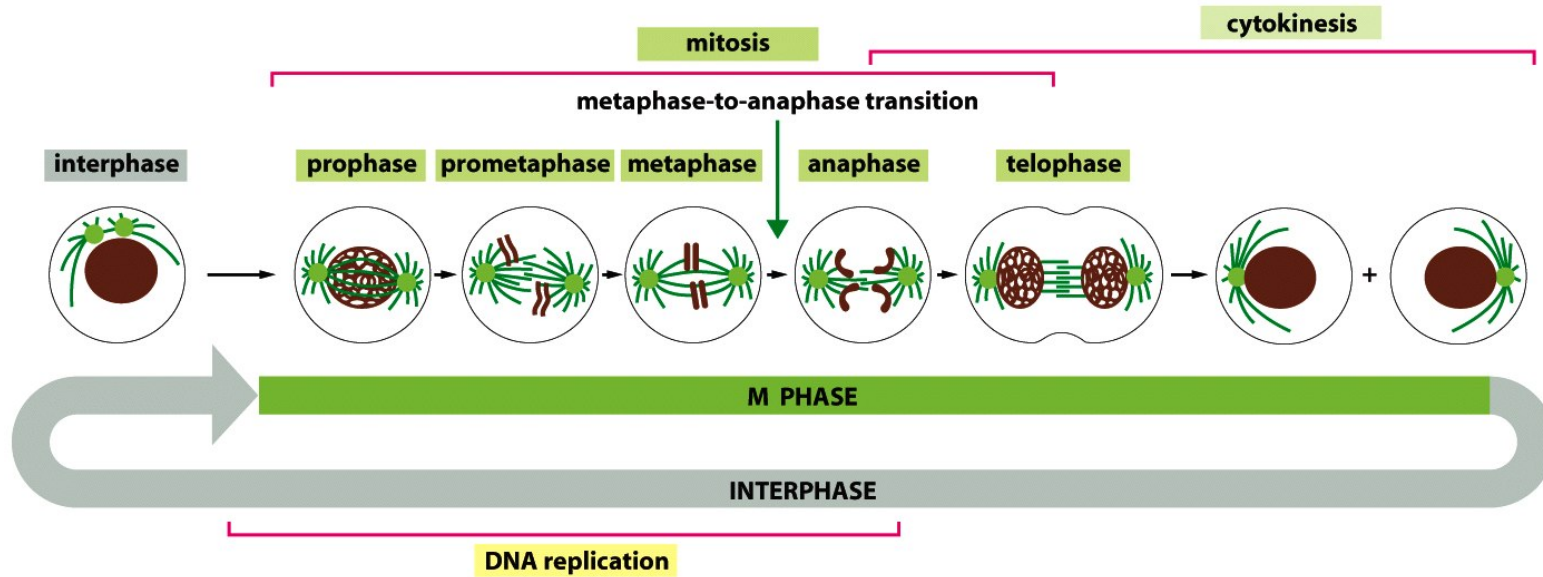


Courtesy of Lee Weiss & Takeo Kanade

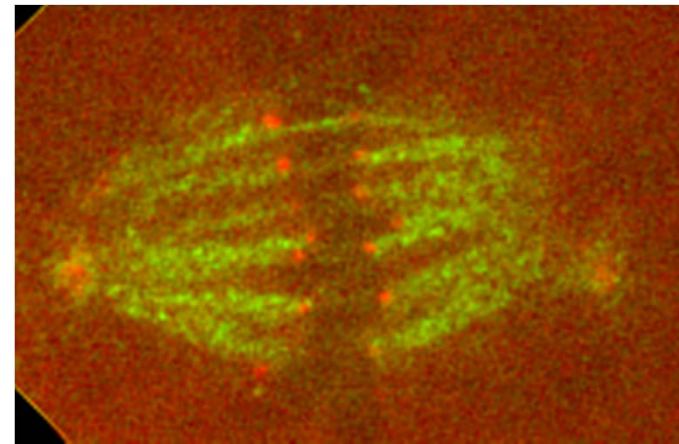
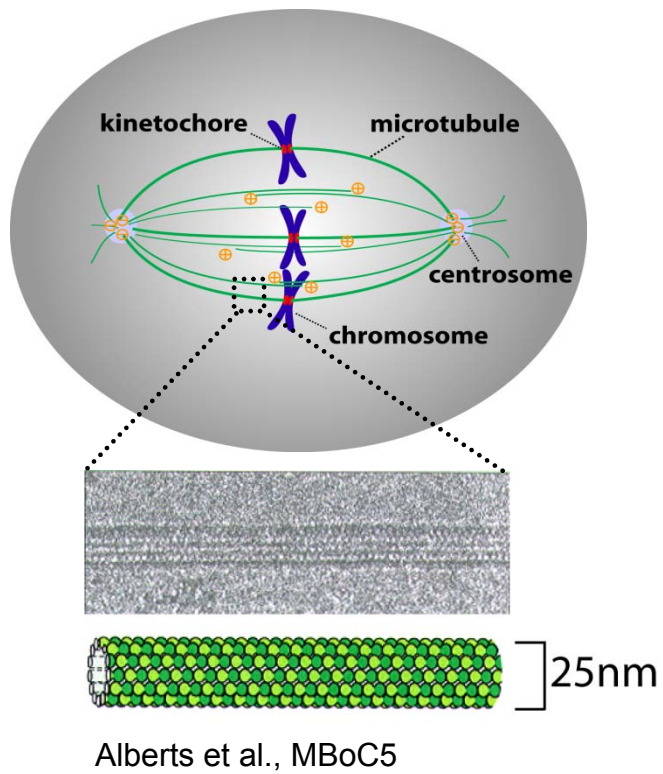
- 
- Overview of single particle tracking techniques
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- **Application I: fluorescence speckle microscopy**



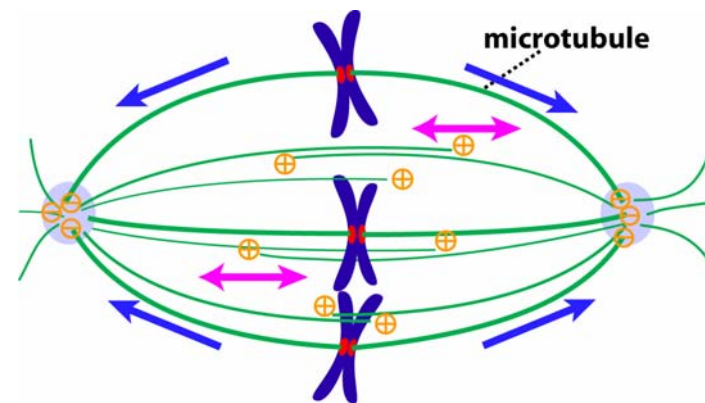
# Overview of Cell Cycle



# Dynamic Microtubules in the Mitotic Spindle

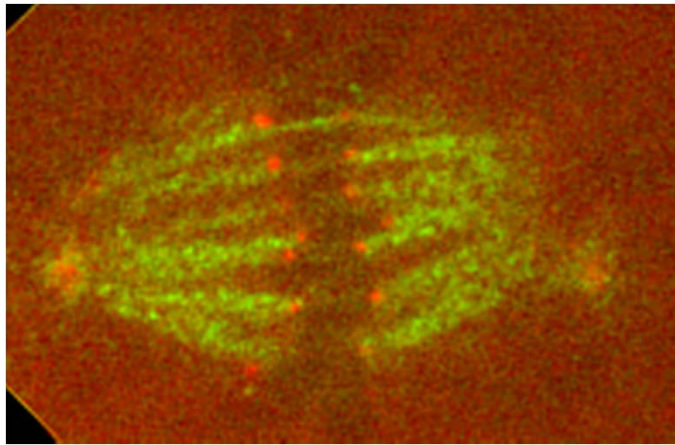


Green: microtubule  
Red: kinetochore



# Confirmation of Poleward Flow of Spindle Microtubules

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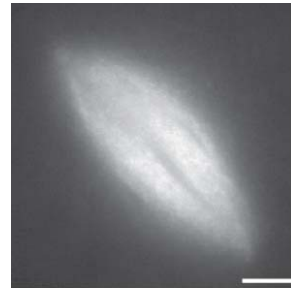
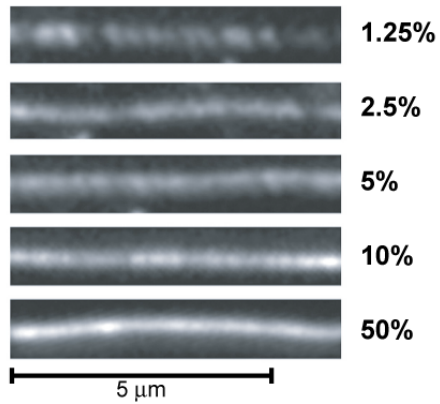
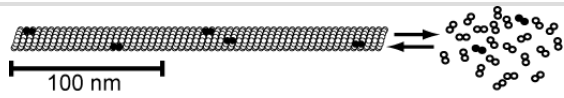
5  $\mu\text{m}$  —————



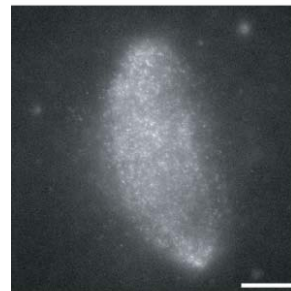
Cameron et al, *JCB*, 173:173-179,2006

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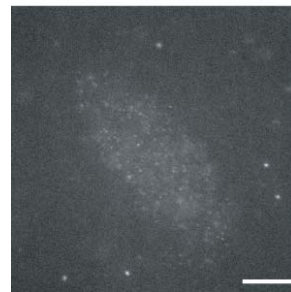
# Fluorescent Speckle Microscopy (FSM)



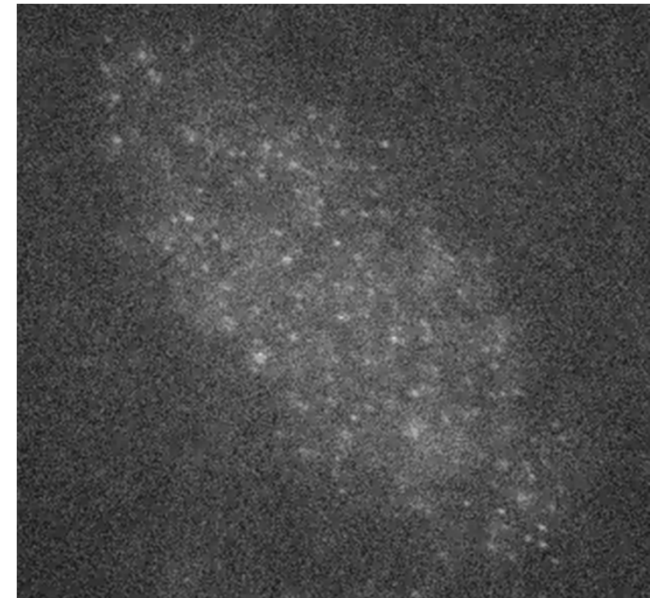
$1.32 \times 10^{-4}$



$1.32 \times 10^{-5}$



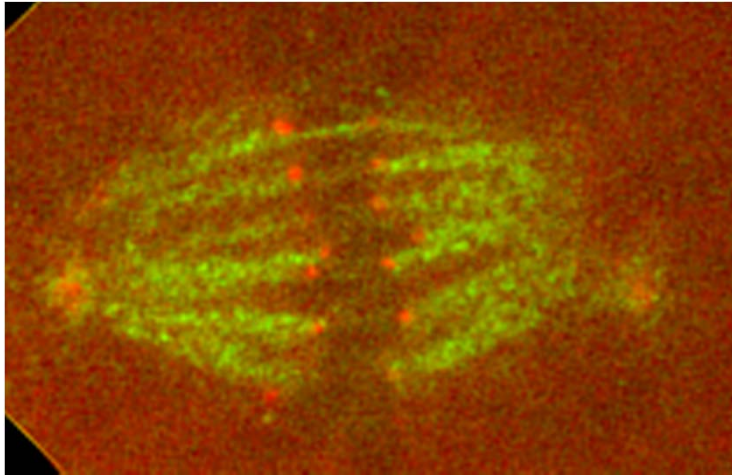
$1.32 \times 10^{-6}$



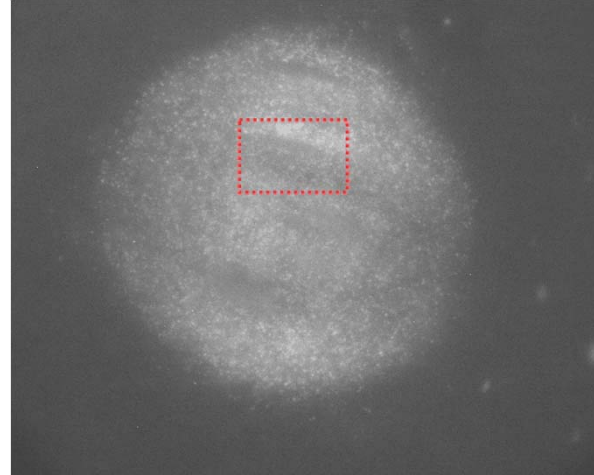
# FSM of Dynamic Spindle Architecture

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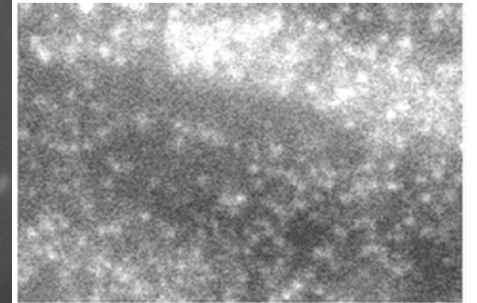
Fluorescent speckle microscopy



5  $\mu\text{m}$  —

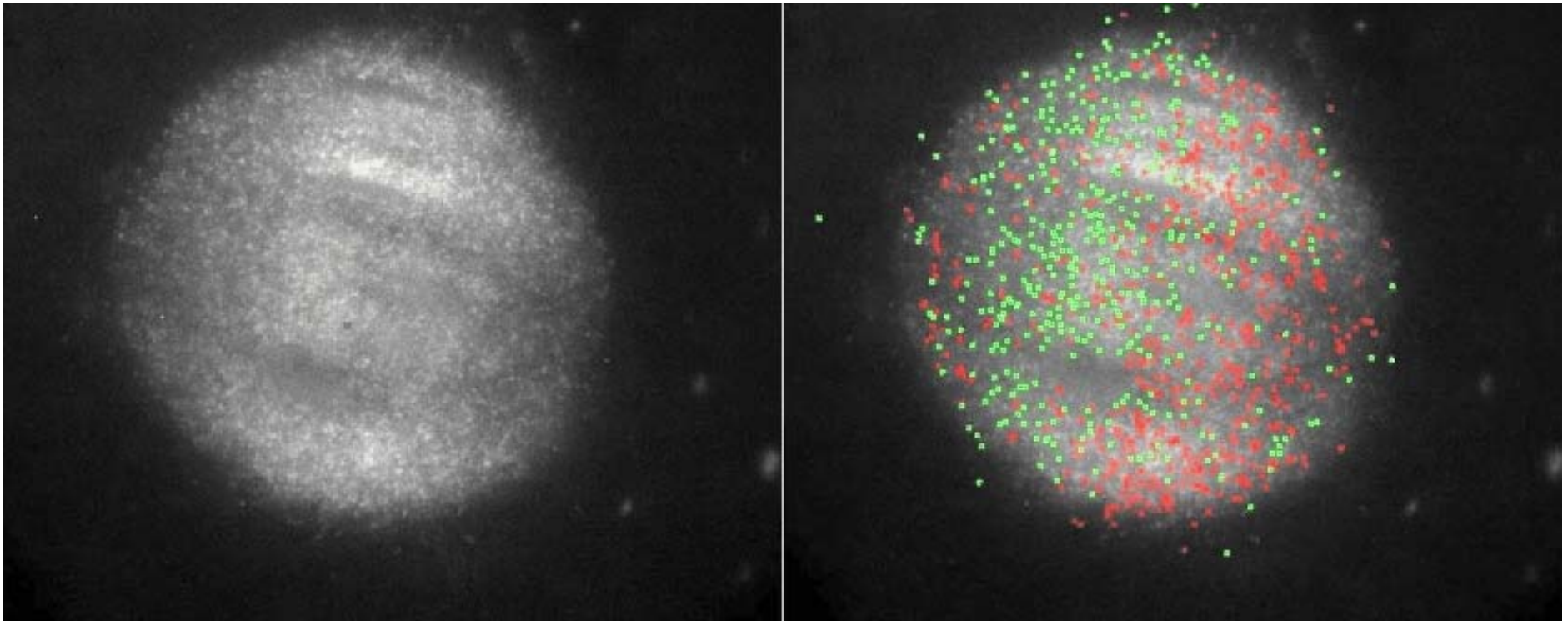


10  $\mu\text{m}$  —



# Quantitative Mapping of Spatial-Temporal Spindle Dynamics

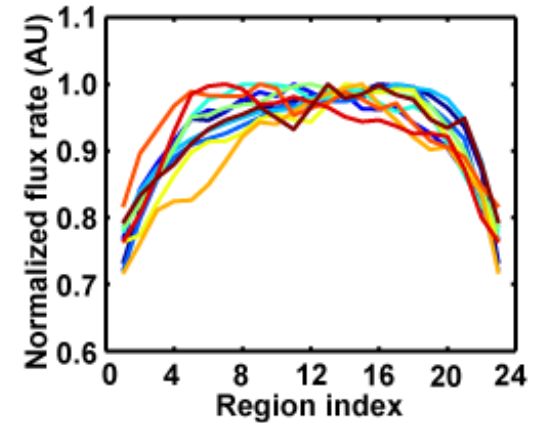
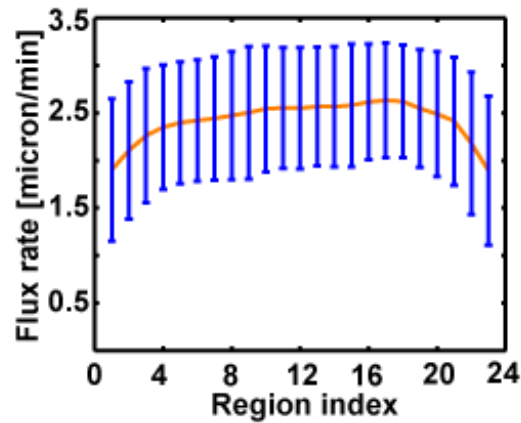
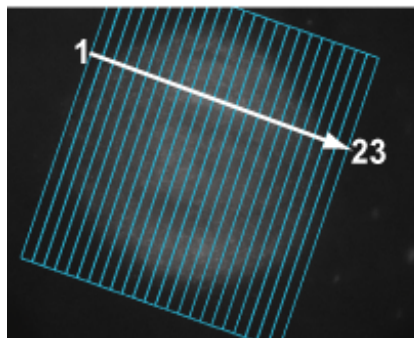
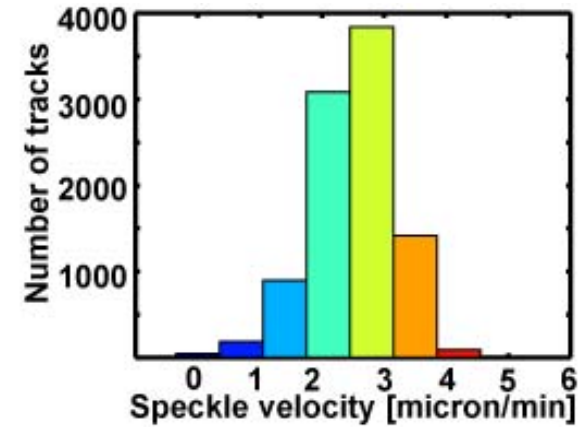
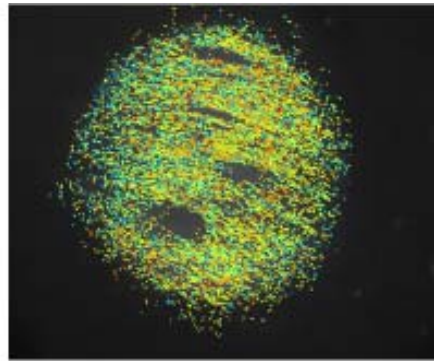
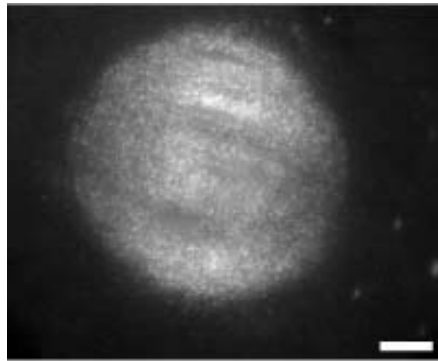
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Yang et al., *J. Cell Biol.*, 182:631-639, 2008

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# Regional Variations of Microtubule Flux



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**Questions?**



# Movement of a Free Molecule (I)

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- The average kinetic energy of a particle of mass  $m$  and velocity  $v_x$  is

$$\left\langle \frac{1}{2} m v_x^2 \right\rangle = \frac{kT}{2}$$

Boltzmann constant =  $1.381 \times 10^{-23}$  J/K

1 Joule = 1 N·m

$t_K = t_C + 273.15$

where  $k$  is Boltzmann's constant and  $T$  is absolute temperature (Einstein 1905).

- Principle of equipartition of energy

$$\left\langle \frac{1}{2} m v^2 \right\rangle = \frac{3 \cdot kT}{2}$$

Howard Berg, Random walks in biology,  
Princeton University Press, 1993

## Movement of a Free Molecule (II)

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- Molecular mass of GFP is 27 kDa. One atomic mass unit (Da) is  $1.6606 \times 10^{-24}$ g. So the mass of one GFP molecule is  $4.4836 \times 10^{-20}$ g.

At 27 degree C,  $kT$  is  $4.1451 \times 10^{-14}$ g·cm<sup>2</sup>/sec<sup>2</sup>.

$$\sqrt{\langle v_x^2 \rangle} = \sqrt{\frac{kT}{m}} = 961.51 \text{ cm/sec}$$

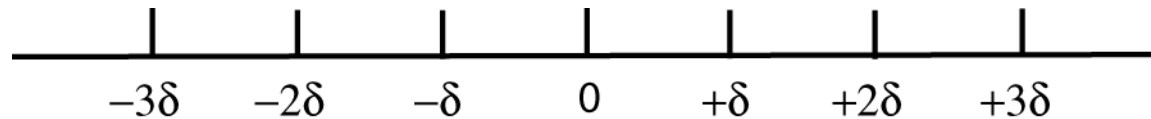
Howard Berg, Random walks in biology,  
Princeton University Press, 1993

# 1D Random Walk in Solution (I)

- Assumptions: consider an ensemble of  $N$  particles,

- (1) A particle  $i$  has equal probabilities to walk to the left and to the right.
- (2) Particle movement at consecutive time points are independent.
- (3) Movement of different particles are independent.
- (4) Each particle moves at a average step size of  $\delta = v_x \cdot \tau$

$$x_i(n) = x_i(n-1) \pm \delta$$



$$\begin{aligned} \langle x(n) \rangle &= \frac{1}{N} \sum_{i=1}^N x_i(n) = \frac{1}{N} \sum_{i=1}^N [x_i(n-1) \pm \delta] \\ &= \frac{1}{N} \sum_{i=1}^N x_i(n-1) = \langle x(n-1) \rangle \end{aligned}$$

- Property 1: The mean position of an ensemble of particles undergoing random walk remains unchanged.

# 1D Random Walk in Solution (II)

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- Property 2: The mean square displacement of a particle undergoing random walk increases linearly w.r.t. time.

$$\begin{aligned}\langle x^2(n) \rangle &= \frac{1}{N} \sum_{i=1}^N x_i^2(n) = \frac{1}{N} \sum_{i=1}^N [x_i^2(n-1) \pm 2\delta x_i(n-1) + \delta^2] \\ &= \langle x^2(n-1) \rangle + \delta^2\end{aligned}$$

$$\langle x^2(n) \rangle = n\delta^2 = \frac{t}{\tau} \delta^2 = 2Dt \quad \langle r^2(n) \rangle = \langle x^2(n) + y^2(n) \rangle = 4Dt$$

$$\langle r^2(n) \rangle = \langle x^2(n) + y^2(n) + z^2(n) \rangle = 6Dt$$

Howard Berg, *Random walks in biology*,  
Princeton University Press, 1993

# Application of the Microscopic Theory (I)

Object	Distance diffused			
	1 $\mu\text{m}$	100 $\mu\text{m}$	1 cm	1 m
K <sup>+</sup>	0.25ms	2.5s	2.5 $\times 10^4$ s (7 hrs)	2.5 $\times 10^8$ s (8 yrs)
Protein	5ms	50s	5.0 $\times 10^5$ s (6 days)	5.0 $\times 10^9$ s (150 yrs)
Organelle	1s	10 <sup>4</sup> s (3 hrs)	10 <sup>8</sup> s (3 yrs)	10 <sup>12</sup> s (31710 yers)

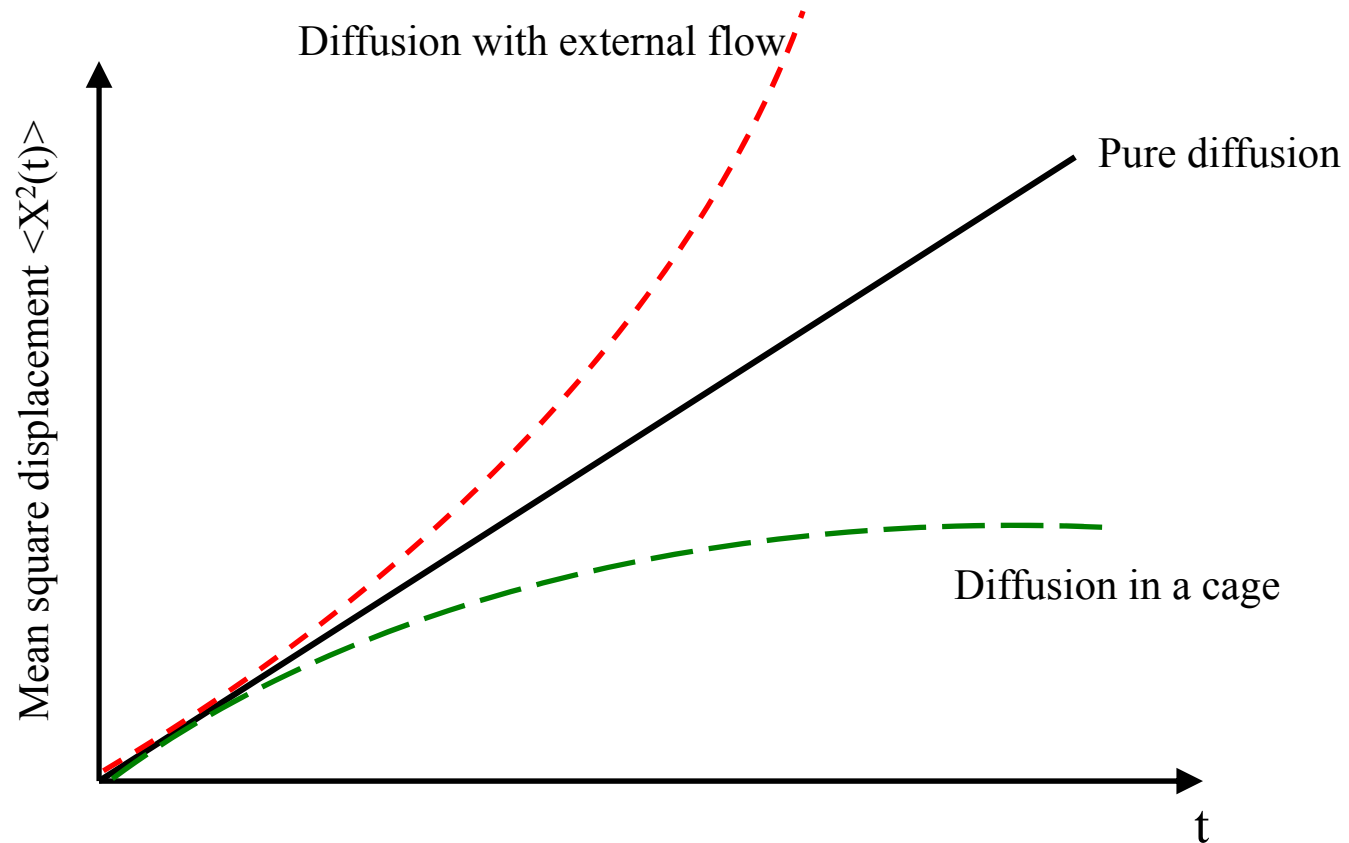
K<sup>+</sup>: Radius = 0.1nm, viscosity = 1mPa·s<sup>-1</sup>; T = 25°C; D=2000  $\mu\text{m}^2/\text{sec}$

Protein: Radius = 3nm, viscosity = 0.6915mPa·s<sup>-1</sup>; T = 37; D = 100  $\mu\text{m}^2/\text{sec}$

Organelle: Radis = 500nm, viscosity = 0.8904mPa·s<sup>-1</sup>; T = 25°C; D = 0.5  $\mu\text{m}^2/\text{sec}$

Jonathon Howard, *Mechanics of motor proteins and the cytoskeleton*, Sinauer, 2001

# Application of the Microscopic Theory (II)



H. Qian, M. P. Sheetz, E. L. Elson, *Single particle tracking: analysis of diffusion and flow in two-dimensional systems*, Biophysical Journal, 60(4):910-921, 1991.

# Application of the Microscopic Theory (III)

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- Calculation of diffusion coefficient (Einstein-Stokes equation)

- diffusion of spherical particles through liquid in which viscous force dominates

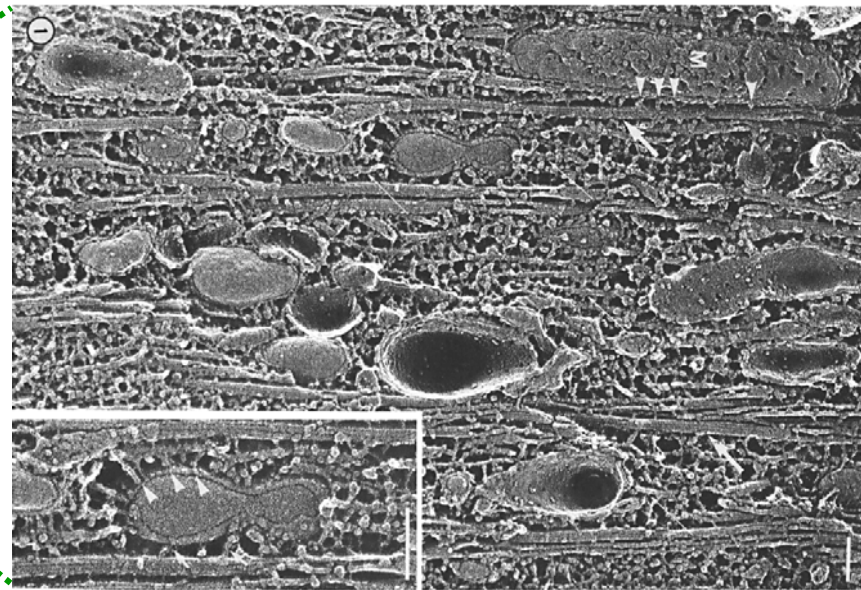
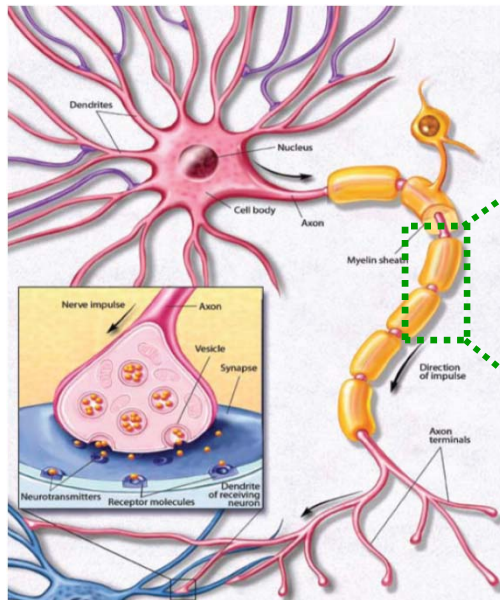
$$D = \frac{kT}{6\pi\eta r}$$

- Boltzmann constant:  $k=1.381 \times 10^{-23} \text{ J/k} = 1.381 \times 10^{-17} \text{ N} \cdot \mu\text{m/k}$
- Absolute temperature:  $T = 273.15 + 25$
- Viscosity:  $\eta = 0.8904 \text{ mPa} \cdot \text{s} = 0.8904 \times 10^{-3} \times 10^{-12} \text{ N} \cdot \mu\text{m}^{-2} \cdot \text{s}$
- Sphere radius:  $r = 500 \text{ nm} = 0.5 \mu\text{m}$
- Calculated diffusion coefficient:  $D = 0.5 \mu\text{m}^2/\text{s}$

Howard Berg, *Random walks in biology*,  
Princeton University Press, 1993

# An Overview of Axonal Transport

From *Brain Facts*, Society for Neuroscience



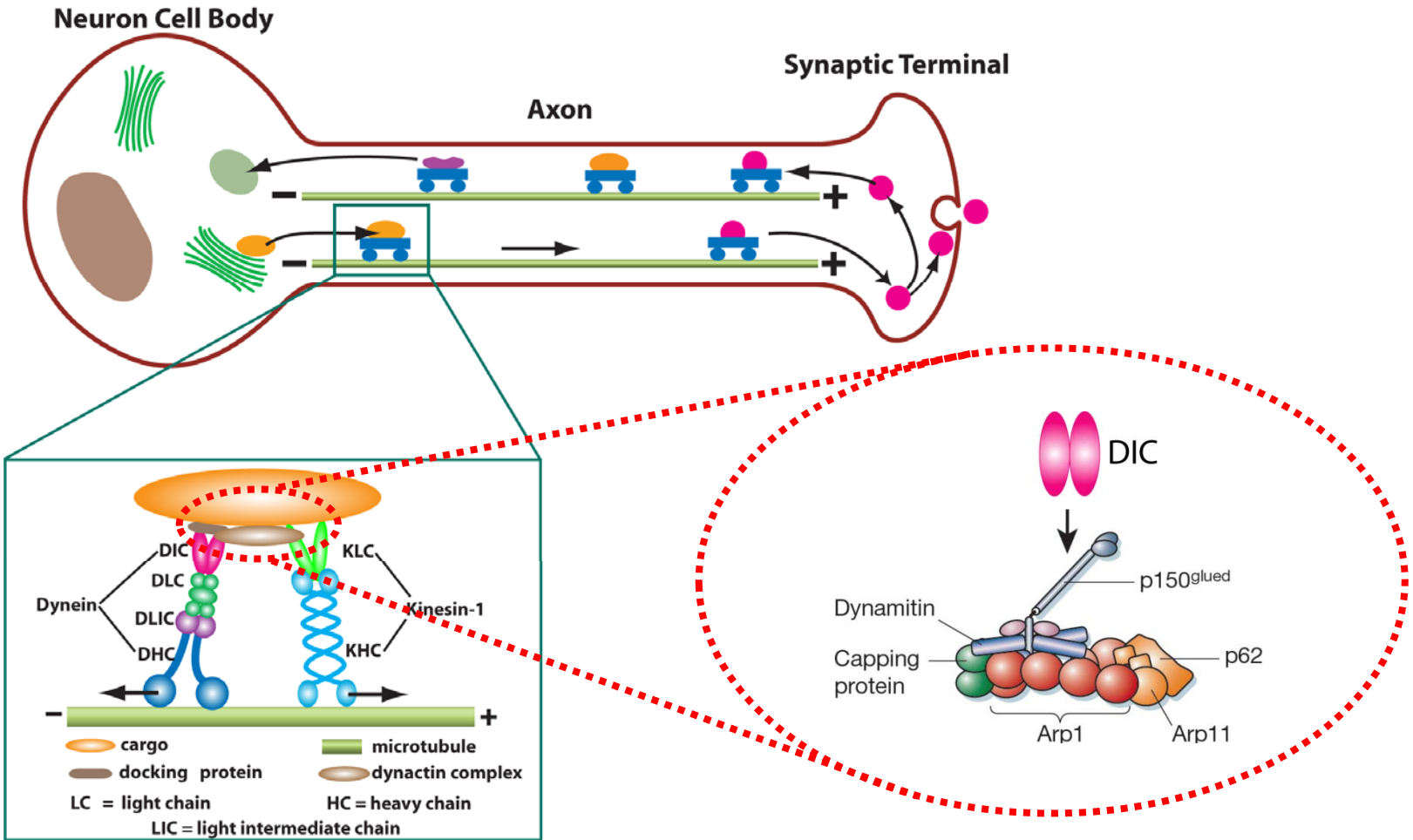
Hirokawa N., *JCB*, 94:129, 1982

Bars: 0.1  $\mu$ m

- Axonal transport is critical to survival and function of neurons.
- Axonal transport is a powerful model of intracellular transport.
- Axonal transport may be a good model to study spatiotemporal cell signaling.
- Many mitotic motors also drive axonal transport.

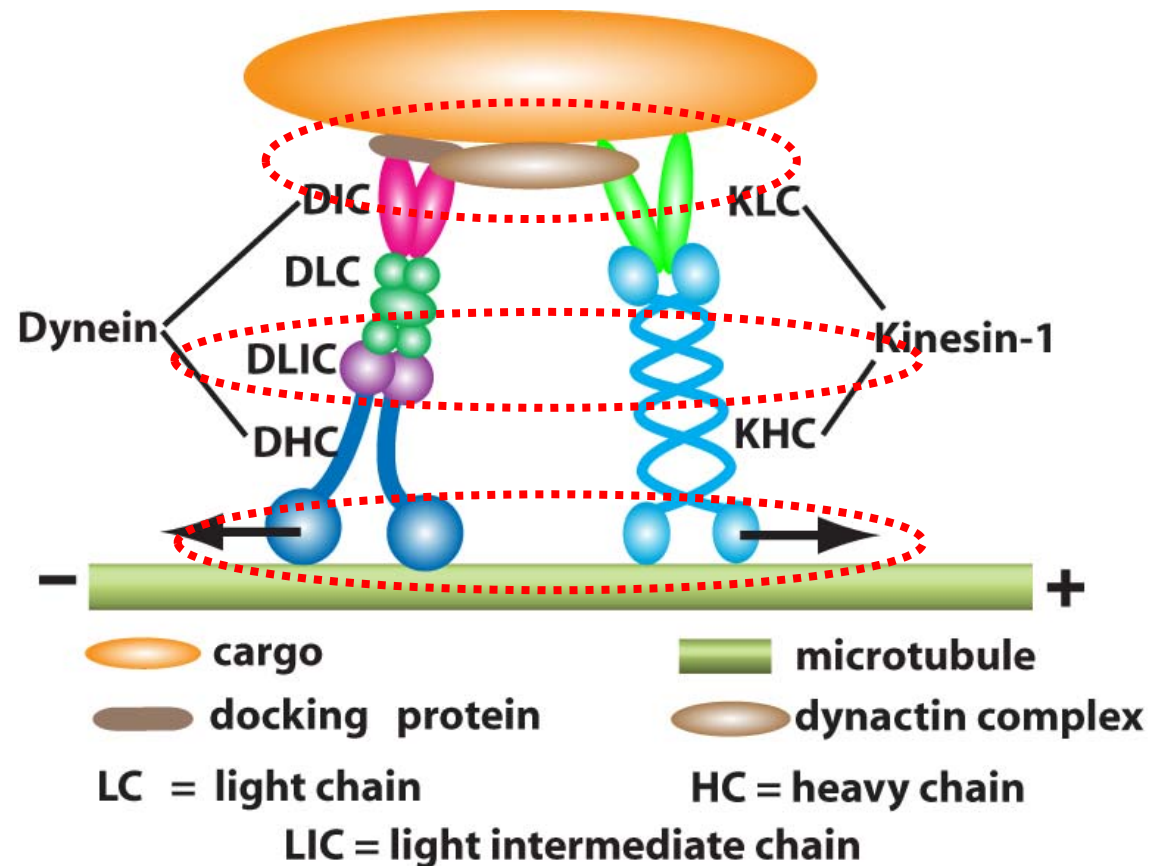


# Molecular Motor Machinery of Axonal Transport



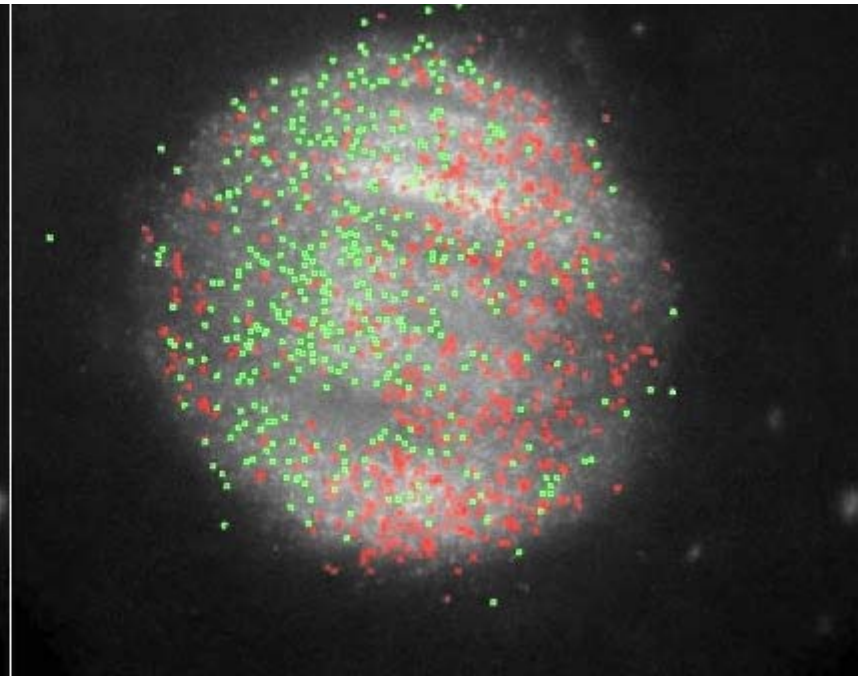
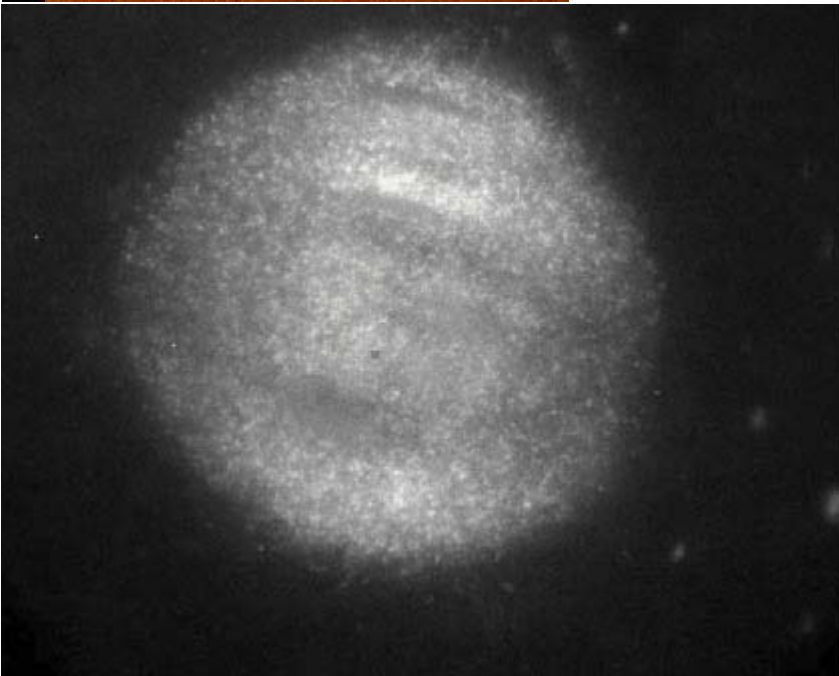
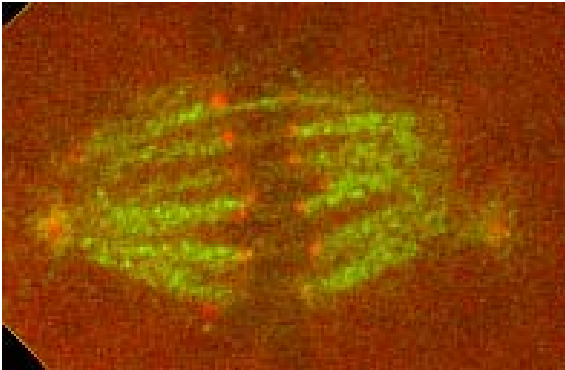
Adapted from Schliwa & Woehlke, *Nature*, 422:759, 2003

# Potential Mechanisms of Axonal Transport Defects



# Tracking Results Demo

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Yang G., Cameron L.A., Danuser G., and Salmon E.D. (2008) Regional variation of microtubule flux reveals microtubule organization in *Xenopus* extract meiotic spindles, *Journal of Cell Biology*, vol. 182, pp. 631-639.