

# Modeling Neck Linker Extension in Kinesin.

John Fricks

Dept of Statistics  
Penn State University  
University Park, PA

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Joint work with Matthew Kutys, John Hughes, and William Hancock.

## Overview

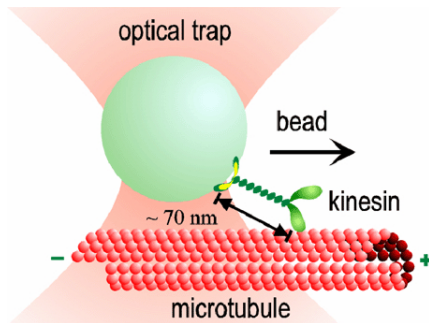
The Kinesin  
Motor.

Important  
Quantities of  
Interest.

The Models.

Extensions.

- The Kinesin Molecular Motor.
- Important Quantities—Asymptotic Velocity, Effective Diffusion, Processivity.
- Common Models.
- Our Model.
- A Numerical Strategy.
- Extensions and Current Work.

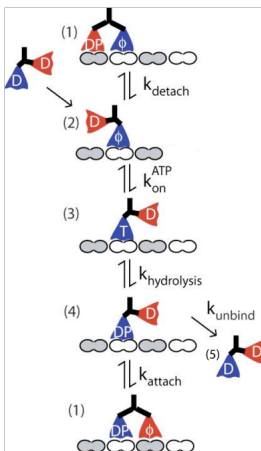


Block Lab: <http://www.stanford.edu/group/blocklab/kinesin/kinesin.html>

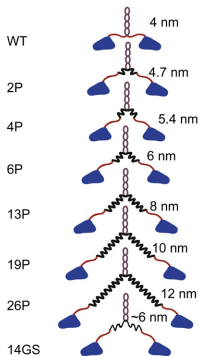
# The Important Biological Points.

- “Hand over hand” stepping mechanism.
- 8 nanometer steps with 1 ATP per step.
- Length of step determined by the physical structure of microtubule.
- Back steps are rare.
- Kinetics + Constrained Diffusion.
  - Free head detachment.
  - ATP binding.
  - ATP hydrolysis.
  - Free head attachment.

# The Kinesin Cartoon.



- Extensions can range from less than 1 nm up to 12 nm.
- Hackney and Hancock—extensions reduced processivity.
- Hancock—velocity was reduced.
- Yildiz et al—processivity was unaffected and velocity was reduced.



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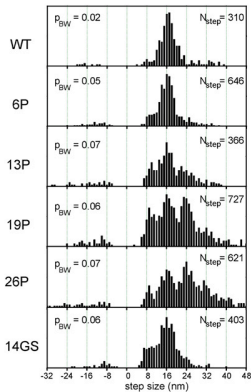
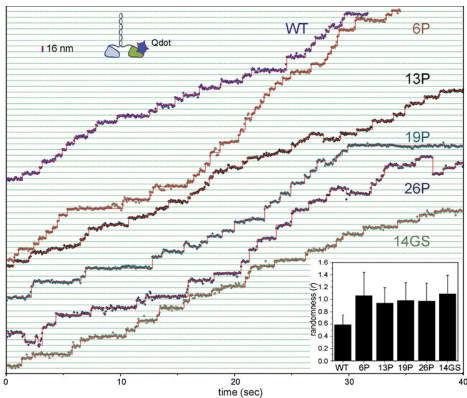
Overview

The Kinesin Motor.

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Yildiz, A. and Tomishige, M. and Gennerich, A. and Vale, R.D.

*Intramolecular Strain Coordinates Kinesin Stepping Behavior along Microtubules.*

- Different measurement methods.
  - Laser Trap.
  - FRET.
  - FIONA.
- What data is collected?
  - Position.
  - Time of Run.
  - Size of Steps.



# Important Quantities of Interest.

- **Asymptotic Velocity**

$$V_a = \lim_{t \rightarrow \infty} \frac{E[X(t)]}{t} \quad \text{or} \quad V_a = \lim_{t \rightarrow \infty} \frac{X(t)}{t}$$

- **Effective Diffusion**

$$D_{eff} = \lim_{t \rightarrow \infty} \frac{Var[X(t)]}{2t}$$

or the quantity which ensures

$$\frac{X(t) - V_a t}{\sqrt{2D_{eff} t}}$$

converges to a standard normal.

- **Randomness Parameter**

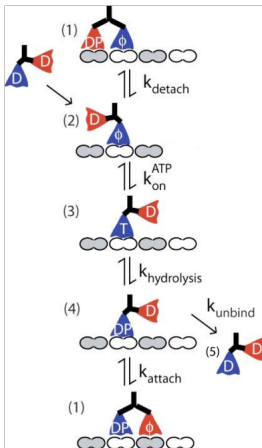
$$R = \frac{2D_{eff}}{LV_a}$$

- **Processivity**

$\nu$  the number of random steps taken before detachment.

Pure kinetics model—a discrete space Markov chain.

- Fails to account for the physical movement of heads.



## Stochastic Differential Equation Model

- Brownian particle in a periodic potential.
- $dX(t) = a(X(t))dt + \sigma dB(t)$
- Fails to account for two individual heads.
- Fails to coordinate physical movement and chemical kinetics.

## Flashing Ratchet

- $dX(t) = a_{K(t)}(X(t))dt + \sigma dB(t)$
- Accounts for both chemical and physical states.
- How can these be coordinated?

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Overview

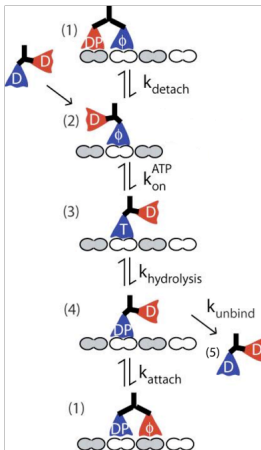
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# The Kinesin Cartoon.



- What about incorporating diffusion of the freehead into the model?
- State 1 corresponds to having both heads bound.
- State 2 corresponds to the head having become free  
Tethered diffusion with a negative or neutral bias.
- State 3 and state 4 mean ATP has been bound  
A conformational change causes there to be a forward bias  
and less compliant spring.

- The position of the free motor head is governed by the following equation.

$$Y(t) = y + \int_0^t a_{K(s)}(Y(s)) ds + \sigma B(s)$$

where  $K(t)$  is the process corresponding to state events.

- Associate with each binding site a binding process

$$N_j \left( \int_0^t g_j(Y(s)) ds \right)$$

where the  $N_j$  are independent standard Poisson processes (independent of  $B$  also).

- The time until we return to (chemical) state one ( $\tau$ ) would then be the time for one of these clocks to fire.
- We define  $Y(\tau)$  to be the location of the binding site associated with the binding process which fires first.

- $Z_i$ ,  $i = 1, 2, \dots$  with mean  $\mu_z$  and variance  $\sigma_z^2$ .

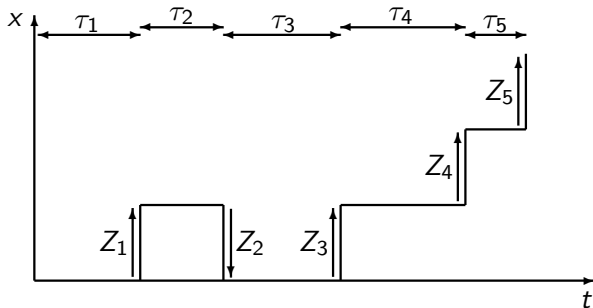
$$X(t) = \sum_{i=1}^{N(t)} Z_i$$

where  $N(t)$  is a renewal process.

- $N(t) = \max\{n : \sum_{i=1}^n \tau_i \leq t\}$
- Time between events are independent and identically distributed,  $\tau_i$ ,  $i = 1, 2, \dots$  ( $\tau_0 = 0$ ).
- The  $\tau_i$  have finite mean ( $\mu_\tau$ ) and variance ( $\sigma_\tau^2$ ).



# Renewal-Reward Process.



# Limits for Renewal-Reward Process.

For motor with backwards/forward steps,

- $$V_a = \lim_{t \rightarrow \infty} \frac{LX(t)}{t} = \frac{L\mu_Z}{\mu_\tau}$$

- $$D_{\text{eff}} = \lim_{t \rightarrow \infty} \frac{L^2 \text{Var}[X(t)]}{2t} = \frac{L^2}{2} \left( \frac{\sigma_Z^2}{\mu_\tau} + \frac{\mu_Z^2 \sigma_\tau^2}{\mu_\tau^3} \right)$$

# Functional Central Limit Theorem.

Define

$$S(t) = \sum_{i=0}^{\lfloor t \rfloor} Z_i \quad T(t) = \sum_{i=0}^{\lfloor t \rfloor} \tau_i$$

$$n^{-1/2} \begin{pmatrix} S(nt) - \mu_Z nt \\ T(nt) - \mu_\tau nt \end{pmatrix} \Rightarrow \begin{pmatrix} B_1(t) \\ B_2(t) \end{pmatrix}$$

where

$$\Sigma = \begin{pmatrix} \sigma_Z^2 & 0 \\ 0 & \sigma_\tau^2 \end{pmatrix}$$

Now, if we define

$$X_n(t) = n^{-1/2} \left( S(T^{-1}(nt)) - \frac{\mu_Z}{\mu_\tau} nt \right)$$

and we apply Theorem 13.7.3 from Whitt; we obtain

$$X_n(t) \Rightarrow B_1 \left( \frac{t}{\mu_\tau} \right) - \frac{\mu_Z}{\mu_\tau} B_2 \left( \frac{t}{\mu_\tau} \right).$$

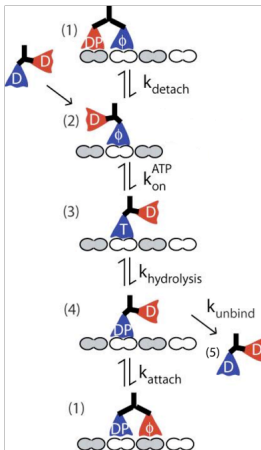
- Note that  $X(t) = S(T^{-1}(t))$
- This is equivalent in law to

$$X_n(t) = n^{-1/2} \left( X(nt) - \frac{\mu_Z}{\mu_T} nt \right) \Rightarrow \sqrt{\frac{\sigma_Z^2}{\mu_T} + \frac{\mu_Z^2 \sigma_T^2}{\mu_T^3}} B(t)$$

- 

$$X(nt) \approx \frac{\mu_Z}{\mu_T} nt + n^{1/2} \sqrt{\frac{\sigma_Z^2}{\mu_T} + \frac{\mu_Z^2 \sigma_T^2}{\mu_T^3}} B(t)$$

# The Kinesin Cartoon.



Relabel the states. Negative means front head became detached first.

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$$Q = \left( \begin{array}{c|c} A & B \\ \hline 0 & 0 \end{array} \right)$$

$$A = \begin{pmatrix} k_{1+,1+} & k_{1+,2+} & 0 & 0 & k_{1+,4-} & 0 & 0 \\ 0 & k_{2+,2+} & k_{2+,3+} & 0 & 0 & 0 & 0 \\ 0 & k_{3+,2+} & k_{3+,3+} & k_{3+,4+} & 0 & 0 & 0 \\ 0 & 0 & k_{4+,3+} & k_{4+,4+} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & k_{4-,4-} & k_{4-,3-} & 0 \\ 0 & 0 & 0 & 0 & k_{3-,4-} & k_{3-,3-} & k_{3-,2-} \\ 0 & 0 & 0 & 0 & 0 & k_{2-,3-} & k_{2-,2-} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad (1)$$

and

$$B = \begin{pmatrix} 0 & 0 & 0 \\ 0 & K_{2+,1*} & 0 \\ 0 & 0 & 0 \\ k_{4+,1++} & 0 & 0 \\ 0 & k_{4-,1*} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & k_{2-,1-} \end{pmatrix}. \quad (2)$$

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# Aggregated States of Markov Chains.

- Wang and Qian on kinetic models for motors.
- Milescu et al on MLE for motor dwell time.
- Fredkin and Rice a comprehensive look.
- Colquhoun and Hawkes with ion channels.
- Queueing Literature—Asmussen, Neuts+others

Using this formulation, the transition matrix can, under suitable conditions, be written as

$$P(t) = e^{Qt}$$

In the decomposition into submatrices, this can be simplified into

$$e^{Qt} = \begin{pmatrix} e^{At} & e^{At}A^{-1}B - A^{-1}B \\ 0 & I \end{pmatrix}$$



This also allows for the time until absorption ( $\tau_i$ )

$$\begin{aligned} F(t) &= P(X(t) = 1_- \text{ or } 1_{++}) \\ &= 1 - P(X(t) \neq 1_- \text{ or } 1_{++}) \\ &= 1 - ae^{At}\mathbf{1}' \end{aligned}$$

The mean and variance for  $\tau_i$  are readily available.

$$\mu_\tau = -aA^{-1}\mathbf{1}'$$

and

$$\sigma_\tau^2 = 2aA^{-1}A^{-1}\mathbf{1}' - (\nu A^{-1}\mathbf{1}')^2$$

- We can also find the probability of a forward or backward step.

- 

$$\begin{aligned} P(X(\tau) = 1_{++}, \tau \leq t) &= P(Z = 1, \tau \leq t) \\ &= a \left( I - e^{At} \right) \left( -A^{-1}B \right) c' \end{aligned}$$

- 

$$P(Z = 1) = \lim_{t \rightarrow \infty} P(Z = 1, \tau \leq t) = a \left( -A^{-1}B \right) c'$$

- This allows us to calculate  $\mu_z$  and  $\sigma_z^2$ .

- The covariance can be calculated from the joint distribution.

- $$P(Z = z, \tau \leq t) = a \left( I - e^{At} \right) \left( -A^{-1}B \right) c'_z$$

- From this we obtain the density

$$f(z, t) = ae^{At} Bc'_z$$

- This allows us to calculate the covariance,  $\sigma_{Z, \tau}$ .

$$-aA^{-1}Bd'$$

- Note we can also calculate the conditional density

$$f(z|t) = \frac{f(z, t)}{f(t)} = \frac{ae^{At} Bc'_z}{-aAe^{At} \mathbf{1}'}$$

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- Thus,  $X_n(t) \Rightarrow B_1 \left( \frac{t}{\mu_\tau} \right) - \frac{\mu_Z}{\mu_\tau} B_2 \left( \frac{t}{\mu_\tau} \right)$ .
- We can multiply out the diffusion coefficient of the resulting Brownian motion

$$\frac{1}{\mu_\tau^2} \begin{pmatrix} 1 & -\frac{\mu_Z}{\mu_\tau} \\ & \end{pmatrix} \begin{pmatrix} \sigma_Z^2 & \sigma_{Z,\tau} \\ \sigma_{Z,\tau} & \sigma_\tau^2 \end{pmatrix} \begin{pmatrix} 1 \\ -\frac{\mu_Z}{\mu_\tau} \end{pmatrix}$$

- So,  $X_n(t) = n^{-1/2} \left( X(nt) - \frac{\mu_Z}{\mu_\tau} nt \right) \Rightarrow$

$$\sqrt{\frac{\sigma_Z^2}{\mu_\tau} + \frac{\mu_Z^2 \sigma_\tau^2}{\mu_\tau^3} - 2 \frac{\mu_Z \sigma_{Z,\tau}}{\mu_\tau^2}} B(t)$$

- This is equivalent in law to

$$X(nt) \approx \frac{\mu_Z}{\mu_\tau} nt + n^{1/2} \sqrt{\frac{\sigma_Z^2}{\mu_\tau} + \frac{\mu_Z^2 \sigma_\tau^2}{\mu_\tau^3} - 2 \frac{\mu_Z \sigma_{Z,\tau}}{\mu_\tau^2}} B(t)$$

# A Matrix Approximation for Our Model.

We can approximate the evolution of a cycle using a similar matrix setup to the purely kinetic. The matrices will have the following block form:

$$\mathbf{A} = \begin{pmatrix} k_{1+,1+} & k_{1+,2+} & 0 & 0 & k_{1+,4-} & 0 & 0 \\ 0 & k_{2+,2+} & k_{2+,3+} & 0 & 0 & 0 & 0 \\ 0 & k_{3+,2+} & k_{3+,3+} & k_{3+,4+} & 0 & 0 & 0 \\ 0 & 0 & k_{4+,3+} & k_{4+,4+} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & k_{4-,4-} & k_{4-,3-} & 0 \\ 0 & 0 & 0 & 0 & k_{3-,4-} & k_{3-,3-} & k_{3-,2-} \\ 0 & 0 & 0 & 0 & 0 & k_{2-,3-} & k_{2-,2-} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad (3)$$

and

$$\mathbf{B} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & K_{2+,1*} & 0 \\ 0 & 0 & 0 \\ k_{4+,1++} & 0 & 0 \\ 0 & k_{4-,1*} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & k_{2-,1-} \end{pmatrix}. \quad (4)$$

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$k_{2+,2+} =$

$$\begin{matrix} y_1 \\ y_2 \\ \dots \\ \dots \\ y_n \end{matrix} \begin{pmatrix} y_1 & y_2 & \dots & \dots & \dots & y_n \\ -\sum_{n+1} & \mathbf{L}_{1,2} & 0 & 0 & \dots & 0 \\ \mathbf{L}_{2,1} & -\sum_{n+2} & \mathbf{L}_{2,3} & 0 & \dots & \dots \\ 0 & \dots & \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \mathbf{L}_{n-2,n-1} & -\sum_{n+(n-1)} & \mathbf{L}_{n-1,n} \\ 0 & \dots & \dots & 0 & \mathbf{L}_{n,n-1} & -\sum_{2n} \end{pmatrix}$$

- $Y(t) = x + \int_0^t a_K(s)(Y(s))ds + \sigma B(s)$

- **Linear Spring**

$$a_k(y) = -\kappa(y - c)$$

- **WLC**

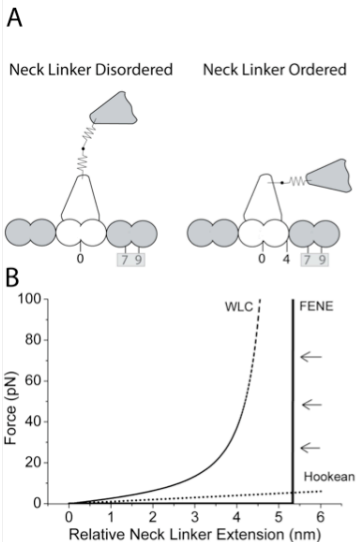
$$a_k(y) = \kappa \left( \frac{1}{4} \left( 1 - \frac{y}{L_c} \right)^{-2} - \frac{1}{4} + \frac{y}{L_c} \right)$$

- **FENE**

$$a_k(y) = -\kappa(y - c)$$

but with reflecting barriers at  $L_c$  and  $-L_c$ .

# Necklinker Models (Drifts).





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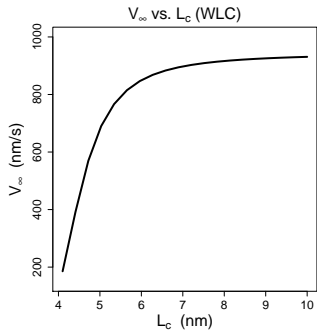
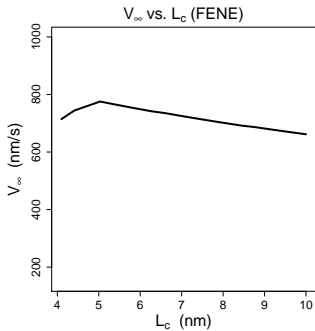
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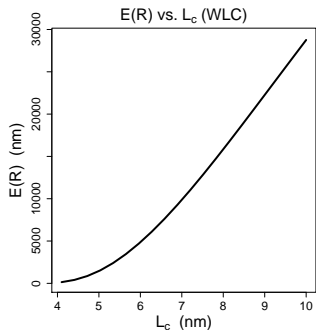
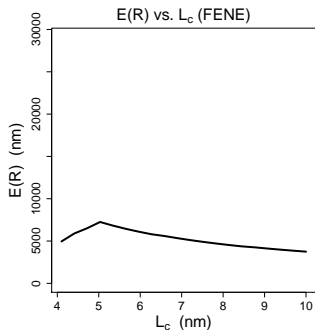
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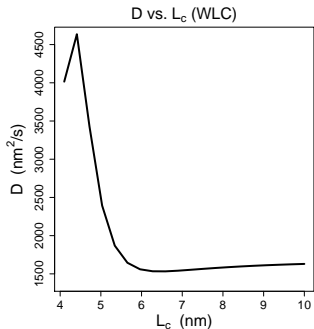
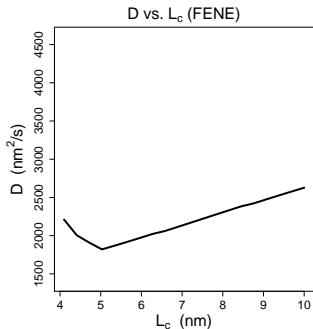
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# Binding Radius and Attachment Rate.

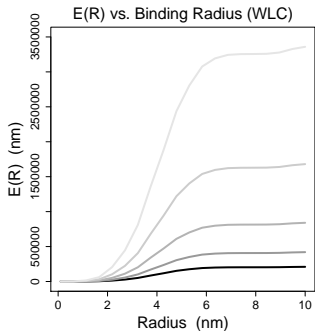
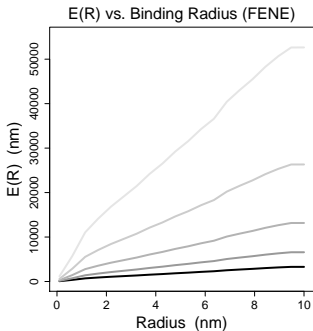
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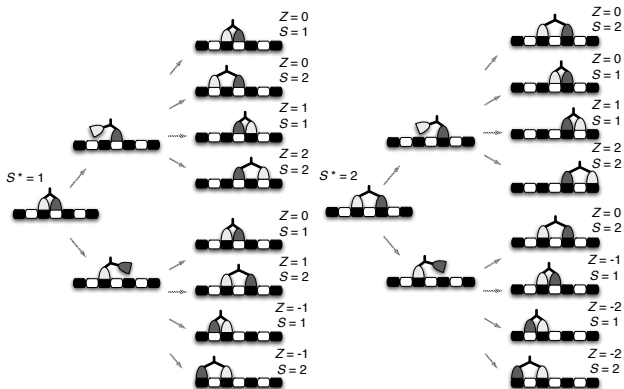
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# Summary for Different Spring Models.

- WLC.
  - When allowed to extend to approximately 4nm, binding constant must be very high.
  - As neck linker is extended, velocity AND processivity increase.
- FENE.
  - Binding constant is reasonable.
  - As neck linker is extended, velocity and processivity decrease as expected.
- Possible Resolutions.
  - Projection is the problem.
  - Weak binding.
  - Mis-specification of neck linker.

- Heads are not necessarily one binding site away at the beginning of each cycle.
- Return to double binding changes initial conditions of next cycle.



The following forms a Markov chain

$$\begin{pmatrix} Z_i \\ \tau_i \\ S_i \end{pmatrix}$$

- $S_i$  is a Markov chain describing the distance between heads after previous cycle.
- The position of the front head after a full cycle

$$X(t) = \sum_{i=1}^{N(t)} Z_i$$

- Take advantage of the simplified structure;  $Z_i$  and  $\tau_i$  depend on the last value of  $S$ .
- Calculate the stationary distribution of  $S_i$  using the matrix approximation.
- Can calculate the other moments based only on the conditional means and variances given  $S_{i-1}$ .
- Central Limit Theorem for stationary Markov chains will lead to FCLT for sums—the result is a bivariate Brownian motion
- We can still use Whitt to give us the correct FCLT.



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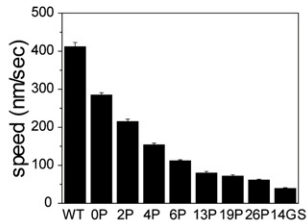
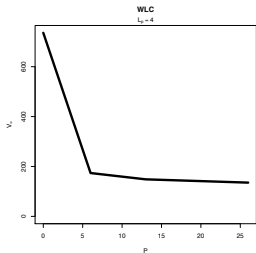
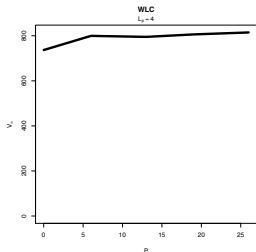
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# Tension vs No Tension.



- Modeling Laser Trap Experiments.
- How does this nanoscale model react to external (and fluctuating) forces?
- How about imposed forces?
- What happens when multiple motors are connected to the same cargo?

- NSF for support (DMS 0714939) through the DMS/NIGMS joint program in mathematical biology.
- Collaborators
  - Matthew Kutys (UNC/NIH)
  - John Hughes (PSU Statistics)
  - Will Hancock. (PSU Bioengineering)