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Exact results for parallel-chain kinetic models of biological transport

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In order to describe the observed behavior of single motor proteins moving along linear molecular tracks, a class of stochastic models is studied which recognizes the possibility of parallel biochemical pathways. Extending the theoretical analysis of Derrida [J. Stat. Phys. **31**, 433 (1983)], exact results are derived for the velocity and dispersion of a discrete one-dimensional kinetic model which consists of two parallel chains of N states and M states, respectively, with arbitrary forward and backward rates. Generalizations of this approach for $g>2$ parallel chains models are briefly sketched. These results and other properties of parallel-chain kinetic models are illustrated by various examples. © *2001 American Institute of Physics.* [DOI: 10.1063/1.1405446]

I. INTRODUCTION

Biological motor proteins such as kinesins, dyneins, myosins, DNA and RNA polymerases have been shown to play crucial roles in cell division, cellular transport, muscle contraction, and genetic transcription.[1,2] These proteins, also known as molecular motors, operate in cells by consuming energy provided by hydrolysis of ATP (adenosine triphosphate) or related compounds, and moving along polarized, periodic linear tracks such as microtubules, actin filaments, or DNA molecules.[3]

The mechanical and biochemical properties of *single* motor proteins can now be studied experimentally with great accuracy under varying conditions.[3–10] Experimental successes have led to attempts to describe and understand the mechanisms of functioning of molecular motor proteins.[11–25]

Most theoretical research on molecular motors follows one of two main directions. One approach is based on the "physical" concept of *thermal ratchets*.[13–16] Here, the motor protein molecule is viewed as a Brownian particle which diffuses in periodic but asymmetric potentials, between which it switches stochastically. An alternative "chemical" approach is based on a kinetic multistate description of the molecular motor transport.[17–25] It assumes that a sequence of chemical transitions between consecutive spatially separated biochemical states or conformations leads to the motion of motor proteins.

In the simplest chemical kinetic model (see Fig. 1), a motor protein molecule moves along a linear periodic track and binds at specific sites $x=ld$ $(l=0,\pm 1,\pm 2,...)$, where d is the distance between neighboring binding sites. There are N discrete states, $j=0,1,...,N-1$, on a biochemical pathway between two consecutive binding sites. The motor protein molecule in state j_l (at site l) can jump forward to state $(j+1)_l$ with rate u_j, or it can step backward to state $(j-1)_l$ at rate w_j, as schematically pictured in Fig. 1.[20,21] In this representation, the model can easily be mapped onto a discrete biased random walk on a periodic one-dimensional lattice. This observation[19] allows one to use the method of Derrida[26] to obtain exact and explicit formulas for the asymptotic (long time) drift velocity

$$V_0=V_0(\{u_j,w_j\})=\lim_{t\to\infty}\frac{d}{dt}\langle x(t)\rangle, \tag{1}$$

and for the dispersion (or effective diffusion constant)

$$D_0=D_0(\{u_j,w_j\})=\tfrac{1}{2}\lim_{t\to\infty}\frac{d}{dt}[\langle x^2(t)\rangle-\langle x(t)\rangle^2], \tag{2}$$

where $x(t)$ is the position of the motor protein along the linear track at time t.

In most experiments on motor protein motility the trajectories of beads (to which motor protein molecules are chemically attached) are monitored.[3–10] This fact stimulated Chen and co-workers[23,24] to develop a formalism that takes into consideration the interactions between the bead and the motor protein molecule. Although the hydrodynamic relaxation and elastic properties of beads are important for transport properties of molecular motors, the experiments suggests that external force fluctuations due to these phenomena are minimal.[8] In addition, this method[23,24] allows numerical calculations only for drift velocities in simplified two-state models. Thus, the application of phenomenological simple chemical kinetic models[20–22,25] (which provide exact analytic expressions for velocities and dispersions for any N-state model) for description of motor protein transport seems more practical at current stage.

While the simple chemical kinetic model in Fig. 1 provides a reasonable description of the motion of a normal two-headed kinesin walking on a microtubule,[27] certain experimental observations on kinesins and other classes of motor proteins demand more elaborate theoretical treatments. To take into consideration the complexity of real biochemical pathways and to account for the irreversible dissociation of molecular motors from the linear track, extensions of the basic N-state periodic sequential kinetic model were recently presented.[22] In addition, the significance of deviations from chemical kinetics in the motion of motor proteins was discussed in detail using generalized kinetic models with *waiting-time distributions*.[25] Moreover, recent experiments on the processivity of single-headed kinesins and dyneins reveal the existence of a second, ATP-independent biochemi-

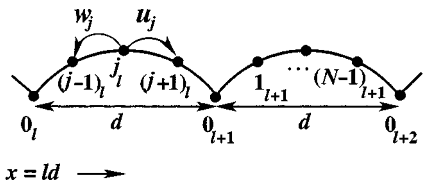

FIG. 1. General scheme for the simplest N-state chemical kinetic model with forward rates u_j and backward rates $w_j (j=0,1,...,N-1)$.

cal pathway.[28–30] Finally, the possibility of parallel biochemical pathways have been demonstrated experimentally for translocating RNA polymerases.[31] These observations call for an extension of the basic chemical kinetic models, which incorporate the existence of parallel biochemical pathways.

In this paper we consider the parallel-chain kinetic model that is illustrated in Fig. 2: The motor protein molecule can be found on the upper biochemical pathway (chain 0), which consists of N discrete states, or it can diffuse along the lower pathway (chain 1), which has M states. The molecular motor in state j_l on chain 0 can make one step forward at rate u_j, or one step backward at rate w_j $(j=0,...,N-1)$. Similarly, the motor protein molecule in state i_l on chain 1 can move forward (backward) with rate $\alpha_i(\beta_i)$ for $i=0,...,M-1$. Note that the extended chemical kinetic model with jumps considered in Ref. 22 corresponds to our parallel-chain model with $M=1$. Our method can be easily generalized for parallel-chain models with more than two chains.

The analysis of different extended chemical kinetic models[22,25] revealed that the corresponding expressions for V and D depend on certain linear sequential products of rate ratios. The same is true for the parallel-chain chemical kinetic model, where we define four types of product. Specifically, for chain 0 we have

$$\Pi_{(0)j}^{k} \equiv \prod_{i=j}^{k} \frac{w_i}{u_i} \quad \text{and} \quad \Pi_{(0),j}^{\dagger k} \equiv \prod_{i=j}^{k} \frac{w_{i+1}}{u_i} = \frac{w_{k+1}}{w_j} \Pi_{(0)j}^{k}, \tag{3}$$

with periodicity $u_{j\pm N}=u_j$ and $w_{j\pm N}=w_j$. Similarly, for chain 1 we have

$$\Pi_{(1)j}^{k} \equiv \prod_{i=j}^{k} \frac{\beta_i}{\alpha_i} \quad \text{and} \quad \Pi_{(1)j}^{\dagger k} \equiv \prod_{i=j}^{k} \frac{\beta_{i+1}}{\alpha_i} = \frac{\beta_{k+1}}{\beta_j} \Pi_{(1)j}^{k}, \tag{4}$$

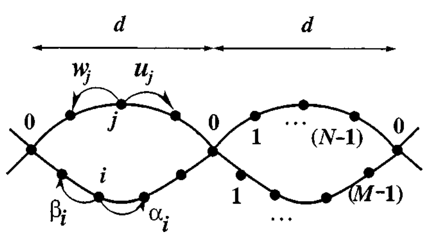

FIG. 2. Schematic illustration for the two chains chemical kinetic model. The upper chain has N discrete states with forward (backward) rates u_j (w_j) for $j=0,1,...,N-1$, while there are M discrete states in the lower chain with rates α_i and $\beta_i (i=0,1,...,M-1)$ for forward and backward transitions, respectively.

with periodicity $\alpha_{j\pm M}=\alpha_j$ and $\beta_{j\pm M}=\beta_j$.

In parallel-chain chemical kinetic model, as shown in Fig. 2, two chains form a loop. If the free energy changes along each chain are equal, then from the principle of detailed balance[32] we have

$$\Pi_{(0)1}^{N} = \Pi_{(1)1}^{M}. \tag{5}$$

However, our analysis is valid for more general situations where detailed balance is not holding. For example, for moving motor proteins, one pathway may correspond to ATP-dependent biochemical cycle, while the second pathway is just simple diffusional slippage of the protein molecule from one site to the other as was discussed by Chen and Yan.[24]

II. RESULTS FOR THE PARALLEL-CHAIN KINETIC MODEL

We present here the explicit formulas for the drift velocity and the dispersion of the two-chain parallel chemical kinetic model. The derivations are outlined in the Appendix.

For the two-chain model, the formal expression for the drift velocity is given as a sum of two terms corresponding to transport across chain 0 and chain 1, namely,

$$V = V_0 + V_1, \tag{6}$$

with

$$V_0 = \frac{d}{r_0^{(0)}} [1 - \Pi_{(0)1}^{N}] \Bigg/ \left[\frac{1}{r_0^{(0)}} R_N + \frac{1}{r_0^{(1)}} R_M - 1 \right], \tag{7}$$

and

$$V_1 = \frac{d}{r_0^{(1)}} [1 - \Pi_{(1)1}^{M}] \Bigg/ \left[\frac{1}{r_0^{(0)}} R_N + \frac{1}{r_0^{(1)}} R_M - 1 \right], \tag{8}$$

where, using the notations introduced above,

$$R_N = \sum_{j=0}^{N-1} r_j^{(0)}, \quad r_j^{(0)} = u_j^{-1} \left[1 + \sum_{k=1}^{N-1} \Pi_{(0)j+1}^{j+k} \right], \tag{9}$$

and

$$R_M = \sum_{j=0}^{M-1} r_j^{(1)}, \quad r_j^{(1)} = \alpha_j^{-1} \left[1 + \sum_{k=1}^{M-1} \Pi_{(1)j+1}^{j+k} \right]. \tag{10}$$

Taking into the consideration the detailed balance [see Eq. (5)], we obtain

$$V = d(1/r_0^{(0)} + 1/r_0^{(1)}) [1 - \Pi_{(0)1}^{N}] \Bigg/ \left[\frac{1}{r_0^{(0)}} R_N + \frac{1}{r_0^{(1)}} R_M - 1 \right]. \tag{11}$$

For a general parallel-chain model with g chains (which satisfy detailed balance conditions), the drift velocity is given by

$$V = d \left(\sum_{i=0}^{g-1} 1/r_0^{(i)} \right) [1 - \Pi_{(0)1}^{N_0}] \Bigg/ \left[\sum_{i=0}^{g-1} \frac{1}{r_0^{(i)}} R_{N_i} - 1 \right], \tag{12}$$

where ith chain has N_i discrete states, and $r_j^{(i)}$ and R_{N_i} are defined similarly to Eqs. (9) and (10).

The expressions for dispersion of the two-chain chemical kinetic model are more complicated, and can be written as

$$D=D_0+D_1+D_2+D_3, \tag{13}$$

with the first term given by

$$D_0=(d/N)\left\{VN\sum_{i=1}^{M-1} b_i^{(1)}-\frac{V(N+2)}{2}\right. \\ \left.-\frac{d(N-2)}{2M}\sum_{j=0}^{M-1}(\alpha_j-\beta_j)b_j^{(1)}+\frac{VJ_0}{1-\Pi_{(0)1}^N}\right\}, \tag{14}$$

with

$$J_0=\frac{1}{M}\sum_{j=0}^{N-1} s_j^{(0)} j\sum_{i=0}^{M-1}(\alpha_i-\beta_i)b_i^{(1)}+U_N+(V/d)S_N \\ -(V/d)\sum_{j=0}^{N-1} s_j^{(0)} j\sum_{i=1}^{M-1} b_i^{(1)}, \tag{15}$$

$$S_N=\sum_{j=0}^{N-1} s_j^{(0)}\sum_{k=0}^{N-1}(k+1)b_{k+j+1}^{(0)}, \\ U_N=\sum_{j=0}^{N-1} u_j b_j^{(0)} s_j^{(0)}, \tag{16}$$

where, using definitions (3) and (4), the new functions are given by

$$s_j^{(0)}=u_j^{-1}\left[1+\sum_{k=1}^{N-1}\Pi_{(0)j-1}^{\dagger j-k}\right], \tag{17}$$

and

$$b_j^{(0)}=\left(\frac{r_j^{(0)}}{r_0^{(0)}}\right)\Bigg/\left[\frac{1}{r_0^{(0)}}R_N+\frac{1}{r_0^{(1)}}R_M-1\right], \tag{18}$$

$$b_j^{(1)}=\left(\frac{r_j^{(1)}}{r_0^{(1)}}\right)\Bigg/\left[\frac{1}{r_0^{(0)}}R_N+\frac{1}{r_0^{(1)}}R_M-1\right]. \tag{19}$$

Note that

$$b_0^{(0)}=b_0^{(1)}=1\Bigg/\left[\frac{1}{r_0^{(0)}}R_N+\frac{1}{r_0^{(1)}}R_M-1\right]. \tag{20}$$

The second term in (13) has a similar structure, namely,

$$D_1=(d/M)\left\{VM\sum_{i=1}^{N-1} b_i^{(0)}-\frac{V(M+2)}{2}\right. \\ \left.-\frac{d(M-2)}{2N}\sum_{j=0}^{N-1}(u_j-w_j)b_j^{(0)}+\frac{VJ_1}{1-\Pi_{(1)1}^M}\right\}, \tag{21}$$

with

$$J_1=\frac{1}{N}\sum_{j=0}^{M-1} s_j^{(1)} j\sum_{i=0}^{N-1}(u_i-w_i)b_i^{(0)}+U_M+(V/d)S_M \\ -(V/d)\sum_{j=0}^{M-1} s_j^{(1)} j\sum_{i=1}^{N-1} b_i^{(0)}, \tag{22}$$

$$S_M=\sum_{j=0}^{M-1} s_j^{(1)}\sum_{k=0}^{M-1}(k+1)b_{k+j+1}^{(1)}, \\ U_M=\sum_{j=0}^{M-1}\alpha_j b_j^{(1)} s_j^{(1)}, \tag{23}$$

and, again recalling the definitions (3) and (4), we have for the new function

$$s_j^{(1)}=\alpha_j^{-1}\left[1+\sum_{k=1}^{M-1}\Pi_{(1)j-1}^{\dagger j-k}\right]. \tag{24}$$

The third term in (13) can be written as

$$D_2=-(d/M)\frac{VJ_2}{1-\Pi_{(1)1}^M}, \tag{25}$$

where

$$J_2=\sum_{j=0}^{M-1}\left[\frac{j\Pi_{(1)1}^j}{N\alpha_0}\sum_{i=0}^{N-1}(u_i-w_i)b_i^{(0)}+\frac{b_j^{(1)}\alpha_j\Pi_{(1)1}^j}{\alpha_0}\right. \\ \left.+\frac{V\Pi_{(1)1}^j}{d\alpha_0}\left(\sum_{i=0}^{M-1}(i+1)b_{j+i+1}^{(1)}-j\sum_{i=0}^{N-1} b_i^{(0)}\right)\right]. \tag{26}$$

Finally, the last term in (13) is given by

$$D_3=d^2\left[\sum_{j=0}^{N-1}\frac{b_j^{(0)}}{r_0^{(1)}}(1-\Pi_{(1)1}^M)-\sum_{j=1}^{M-1}\frac{b_j^{(1)}}{r_0^{(0)}}(1-\Pi_{(0)1}^N)\right] \\ \times\left(\frac{J_2}{M(1-\Pi_{(1)1}^M)}-\frac{J_3}{N(1-\Pi_{(0)1}^N)}\right), \tag{27}$$

where

$$J_3=\sum_{j=0}^{N-1}\left[\frac{j\Pi_{(0)1}^j}{Mu_0}\sum_{i=0}^{M-1}(\alpha_i-\beta_i)b_i^{(1)}+\frac{b_j^{(0)}u_j\Pi_{(0)1}^j}{u_0}\right. \\ \left.+\frac{V\Pi_{(0)1}^j}{du_0}\left(\sum_{i=0}^{N-1}(i+1)b_{j+i+1}^{(0)}-j\sum_{i=0}^{M-1} b_j^{(1)}\right)\right]. \tag{28}$$

Note that when $M=1$, the results for the drift velocity and for the dispersion reduce to corresponding expressions for the chemical kinetic model with jumps.[22] For a single-chain model, the original results of Derrida[26] are recovered, as expected.

III. ILLUSTRATIVE EXAMPLES

In order to illustrate these exact results and other properties of parallel-chain kinetic models, we consider several simple examples. First, we discuss a simple, although unphysical, $N=2$ and $M=2$ model with only forward rates, and $u_0=\alpha_0$ and $u_1=\alpha_1$. The expression for the drift velocity can then be easily found:

$$V=V_0+V_1=2V_0=d\frac{2u_0u_1}{2u_0+u_1}, \tag{29}$$

and the expression for dispersion yields

$$D=\frac{d^2}{2}\frac{2u_0u_1(u_1^2+4u_0^2)}{(2u_0+u_1)^3}. \tag{30}$$

For the model with only one chain with the same forward rates, the expression for the drift velocity is given by[26]

$$V^* = d\,\frac{u_0 u_1}{u_0+u_1}, \tag{31}$$

while the dispersion is equal to

$$D^* = \frac{d^2}{2}\,\frac{u_0 u_1 (u_1^2+u_0^2)}{(u_0+u_1)^3}. \tag{32}$$

It is clear that $V_0 < V^* < V$. This example illustrates one of the properties of general parallel-chains chemical models: with the addition of parallel chains with intermediate states $(M>1)$, the transport in the positive direction *increases* in accord with intuition, however the current per chain *decreases*. Similar behavior is found for dispersion.

Measurements of mechanical and biochemical properties of motor proteins as a function of external load are important tools in studying mechanisms of protein motility. In the second example, we will illustrate how external load affects the drift velocity in parallel-chain chemical kinetic model. Consider $N=2$ and $M=1$ model with arbitrary forward and backward rates which satisfy the detailed balance. Then the expression for the drift velocity is given by

$$V = d\,\frac{u_0 u_1 - w_0 w_1 + (\alpha_0-\beta_0)(u_1+w_1)}{u_0+u_1+w_0+w_1}. \tag{33}$$

External load F modifies the rate constants as discussed in Refs. 20–22,

$$u_j(F) = u_j(0) e^{-\theta_j^+ F d/k_B T}, \quad w_j(F) = w_j(0) e^{+\theta_j^- F d/k_B T},$$
$$\tag{34}$$
$$\alpha_0(F) = \alpha_0(0) e^{-\theta_\alpha F d/k_B T}, \quad \beta_0(F) = \beta_0(0) e^{+\theta_\beta F d/k_B T},$$

where $\Sigma_{j=0}^{1}(\theta_j^+ + \theta_j^-) = \theta_\alpha + \theta_\beta = 1$.[20–22] The resulting force-velocity curves for the parallel-chain and for the single-chain $(\alpha_0=\beta_0=0)$ models are presented in Fig. 3. It shows that, although the addition of chains increases the drift velocity and dispersion, the stalling force (when $V=0$) remains unchanged. This is due to the fact that stalling force for motor proteins is determined by free-energy change between two binding states, say states 0_l and 0_{l+1}.[20] The addition of chains does not change free energy in the system because of detailed balance conditions. This is similar to the action of catalyst in chemical reactions when it opens a new reaction channel but does not change an equilibrium constant.

To summarize, parallel-chain kinetic models are introduced and explicit expressions are found for the drift velocity and the dispersion. It is found that the velocity is given by the sum of the currents across the corresponding chains. However, the expression for the dispersion cannot be presented as a linear combination of chain terms. These results together with some properties of the parallel-chain kinetic models, are illustrated on simple examples. It is proposed that these results can be used to describe the complex mechanism of the motion of several classes of motor proteins.

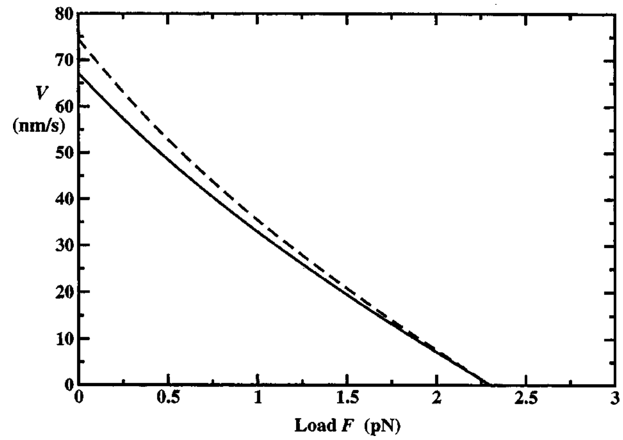

FIG. 3. Force-velocity curves for single-chain (solid line) and parallel-chain (dashed line) models. Parameters used for parallel-chain model calculations are: $u_0=10\ \mathrm{s}^{-1}$, $u_1=100\ \mathrm{s}^{-1}$, $w_0=1\ \mathrm{s}^{-1}$, $w_1=10\ \mathrm{s}^{-1}$, $\alpha_0=1\ \mathrm{s}^{-1}$, $\beta_0=0.01\ \mathrm{s}^{-1}$, $\theta_0^+=\theta_0^-=\theta_1^+=\theta_1^-=0.5$, $\theta_\alpha=\theta_\beta=0.5$, and $d=8.2$ nm. For the single-chain models we assumed that $\alpha_0=\beta_0=0$, and for other parameters we used the same values as above. The step size d used in our calculations corresponds to distance between binding sites in microtubules.

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APPENDIX A: PARALLEL-CHAIN CHEMICAL KINETIC MODEL

In order to derive the results presented in Sec. II, we consider the two-chains kinetic model as shown in Fig. 2. We introduce the probability $P_j^{(k)}(l,t)$ of finding the motor protein particle at site l in state j on chain k $k(k=0,1)$ at time t, which satisfies the master equations

$$\frac{d}{dt} P_j^{(0)}(l,t) = u_{j-1} P_{j-1}^{(0)}(l,t) + w_{j+1} P_{j+1}^{(0)}(l,t) - (u_j+w_j) P_j^{(0)}(l,t), \tag{A1}$$

$$\frac{d}{dt} P_j^{(1)}(l,t) = \alpha_{j-1} P_{j-1}^{(1)}(l,t) + \beta_{j+1} P_{j+1}^{(1)}(l,t) - (\alpha_j+\beta_j) P_j^{(1)}(l,t), \tag{A2}$$

for $j\neq 0$, while $j=0$ is a special state, and $P_0^{(0)}(l,t) = P_0^{(1)}(l,t) = P_0(l,t)$. In this case, the master equation can be written as

$$\frac{d}{dt} P_0(l,t) = u_{N-1} P_{N-1}^{(0)}(l-1;t) + w_1 P_1^{(0)}(l,t) + \alpha_{M-1} P_{M-1}^{(1)}(l-1;t) + \beta_1 P_1^{(1)}(l;t) - (u_0 + w_0 + \alpha_0 + \beta_0) P_0(l,t). \tag{A3}$$

Following[22,25] we can assume that at $t=0$ the particle starts at the origin $x=l=0$. Also, because of conservation of probability, we have

$$\sum_{l=-\infty}^{+\infty}\left(\sum_{j=0}^{N-1} P_j^{(0)}(l,t)+\sum_{j=0}^{M-1} P_j^{(1)}(l,t)\right)=1 \quad (\text{all } t). \tag{A4}$$

Next Derrida's approach[26] is extended by defining four auxiliary functions for each state, j, namely,

$$B_j^{(0)}(t)\equiv\sum_{l=-\infty}^{+\infty} P_j^{(0)}(l,t),$$
$$C_j^{(0)}(t)\equiv\sum_{l=-\infty}^{+\infty} (j+Nl)P_j^{(0)}(l,t), \tag{A5}$$

$$B_j^{(1)}(t)\equiv\sum_{l=-\infty}^{+\infty} P_j^{(1)}(l,t),$$
$$C_j^{(1)}(t)\equiv\sum_{l=-\infty}^{+\infty} (j+Ml)P_j^{(1)}(l,t). \tag{A6}$$

Note that

$$B_0^{(0)}(t)=B_0^{(1)}(t)=B_0(t), \quad C_0^{(0)}(t)/N=C_0^{(1)}(t)/M. \tag{A7}$$

The master equations (A1) and (A2) then give for $j\neq 0$

$$\frac{d}{dt}B_j^{(0)}(t)=u_{j-1}B_{j-1}^{(0)}+w_{j+1}B_{j+1}^{(0)}-(u_j+w_j)B_j^{(0)}, \tag{A8}$$

$$\frac{d}{dt}B_j^{(1)}(t)=\alpha_{j-1}B_{j-1}^{(1)}+\beta_{j+1}B_{j+1}^{(1)}-(\alpha_j+\beta_j)B_j^{(1)}, \tag{A9}$$

and for $j=0$ we obtain

$$\frac{d}{dt}B_0(t)=u_{N-1}B_{N-1}^{(0)}+\alpha_{M-1}B_{M-1}^{(1)}+w_1B_1^{(0)}+\beta_1B_1^{(1)} -(u_0+w_0+\alpha_0+\beta_0)B_0. \tag{A10}$$

Similarly, for $j\neq 0$ we derive

$$\frac{d}{dt}C_j^{(0)}(t)=u_{j-1}C_{j-1}^{(0)}+w_{j+1}C_{j+1}^{(0)}-(u_j+w_j)C_j^{(0)} +u_{j-1}B_{j-1}^{(0)}-w_{j+1}B_{j+1}^{(0)}, \tag{A11}$$

$$\frac{d}{dt}C_j^{(1)}(t)=\alpha_{j-1}C_{j-1}^{(1)}+\beta_{j+1}C_{j+1}^{(1)}-(\alpha_j+\beta_j)C_j^{(1)} +\alpha_{j-1}B_{j-1}^{(1)}-\beta_{j+1}B_{j+1}^{(1)}, \tag{A12}$$

while for $j=0$ the results are

$$\frac{d}{dt}C_0^{(0)}(t)=u_{N-1}C_{N-1}^{(0)}+w_1C_1^{(0)}-(u_0+w_0)C_0^{(0)} +u_{N-1}B_{N-1}^{(0)}-w_1B_1^{(0)}+\frac{N}{M}[\alpha_{M-1}C_{M-1}^{(1)} +\beta_1C_1^{(1)}-(\alpha_0+\beta_0)C_0^{(1)}+\alpha_{M-1}B_{M-1}^{(1)} -\beta_1B_1^{(1)}], \tag{A13}$$

$$\frac{d}{dt}C_0^{(1)}(t)=\alpha_{M-1}C_{M-1}^{(1)}+\beta_1C_1^{(1)}-(\alpha_0+\beta_0)C_0^{(1)} +\alpha_{M-1}B_{M-1}^{(1)}-\beta_1B_1^{(1)}+\frac{M}{N}[u_{N-1}C_{N-1}^{(0)} +w_1C_1^{(0)}-(u_0+w_0)C_0^{(0)}+u_{N-1}B_{N-1}^{(0)} -w_1B_1^{(0)}]. \tag{A14}$$

Following Derrida's arguments,[26] we introduce the ansatz

$$B_j(t)^{(k)}\to b_j^{(k)}, \quad C_j^{(k)}(t)-a_j^{(k)}t\to T_j^{(k)} \quad (k=0,1), \tag{A15}$$

which should be valid at large times. The parameters $b_j^{(k)}$, $a_j^{(k)}$ and $T_j^{(k)}$ are periodic

$$b_{j+N}^{(0)}=b_j^{(0)}, \quad a_{j+N}^{(0)}=a_j^{(0)}, \quad T_{j+N}^{(0)}=T_j^{(0)}, \tag{A16}$$

$$b_{j+M}^{(1)}=b_j^{(1)}, \quad a_{j+M}^{(1)}=a_j^{(1)}, \quad T_{j+M}^{(1)}=T_j^{(1)}. \tag{A17}$$

At steady state $dB_j^{(k)}/dt=0$ and for $j\neq 0$, Eqs. (A9) and (A10) yield

$$0=u_{j-1}b_{j-1}^{(0)}+w_{j+1}b_{j+1}^{(0)}-(u_j+w_j)b_j^{(0)}, \tag{A18}$$

$$0=\alpha_{j-1}b_{j-1}^{(1)}+\beta_{j+1}b_{j+1}^{(1)}-(\alpha_j+\beta_j)b_j^{(1)}, \tag{A19}$$

while for $j=0$, Eq. (A10) give us

$$0=u_{N-1}b_{N-1}^{(0)}+w_1b_1^{(0)}+\alpha_{M-1}b_{M-1}^{(1)} +\beta_1b_1^{(1)}-(u_0+w_0+\alpha_0+\beta_0)b_0, \tag{A20}$$

where $b_0^{(0)}=b_0^{(1)}=b_0$. Again following Derrida's method,[26] the solutions of Eqs. (A18)–(A20) can be written in the form

$$b_j^{(k)}=e_kr_j^{(k)}, \qquad \text{for } k=0,1, \tag{A21}$$

where $r_j^{(k)}$ are defined in Eqs. (9) and (10) and the unknown constants e_k can be determined using the conservation of probability requirement [see (A4)],

$$\sum_{j=0}^{N-1} b_j^{(0)}+\sum_{j=0}^{M-1} b_j^{(1)}=1, \tag{A22}$$

which yield the expressions for $b_j^{(k)}$ given in (18) and (19).

To find the coefficients $a_j^{(k)}$ and $T_j^{(k)}$, the ansatz (A15) is substituted into the asymptotic $(t\to\infty)$ expressions (A11)–(A14), yielding for the coefficients $a_j^{(k)}$ $(j\neq 0)$

$$0=u_{j-1}a_{j-1}^{(0)}+w_{j+1}a_{j+1}^{(0)}-(u_j+w_j)a_j^{(0)}, \tag{A23}$$

$$0=\alpha_{j-1}a_{j-1}^{(1)}+\beta_{j+1}a_{j+1}^{(1)}-(\alpha_j+\beta_j)a_j^{(1)}, \tag{A24}$$

while the coefficients $T_j^{(k)}$ (for $j\neq 0$) then satisfy

$$a_j^{(0)}=u_{j-1}T_{j-1}^{(0)}+w_{j+1}T_{j+1}^{(0)}-(u_j+w_j)T_j^{(0)} +u_{j-1}b_{j-1}^{(0)}-w_{j+1}b_{j+1}^{(0)}, \tag{A25}$$

$$a_j^{(1)}=\alpha_{j-1}T_{j-1}^{(1)}+\beta_{j+1}T_{j+1}^{(1)}-(\alpha_j+\beta_j)T_j^{(1)} +\alpha_{j-1}b_{j-1}^{(1)}-\beta_{j+1}b_{j+1}^{(1)}. \tag{A26}$$

Similarly, for $j=0$ we obtain

$$0=u_{j-1}a_{N-1}^{(0)}+w_1a_1^{(0)}-(u_0+w_0)a_0^{(0)}, \tag{A27}$$

$$0=\alpha_{M-1}a_{M-1}^{(1)}+\beta_1 a_1^{(1)}-(\alpha_0+\beta_0)a_j^{(1)}, \tag{A28}$$

and

$$a_0^{(0)}=\frac{N}{M}a_0^{(1)}=u_{N-1}T_{N-1}^{(0)}+w_1T_1^{(0)}-(u_0+w_0)T_0^{(0)} +u_{N-1}b_{N-1}^{(0)}-w_1b_1^{(0)}+\frac{N}{M}[\alpha_{M-1}T_{M-1}^{(1)} +\beta_1T_1^{(1)}-(\alpha_0+\beta_0)T_0^{(1)}+\alpha_{M-1}b_{M-1}^{(1)}-\beta_1b_1^{(1)}]. \tag{A29}$$

Comparing (A23), (A24), (A27), and (A28) with expressions (A18)–(A20), we conclude that

$$a_j^{(k)}=A_kb_j^{(k)}, \quad k=0,1, \tag{A30}$$

with the constants A_k related to each other by $A_0/N=A_1/M$. These constants can be found by considering the expression $M\Sigma_{j=0}^{N-1}a_j^{(0)}+N\Sigma_{j=1}^{N-1}a_j^{(1)}$ [using (A25) and (A26) for summations over $a_j^{(k)}$] and recalling the normalization Eq. (A22)

$$A_0=\sum_{j=0}^{N-1}a_j^{(0)}+\frac{N}{M}\sum_{j=1}^{M-1}a_j^{(1)} =\sum_{j=0}^{N-1}(u_j-w_j)b_j^{(0)}+\frac{N}{M}\sum_{j=0}^{M-1}(\alpha_j-\beta_j)b_j^{(1)}. \tag{A31}$$

To determine the coefficients $T_j^{(k)}$, we introduce, following,[22,25,26]

$$y_j^{(0)}\equiv w_{j+1}T_{j+1}^{(0)}-u_jT_j^{(0)}, \quad y_j^{(1)}\equiv \beta_{j+1}T_{j+1}^{(1)}-\alpha_jT_j^{(1)}. \tag{A32}$$

Now (A25) and (A26) can be rewritten as

$$y_j^{(0)}-y_{j-1}^{(0)}=a_j^{(0)}-u_{j-1}b_{j-1}^{(0)}+w_{j+1}b_{j+1}^{(0)},$$
$$y_j^{(1)}-y_{j-1}^{(1)}=a_j^{(1)}-\alpha_{j-1}b_{j-1}^{(1)}+\beta_{j+1}b_{j+1}^{(1)}, \tag{A33}$$

while expression (A29) gives us

$$y_0^{(0)}-y_{N-1}^{(0)}=a_0^{(0)}-u_{N-1}b_{N-1}^{(0)}+w_1b_1^{(0)}-\frac{N}{M}(y_0^{(1)} -y_{M-1}^{(1)}+\alpha_{M-1}b_{M-1}^{(1)}-\beta_1b_1^{(1)}), \tag{A34}$$

$$y_0^{(1)}-y_{M-1}^{(1)}=a_0^{(1)}-\alpha_{M-1}b_{M-1}^{(1)}+\beta_1b_1^{(1)}-\frac{M}{N}(y_0^{(0)} -y_{M-1}^{(0)}+u_{N-1}b_{N-1}^{(0)}-w_1b_1^{(0)}). \tag{A35}$$

Following the discussions in Refs. 22 and 25, these equations can be solved, yielding

$$y_j^{(0)}=(j/M)\sum_{i=0}^{M-1}(\alpha_i-\beta_i)b_i^{(1)}+u_jb_j^{(0)} +(A_0/N)\left[\sum_{i=0}^{N-1}(i+1)b_{j+1+i}^{(0)}-j\sum_{i=1}^{M-1}b_i^{(1)}\right]+c_0, \tag{A36}$$

$$y_j^{(1)}=(j/N)\sum_{i=0}^{N-1}(u_i-w_i)b_i^{(0)}+\alpha_jb_j^{(1)}+(A_1/M)\left[\sum_{i=0}^{M-1}(i +1)b_{j+i+1}^{(1)}-j\sum_{i=1}^{N-1}b_i^{(0)}\right]+c_1, \tag{A37}$$

where c_k ($k=0,1$) are arbitrary constants which will be canceled in final expressions for the dispersion D. These expressions allow us to find the formulas for $T_j^{(k)}$ (see Refs. 22, 25, and 26)

$$T_j^{(0)}=-\frac{1}{u_j}\left[y_j^{(0)}+\sum_{k=1}^{N-1}y_{j+k}^{(0)}\Pi_{j+1}^{j+k}(0)\right]\Bigg/(1-\Pi_1^N(0)), \tag{A38}$$

$$T_j^{(1)}=-\frac{1}{\alpha_j}\left[y_j^{(1)}+\sum_{k=1}^{M-1}y_{j+k}^{(1)}\Pi_{j+1}^{j+k}(1)\right]\Bigg/(1-\Pi_1^M(1)). \tag{A39}$$

It is now possible to calculate explicitly the drift velocity, V, and the dispersion, D, using the steady-state definitions (1) and (2). The mean particle position can be written as

$$\langle x(t)\rangle=\frac{d}{N}\sum_{l=-\infty}^{+\infty}\sum_{j=0}^{N-1}(j+Nl)P_j^{(0)}(l,t) +\frac{d}{M}\sum_{l=-\infty}^{+\infty}\sum_{j=1}^{M-1}(j+Ml)P_j^{(1)}(l,t) =\frac{d}{N}\sum_{j=0}^{N-1}C_j^{(0)}(t)+\frac{d}{M}\sum_{j=1}^{M-1}C_j^{(1)}(t). \tag{A40}$$

Using the master Eqs. (A1) and (A2), the following expression can be derived

$$\lim_{t\to\infty}\frac{d}{dt}\langle x(t)\rangle=\frac{d}{N}A_0\sum_{j=0}^{N-1}b_j^{(0)}+\frac{d}{M}A_1\sum_{j=1}^{M-1}b_j^{(1)} =\frac{d}{N}A_0=\frac{d}{M}A_1. \tag{A41}$$

Using result (A31) and definitions (18) and (19), we obtain the final results for the drift velocity, which are given in Eqs. (6)–(11). Note that the final explicit formula for the drift velocity consists of two terms which correspond to transport across each of the chains. This result can be easily generalized for a model with more than two parallel chains [see Eq. (12)].

A similar method can be used to determine the dispersions. Starting from

$$\langle x^2(t)\rangle=\frac{d^2}{N^2}\sum_{l=-\infty}^{\infty}\sum_{j=0}^{N-1}(j+Nl)^2P_j^{(0)}(l,t) +\frac{d^2}{M^2}\sum_{l=-\infty}^{\infty}\sum_{j=1}^{M-1}(j+Ml)^2P_j^{(1)}(l,t), \tag{A42}$$

and again appealing to the master Eqs. (A1) and (A2), we obtain

$$\lim_{t\to\infty}\frac{d}{dt}\langle x^2(t)\rangle=\frac{d^2}{N^2}\left[2\sum_{j=0}^{N-1}(u_j-w_j)(a_j^{(0)}t+T_j^{(0)})+\sum_{j=0}^{N-1}(u_j+w_j)b_j^{(0)}\right]+\frac{d^2}{M^2}\left[2\sum_{j=0}^{M-1}(\alpha_j-\beta_j)(a_j^{(1)}t+T_j^{(1)})+\sum_{j=0}^{M-1}(\alpha_j+\beta_j)b_j^{(1)}\right]. \tag{A43}$$

By using Eq. (A41) and definition (2), we find

$$D=\frac{d^2}{N^2}\left[\sum_{j=0}^{N-1}(u_{j-w_j})T_j^{(0)}+\frac{1}{2}\sum_{j=0}^{N-1}(u_j+w_j)b_j^{(0)}-A_0\sum_{j=0}^{N-1}T_j^{(0)}\right]+\frac{d^2}{M^2}\left[\sum_{j=0}^{M-1}(\alpha_j-\beta_j)T_j^{(1)}+\frac{1}{2}\sum_{j=0}^{M-1}(\alpha_j+\beta_j)b_j^{(1)}-A_1\sum_{j=0}^{M-1}T_j^{(1)}\right]+\frac{d^2}{M^2}A_1T_0^{(1)}. \tag{A44}$$

By substituting the expressions for $T_j^{(k)}$ [using (A38), (A39) and (A36), (A37)] into (A44), the constants c_k cancel and we obtain the final expressions (13)–(28) for the dispersion. Note that the dispersion has four contributions: two of them [square brackets terms in (A44)] are due to transport along the corresponding chains 0 and 1, the third contribution [which is associated with the last term in (A44)] is due to chain connectivity, and the last term arises from algebraic equations relating the constants c_0 and c_1.

[1] H. Lodish *et al.*, *Molecular Cell Biology*, 3rd ed. (Scientific American Books, New York, 1995), Chapter 23.
[2] B. Alberts *et al.*, *Molecular Biology of the Cell*, 3rd ed. (Garland, New York, 1994) Chapter 16.
[3] J. Howard, *Mechanics of Motor Proteins and the Cytoskeleton* (Sinauer Associates, Sunderland, MA, 2001).
[4] K. Svoboda, P. P. Mitra, and S. M. Block, Proc. Natl. Acad. Sci. U.S.A. **91**, 11782 (1994).
[5] H. Kojima, E. Muto, H. Higuchi, and T. Yanagida, Biophys. J. **73**, 2012 (1997).
[6] C. M. Coppin, D. W. Pierce, L. Hsu, and R. D. Vale, Proc. Natl. Acad. Sci. U.S.A. **94**, 8539 (1997).
[7] H. Higuchi, E. Muto, Y. Inoue, and T. Yanagida, Proc. Natl. Acad. Sci. U.S.A. **94**, 4395 (1997).
[8] K. Visscher, M. J. Schnitzer, and S. M. Block, Nature (London) **400**, 184 (1999).
[9] M. D. Wang, M. J. Schnitzer, H. Yin, R. Landick, J. Gelles, and S. M. Block, Science **282**, 902 (1998).
[10] G. J. L. Wuite, S. B. Smith, M. Young, and C. Bustamante, Nature (London) **404**, 103 (2000).
[11] S. Leibler and D. A. Huse, J. Cell Biol. **121**, 1357 (1993).
[12] T. Duke and S. Leibler, Biophys. J. **71**, 1235 (1996).
[13] F. Jülicher, A. Ajdari, and J. Prost, Rev. Mod. Phys. **69**, 1269 (1997).
[14] T. Harms and R. Lipowsky, Phys. Rev. Lett. **79**, 2895 (1997).
[15] F. Julicher, in *Transport and Structure in Biophysical and Chemical Phenomena*, Lecture Notes in Physics, edited by S. C. Müller, J. Parisi, and W. Zimmerman, (Springer, Heidelberg, 1999).
[16] D. Keller and C. Bustamante, Biophys. J. **78**, 541 (2000).
[17] H. Qian, Biophys. Chem. **67**, 263 (1997).
[18] H. Wang, T. Elston, A. Mogilner, and G. Oster, Biophys. J. **74**, 1186 (1998).
[19] A. B. Kolomeisky and B. Widom, J. Stat. Phys. **93**, 633 (1998).
[20] M. E. Fisher and A. B. Kolomeisky, Proc. Natl. Acad. Sci. U.S.A. **96**, 6597 (1999).
[21] M. E. Fisher and A. B. Kolomeisky, Physica A **274**, 241 (1999).
[22] A. B. Kolomeisky and M. E. Fisher, Physica A **279**, 1 (2000).
[23] Y. Chen, Biophys. J. **78**, 313 (2000).
[24] Y. Chen and B. Yan, Biophys. Chem. **91**, 79 (2001).
[25] A. B. Kolomeisky and M. E. Fisher, J. Chem. Phys. **113**, 10867 (2000).
[26] B. Derrida, J. Stat. Phys. **31**, 433 (1983).
[27] M. E. Fisher and A. B. Kolomeisky, Proc. Natl. Acad. Sci. U.S.A. **98**, 7748 (2001).
[28] Y. Okada and N. Hirokawa, Science **283**, 1152 (1999).
[29] Y. Okada and N. Hirokawa, Proc. Natl. Acad. Sci. U.S.A. **97**, 640 (2000).
[30] H. Sakakibara, H. Kojima, Y. Sakai, E. Katayama, and K. Oiwa, Nature (London) **400**, 586 (1999).
[31] M. Guthold, X. Zhu, C. Rivetti *et al.*, Biophys. J. **77**, 2284 (1999).
[32] T. Hill, *Free Energy Transduction and Biochemical Cycle Kinetics* (Springer, New York, 1989).