Drift coefficients of motor proteins moving along sidesteps*

Li Jing-Hui(李静辉)†

Faculty of Science, Ningbo University, Ningbo 315211, *China*

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In the paper, we investigate two motor proteins moving along the sidesteps: a motor protein moving along a two-dimensional sidestep and another protein moving along a three-dimensional sidestep. The drift coefficients (or stationary average velocities) of these two motor proteins are calculated. We believe that our investigation of the motor proteins moving along the sidesteps in the present paper can benefit the investigation of the transport of the motor proteins to some extent.

Keywords: motor protein, drift, master equation, stationary average velocity

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1. Introduction

Every day in the world, almost everyone needs to walk up and down the stairs of buildings. Here, one probably wants to ask a question: if a motor protein moves along the stairs of the buildings in biological bodies, how will it move (or what about its probability density and average velocity)?

Nowadays, (both theoretically and experimentally) the investigation of the transport of motor proteins shows that, when some motor proteins transport the loads (which are needed by biological bodies), their movements are basically like some random walks.[1–4] This is the reason why we now began to use the random-walk models to express the movements of these motor proteins.[1–4] Sometimes, the motor proteins also want to climb the stairs in biological bodies, even though they should move along the rigid linear tracks, such as the cytoskeleton filaments, the DNA molecular tubes, and so on. This also motivates us to investigate the motor proteins moving along the stairs of the buildings in biological bodies. The stationary average velocity (or drift coefficient) and dispersion constant (or diffusion coefficient) of the one-dimensional continuous-time random walk were investigated in Ref. [5]. Now, researchers are not only interested in the transport behaviors of the one-dimensional continuous-time random walk,[1–4,6] but also in the coupled continuous-time random walks[7,8] and the continuous-time quantum random walks.[9,10]

In this paper, we will consider two motor proteins moving along the sidesteps: a motor protein moving along a two-dimensional sidestep (see Fig. 1) and a motor protein moving along a three-dimensional sidestep (see Fig. 2). We will derive the drift coefficients (or stationary average velocities) of these two motor proteins respectively. I think that this work can benefit the investigation of the transport of the motor proteins to some extent.

2. Motor protein I: A motor protein moving along a two-dimensional sidestep

We consider a motor protein moving along a two-dimensional sidestep as plotted in Fig. 1(a) in which the motor protein can move between the nearest sites of the solid fold lines (this case is abbreviated as protein I). The sites of the solid fold lines in the figure can be denoted by the configuration (l,m) with $l,m=0,\pm1,\pm2,\pm3,\pm4,\ \ldots,\pm\infty$ [see Fig. 1(a)]. The transition rate of the motor protein from the site (l,m) to $(l\pm1,m)$ is $\lambda^{(m)}_{l,l\pm1}$, and that from the site (l,m) to $(l,m\pm1)$ is $\gamma^{(l)}_{m,m\pm1}$.

From Fig. 1(a), we can obtain the master equations of the probability densities of this motor protein

$$\begin{aligned}&\partial_t P(l,m;t)\\ =\ &-(\lambda^{(m)}_{l,l+1}+\gamma^{(l)}_{m,m-1})P(l,m;t)+\lambda^{(m)}_{l+1,l}P(l+1,m;t)\\ &+\gamma^{(l)}_{m-1,m})P(l,m-1;t),\end{aligned}\tag{1}$$

$$\begin{aligned}&\partial_t P(l+1,m;t)\\ =\ &-(\lambda^{(m)}_{l+1,l}+\gamma^{(l+1)}_{m,m+1})P(l+1,m;t)+\lambda^{(m)}_{l,l+1}P(l,m;t)\\ &+\gamma^{(l+1)}_{m+1,m})P(l+1,m+1;t),\end{aligned}\tag{2}$$

where $P(l,m;t)$ is the probability density to find the motor protein in the configuration (l,m) at the time t.

Here, we simply believe $l=m$ (the other cases can be considered in the same way, see below) and set $\lambda^{(m)}_{l,l+1}=\lambda_1$, $\lambda^{(m)}_{l+1,l}=\lambda_2$, $\gamma^{(l)}_{m-1,m}=\gamma^{(l+1)}_{m,m+1}=\gamma_1$, and $\gamma^{(l)}_{m,m-1}=\gamma^{(l+1)}_{m+1,m}=\gamma_2$. Then, equations (1) and (2) can be written as

$$\begin{aligned}&\partial_t P(l,l;t)\\ =\ &-(\lambda_1+\gamma_2)P(l,l;t)+\lambda_2P(l+1,l;t)+\gamma_1P(l,l-1;t),\end{aligned}\tag{3}$$

$$\begin{aligned}&\partial_t P(l+1,l;t)\\ =\ &-(\lambda_2+\gamma_1)P(l+1,l;t)+\lambda_1P(l,l;t)\end{aligned}$$

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†Corresponding author. E-mail: lijinghui@nbu.edu.cn

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$$+\gamma_2 P(l+1,l+1;t), \tag{4}$$

with the normalization condition

$$\sum_l [P(l,l;t)+P(l+1,l;t)]=1.$$

When the motor protein moves along the sites of the stairs in Fig. 1(a), its average velocity is

$$\begin{aligned} V(t) &= \frac{\mathrm{d}}{\mathrm{d}t}\langle l\rangle = \frac{\mathrm{d}}{\mathrm{d}t}\sum_l l[P(l,l;t)+P(l+1,l;t)] \\ &= \sum_l l[\partial_t P(l,l;t)+\partial_t P(l+1,l;t)]. \end{aligned} \tag{5}$$

Substituting Eqs. (3) and (4) into Eq. (5), we can get

$$\begin{aligned} V(t) &= -\gamma_2\sum_l lP(l,l;t)+\gamma_1\sum_l lP(l,l-1;t) \\ &\quad -\gamma_1\sum_l lP(l+1,l;t)+\gamma_2\sum_l lP(l+1,l+1;t) \\ &= \gamma_1\sum_l P(l+1,l;t)-\gamma_2\sum_l P(l,l;t). \end{aligned} \tag{6}$$

In the stationary state, i.e. in the limit of $t\to\infty$, the average velocity of the motor protein is

$$V_\mathrm{s}=\gamma_1 P_2-\gamma_2 P_1, \tag{7}$$

where $P_1=\sum_l P(l,l)$ and $P_2=\sum_l P(l+1,l)$, and the subscript "s" means that the system is in the stationary state. The stationary average velocity V_s is just the drift coefficient.

Below we derive P_1 and P_2. From Eqs. (3) and (4), we can get

$$-(\lambda_1+\gamma_2)P_1+\lambda_2 P_2+\gamma_1 P_2=0, \tag{8}$$

$$-(\lambda_2+\gamma_1)P_2+\lambda_1 P_1+\gamma_2 P_1=0. \tag{9}$$

In addition, in the limit of $t\to\infty$, the normalization condition of the probability densities is

$$P_1+P_2=1. \tag{10}$$

From Eqs. (8)–(10), we can solve

$$P_1=\frac{\lambda_2+\gamma_1}{\lambda_1+\lambda_2+\gamma_1+\gamma_2}, \tag{11}$$

$$P_2=\frac{\lambda_1+\gamma_2}{\lambda_1+\lambda_2+\gamma_1+\gamma_2}. \tag{12}$$

Substituting Eqs. (11) and (12) into Eq. (7), we can get the stationary average velocity (or drift coefficient) of the motor protein moving along the two-dimensional sidestep as plotted in Fig. 1(a)

$$V_\mathrm{s}=\frac{\lambda_1\gamma_1-\lambda_2\gamma_2}{\lambda_1+\lambda_2+\gamma_1+\gamma_2}. \tag{13}$$

Equation (13) illustrates that the drift coefficient of the motor protein in Fig. 1(a) can be negative, zero, and positive. Controlling the values of the transition rates λ_1, λ_2, γ_1, and γ_2 can reverse the stationary drift of the motor protein (i.e. the value of the stationary average velocity can be reversed from the negative to the positive or *vice versa* by controlling the transition rates).

Now, we know that, for the spatially periodic systems, the symmetry breaking is the ingredient for the drift transport in these systems.[1–4,11–16] For the motor protein in Fig. 1(a), after we set $\lambda^{(m)}_{l,l+1}=\lambda_1$, $\lambda^{(m)}_{l+1,l}=\lambda_2$, $\gamma^{(l)}_{m-1,m}=\gamma^{(l+1)}_{m,m+1}=\gamma_1$, and $\gamma^{(l)}_{m,m-1}=\gamma^{(l+1)}_{m+1,m}=\gamma_2$, if we consider l and m as the space variables, it is a spatially periodic system. Below, let us analyze the symmetry breaking condition for the motor protein in Fig. 1(a). If $\lambda_1=\lambda_2$ and $\gamma_1=\gamma_2$, it is clear that, in this case, the motor protein is wholly symmetric. Now, from Eq. (13), we can immediately get $V_\mathrm{s}=0$. But our result [i.e. the formula Eq. (13), see Eq. (13)] shows that, even if $\lambda_1\neq\lambda_2$ and $\gamma_1\neq\gamma_2$, as long as $\lambda_1\gamma_1=\lambda_2\gamma_2$, the stationary drift of the motor protein is absent. So, for the motor protein in Fig. 1(a), its symmetry breaking condition is $\lambda_1\gamma_1\neq\lambda_2\gamma_2$.

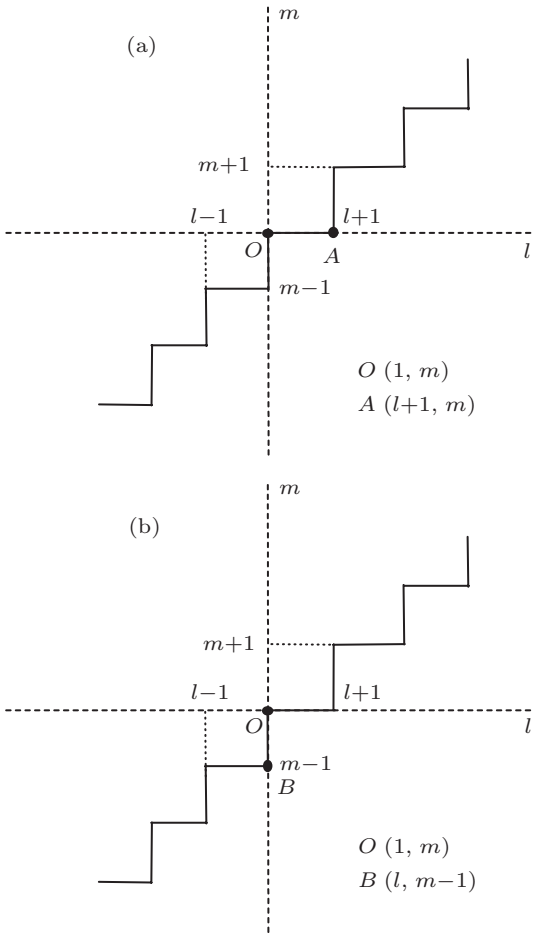


Fig. 1. Schematic view of a motor protein moving along a two-dimensional sidestep. (a) Two independent sites O and A are marked (the other sites of the motor protein can be described by using these two sites' probability-density equations). (b) Two independent sites O and B are marked (the other sites of the motor protein can be described by using these two sites' probability-density equations).

Here, we only considered the case when $l=m$. If $l\neq m$,

such as $l = m + m_0$, for this case, we should replace m in Eqs. (1) and (2) with $m = l - m_0$. Then, all our derivations and the result formula are still valid. In addition, for our motor protein, besides the drift transport, it still has the diffusive transport. We will consider the diffusive coefficient of the motor protein in Fig. 1(a) elsewhere. Moreover, in the present paper, we used the probability density equations of the sites O and A in Fig. 1(a) [i.e. Eqs. (1) and (2)] to express the motor protein in Fig. 1(a). Here, we can also use the probability density equations of the sites O and B in Fig. 1(b) to express this motor protein. If we use the probability density equations of the sites O and B in Fig. 1(b) to express the motor protein, the master equations of the motor protein are

$$\begin{aligned}&\partial_t P(l,m;t)\\ =\ &-(\lambda^{(m)}_{l,l+1}+\gamma^{(l)}_{m,m-1})P(l,m;t)\\ &+\lambda^{(m)}_{l+1,l}P(l+1,m;t)+\gamma^{(l)}_{m-1,m})P(l,m-1;t), \quad (14)\\ &\partial_t P(l,m-1;t)\\ =\ &-(\lambda^{(m-1)}_{l,l-1}+\gamma^{(l)}_{m-1,m})P(l,m-1;t)\\ &+\lambda^{(m-1)}_{l-1,l}P(l-1,m-1;t)+\gamma^{(l)}_{m,m-1})P(l,m;t). \quad (15)\end{aligned}$$

Superficially, although equation (15) is very different from Eq. (2), equation (15) can be obtained from Eq. (2), which will be given below. If we substitute $l+1 = l'$ and $m = m'-1$ into Eq. (2), equation (2) becomes

$$\begin{aligned}&\partial_t P(l',m'-1;t)\\ =\ &-(\lambda^{(m'-1)}_{l',l'-1}+\gamma^{(l')}_{m'-1,m'})P(l',m'-1;t)\\ &+\lambda^{(m'-1)}_{l'-1,l'}P(l'-1,m'-1;t)+\gamma^{(l')}_{m',m'-1})P(l',m';t). \quad (16)\end{aligned}$$

Since l, l', m, and m' all take the values from the infinite negative integer to the infinite positive integer (i.e. l, l', m, $m' = \pm1, \pm2, \pm3, \pm4, \ldots, \pm\infty$), equations (15) and (16) are wholly identical. So, if we only consider the probability densities of the motor protein in Fig. 1, using Eqs. (1) and (2) to express the motor protein is the same as using Eqs. (14) and (15). We also calculated the drift coefficient using Eqs. (14) and (15). The result formula derived by us is the same as Eq. (13). Here, there is a question: if we use Eqs. (1) and (2) differently, and use Eqs. (14) and (15), could we get the same result for the diffusive coefficient? We will consider this question elsewhere.

Of course, for real motor proteins, our model is too simple, since the transition rates between the nearest sites for the motor proteins are determined by the temperature of the system, the chemical potential energy differences between the nearest sites, and the gravitational potential energy differences between the nearest sites. Here, the ATP concentration can determine the chemical potential energy differences between the nearest sites, and the height differences between the nearest sites from the earth can determine the gravitational potential energy differences between the nearest sites. So, for the processing motor proteins that move along a track similar to the solid fold lines in Fig. 1, according to our result [i.e. Eq. (13)], their movement can be controlled by suitably selecting the differences of the temperature of the system, the ATP concentration and the height of sites from the earth. Controlling these conditions can lead to a reversal of the stationary average velocity of the processing motor proteins, which are now intensively investigated and well known as "current reversal".[17,18]

In addition, we should mention that, for the positive direction of the stationary average velocity [see Eqs. (7) and (13)], it takes the one along the diagonal line of the axes l and m from the negative numbers of l and m to the positive numbers of l and m.

3. Motor protein II: A motor protein moving along a three-dimensional sidestep

Below, we consider a motor protein (this case is abbreviated as protein II) moving along a three-dimensional sidestep, wherein the motor protein can move between the nearest sites along the solid fold lines in Fig. 2. The sites of the solid fold lines in Fig. 2 are described by the configuration (l,m,n) with $l,m,n = 0, \pm1, \pm2, \pm3, \pm4, \ldots, \pm\infty$ [see Fig. 2]. The transition rate from (l,m,n) to $(l\pm1,m,n)$ is $\lambda^{(m,n)}_{l,l\pm1}$, that from (l,m,n) to $(l,m\pm1,n)$ is $\gamma^{(l,n)}_{m,m\pm1}$, and that from (l,m,n) to $(l,m,n\pm1)$ is $\mu^{(l,m)}_{n,n\pm1}$.

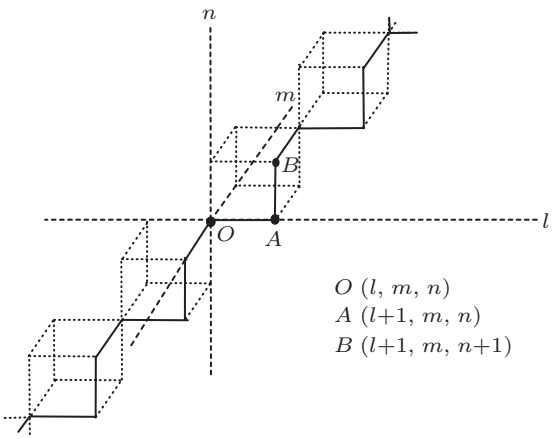


Fig. 2. Schematic view of a motor protein moving along the three-dimensional sidestep, where three independent sites are marked (the other sites of the motor protein can be described by using these three sites' probability-density equations).

The master equations of the probability densities of the motor protein in Fig. 2 are

$$\begin{aligned}&\partial_t P(l,m,n;t)\\ =\ &-(\lambda^{(m,n)}_{l,l+1}+\gamma^{(l,n)}_{m,m-1})P(l,m,n;t)\\ &+\lambda^{(m,n)}_{l+1,l}P(l+1,m,n;t)+\gamma^{(l,n)}_{m-1,m})P(l,m-1,n;t), \quad (17)\end{aligned}$$

$$\begin{aligned}
&\partial_t P(l+1,m,n;t)\\
=\ &-(\lambda_{l+1,l}^{(m,n)}+\mu_{n,n+1}^{(l+1,m)})P(l+1,m,n;t)\\
&+\lambda_{l,l+1}^{(m,n)}P(l,m,n;t)+\mu_{n+1,n}^{(l+1,m)}P(l+1,m,n+1;t), \quad (18)\\
&\partial_t P(l+1,m,n+1;t)\\
=\ &-(\gamma_{m,m+1}^{(l+1,n+1)}+\mu_{n+1,n}^{(l+1,m)})P(l+1,m,n+1;t)\\
&+\gamma_{m+1,m}^{(l+1,n+1)}P(l+1,m+1,n+1;t)\\
&+\mu_{n,n+1}^{(l+1,m)}P(l+1,m,n;t), \quad (19)
\end{aligned}$$

where $P(l,m,n;t)$ is the probability density to find the motor protein in the configuration (l,m,n) at the time t.

Here, we only consider the case of $l=m=n$, and set $\lambda_{l,l+1}^{(m,n)}=\lambda_1$, $\lambda_{l+1,l}^{(m,n)}=\lambda_2$, $\gamma_{m-1,m}^{(l,n)}=\gamma_{m,m+1}^{(l+1,n+1)}=\gamma_1$, $\gamma_{m,m-1}^{(l,n)}=\gamma_{m+1,m}^{(l+1,n+1)}=\gamma_2$, $\mu_{n,n+1}^{(l+1,m)}=\mu_1$, and $\mu_{n+1,n}^{(l+1,m)}=\mu_2$. Then, equations (17)–(19) become

$$\begin{aligned}
&\partial_t P(l,l,l;t)\\
=\ &-(\lambda_1+\gamma_2)P(l,l,l;t)+\lambda_2 P(l+1,l,l;t)\\
&+\gamma_1 P(l,l-1,l;t), \quad (20)\\
&\partial_t P(l+1,l,l;t)\\
=\ &-(\lambda_2+\mu_1)P(l+1,l,l;t)\\
&+\lambda_1 P(l,l,l;t)+\mu_2 P(l+1,l,l+1;t), \quad (21)\\
&\partial_t P(l+1,l,l+1;t)\\
=\ &-(\gamma_1+\mu_2)P(l+1,l,l+1;t)\\
&+\gamma_2 P(l+1,l+1,l+1;t)+\mu_1 P(l+1,l,l;t), \quad (22)
\end{aligned}$$

with the normalization condition

$$\sum_l [P(l,l,l;t)+P(l+1,l,l;t)+P(l+1,l,l+1;t)]=1.$$

The average velocity of the motor protein is

$$\begin{aligned}
V(t)\ &=\ \frac{\mathrm{d}}{\mathrm{d}t}\langle l\rangle=\frac{\mathrm{d}}{\mathrm{d}t}\sum_l l[P(l,l,l;t)+P(l+1,l,l;t)\\
&\quad +P(l+1,l,l+1;t]\\
&=\ \sum_l l[\partial_t P(l,l,l;t)+\partial_t P(l+1,l,l;t)\\
&\quad +\partial_t P(l+1,l,l+1;t)]. \quad (23)
\end{aligned}$$

Substituting Eqs. (20)–(22) into Eq. (23) and only considering the case in the limit of $t\to\infty$, we can get the stationary average velocity of the motor protein in Fig. 2

$$V_{\mathrm{s}}=\gamma_1 P_3'-\gamma_2 P_1', \quad (24)$$

where $P_1'=\sum_l P(l,l,l)$ and $P_3'=\sum_l P(l+1,l,l+1)$ with $P(l,l,l)=\lim_{t\to\infty}P(l,l,l;t)$, and $P(l+1,l,l+1)=\lim_{t\to\infty}P(l+1,l,l+1;t)$.

In the limit of $t\to\infty$, from Eqs. (20)–(22), we can get

$$-(\lambda_1+\gamma_2)P_1'+\lambda_2 P_2'+\gamma_1 P_3'=0, \quad (25)$$

$$-(\lambda_2+\mu_1)P_2'+\lambda_1 P_1'+\mu_2 P_3'=0, \quad (26)$$

$$-(\gamma_1+\mu_2)P_3'+\gamma_2 P_1'+\mu_1 P_2'=0, \quad (27)$$

with $P_2'=\sum_l P(l+1,l,l)$ and $P(l+1,l,l)=\lim_{t\to\infty}P(l+1,l,l;t)$.

Now, the normalization condition of the probability densities is

$$P_1'+P_2'+P_3'=1. \quad (28)$$

From Eqs. (25)–(28), we can solve P_1', P_2', and P_3'. Then, substituting P_1' and P_3' into Eq. (24), we can get

$$\begin{aligned}
V_{\mathrm{s}}\ =\ &(\lambda_1\gamma_1\mu_1-\lambda_2\gamma_2\mu_2)/(\lambda_1\mu_1+\lambda_1\mu_2+\gamma_1\lambda_2+\gamma_1\mu_1\\
&+\gamma_2\lambda_2+\gamma_2\mu_1+\gamma_2\mu_2+\mu_2\lambda_2+\lambda_1\gamma_1). \quad (29)
\end{aligned}$$

Equation (29) shows that i) the stationary drift of the motor protein in Fig. 2 can be negative, zero, and positive, and ii) the "current reversal" phenomenon[7] can be obtained by controlling the values of the transition rates of the motor protein in Fig. 2.

For the positive direction of the stationary average velocity [see Eqs. (24) and (29)], it takes the one along the diagonal line of the axes l, m, and n from the negative numbers of l, m, and n to the positive numbers of l, m, and n.

For the further discussion of the stationary drift of the motor protein moving along the three-dimensional sidestep in Fig. 2, since they are almost the same as the ones of the motor protein moving along the two-dimensional sidestep in Fig. 1, here, to avoid the repetition, we no longer give them [see the discussion after Eq. (13) for the transport of the motor protein moving along the two-dimensional sidestep in Fig. 1].

Here, it is worthwhile to plot a figure for the comparison of the drift coefficients of the motor protein discussed in Section 2 and the motor protein in Section 3. To do so, we should make some simplifications for our results [i.e. Eqs. (13) and (29)]. First, we simplify the result of the motor protein I [i.e. Eqs. (13)]. For the motor protein I, because of the absorbtion of the energy of ATPs, when the motor protein is in the configuration (l,m), we believe that the filled position in the configuration (l,m) has more energy ε_1 than the empty position in the configuration $(l+1,m)$, and has more energy ε_2 than the empty position in the configuration $(l,m-1)$; when the motor protein is in the configuration $(l+1,m)$, we believe that the filled position in the configuration $(l+1,m)$ has more energy ε_1 than the empty position in the configuration $(l+1,m+1)$, and has more energy ε_2 than the empty position in the configuration (l,m). Then, we can get the transition rates of the motor protein I[1–4]

$$\begin{aligned}
&\lambda_{l,l+1}^{(m)}=\lambda_{l,l+1}^{(m)}(0)\,\mathrm{e}^{\varepsilon_1/kT},\quad \lambda_{l+1,l}^{(m)}=\lambda_{l+1,l}^{(m)}(0)\,\mathrm{e}^{\varepsilon_2/kT},\\
&\gamma_{m,m+1}^{(l+1)}=\gamma_{m,m+1}^{(l+1)}(0)\,\mathrm{e}^{\varepsilon_1/kT},\\
&\gamma_{m,m-1}^{(l)}=\gamma_{m,m-1}^{(l)}(0)\,\mathrm{e}^{\varepsilon_2/kT},
\end{aligned}$$

where k is the Boltzmann constant, T is the temperature of the system, $\lambda^{(m)}_{l,l+1}(0)$ is the transition rate $\lambda^{(m)}_{l,l+1}$ with $\varepsilon_1 = 0$ which is related with T, and $\lambda^{(m)}_{l+1,l}(0)$, $\gamma^{(l+1)}_{m,m+1}(0)$, and $\gamma^{(l)}_{m,m-1}(0)$ have the same understandings as $\lambda^{(m)}_{l,l+1}(0)$. To further the simplification of our result [i.e. Eqs. (13)], here, we take the dimensionless form and set $kT = 1$ and $\lambda^{(m)}_{l,l+1}(0) = \lambda^{(m)}_{l+1,l}(0) = \gamma^{(l+1)}_{m,m+1}(0) = 1$. After that, from Eq. (13), we can get

$$V_{\rm s} = \frac{{\rm e}^{2\varepsilon_1} - {\rm e}^{2\varepsilon_2}}{2\left({\rm e}^{\varepsilon_1} + {\rm e}^{\varepsilon_2}\right)}. \tag{30}$$

Second, for the motor protein II, after the same simplifications as motor protein I, we can get

$$V_{\rm s} = \frac{{\rm e}^{3\varepsilon_1} - {\rm e}^{3\varepsilon_2}}{3\left({\rm e}^{2\varepsilon_1} + {\rm e}^{2\varepsilon_2} + {\rm e}^{\varepsilon_1+\varepsilon_2}\right)}. \tag{31}$$

In Fig. 3, from Eqs. (30) and (31), we plot the curves of $V_{\rm s}$ as a function of ε_1 with parameter $\varepsilon_2 = 2.5$ for the motor protein I and motor protein II respectively, in the dimensionless form. From this figure, we can see that, under the above simplifications, the motor protein I drifts faster than the motor protein II. In addition, figure 3 also shows that, by fixing the parameter ε_2, the drift reversal[17,18] can be obtained by controlling the value of ε_1.

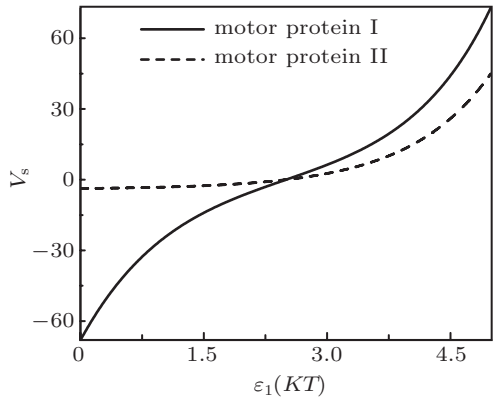


Fig. 3. $V_{\rm s}$ versus ε_1 with $\varepsilon_2 = 2.5$ plotted from Eqs. (30) and (31), wherein the solid curve is for the motor protein I and the dashed curve is for the motor protein II.

Finally, we should mention the differences between this paper and its relevant references.[1–4,6] First, we give the difference between this paper and Refs. [1]–[4]. In the present paper, we considered the movement of the motor proteins moving along the two-dimensional and three-dimensional sidesteps in Figs. 1 and 2; While in Refs. [1]–[4], we considered the motions of the single motor protein and two coupled motor proteins moving along the straight lines. Secondly, we give the differences between this paper and Ref. [6]. (i) The motor proteins in the present paper go between the nearest sites of a two-dimensional sidestep and a three-dimensional sidestep; while the random walk in Ref. [6] moves between the nearest sites of a network of the squares with the same diagonals (see Fig. 1 of Ref. [6]). (ii) For the processive motor proteins, owing to the complexity and variety of the biological bodies, there are fewer cases where the motor proteins move along the network in Fig. 1 of Ref. [6], but there are more cases where the motor proteins want to move along the sidesteps in Figs. 1 and 2 (in comparison with the ones in Ref. [6]).

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