Mean-field analysis of two-species totally asymmetric simple exclusion process (TASEP) with attachment and detachment
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Abstract: In the field of statistical physics, unidirectional motion of a large number of particles along a single track can be described by totally asymmetric simple exclusion process (TASEP), from which many meaningful properties, such as the appearance of domain wall (defined as the borderline of high particle density and low particle density along the motion track) and boundary layers, can be obtained. However, it is biologically general that a single track may be occupied by different particle species. For example, in cells each microtubule protofilament is usually occupied by different species of motor protein. So previous studies about TASEP that included only one particle species may not be reasonable enough to describe more detailed properties of particle motion processes in a real cell environment. To address this problem, TASEP including two particle species is discussed in this study. Theoretical methods to get particle densities of each species are provided. By which, phase transition related properties of particle densities are obtained. Our analysis shows that domain wall and boundary layers of single species densities always appear simultaneously with those of the total particle density. The height of the domain wall of total particle density is equal to the summation of those of single particle species. Phase diagrams for typical model parameters are also presented. The methods presented in this study can be generalized to analyze TASEP with more particle species.

Key words: two-species TASEP, domain wall, boundary layer, molecular motor, phase transition.

1. Introduction

In the last decades, several theoretical models have been developed to describe the unidirectional motion of a large number of particles, including the motion of motor proteins along microtubules, the motion of RNA polymerases along DNA template during gene transcription, the motion of ribosomes along mRNA transcript during translation, as well as the bus traffic process in our daily life [1–4]. Most of these can be regarded as generalizations of the one-dimensional totally asymmetric simple exclusion process (TASEP) [5, 6].

In TASEP, motion tracks of particles are simplified to a one-dimensional lattice with length N + 1: particles enter the track from the first site 0, provided this site is not occupied, and leave the track from the last site N. If lattice site i + 1 is empty, the particle at lattice site i will hop forward to site i + 1 with given rate. Generally, particles may also detach to any unoccupied bulk site. In recent years, TASEP has been studied extensively, especially for its phase transition related properties (i.e., the appearance of domain wall (DW) and boundary layers (BLs)), which are usually driven by boundary conditions [7–14]. However, in most previous studies, the self-propelled particles are usually assumed to be the same species (i.e., they all have the same properties, including the hopping rate, attachment and detachment rate, as well as the entering rate and leaving rate). But in real cells, one microtubule protofilament (which is the main highway to transport cargos in
cells) is usually occupied by motor proteins from different species [15]. So, to know more detailed properties about the particle motion process in reality, the usual TASEP should be generalized to include particles from different species [16-19].

The simplest generalization is the two-species ASEP, which has been discussed in recent studies [20-30]. However, to our knowledge, in most of the previous studies (except refs. 24, 27, 28) no particle attachment or detachment to or from bulk sites of the track (which is usually called the Langmuir kinetics) is included, whereas here sites 1, 2, ..., N−1 are considered bulk sites. Furthermore, previous studies usually assumed that one particle species enters the motion track from site 0 and leaves from site N, while the other one enters from site N and leaves from site 0. Meanwhile, it is also assumed that two-species pair \((P_1)(P_2)_{i+1}\) can change to \((P_2)(P_1)_{i+1}\) (i.e., forward hopping of one species will never be blocked by the other species). For convenience, the two particle species are denoted \(P_1\) and \(P_2\) and \((P_1)\) means there is a particle \(P_1\) at site \(i\).

The TASEP discussed in this study also includes two particle species, but both of them enter the motion track from the first site 0 and leave from last site N (i.e., they not only travel along the same track, but also move in the same direction). Previous studies about one species TASEP have shown that nontrivial attachment and detachment (i.e., the Langmuir kinetics) is one of the key driven factors to the appearance of DW in particle density [3, 9, 13, 31-33]. So, in this study, both of the two particle species are allowed to attach to (and detach from) bulk sites of the track. Like in the one species cases, we also called this process "TASEP-Langmuir kinetics (LK)" [9].

2. Models for two-species TASEP

Let \(n_i\) and \(m_i\) be occupation numbers of particle species \(P_1\) and \(P_2\) at site \(i\), respectively. Specifically \(n_i = 1\) means site \(i\) is occupied by a particle \(P_1\), while \(m_i = 0\) means site \(i\) is not occupied by particle \(P_2\). Because of the hard-core exclusion, \(n_i + m_i = 0\) or 1. For \(1 \leq i \leq N-1\), the time evolution of \(n_i\) and \(m_i\) are governed by following equations:

\[
\frac{dn_i}{dt} = n_{i-1}(1 - n_i - m_i) - n_i(1 - n_{i+1} - m_{i+1}) + \omega_{i+1}(1 - n_i - m_i) - \omega_{i+1}n_i
\]

\[
\frac{dm_i}{dt} = qm_{i-1}(1 - n_i - m_i) - qm_i(1 - n_{i+1} - m_{i+1}) + \omega_{i+1}(1 - n_i - m_i) - \omega_{i+1}m_i
\]

where, for convenience, the forward hopping rate of species \(P_1\) is normalized to be a unit, and the forward hopping rate of species \(P_2\) is assumed to be \(q\). The attachment rate of species \(P_2\) to any unoccupied bulk site \(i\) is denoted \(\omega_{b,i}\), and the detachment rate of species \(P_1\) from bulk sites is denoted by \(\omega_{b,D}\). At the first site \(i = 0\) (left boundary),

\[
\frac{dn_0}{dt} = \alpha_1(1 - n_0 - m_0) - n_0(1 - n_1 - m_1)
\]

\[
\frac{dm_0}{dt} = \alpha_2(1 - n_0 - m_0) - qm_0(1 - n_1 - m_1)
\]

where \(\alpha_1\) is the entry rate of particle \(P_1\) to the first site 0. While at the last site \(i = N\) (right boundary),

\[
\frac{dn_N}{dt} = n_{N-1}(1 - n_N - m_N) - \beta n_N
\]

\[
\frac{dm_N}{dt} = q n_{N-1}(1 - n_N - m_N) - \beta m_N
\]

\[
\frac{dm_N}{dt} = q m_{N-1}(1 - n_N - m_N) - \beta m_N
\]

with \(\beta\) the leaving rate of particle \(P_2\) from the last site \(N\).

In cells, the hopping rate of particles is usually determined by their biochemical properties. For example, forward hopping of motor proteins, such as conventional kinesin, is mechanochemically coupled with hydrolysis of adenosine triphosphate (ATP). Each forward mechanical step is tightly coupled with one ATP hydrolysis. Therefore, hopping rate is determined by the rate of ATP hydrolysis. Meanwhile, leaving rate of particles from the motion track is also determined by their biochemical properties, or even the rate of ATP hydrolysis. Therefore it is biophysically reasonable to assume that the ratio of leaving rate of the two species \(\beta_2/\beta_1\) is equal to the ratio of their forward hopping rate \(1/q\). Meanwhile, experiments found that, if the two heads of motor protein kinesin both bind adenosine diphosphate (ADP), then it will soon detach from the microtubule. This means that detachment rate of motor proteins is also determined by their biochemical properties and the rate of ATP hydrolysis. So, for convenience of theoretical analysis, this study also assumes that \(\omega_{b,D}/\omega_{b,i} = 1\). However, along with their biochemical properties, entry rate \(\alpha_2\) and attachment rate \(\omega_{b,D}\) of particle \(P_1\) and \(P_2\) are also influenced by environmental conditions, especially their concentrations. So, the corresponding rate ratios, \(\alpha_2/\alpha_1\) and \(\omega_{b,D}/\omega_{b,i}\) may be different from the ratio \(1/q\).

Define \(\rho_1(0) = (n_0)\) and \(\rho_2(0) = (m_0)\). Using the mean-field approximation, for large \(N\) limit, equations for steady state values of particle densities \(\rho_1\) and \(\rho_2\) can be obtained from (1) and (2),

\[
\frac{dJ_k}{dt} = q^2 \frac{\Omega_{b,i}}{2} (1 - \rho_1 - \rho_2) - \Omega_{b,D} \frac{\rho_1}{k = 1, 2}
\]

where \(J_k = \rho_0(1 - \rho_1 - \rho_2), \Omega_{b,i} = N \omega_{b,i}, \Omega = N \omega_{b,D} = N \omega_{b,D}/q = N \omega_0, 0 < x < 1\). Note, this study assumes that \(\alpha_1(n_i, n_{i+1}) = \alpha_2(n_i, n_{i+1}) + 1\), and in the analysis of mean-field approximation, the length of the motion track is normalized to 1. Meanwhile, this study also assumes that the unbinding–binding rate \(\omega_{b,D}/\omega_{b,i}\) scales inversely with track length \(N\), which is the most interesting case. For other cases, one can discuss similarly as in [34, 35]. From (7), one can show that total particle density \(\rho = \rho_1 + \rho_2\) satisfies

\[
\frac{dJ}{dt} = K\Omega (1 - \rho) - \Omega \frac{\rho_1}{k = 1, 2}
\]

where \(K = K_1 + K_2 = (\omega_{b,D} + \omega_{b,i})/\omega_0\) and \(J = \rho(1 - \rho)\). From (3)-(6), one can obtain that at boundaries \(x = 0\), particle densities \(\rho_1, \rho_2\), and \(\rho\) satisfy \(\rho(0) = \rho_1(0) = \rho_2(0)\), and \(\rho(1) = \rho_1(1) + \rho_2(1) = 1 - \beta + \beta = \beta_2/\beta_1\).

We need to point out that, with notations defined previously, the density current of the first particle species is \(J_1\). However, the density current of the second particle species should be \(qJ_2\), and so the total density current is \(J_1 + qJ_2 = (\rho_1 + q\rho_2)(1 - \rho)\). which is different from \(J\).

Equation (8) implies that the governing equation for total particle density \(\rho\) is the same as the one obtained for one-species TASEP-LK process [36], but with effective detachment rate \(\Omega_{b,D} = \Omega\), effective attachment rate \(\Omega_{b,i} = K\Omega\), initiation (entry) rate \(\alpha = \alpha_1 + \alpha_2, \rho\) and termination (leaving) rate \(\beta = \beta_1 + \beta_2\) (see Fig. 1). So total particle density \(\rho\) can be obtained using the same methods as described in one-species TASEP-LK process. But the main difficulty for the two-species case is how to get single species densities \(\rho_1\) and \(\rho_2\). Actually, no reasonable boundary conditions at \(x = 1\) (i.e., values of \(\rho_1(1)\) and \(\rho_2(1)\)) can be derived from (5) and (6). Meanwhile, properties of densities \(\rho_1\) and \(\rho_2\) are different from those in one-species cases. For example, in one-species TASEP-LK process, particle densities before and after DW location \(x_0\) satisfy \(\rho(x_0) + \rho(x_0) = 1\).
Fig. 1. Mean density profiles obtained from (1–6) (black dotted line), and their mean-field approximations obtained from (7), (8) (solid lines for \( \rho \), dash-dot lines for \( \rho_1 \), and dashed line for \( \rho_2 \)). Parameter values used in calculations are \( \Omega_{1,2} = 0.01, \Omega = 0.14, \alpha_1 = 0.2, \alpha_2 = 0.09 \) and \( \Omega_{1,2} = 0.1, \Omega = 0.05, \alpha_1 = 0.1, \alpha_2 = 0.18 \). Other parameter values are \( N = 10^4, q = 0.9, \Omega_{1,2} = 0.1, \beta = 0.1 \). Total particle density \( \rho \) in both (a) and (b) is the same as the one in usual TASEP-LK with \( \alpha = \beta = 0.3 \), and \( \Omega_{1,2} = 0.1, \Omega = 0.15 \). Locations of DW for total density \( \rho \) and single species densities \( \rho_1, \rho_2 \) are the same. Across DW location, \( J(1-\rho) \) and \( J_k(1-\rho) \) for \( k = 1, 2 \) are all conserved. [Colour online.]

[37]. This is because across DW location \( x_{\omega}J = \rho(1-\rho) \) is conserved. But for two-species cases, particle densities \( \rho_1, \rho_2 \) do not satisfy this relation. However, the plots in Fig. 1 imply that DWs of density \( \rho \), \( \rho_1, \rho_2 \) appear at the same location. Actually, further numerical calculations show that their BLs also appear simultaneously, see Sect. 5.

Along the motion track, \( J_1, J_2 \), and consequently \( J \), always change continuously, even if corresponding densities \( \rho_1, \rho_2 \), and \( \rho \) are discontinuous. At any location \( x \) of the track, \( \rho(x)[1-\rho(x)] = J_1(x)[1-\rho(x)] + \rho_1(x)[1-\rho(x)] + \rho_2(x)[1-\rho(x)] \). Through simple analysis, we obtain \( \rho(x)[1-\rho(x)] = \rho(x)[1-\rho(x)] \). Particularly, this relation also holds at location \( x_{\omega} \), of DW.

As we have mentioned before, total particle density \( \rho \) can be obtained from (8) with boundary conditions \( \rho(0) = \rho(0) + \rho_2(0) = \alpha_1 + \alpha_2q \) and \( \rho(1) = 1 - \beta \). But, if there exists DW between boundaries \( x = 0 \) and \( x = 1 \), then without boundary value \( \rho_0(1) \), single species density \( \rho_0 \) cannot be obtained simply by (7). Actually, with boundary value \( \rho_0(0) \), only the value of density \( \rho_0 \) before DW location \( x_{\omega} \) (i.e., in interval \( [0, x_{\omega}] \)) can be directly obtained using (7). One of the main aims of this study is to find methods to get single species density \( \rho_0 \) along the whole track (i.e., in interval \( [0, 1] \)) but using only boundary condition at \( x = 0 \).

Let \( \Delta = \rho(x_{\omega}) - \rho(x_{\omega}) \) (i.e., the DW height of total density \( \rho \)). Then the DW height of single species density is

\[
\Delta = \rho(x_{\omega}) - \rho(x_{\omega}) - \rho(x_{\omega}) - \rho(x_{\omega}) = \rho(x_{\omega}) - \rho(x_{\omega}) = \rho(x_{\omega}) - \rho(x_{\omega})
\]

So, \( \Delta_1 + \Delta_2 = \Delta \), and \( \Delta > 0 \) if \( \Delta > 0 \). Therefore, DWs of total density \( \rho \) and single species densities \( \rho_1, \rho_2 \) always appear at the same location, which is consistent with the finding through numerical calculations (see Fig. 1).

The value \( \rho_0(x_{\omega}) \) can be obtained as follows:

\[
\rho_0(x_{\omega}) = \rho(x_{\omega}) + \Delta = \rho(x_{\omega}) + \rho(x_{\omega}) - \rho(x_{\omega}) - \rho(x_{\omega}) = \rho(x_{\omega}) = \rho(x_{\omega})
\]

Using \( \rho_0(x_{\omega}) \) as the left boundary condition, the value of single species density \( \rho_0 \) after DW location \( x_{\omega} \) (i.e., in interval \( [x_{\omega}, 1] \)) can be obtained from (7). Note, the preceding method to get single species density \( \rho_0 \) is also available when there exist BLs at either boundary \( x = 0 \) or boundary \( x = 1 \). BSls of single species densities \( \rho_1, \rho_2 \) and total density \( \rho \) also appear simultaneously.

3. Methods to obtain particle densities \( \rho_1, \rho_2 \): special cases \( K = 1 \)

The basic idea to obtain single species densities \( \rho_1, \rho_2 \) is to use (7) and the expression of total density \( \rho \). Therefore, the first step is to get \( \rho_0 \) from (8).

For \( K = 1, (8) \) is reduced to

\[
(\rho_0 - \Omega)(2\rho - 1) = 0
\]

with boundary conditions \( \rho(0) = \alpha \) and \( \rho(1) = 1 - \beta \). The method to get density \( \rho \) from (9) has been discussed previously in ref. 36. For the sake of convenience, we introduced briefly as follows.

Equation (9) has two general solutions, \( \rho(x) = 1/2 \) and \( \rho(x) = \Omega x + C \) with \( C \) a constant determined by boundary conditions. The constant solution \( \rho(x) = 1/2 \) coincides with the density \( \rho_i = K/(K + 1) \) given by IK, and corresponds to the maximal current (MC) phase. For convenience, the solution \( \rho(x) = \Omega x + C \), which satisfies the left boundary condition \( \rho(0) = \alpha \) is denoted by \( \rho_1(x) = \Omega x + \alpha \), and the solution \( \rho(x) \), which satisfies the right boundary condition \( \rho(1) = 1 - \beta \) is denoted by \( \rho_2(x) = \Omega x + 1 - \beta - \Omega \).

If expanding solution domain \([0, 1]\) to the whole space (i.e., \( -\infty, \infty \)) then both \( \rho_1(x) \) and \( \rho_2(x) \) cross the line \( \rho = \rho_1 = 1/2 \). Denote corresponding intersection points by \( x_{\omega} \) and \( x_{\omega} \), respectively. It can be easily obtained that \( x_{\omega} = (1 - 2\alpha)/2\Omega \) and \( x_{\omega} = (2\beta + 2\Omega - 1)/2\Omega \). The solution \( \rho(x) \) of (9) is obtained by the following process. If \( x_{\omega} < x_{\omega} \), then \( \rho_1(x) \) is on the left of \( \rho_2(x) \). So a MC phase appears between \( x_{\omega} \) and \( x_{\omega} \). For such cases,

\[
\rho(x) = \begin{cases} 
\rho_1(x) & 0 < x \leq x_{\omega} \\
1/2 & x_{\omega} \leq x \leq x_{\omega} \\
\rho_2(x) & x_{\omega} < x < 1
\end{cases}
\]

On the other hand, if \( x_{\omega} > x_{\omega} \), then \( \rho_1(x) \) is on the right of \( \rho_2(x) \). For these cases, a DW will appear between \( x_{\omega} \) and \( x_{\omega} \). Based on the continuity of \( f = \rho(1-\rho) \) (i.e., \( J_1(x_{\omega}) = J_2(x_{\omega}) \)) the location of DW can be obtained as follows:

\[
x_{\omega} = \frac{\Omega + \beta - \alpha}{2\Omega}
\]
The solution $\rho(x)$ of (9) can then be obtained,

$$
\rho(x) = \begin{cases} 
\rho_{i}(x) & 0 < x < x_{w} \\
\rho_{i}(x) & x_{w} < x < 1 
\end{cases}
$$

Finally, single species density $\rho(x)$ in the main body of the motion track (i.e., for $0 < x < 1$) can be obtained from $\rho_{MC}(x)$ and $\rho_{i}(x).$ If $x_{w} < x_{i}$ then

$$
\rho(x) = \begin{cases} 
\rho_{i}(x) & 0 < x < x_{w} \\
\rho_{MC}(x) & x_{w} < x < x_{i} \\
\rho_{i}(x) & x_{i} < x < 1 
\end{cases}
$$

On the other hand, if $x_{i} < x_{w}$ then

$$
\rho(x) = \begin{cases} 
\rho_{i}(x) & 0 < x < x_{w} \\
\rho_{MC}(x) & x_{w} < x < x_{i} \\
\rho_{i}(x) & x_{i} < x < 1 
\end{cases}
$$

Like in the expression of total density $\rho$, see (10) and (12), locations $x_{i}, x_{w}, x_{u}$ may not lie in interval [0, 1]. For those cases, corresponding BLs will appear. For example, if $x_{i} < 0$ then there will exist left BL.

After getting total density $\rho$, single species densities $\rho_1$ and $\rho_2$ can be obtained by four steps: (i) Get left solutions $\rho_{i,1}(x)$ and $\rho_{i,2}(x)$ in interval $[0, x_{w}]$ from (7) by matching boundary conditions $\rho_{i,1}(0) = \alpha_1$ and $\rho_{i,2}(0) = \alpha_2/q$, respectively; (ii) get solutions $\rho_1(x)$ and $\rho_2(x)$ in interval $[\min(x_{w}, x_{MC}), \max(x_{w}, x_{MC})]$ from (7) by matching boundary conditions $\rho_1(x_{w}) = \rho_{i,1}(x_{w})$; (iii) get solutions $\rho_1(x)$ and $\rho_2(x)$ in interval $[x_{MC}, \infty)$ by matching $\rho_1(x_{MC}) = \rho_1(x_{MC})$; (iv) get single species densities by confining the obtained $\rho_1$ and $\rho_2$ in interval [0, 1]. Note, if $x_{i} > x_{w}$ and $0 < x_{i} < 1$, then there will exist DW for both $\rho_1$ and $\rho_2$ at $x_{w}$, see detailed discussion later.

If the solution $\rho(x)$ of (9) is $\rho(x) = 1+\alpha x + C$, then from (7), single species density $\rho_1$ can be obtained as follows,

$$
\rho_1 = \frac{\Omega_{1} x + C_1}{q}
$$

On the other hand, if the solution $\rho(x)$ of (9) is $\rho(x) = 1/2$, then $\rho_1$ and $\rho_2$ satisfy

$$
\begin{align*}
\frac{\partial \rho_1}{\partial x} &= \frac{\Omega_{1} x + C_1}{q} - 2\Omega \\
\frac{\partial \rho_2}{\partial x} &= -\frac{\Omega_{1} x + C_1}{q} + 2\Omega
\end{align*}
$$

Their solutions are

$$
\begin{align*}
\rho_1 &= \frac{\Omega_{1} x - \exp(\Omega_{1} x - 2\Omega x)}{2\Omega} \\
\rho_2 &= \frac{(\Omega_{1} x/q) - \exp(\Omega_{1} x - 2\Omega x)}{2\Omega}
\end{align*}
$$

Constants $C_1$ and $C_2$ are determined by boundary conditions.

By matching boundary conditions at $x = 0$, left solutions $\rho_{i,1}(x)$ and $\rho_{i,2}(x)$ in interval $[0, x_{w}]$ are given as follows:

$$
\begin{align*}
\rho_{i,1}(x) &= \Omega_{1} x + a_1 \\
\rho_{i,2}(x) &= \Omega_{2} x + a_2
\end{align*}
$$

Then values of $\rho_{i,1}(x_{w})$ and $\rho_{i,2}(x_{w})$ can be obtained. Using $\rho_{i,1}(x)$ as boundary conditions, single species density $\rho_{MC}(x)$ in interval $[\min(x_{w}, x_{MC}), \max(x_{w}, x_{MC})]$ can be obtained by (15) and (16). Where constants $C_1$ and $C_2$ are

$$
\begin{align*}
\alpha_1 &= 2\Omega x_w + \ln(\Omega_{1} x - 2\Omega \rho_{i,2}(x_{w})) \\
\alpha_2 &= 2\Omega x_w + \ln(\Omega_{2} x - 2\Omega \rho_{i,2}(x_{w}))
\end{align*}
$$

Using $\rho_{MC}(x)$ as boundary condition of $\rho_{MC}(x)$ (i.e., $\rho_{MC}(x_{w}) = \rho_{MC}(x_{MC})$) the constant $C_1$ in (13) and (14) can be determined. Therefore, right solution $\rho_{MC}(x)$ of (7) can be obtained,

$$
\begin{align*}
\rho_{i,1}(x) &= \frac{\Omega_{1} x - x_{i} + \rho_{MC}(x_{w})}{q} \\
\rho_{i,2}(x) &= \frac{\Omega_{2} x - x_{i} + \rho_{MC}(x_{w})}{q}
\end{align*}
$$

4. MC phase of total density $\rho$ for special cases $K = 1$

In this section, we will show that if effective initiation rate $\alpha$ and leaving rate $\beta$ satisfy

$$
\alpha > \frac{1}{2} - \Omega \quad \text{and} \quad \alpha + \beta > 1 - \Omega
$$

then total particle density $\rho$ will be in the MC phase near the right boundary $x = 1$, in which $\rho = 1/2$ and $\rho = 1/2$.

The MC phase of density $\rho$ may appear in four cases: LD–MC, LD–MC–HD, MC–HD, and MC, see Figs. 3a, 3d. Based on the continuity of $J$ and $J_{F}$ at locations $x_{s} = (1 - 2\alpha)/21$ and $x_{f} = (2\beta + 21 - 1)/21$, we have the following conclusions:

1. If $\mathcal{F}$ appears at left boundary $x = 0$, then $x_{s} \leq 0$ and $x_{f} > 0$, which means that $\alpha < 1/2$, and $\beta > 1/2$.

2. If $\mathcal{F}$ appears at right boundary (i.e., phase LD–MC or MC), then $x_{s} < 1$ and $x_{f} \geq 1$, which means $\beta > 1/2$ and $\alpha > 1/2$.

3. If $\mathcal{F}$ appears only in part of the main body of motion track (i.e., in LD–MC–HD phase), then $0 < x_{s} < x_{f} < 1$, which means $\alpha < 1/2, \beta < 1/2$, and $\alpha + \beta < 1$.
Based on the preceding three conclusions, we then obtain conditions listed in (23) for the existence of MC phase.

From (15) and (16), one can verify that in MC phase, derivatives of single species density $\rho_1$ and $\rho_2$ are as follows:

$$
\dot{\rho}_1(x) = \exp[2\Omega(x_{\alpha} - x)](\Omega_{\alpha A} - 2\Omega_{\alpha B} x)
$$

$$
\dot{\rho}_2(x) = \exp[2\Omega(x_{\alpha} - x)]\left(\frac{\Omega_{\alpha A}}{q} - 2\Omega_{\alpha B} x\right)
$$
Fig. 4. Typical examples of densities \( \rho_1, \rho_2, \rho_{2s} \) in which MC phase appears in total density \( \rho \). In the MC phase of \( \rho \) (i.e. \( \rho \geq 1/2 \)) densities \( \rho_1, \rho_2 \) of single particle species may be constant, or increase or decrease along the motion track, which depends on the sign of \( \Omega_{1A}x_1 - \Omega_{2A}x_2 \).

(a) For \( \Omega_{1A}x_1 - \Omega_{2A}x_2 > 0 \), \( \rho_1 \) increases along the track. (b) While for \( \Omega_{1A}x_1 - \Omega_{2A}x_2 < 0 \), \( \rho_2 \) decreases along the track. (c, d) For special cases, \( \Omega_{1A}x_1 - \Omega_{2A}x_2 = 0 \), both \( \rho_1 \) and \( \rho_2 \) are constants when total density \( \rho \) is in the MC phase. Line types in this figure are the same as in Fig. 1.

[Colour online.]

By substituting expressions of \( x_1, x_2, \) and \( \rho_{2s,1}(x) \), see (17) and (18), we obtain

\[
\begin{align*}
\partial_x \rho_1(x) &= 2 \exp[2\Omega_1(x_1 - x)] \frac{\Omega_{1A}x_1 - \Omega_{2A}x_2}{q} \\
\partial_x \rho_2(x) &= 2 \exp[2\Omega_1(x_2 - x)] \frac{\Omega_{2A}x_2 - \Omega_{1A}x_1}{q}
\end{align*}
\]

which implies that, if total density \( \rho \) is in MC phase (i.e., \( \rho \geq 1/2 \); see Fig. 4), the value of \( \Omega_{1A}x_1 - \Omega_{2A}x_2 \) is essential to determine the monotonicity of single species densities \( \rho_1 \) and \( \rho_2 \).

Depending on values of rates \( \alpha_1 \) and \( \Omega_{1A} \), even if the total density \( \rho \) is constant in a certain interval, the single species density \( \rho_1 \) may not be, and they may increase or decrease in this interval. This is different from the cases in which density \( \rho \) is in LD or HD phase. For those cases, both \( \rho_1 \) and \( \rho_2 \) increase with \( x \), and with slopes \( \Omega_{1A} \) and \( \Omega_{2A} \), respectively, see (13) and (14). For the cases in which total density \( \rho \) is constant, if \( \Omega_{1A}x_1 - \Omega_{2A}x_2 > 0 \) then \( \rho_1 \) has positive slope (i.e., increases along the motion track), while \( \rho_2 \) has negative slope. Both \( \rho_1, \rho_2 \) are all constants iff \( \Omega_{1A}x_1 - \Omega_{2A}x_2 = 0 \), see Fig. 4. Finally, previous analysis shows that, for \( K = 1 \), there exists DW iff \( |\alpha - \beta| < \Omega \) and \( \alpha + \beta > \Omega < 1 \). The DW lies at \( x_w = (\Omega + \beta - \alpha)/2\Omega \) with height \( \Delta = \rho_2(x_w) - \rho_1(x_w) \). The DW height of single species density \( \rho_1 \) can be obtained by \( \Delta_1 = \rho_1(x_w)\Delta \), see (10), (11), (13), and (14).

5. Methods to obtain particle densities \( \rho_1, \rho_2 \): general cases \( K > 1 \)

As mentioned in ref. 9, due to particle–hole symmetry, this study only discusses the TASEP-1K process with \( K > 1 \). For these general cases, the idea used in the special cases with \( K = 1 \) can also be employed to get the single special density \( \rho_c \). Roughly speaking, the method of obtaining densities \( \rho_1 \) and \( \rho_2 \) of the two particle species is to use (7) and the solution of total density \( \rho \), as well as the key relationship \( \rho_2(x_w)\rho_2(x_w') = \rho_1(x'_w)\rho_1(x'_w') \) at locations \( x_w \) of DW or BLs.

After the total density \( \rho(x) \) has been obtained, there are also four steps needed to get single species density \( \rho_{1,2}(x) \): (i) Get left solutions \( \rho_{1,2}(x) \) in interval \([-x_w, x_w] \) from (7) with boundary conditions \( \rho_{1,2}(0) = \alpha_1 \) and \( \rho_{1,2}(x) = \alpha_1q^{|x|} \), respectively; (ii) use \( \rho_{1,2}(x_0') = \rho_{1,2}(x_0') + \Delta_1 = \rho_2(x'_w)\rho_1(x'_w')\rho_1(x'_w') \) to get the value of density \( \rho_{1,2}(x) \) at \( x = x'_w \); (iii) use \( \rho_{1,2}(x_0) \) as the boundary condition to get the right solutions \( \rho_{1,2}(x) \) in interval \([x_w, 1]\); and (iv) get single species density by confining \( \rho_{1,2} \) and \( \rho_{1,2} \) in interval \([0, 1]\), and connect them at location \( x_w \).

The method to get total particle density \( \rho \) is similar to that used in special cases \( K = 1 \), but with the help of the Lambert W function, see Fig. 5 and for details see ref. 36. In brief, left solution \( \rho_{1,2}(x) \) and right solution \( \rho_{1,2}(x) \), which satisfy (8) with left and right boundary conditions, respectively, should be obtained firstly. Then based on the continuity of \( J \) and \( J_b \), location \( x_w \) of DW can be determined \( x_w \) may lie outside the interval \([0, 1]\). Finally total density \( \rho \) is obtained by linking \( \rho_{1,2}(x) \) and \( \rho_{1,2}(x) \) at location \( x_w \) and restricting the new linked function in interval \([0, 1]\).
It can be easily verified that
\[ x = \frac{\rho - \rho_1}{\rho_2 - \rho_1} \]
where \( K_2\Omega = \Omega_{2,\lambda} \) and \( K_2\Omega = \Omega_{2,\lambda}/q \). From (24), we get
\[ \frac{\partial}{\partial \rho} \rho = \frac{K - (K + 1)\rho}{1 - 2\rho} \Omega \] (27)
Substituting (27) into (25) and (26) we then obtain
\[ \frac{\partial}{\partial \rho} \rho_1 + P(x)\rho_1 = K_2\Omega \quad \frac{\partial}{\partial \rho} \rho_2 + P(x)\rho_2 = K_2\Omega \]
where \( P(x) = |K - 1|/(2\rho - 1) \). So the general solutions of \( \rho_1 \) and \( \rho_2 \) are
\[ \rho_1 = \exp\left(-\int P(x)dx\right) + \int K_2\Omega \exp\left(\int P(x)dx\right) \] (28)
\[ \rho_2 = \exp\left(-\int P(x)dx\right) + \int K_2\Omega \exp\left(\int P(x)dx\right) \] (29)
where constant \( c \) can be determined by the boundary condition at \( x = 0 \) or \( x = 1 \).

Similar to that in ref. 36, to obtain the total density \( \rho(x) \), a rescaled density \( \sigma(x) \) is introduced as follows:
\[ \sigma(x) = \frac{K + 1}{K - 1}(2\rho(x) - 1) - 1 \] (30)
It can be easily verified that \( \sigma(x) \) satisfies
\[ \frac{\partial}{\partial \rho} \sigma(x) + \frac{\partial}{\partial \ln[\sigma(x) = \frac{(K + 1)^2}{K - 1} \Omega] \]
By integration we get
\[ \sigma(x) = Y(x) \]
where the function \( Y(x) \) is
\[ Y(x) = |\sigma(0)| \exp\left(\frac{(K + 1)^2}{K - 1}(x - x_0) + \sigma(0)\right) \]
In which, \( x_0 \) is usually chosen as \( x_0 = 0 \) or \( x_0 = 1 \), where the density \( \rho(x_0) \) and consequently \( \sigma(x_0) \) is known. By matching left or right boundary condition, corresponding expression of \( Y(x) \) can be obtained, denoted \( Y_L(x) \) or \( Y_R(x) \), respectively. Then the function \( \sigma(x) \), denoted \( \sigma_L(x) \) and \( \sigma_R(x) \) correspondingly, can be obtained from (31). Note that the special case \( \sigma(x) = 0 \) corresponds to the Langmuir isotherm \( \rho(x) = \rho_o = K(K + 1) \).

Equations like (31) are known to have an explicit solution written in terms of a special function called the \( W \) function, see refs. 36, 38 and Fig. 5. The \( W \) function, obtained by \( W_1\exp(W(x)) = \xi \), is a multivalued function with two real branches, which are usually denoted \( W_+(\xi) \) and \( W_-(\xi) \). The first branch, \( W_+(\xi) \), is defined for \( \xi \geq -1/e \); it diverges at infinity sub-logarithmically. The second branch, \( W_-(\xi) \), is always negative and defined in the domain \(-1/e \leq \xi \leq 0 \). Using these properties of the \( W \) function, the branch of \( W \) is selected according to the value of rescaled density \( \alpha \).

As has been discussed in refs. 13, 36, there exists a left BL if \( \alpha > 1/2 \). Therefore, we have the following left rescaled solution only when \( 0 \leq \alpha \leq 1/2 \).
\[ \sigma_L(x) = W_+(\xi(x)) < 0 \] (32)
For the right rescaled solution \( \sigma_R(x) \), we have
\[ \sigma_R(x) = \left\{ \begin{array}{ll}
W_+(\xi(x)) > 0 & 0 \leq \beta < 1 - \rho_l \\
0 & \beta = 1 - \rho_l \\
W_+(\xi(x)) < 0 & 1 - \rho_l < \beta \leq 1/2 \\
W_+(\xi(x)) < 0 & \beta > 1/2 
\end{array} \right. \] (33)
We note that, due to the existence of the right BL, when \( \beta > 1/2 \), the right solution \( \sigma_R(x) \) is only an approximation.

So far, total densities \( \rho_L(x) \) and \( \rho_R(x) \), which satisfy left and right boundary conditions, respectively, can be obtained from (32) and (33). The DW location \( x_o \) can be determined by the continuity of \( j_L \) and \( j_R \), which implies \( \rho_L(x_o) + \rho_R(x_o) = 1 \), or equivalently \( \sigma_L(x_o) + \sigma_R(x_o) = -2 \). If there exists left BL, especially when \( \alpha > 0.5 \), we set \( x_o = 0 \). Meanwhile, if there exists a right BL, especially in the LD phase, we set \( x_o = 1 \).

The continuity of \( j \) at \( x_o \) gives
\[ \rho_L(x_o)[1 - \rho_R(x_o)] = j_L(x_o) = j_R(x_o) = \rho_R(x_o)[1 - \rho_L(x_o)] \]
while the continuity of \( j_L \) at \( x_o \) means
\[ \rho_L(x_o)[1 - \rho_R(x_o)] = j_L(x_o) = j_L(x_o) = \rho_L(x_o)[1 - \rho_R(x_o)] \]
Therefore,
\[ \frac{\rho_L(x_o)}{\rho_R(x_o)} = \frac{\rho_L(x_o)}{\rho_R(x_o)} \] (34)
and the height of DWs \( \Delta \), \( \Delta_o \) of total density and single species density satisfy
\[ \Delta = \rho_L(x_o) - \rho_R(x_o) = \rho_L(x_o) - \rho_L(x_o) \]
\[ = \frac{\rho_L(x_o)}{\rho_R(x_o)}(\rho_R(x_o) - \rho_R(x_o)) = \rho_L(x_o)(\rho_L(x_o) - \rho_R(x_o)) \]
\[ = \rho_L(x_o)(\rho_L(x_o) - \rho_R(x_o)) = \rho_L(x_o)(\rho_L(x_o) - \rho_R(x_o)) \] (35)

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Fig. 6. Typical examples of densities $\rho_1$, $\rho_2$, and $\rho_3$, for general cases $K > 1$. In all calculations $K_1 = 1$, $K_2 = 0.5$, $\Omega = 0.1$ are used. The four figures in the first row show that, with the decrease of leaving rate $\beta$, densities $\rho_1$, $\rho_2$, and $\rho_3$ change from LD phase to phase with DW. The figures in the second row show that, with the decrease of $\beta$, the location $x_{\omega}$ of DW moves to the left, see ref. 37. The last row includes examples with effective entrance rate $\alpha > 0.5$. The phase of density $\rho$ in each figure is as follows: (a) LD–BL, (b, c) LD–BL, (d) LD–DW–HD, (e) LD–DW–HD, (f, g) LD–DW–HD, (h) LD–DW–BL, (i) BL, –M–BL, (j) BL, –M, (k) BL, –M. Line types in this figure are the same as in Fig. 1. [Colour online.]

![Figure 6](image-url)

After getting total density $\rho$ and its DW location $x_{\omega}$, single species density $\rho_3$ and $\rho_2$ can be obtained by the following process. The left solution $\rho_{1,3}(x)$ in domain $[0, x_{\omega}]$ can be obtained from (28) and (29) by matching left boundary conditions,

$$
\rho_{1,3}(x) = \exp \left( -\int_0^x P_0(x)dx \right) \left[ \alpha_1 + \int_0^x K_1 \Omega \exp \left( \int_0^x P_0(x)dx \right) dx \right] \frac{\alpha_3}{q} \exp \left( -\int_0^x P_0(x)dx \right)
$$

Substituting the expression of $P_0(x)$ into the preceding two equations, and using (27), we obtain that, for $0 < \alpha < 0.5 \neq \rho_3$,

$$
\rho_{1,3}(x) = \frac{K_1}{K} \rho_3(x) + \gamma_1 |\rho_3(x) - \rho_1^{[1-K\Omega]}(1+K^{[1-K]}(x-x_{\omega}))
$$

where

$$
\gamma_1 = |\alpha - \rho_1^{[1-K\Omega]}| K_1 \frac{\alpha_1}{q} \frac{K}{K}
$$

$$
\gamma_2 = |\alpha - \rho_2^{[1-K\Omega]}| K_2 \frac{\alpha_2}{q} \frac{K}{K}
$$

Now, using $\rho_{1,3}(x_{\omega}) = (\rho_{1,3}(x_{\omega})/\rho_3(x_{\omega})) \rho_3(x_{\omega})$ as the boundary condition, the right solution $\rho_{0,3}(x)$ in interval $[x_{\omega}, 1]$ can be obtained. For $\beta \neq 1 - \rho_3$, we obtain that

$$
\rho_{0,3}(x) = \frac{K_3}{K} \rho_3(x) + \delta_1 |\rho_3(x) - \rho_1^{[1-K\Omega]}(1+K^{[1-K]}(x-x_{\omega}))
$$

where

$$
\delta_1 = |\rho_3(x_{\omega}) - \rho_3^{[1-K\Omega]}| K_3 \frac{\alpha_2}{q} \frac{K}{K}
$$

$$
\delta_2 = |\rho_3(x_{\omega}) - \rho_3^{[1-K\Omega]}| K_2 \frac{\alpha_2}{q} \frac{K}{K}
$$

When $\beta = 1 - \rho_3$, the right solution in domain $[x_{\omega}, 1]$ will be

$$
\rho_{0,3}(x) = \frac{K_3}{K} \rho_3(x) + \exp[(K + 1)\Omega(x_{\omega} - x)] \rho_3^{[1-K\Omega]}(x_{\omega}) - K_3 \frac{\rho_3}{K}
$$

$$
\rho_{0,3}(x) = \frac{K_2}{K} \rho_3(x) + \exp[(K + 1)\Omega(x_{\omega} - x)] \rho_3^{[1-K\Omega]}(x_{\omega}) - K_2 \frac{\rho_3}{K}
$$

Finally, we want to point out that the relationship presented in (34) also holds at the left BL, which is needed to get single species density $\rho_3$ when there exist left BL in total density $\rho$. To get intuitive impressions of properties of the two-species TASEP for general cases $K > 1$, typical examples of density $\rho_3$, $\rho_2$, and $\rho_3$ are plotted in Fig. 6.

In summary, the main process to obtain single species densities $\rho_1(x)$, $\rho_2(x)$ is as follows. Total density $\rho$, as well as locations of its
Fig. 7. Typical examples of densities $\rho_1, \rho_2$ for $\beta = 1 - \rho_2$. For these cases, near right boundary $x = 1$, total density $\rho$ is constant. Besides parameter values given in the legends, we set $\Omega = 0.1$ and $K = 1.5$, therefore $\rho_2 = K(1 + \Omega) = 1.6$. Although total density $\rho$ is constant, single species densities $\rho_1$ and $\rho_2$ may not be. In the same way as in special cases $K = 1$, the monotonicity of $\rho_1$ is determined by the sign of $\Omega l_1(0) - \Omega l_2(0)$; for a positive value, $\rho_1$ will increase, while $\rho_2$ will decrease, along the track (when $\rho$ is constant). In (a, b, c, $\rho_1$ increases while $\rho_2$ decreases. In (d, e), the same as the total density $\rho$, both $\rho_1$ and $\rho_2$ are also constants. In contrast, in (f), $\rho_2$ decreases while $\rho_1$ increases. (c, e) are examples with DW, and (b) is an example where there exists BL. Line types in this figure are the same as in Fig. 1. [Colour online.]

DW and BLs, can be obtained from (8) with boundary conditions $\rho(0) = \alpha = \alpha_1 + \alpha_2 q/y$ and $\rho(t) = 1 - \beta = 1 - \beta_1 - \beta_2 q/y$. Then single species density $\rho_1$ and $\rho_2$ in interval $[x_w, 1]$ can be obtained from (7) with left boundary condition $\rho_l(0) = \alpha_1$, and $\rho_r(0) = \alpha_2 q/y$, respectively. Finally, density $\rho_l$ in interval $[x_w, 1]$ can be obtained from (7) with left boundary condition $\rho_l(x_l^K)$, which is given by $\rho_l(x_l^K) = \rho_l(x_l^K) + \Delta l$. The main difference from that in special cases $K = 1$ is that Lambert function [38] should be employed to help to get densities $\rho$ and $\rho_2$.

For $K > 1$, properties of total density $\rho$ are similar as those of the one-species TASEP-LK process [9, 13] (i.e., there may exist left or right BL, DW, or “Meissner” (M) phase). Here Meissner phase means that density $\rho$ satisfies $1/2 < \rho < \rho_l = K/(K + 1)$, and is independent of initiation rate $\alpha$ and leaving rate $\beta$, see Figs. 6i and 6j). Properties of single species density $\rho_l$ may differ from $\rho$. For example, if $\rho$ lies in $[0, 1/2]$ or $[\rho_l, 1]$, it will increase along the track. Otherwise, $\rho$ will decrease along the track. This is because that $\rho_\Omega = \lceil K(1 + \Omega|\rho - \rho_l)|/(2K - 1)\rceil$, see (27). Therefore, if there exists DW in $[0, 1]$ and the leaving rate $1 - \beta_1 < 1$, then after DW location $x_w$, density $\rho$ decreases monotonically. Otherwise, if $0 < \beta_1 < 1 - \rho_2$, $\rho$ will increase after DW location $x_w$. However, the numerical results show that, after DW location $x_w$, the monotonicity of $\rho_2$ may be different from those of $\rho$.

6. Monotonicity of single species density $\rho_1$ and $\rho_2$

When total density $\rho = \rho_1$ is constant for general cases $K > 1$.

Previous analysis about special cases $K = 1$ has shown that, if total density $\rho$ is in M phase (i.e., $\rho = 1/2$ is constant), then single species density $\rho_l$ may not be constant. Similar results hold for the general $K > 1$ cases. For $K > 1$, if $\beta = 1 - \rho_2$, then total density $\rho(0) = \rho_l(x)$ is constant in interval $[x_w, 1]$, $\rho = \rho_l$ with $\rho_l = K/(K + 1)$. But, similar to those in special cases $K = 1$, the corresponding single species densities $\rho_1$ and $\rho_2$ may not be constant. From (40) and (41), we have

$$\frac{\partial \rho_1}{\partial x}(x) = -(K + 1)\left[ \frac{\rho_1(x)}{K} + \frac{K}{K + 1} \exp[(K + 1)(K - x) - 1] \right]$$

$$\frac{\partial \rho_2}{\partial x}(x) = -(K + 1)\left[ \frac{\rho_2(x)}{K} + \frac{K}{K + 1} \exp[(K + 1)(K - x) - 1] \right]$$

For these special cases, $\rho_1(x) = \rho_l = K/(K + 1)$, $\rho_2(x) = 1 - \rho_1(x) = 1 - \rho_l = 1/(K + 1)$. So $\rho_2(x) = \rho_2(x_l^K)\rho_2(x_\infty^K) = K\rho_1(x_l^K)$. From (36) and (37), we get

$$\rho_2(x_\infty^K) = \frac{K}{K + 1}\rho_2(x_l^K) + \gamma \left[ \frac{\alpha_2}{K} - \frac{\alpha_1}{q} \right] K - \left( K + 1 \right) \exp \left( K - x_\infty^K + 1 \right)$$

Therefore,

$$\rho_1(x_w) = \frac{K}{K + 1} \rho_2(x_w) = \frac{K}{K + 1} \left[ \frac{\alpha_2}{K} - \frac{\alpha_1}{q} \right] K - \left( K + 1 \right) \exp \left( K - x_\infty^K + 1 \right)$$

where $C(a, K) > 0$ for $K > 1$ and $\alpha < \rho_l = K/(K + 1)$. So

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Fig. 8. Phase diagrams of total density $\rho$ obtained by stationary mean-field equation (8) for $K > 1$. Parameter values used in calculations are $\Omega = 0.1$, $K = 1.5$ for ($a$, $d$), $\Omega = 0.15$, $K = 1.5$ for ($b$, $e$), and $\Omega = 0.1$, $K = 4$ for ($c$, $f$). ($d$, $e$, $f$) are phase diagrams in ($\alpha$, $\phi$)-plane with leaving rate $\beta = 0.45$, $0.7$, $0.3$, corresponding to horizontal dotted lines in ($a$, $b$, $c$), respectively. The meanings of Roman numerals in each area are as follows: I, LD–BL, which means that density $\rho$ is in LD phase, and there exists right BL in which $\rho$ increases sharply (i.e., $p(\Omega) > p(\Omega - \epsilon)$ for small real number $\epsilon$); II, LD–BL, (i.e., $\rho$ is in LD phase, and it decreases sharply at right boundary); III, LD–DW–HD$_2$, near left boundary density $\rho$ is in LD phase, while near right boundary $\rho$ is in HD phase, and there exists DW between these two phases (here “HD$_1$” means $\rho > \rho_l$, i.e., $\beta < 1 - \rho_l$); IV, LD–DW–HD$_2$, where HD$_2$ means that density $\rho$ is between 0.5 and $p_l$ (i.e., $1 - p_l < \beta < 0.5$); V, LD–DW–M, where $M$, means that density $\rho$ is between 0.5 and $p_l$ but its value is independent of right boundary condition, therefore right BL appears ($M$, can be regarded as the right half part of “Meissner” phase) and for this phase, $\beta > 0.5$; VI, BL–HD, (i.e., $\rho > \rho_l$ and $\rho$ increases in left BL); VII, BL–HD$_2$, VIII, M*, which means that $\rho$ is in “Meissner” phase and it increases in left BL; IX, BL–HD$_1$–X, BL–HD$_2$–XL, BL–M; and VIII and XI are two species cases of “Meissner” phase. For examples of density $\rho$ in one of the eleven phases, see Fig. 6. (Colour online.)

\[
\begin{align*}
\rho_{\alpha,1}(x) &= \frac{K_1}{K} \left( K_2 \alpha_1 - \frac{K_1 \alpha_1}{q} \right) C(\alpha, K) = \frac{\Omega \alpha_1 \alpha_1 - \Omega \lambda_2 \alpha_2}{q\Omega} C(\alpha, K) \\
\text{and} \quad \rho_{\alpha,2}(x) &= \frac{K_2}{K} \left( K_2 \alpha_2 - \frac{K_1 \alpha_2}{q} \right) C(\alpha, K) = \frac{\Omega \alpha_1 \alpha_2 - \Omega \lambda_2 \alpha_1}{q\Omega} C(\alpha, K)
\end{align*}
\]

Finally, from (42), (46) and (43), (47), we concluded that, when total density $\rho = \rho_1$ is constant, the monotonicity of $\rho_2$ and $\rho_2$ depends on the value of $\Omega_1 \lambda_1 \alpha_1 - \Omega_2 \lambda_2 \alpha_2$. The same as in the special $K = 1$ case, if $\Omega_1 \lambda_1 \alpha_1 - \Omega_2 \lambda_2 \alpha_2 > 0$ then $\rho_1$ increases while $\rho_2$ decreases along the motion track. In contrast, if $\Omega_1 \lambda_1 \alpha_1 - \Omega_2 \lambda_2 \alpha_2 < 0$ then $\rho_1$ decreases while $\rho_2$ increases. Both $\rho_1$ and $\rho_2$ are constants iff $\Omega_1 \lambda_1 \alpha_1 - \Omega_2 \lambda_2 \alpha_2 = 0$, and in such cases $\rho_1 = K_0[\Omega + 1]$ and $\rho_2 = K_0[\Omega + 1]$ in interval $[\alpha_1, 1]$, see Fig. 7.

For these general cases $K > 1$, examples of phase diagram of total density $\rho$ in ($\alpha$, $\beta$) plane are plotted in Figs. 8a, 8b, and 8c. The same as in the one-species TASEP-LK, BL may appear at one or both of the two boundaries. DW may appear in interval (0, 1), and density $\rho$ may be in LD phase ($\rho < 1/2$) or HD phase ($\rho > 1/2$). To show more details about the TASEP-LK process, in Fig. 8 the HD phase is divided into two different cases, HD$_1$ phase ($1/2 < \rho < \rho_l = K[\Omega + 1]$) and HD$_2$ phase ($\rho > \rho_l$). From the phase diagram in the ($\alpha$, $\beta$) plane, phase diagrams in any planes of parameter pair ($\alpha$, $\beta$) can be easily obtained, where $\alpha_1 = \alpha_2$, $\alpha_2$, $\beta_1$, $\beta_2$. Examples of phase diagrams in the ($\alpha$, $\beta$) plane are plotted in Figs. 8d, 8e, 8f, which correspond to the dotted horizontal lines in Figs. 8a, 8b, 8c, respectively. The preceding discussion about the relationship between total density $\rho$ and single species density $\rho_1$ implies that phase diagrams of density $\rho_1$ are topologically equivalent to those of the total density $\rho$.

7. Conclusion

In summary, TASEP-LK process with two particle species is discussed in this study. Unlike the previous studies about two-species TASEP, particle attachment to or detachment from bulk sites of motion track is allowed. Both of the two-particle species enter the track from the same boundary, and move unidirectionally to the same direction. The two particle species do not change to each other, and do not exchange their locations even if they are adjacent to each other [20, 21, 23, 29]. This study found that, DWs and BLs of total particle density and single species densities always appear simultaneously. The height of DW of total density is equal to the summation of those of the two single species. More interestingly, the ratio of particle densities from different species does not change when coming across the DW, which implies that the motion of different particle species along the same track will be jammed at the same position, and with the same probability. Based on these properties, theoretical methods to obtain steady
state densities of the two particle species are presented. Our results show that properties of single species densities may be different from that of the total particle density.

In this study, phase diagrams of particle density in typical parameter planes are also presented. The methods presented in this study are also applicable to the analysis of TASEP-LK processes including more than two particle species, because for any particle species, the DW of its density will always appear at the same position, and ratios of densities of any two particle species always hold unchanged before and after the position of DW. The results of this study are also helpful to further understandings of the biophysical process of cargo transportation in living cells, where one single protofilament of microtubule is actually occupied by various kinds of cargos and motor proteins [15, 39].

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