Phase transition and phase coexistence in coupled rings with driven exclusion process

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We study one-dimensional exclusion processes in two coupled closed rings consisting of a common diffusive channel and two parallel active (driven) channels. Our model displays bulk-driven phase transition and phase coexistence in the form of a localised domain wall (DW) in one of the active channels in a limit where the diffusive and driven dynamics compete. By controlling a splitting parameter which tunes the in-coming currents into the active channels, the system can be brought to a delocalisation transition, when delocalised DWs are formed in both the active channels. We characterise the DW fluctuations numerically.

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I. INTRODUCTION

Totally Asymmetric Simple Exclusion Process (TASEP) [1] serves as a paradigmatic example of open non-equilibrium systems in one dimension (1d). Its practical realizations include quasi-1d motion of molecular motors along with microtubules in intra-cellular transport [2], protein synthesis [3] or motion in geometrical confinement, e.g., nuclear pore complex of cells [4]. In contrast, Symmetric Exclusion Process (SEP) [5] is a typical example of 1d diffusion. Well-known examples of SEP include diffusion through artificial crystalline zeolites [6]. In both passive (SEP) and active (TASEP or TASEP-like) systems, prohibition of mutual passage of particles or exclusion gives rise to nontrivial collective effects, whose details of course depend upon whether the dynamics in question is TASEP or SEP. Active systems with open boundaries generally display spatially nontrivial steady state density distributions.

In this paper, we propose a closed model that consists of two overlapping rings with a common diffusive part (SEP) and two parallel active (driven) channels (marked $T_A$ and $T_B$ hereafter). In order to ensure competition between driven and diffusive dynamics, we consider a particular limit of the model. Our principal result includes identification of a model parameter $\theta$, having values between 0 and 1 (see below), as a switch, by tuning which continuously keeping everything else unchanged (i) one may de-pin pinned domain walls (DW) and (ii) as $\theta$ crosses 1/2, a localised DW in one of the active channels disappears and appears in the other. Our model should serve as a paradigmatic example of localisation-delocalisation transition in a 1d closed model with coupled diffusive and driven dynamics. In addition to its direct theoretical relevance, it is phenomenologically motivated by the movement of molecular motors in closed compartments [7], the dynamics of colloidal particles in optical traps [8] and the dynamics for multiple mRNAs competing for finite resources (ribosomes), where the ribosomes in turn are bounded by a certain trajectory and a diffusion rate outside the mRNA (during recycling) [9, 10]. In particular, protein synthesis involves two stages: transcription of genetic information from DNA to messenger RNA (mRNA) by RNA polymerase and translation from mRNA to proteins through ribosome translocation. In most bacteria such as E.coli, translation involves three main players: the mRNA (genetic template), the ribosome (assembly machinery), and aminoacyl transfer RNAs (aa-tRNAs), i.e., transfer RNAs “charged” with the corresponding amino acid. The process of translation consists of ribosomes moving along the mRNA without backtracking. This is modeled by TASEP. It is well-known that ribosomes that move along mRNA strand are recycled in a cell. For instance, in eukaryotic cells, after each round of protein synthesis, the ribosomes are released from the mRNA and they join the common pool of ribosomes in cytoplasm, where they execute diffusion and may rejoin the mRNA to restart protein synthesis. In our model, the SEP channel models the “common pool” of diffusive ribosomes in the cytoplasm of an eukaryotic cell, which in our model can come back to the entry point of the TASEP lanes due to the feedback from the SEP channel. However, although ribosome translocation along mRNA forms physical motivation of the present work, the analogy between our model and the actual biological process of ribosome translocation along mRNA strands is not strict due to various limitations of our model, as we discuss below. In both SEP and TASEP, each lattice site has maximum unit occupancy and a particle can only move to the nearest neighbour site (in both directions for SEP or in one direction only for TASEP), only if that site is empty. Thus the dynamics obeys the exclusion principle. For SEP with open boundaries, the density profile is always linear with the slope being determined by the boundary conditions at the two ends [5]. In contrast TASEP with open boundaries displays three distinct phases [11] characterized by their average densities (low and high) and a third phase marked by a maximal current (MC). Unlike with open boundary conditions, individual SEP and TASEP dynamics with closed boundaries (say, closed rings) exhibit only uniform density profile in the steady
state due to spatial translational invariance. The rest of the paper is organised as follows: In Sec. II we discuss our model in details. Then in Sec. III we set up our mean-field theory (MFT) and discuss the steady state density profiles by using our MFT, complemented by extensive Monte-Carlo simulation (MCS) studies. In Sec. IV we go beyond MFT, and discuss domain wall fluctuations and delocalisation transition at $\theta = 1/2$. Finally, in Sec. V we summarize our results.

**III. STEADY STATE DENSITY PROFILES**

We use mean-field theory (MFT) together with extensive Monte-Carlo simulation (MCS) of our model to obtain the steady state density profiles. In the MFT, the system is considered as a collection of three channels (two TASEP and one SEP) with effective entry and exit rates. Once these effective rates are determined from the condition of constancy of particle currents, one may use them in conjunction with the known results for TASEP and SEP with open boundaries to obtain the density profiles here. Since an isolated TASEP in steady state can be in three different states, the low density (LD), high density (HD) and maximal current (MC) phases, and we have two active (TASEP) channels, there are a number of possibilities for the overall density profile of the two active channels. In order to ensure that the diffusive current does not vanish in the thermodynamic limit (TL, see Ref. [12]), see below also) we let diffusivity $D$ scales with system size $L$ and define a parameter $d = D/L$ which is the same for any arbitrary system size. Thus steady states of the model are to be parametrised by $(d, n_p, \theta)$. Let us now set the notations: for discrete lattice, density at a particular site $m$ is defined as $\rho_i^m = \langle n_i^m \rangle$, where $i = A$ and $B$ refer to $T_A$ and $T_B$, and $i = S$ for the mean density in the SEP channel $S$. Further in MFT considering continuum limit the density is defined as $\rho_i(x)$, where $x = m/L$, and in TL, $L \gg 1$, $x$ lies in the range $0 \leq x \leq 1$. In all our MFT analysis we use the continuum labelling $x$ for the lattice in one dimension. Our main results are summarized in the phase diagrams (parametrised by $n_p$ and $d$) for $\rho_A(x)$ and $\rho_B(x)$, as shown in Fig. 2, for a representative value of $\theta = 0.8$, which are obtained by extensive Monte-Carlo simulations of our 1d lattice-gas model and the corresponding 1d MFT; see below for details. The Monte-Carlo simulations were realized by random sequential update. For any value of $\theta$ (except $\theta = 0$, 1, when one of the active channels is closed), the phase diagrams of both $T_A$ and $T_B$ may display a combination of the usual LD, HD and MC phases and a region of co-existence of LD and HD phases, i.e., when the density profiles show localised domain walls (DW). The phase co-existence regions are non-overlapping for $T_A$ and $T_B$, i.e., they do not appear for the same values of $d$ and $n_p$, for a given $\theta \neq 1/2$. At $\theta = 1/2$, for which $T_A$ and $T_B$ are statistically symmetric, the density profiles $\rho_A(x)$ and $\rho_B(x)$ of $T_A$ and $T_B$, respectively, are naturally identical. The crucial difference with $\theta \neq 1/2$ is that the co-existence region now corresponds to delocalised DWs, i.e., the frac-

Figure 1: (color online) Schematic diagram of the model; LJ/RJ refer to the left/right junctions. Site labels run from $m = 1$ to $L$ from LJ to RJ for $T_{A,B}$ and for SEP from RJ to LJ, superscripts denote site numbers for the corresponding channel $T_A$, $T_B$ and $S$. Our proposed 1d model is a closed system of two overlapping rings consisting of three channels of equal number of sites designated by $m = 1, 2, ..., L$, as shown in Fig. 1. Dynamics of the two channels $T_A$ and $T_B$ are governed by TASEP and the particles in the third channel $S$ execute SEP. Thus in $S$ particles can hop to both direction with rate $D$, whereas in $T_A$ and $T_B$ particles can only hop to its right neighbour if empty with rate unity setting the time scale. At the left junction of $T_A$ and $T_B$ particles can either enter from SEP channel with rate $D\theta$ and $D(1 - \theta)$ respectively if those sites are vacant or can hop to the other side with rate $D$. If both $T_A$ and $T_B$ try to inject a particle into SEP, then one of the TASEP channels ($T_A$ or $T_B$) is selected randomly for injecting a particle to the target site i.e., the first site of SEP if it is empty. If $N_p$ be the total number of particles then, the global particle density $n_p = N_p/3L$. In Fig. 1, symbols $LJ$ and $RJ$ refer to the left and right junctions in the model. In addition, for the purpose of clarity, the site number for a particular channel (i.e., $T_A$, $T_B$ or $S$) are given as a superscript, e.g., at $LJ$, the first sites of $T_A$ and $T_B$ are denoted as $T_A^1$ and $T_B^1$, respectively, and the $L$-th site of $S$ is denoted as $S^L$. Similarly for the right junction $RJ$. In this model, the three bulk parameters ($\theta, n_p, D$) control different phase transitions. Thus we observe bulk induced phase transitions unlike the usual TASEP with open boundaries which display boundary induced phase transition. The steady state current in each of SEP, $T_A$ or $T_B$ is a function of $\theta, n_p, D$ and is spatially constant. Notice that our model is a variant and extension of that in Ref. [12]. In particular, for $\theta = 1$ or 0, $T_B$ or $T_A$ is blocked and our model explicitly reduces to that of Ref. [12]. Evidently, for $\theta > 1/2$ and $\theta < 1/2$ the behaviour of the two channels are simply interchanged.
Evidently, $J_s$ remains finite in TL provided $D$ scales with $L$ linearly, else, for a fixed $D$ the SEP current $J_s$ vanishes for $L \rightarrow \infty$. This provides a posteriori justification for the scale-dependent $D$ that we have mentioned before. Noting that the current in each of $T_A$ and $T_B$ is given by $J_i = \rho_i (1 - \rho_i)$, $i = A, B$ (assuming no boundary layer at $i = A, B$, i.e., $T_A, T_B$ are in their LD/coexistence phases) and using conservation of total current at the left and right junctions for the individual incoming/outgoing currents to/from $T_A$ and $T_B$ from/to the SEP channel we obtain

$$J_A^{in}(0) = \delta (1 - \alpha_A) \delta D, \quad J_B^{in}(0) = \delta (1 - \alpha_B) (1 - \theta) D.$$

Next, the individual outgoing currents at the sites 1 in $T_A$ and $T_B$ are (again assuming that the channels are in LD or coexistence phase)

$$J_A^{out}(0) = \alpha_A (1 - \alpha_A), \quad J_B^{out}(0) = \alpha_B (1 - \alpha_B).$$

Conservation of current then yields $J_A^{in}(1) = J_A^{out}(1)$. As expected, this holds so long as $T_A, T_B$ are in their LD or coexistence phase.

In contrast, if $T_A, T_B$ are in their HD or coexistence phases the total outgoing current from $T_A$ and $T_B$ to the SEP channel is given by

$$J_T^{out}(1) = (1 - \beta_A)(1 - \gamma) + (1 - \beta_B)(1 - \gamma).$$

Conservation of total current at the right junction then yields (assuming $T_A, T_B$ to be in HD or coexistence phases)

$$J_T^{out}(1) = \beta_A (1 - \beta_A) + \beta_B (1 - \beta_B).$$

Further, again assuming HD or coexistence phases for $\rho_{A,B}$, and separately considering the currents from $T_{A,B}(x = 1)$ to $S(x = 0)$ yields $\beta_A = \beta_B$. This is corroborated by our MCS simulations (see below). This immediately yields that the bulk currents are equal. This is possible only when the bulk currents in $T_{A,B}$ are controlled by RJ, i.e., $T_A$ or $T_B$ are both in HD or a combination of coexistence and HD phases. Notice that the conditions obtained for $\rho_{A,B}(0)$ and $\rho_{A,B}(1)$ by using current conservations at the respective sites do not hold simultaneously, unless $T_A$ or $T_B$ are in coexistence phases, such that there are no boundary layers at $x = 0,1$ with $\rho_{A,B}$ being piecewise continuous. Having defined effective entry and exit rates (valid separately for LD/coexistence or HD/coexistence phases in $T_{A,B}$) for the active channels, we can now apply the known results of TASEP here. One obtains the low (high) density phases in the periodic system equally and are characterized by a uniform density below (above) $1/2$ and a boundary layer at the right (left). However for $\alpha_{A,B} = \beta_{A,B}$, the boundaries are matched by a piecewise constant density profile with

$$J_s = (\gamma - \delta) d.$$ 

(1)

Figure 2: (color online) Phase diagram with $\theta = 0.8$ for densities $\rho_A$ and $\rho_B$ for channels $T_A$ and $T_B$ respectively obtained from our MFT (dashed and dotted lines) and MCS (circles, squares and triangles) analysis. Staying up to $d = 1$, $T_A$ has four phases (all marked by suffix A in the phase diagram), LD, LD-HD, HD and MC phase, where as, $T_B$ has only three phases (marked by suffix B) without any MC phase. The dotted blue and the dashed black lines correspond to the phase boundaries obtained for $T_A$, whereas the dashed-dotted orange line for $T_B$ from MFT calculations. The red circles and grey triangles correspond to the phase boundaries obtained from MCS for $T_A$ and the green squares for that of $T_B$.

Figure 3: (color online) Phase diagram for both $T_A$ and $T_B$ for $\theta = 1/2$. There are four distinct phases; $T_A$ and $T_B$, being statistically identical, have identical phase behaviour (see text). The LD-HD phases in both $T_A$ and $T_B$ now have delocalised DWs. Numerical data are shown by circles and triangles and the phase boundaries obtained analytically are shown by solid lines.

To begin with, we denote densities at the junction site by $\alpha_{A,B} = \rho_{A,B}(0)$ and $1 - \beta_{A,B} = \rho_{A,B}(1)$ for the active channels, and $\gamma = \rho_S(0)$ and $\delta = \rho_S(1)$ in the passive SEP channel. The SEP current then takes the well-known linear form,

$$J_s = (\gamma - \delta) d.$$ 

(1)
an intervening DW. For TASEP with open boundaries, particle entry and exit events are uncorrelated, and as a result, the DW is delocalised and undergoes random walks covering the entire span of the system in the long time limit. However in the present model, as in Ref. [12], entry and exit of particles are not uncorrelated; they get correlated by the fact that the ends of the active channels are connected by the passive channel. Consequently, as revealed by our Monte Carlo simulation studies, we find localised DW in the active channels, which is similar to Ref. [12]. However, rather surprisingly for the special case of $\theta = 1/2$, i.e., when each of the active channels carry equal current on average, we obtain delocalised DWs in both channels. Our MFT formulated above may now be used to analyse the density profiles in the different channels of the model quantitatively.

A. DW in one active channel and LD in other

First, let us consider a situation when there is a DW in one of the active channels (say $T_A$ with $\theta > 1/2$) and the other active channel ($T_B$) is in the LD phase with a uniform density $\alpha_B$ (within MFT neglecting any boundary layer). Following the phenomenology of TASEP with open boundaries, we set $\alpha_A = \beta_A$ as a requirement of a DW in $T_A$. Possibilities of simultaneous DWs in $T_A$ and $T_B$ will be discussed later. Within MFT, $\rho_A$ may be represented by a Heaviside function that connects the two regions of constant density through a localized DW at position $x_w^A$ (say) as,

$$\rho_A(x) = \alpha_A + \Theta(x-x_w^A)(1-\alpha_A - \beta_A). \quad (6)$$

Since $T_B$ is assumed to be in the LD region, density $\rho_B(x)$ can be written as,

$$\rho_B(x) = \alpha_B, \quad (7)$$

neglecting the boundary layer at the right boundary. For the SEP channel the linear density distribution gives,

$$\rho(x) = \delta + (\gamma - \delta)x. \quad (8)$$

Further, the particle number conservation can be expressed as

$$3n_p = \int_0^1 dx[\rho(x) + \rho_A(x) + \rho_B(x)], \quad (9)$$

following the conditions as above and disregarding the discontinuities at the right boundaries. Again from Eq. (6) and Eq. (10) we have,

$$\alpha_B = \alpha_A \left( \frac{1}{\theta} - 1 \right) = \alpha_A q, \quad (10)$$

where $q = (1/\theta-1)$. Now by solving Eq. (10) in TL ($\delta \to 0$) we get

$$x_w^A = \frac{1 + \frac{\gamma}{2} - 3n_p - \alpha_A(1-q)}{1 - 2\alpha_A}. \quad (11)$$

Again Eqs. (4), (5), (10) and the relations $\beta_A = \alpha_A$ and $\beta_B = 1 - \alpha_B$ yield for $\gamma$ as,

$$\gamma = \frac{\alpha_A^2(1+q^2) - 2\alpha_A + 1}{1 - \alpha_A(1-q)}. \quad (12)$$

In TL $\delta \to 0$ and $\gamma = J_A/d$. Since the model considered here is closed, $J_A = J_A^{out}(0) + J_B^{out}(0)$. Again from Eq. (4) we have,

$$d = \alpha_A(1-\alpha_A) + (1-\alpha_A)q\alpha_A. \quad (13)$$

Hence, the position of the DW depends on the two control parameters $n_p$ and $d$ for a given $\theta$. When the DW in $T_A$ is localised within the system ($0 < x_w^A < 1$), it connects the LD and HD phases of $T_A$ through a phase of coexistence (LD-HD). The boundaries between the LD, LD-HD phases and LD-HD, HD phases of $T_A$ are obtained by setting $x_w^A = 0$ and $x_w^A = 1$ respectively. Setting $x_w^A = 0$ from Eq. (11) we get a quadratic equation in $\alpha_A$. For a particular value of $n_p$, the feasible values will be ($0 < \alpha_A < 1/2$). Now putting that $\alpha_A$ in Eq. (13) we get the corresponding $d$ value. Thus we get the boundary between LD and LD-HD coexistence phase in the $(n_p, d)$-plane. Similar exercise for $x_w^A = 1$ gives the right boundary between LD-HD and HD phase. See Fig (2) for details. In Fig (2) the phases of channel $T_A$ and $T_B$ are spanned by $d \leq 1$ and $n_p \leq 1$. The phase diagrams for $T_A$ and $T_B$ are drawn corresponding to a situation when $T_A$ displays a variety of phases (LD,LD-HD,HD AND MC), while $T_B$ remains in its LD phase. For $d > 1$, this part of the phase diagram remains qualitatively unchanged, with the phase marked as $MC_A,LDB$ (i.e., $T_A$ in MC and $T_B$ in LD) should expand to a larger area. Similarly, the phases of $T_B$ are shown when channel $T_A$ remains in its HD phase. The condition for the latter is mathematically given by $\rho_A(x) = 1 - d/2$ in the bulk. For $1 < d < 2$, $\rho_A(x) < 1/2$ and hence $T_A$ is no longer in its HD phase. Hence, we do not consider the $d > 1$ region while presenting our phase diagram. A DW in $T_A$ obtained from our MCS studies are shown in Fig. (3) (top) with $\theta = 0.80$, $n_p = 0.40$ and $d = 0.15$. We have taken $L = 100$ and $200$ for determining the position of the domain walls and phase diagram. We do not find any significant dependence of our results on $L$.

B. DW in one active channel and HD in other

Let us now consider the case when there is a DW in $T_B$, and $T_A$ is in HD phase for $\theta > 1/2$, thus having a boundary wall at the left end. As discussed above, within MFT, $\rho_B$ may be represented by Heaviside $\theta$-function as

$$\rho_B(x) = \alpha_B + \Theta(x-x_w^B)(1-\beta_B), \quad (14)$$

and $T_A$ is in HD phase having a uniform density of ($1-\beta_A$), neglecting the boundary layer. To have a DW in $T_B$
we must have $\alpha_B = \beta_B$. Now from Eqs. (4) and (5), we get

$$\gamma = \frac{(1 - \beta_A)^2 + (1 - \beta_B)^2}{2 - \beta_A - \beta_B}. \quad (15)$$

Hence Eq. (15) and $\beta_A = \beta_B$ yield $\gamma = (1 - \alpha_B)$. In TL $\gamma = J_s/d$, and hence, $\alpha_B = d/2$. Again, by using the particle number conservation and as $\beta_A = \beta_B = \alpha_B$ and $\rho_A(x) = 1 - d/2$ we obtain,

$$x^B_w = 1 - \frac{3n_p - \frac{3}{2} + \frac{d}{4}}{1 - d/2}. \quad (16)$$

From the above expression we get the boundaries between the LD, LD-HD ($x^B_w = 0$) and LD-HD, HD phases ($x^B_w = 1$) of $T_B$. A DW in $T_B$, obtained in our MCS studies, is given in Fig. (4) bottom. There is a crucial difference between the DWs in $T_A$ and $T_B$: The LD part of the DW in $T_A$ has density $\alpha_A$, different from the density $\alpha_B$ of $T_B$ (fully in LD), thus $\rho_A(x)$ has no overlap with $\rho_B(x)$. In contrast, $\rho_A(x)$ (fully in HD) overlaps with $\rho_B(x)$ in the HD part of the DW in $T_B$. This is due to $\beta_A = \beta_B$ and is clearly visible in Fig. (4).

### C. Delocalised domain wall at $\theta = 1/2$

Let us now carefully consider the properties for $\theta = 1/2$, when both the active channels are symmetric and statistically identical. Thus, if $\alpha_A = \beta_A$, then automatically $\alpha_B = \beta_B$. Hence, if $T_A$ has a DW, $T_B$ too will have a DW, or is in its LD-HD (co-existence) phase as well, such that its density may be represented by a Heaviside $\theta$-function that connects the two regions of constant density through a localized DW at $x^B_w$ (say). Hence, $\rho_A(x)$ and $\rho_B(x)$ are given by the expressions (3) and (5) respectively. As both $T_A$ and $T_B$ show DWs, thus $\alpha_A = \beta_A$ and $\alpha_B = \beta_B$, and for $\theta = 1/2$ from Eq. (2) we have, $\alpha_A = \beta_A = \alpha_B = \beta_B = \alpha$ (say). Again, from Eq. (3) and Eq. (4) we have $\gamma = 1 - \alpha$. Therefore, in TL, $\delta \to 0$ and thus $\alpha = d/2$. Now by particle number conservation we have,

$$3n_p = 1/2 + 3d/4 + (2 - x^A_w - x^B_w)(1 - d). \quad (17)$$

Thus for $\theta = 1/2$ we get a relation given by Eq. (17) between $x^A_w$ and $x^B_w$ for a particular value of $n_p$ and $d$. In other words $x^A_w$ and $x^B_w$ are not uniquely determined. In this case both DWs are delocalized and perform random walk along the active channels. As $T_A$ and $T_B$ are identical, the condition for DW is satisfied for both the channels simultaneously. Thus, $x^A_w = x^B_w = 0$ and $x^A_w = x^B_w = 1$ in Eq. (17) can give the boundaries of LD-HD phase in both channels with the LD and HD phases respectively. In Fig. (4) we have shown this mean-field result as well as that obtained from MCS which shows distinct four phases with phase boundaries for both channels are identical. However, symmetry between the two active channels dictate that the long-time averaged po-

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Figure 4: (color online) (top) For $L = 200$, $\theta = 0.8$, $n_p = 0.40$ and $d = 0.15$, $T_B$ is in LD phase and DW appears in $T_A$ at $x^A_w \sim 0.21$, whereas from MFT Eq. (16) $x^A_w = 0.19$. (bottom) For $L = 200$, $\theta = 0.8$, $n_p = 0.65$ and $d = 0.20$, $T_A$ is in HD phase and DW appears in $T_B$ at $x^B_w \sim 0.38$, whereas from MFT Eq. (16) $x^B_w = 0.375$. The black continuous lines display the domain walls obtained from MFT.

Figure 5: (color online) Plots of $\rho = \rho_A, \rho_B$ versus site $(x)$ for $\theta = 1/2$ with $n_p = 0.52, d = 0.19$ and $L = 2 \times 10^3$. Clearly, both $\rho_A$ and $\rho_B$ display overlapping delocalised DWs.
D. Both the active channels in MC phase

Lastly, we consider the possibility of the MC phases in the active channels. Let us first consider the conditions for obtaining MC phases in both the active channels. Condition for MC in isolated TASEPs are \( \rho_A = \rho_B = 1/2 \) and \( J_A = J_B = 1/4 \), and this happens when all the boundary densities \( \alpha_A, \alpha_B, \beta_A, \beta_B > 1/2 \). Furthermore, \( T_A, T_B \) have boundary layers at both the ends. This precludes usage of Eq. (3) to determine the boundary densities. Using similar considerations at RJ, and again assuming no density discontinuity between \( \rho_S(0) \) and \( \rho_{A,B}(0) \), we find \( \delta (1-\alpha_A) \theta D = 1/4, \delta (1-\alpha_B)(1-\theta)D = 1/4 \). Since \( \alpha_A, \beta_B > 1/2 \)

\[
\delta > \max \left\{ 1 \over 2dL\theta, 1 \over 2dL(1-\theta) \right\}
\]

Using similar considerations at RJ, and again assuming no density discontinuity between \( \rho_S(0) \) and \( \rho_{A,B}(1) \), which means \( 1-\gamma = \beta_A = \beta_B \), together with \( \beta_A, \beta_B > 1/2 \), Eq. (1) and \( J_s = 1/2 \) we have,

\[
\delta < 1 \over 2 \, \delta < 1 \over 2 - 1 \over 2d.
\]

From particle conservation we have,

\[
3n_p = \delta + 1 \over 4d + 1
\]

Eqs. (18), (19) and (20) yield boundaries of the MC phase with LD and HD phase as, \( d = 1/(12n_p - 4) \) and \( d = 1/(6 - 12n_p) \) which indicates the presence of such phase for \( d > 1 \) and bounded by the two above mentioned lines. Thus, the demarcating lines are independent of \( \theta \). They are shown in Fig. (3). We now consider the case when one of the channels (say, \( T_A \)) is in MC phase and the other one (\( T_B \)) in the LD phase. Therefore, we have \( J_A = 1/4 \), \( \rho_A = 1/2 \) and \( \alpha_A, \beta_A > 1/2 \). From Eqn. (2) and (3) we have \( \alpha_A = D\delta \theta \). Again using the MC phase condition \( \alpha_A, \beta_A > 1/2 \) we have (arguing as before),

\[
\delta > 1 \over 2d, \delta < 1 \over 2 - J_s \over d.
\]

The maximal current condition gives \( J_s = (1/4 + q/2 - q^2/4) \), then from particle conservation we have,

\[
3n_p = \delta + J_s \over 2d + 1 \over 2 + q \over 2
\]

The two inequalities (21) together with Eq. (22) then yield boundaries of the MC phase with the LD and HD phase respectively as, \( d = J_s/(6n_p - q - 1) \) and \( d = J_s/(q + 2 - 6n_p) \). In Fig. (2) we have shown the MC phase boundaries. Our MCS studies also reveal a small MC phase within the region obtained from MFT. Not surprisingly, for \( \theta = 1 \) and \( \theta = 0 \), the MC phase regions obtained from our MFT match exactly with that of Ref. [12]. In addition, one may argue that the coexistence of \( T_A \) in HD and \( T_B \) in MC is not possible. For \( T_A \) to be in HD phase \( 1 - \beta_A > 1/2 \) or \( \beta_A < 1/2 \). Again \( \beta_B = \beta_A < 1/2 \), so long as \( T_A, T_B \) are in HD or coexistence phases. But condition for MC phase in \( T_B \) is \( \alpha_A, \beta_B > 1/2 \). Thus, an MC phase in \( T_B \) (when \( T_A \) in HD) is not allowed.

IV. DOMAIN WALL FLUCTUATIONS AND DELOCALISATION TRANSITION

Until now we have considered the MFT for the model, where all fluctuations are neglected. However, the DWs fluctuate about their MF DW (mean) positions \( x^0_w \) or \( x^D_w \). We have studied these fluctuations numerically and characterise them by measuring the scaling of the fluctuations with \( \theta \) and system size \( L \). In particular as

\[
\delta \sim (\theta_c - \theta)^\gamma
\]

\[
\sigma \sim 1/\sqrt{L}
\]

Figure 6: (color online) Log-log plot of DW width \( \sigma \) versus \( |\theta - \theta_c| \) for \( L = 200, n_p = 0.40 \) and \( d = 0.15 \) with the exponent \( \beta = 3/4 \) (see text).

\[
\theta \to \theta_c = 1/2 \text{ from above or below, the localised DW in } T_A \text{ or } T_B \text{ shows a delocalisation transition at which DW fluctuations diverge. The width } \sigma \text{ of the distribu-}
\]

\[
\sigma \sim 1/\sqrt{L}
\]

\[
\theta \to \theta_c = 1/2 \text{ from above or below, the localised DW in } T_A \text{ or } T_B \text{ shows a delocalisation transition at which DW fluctuations diverge. The width } \sigma \text{ of the distribu-}
\]
tion of DW fluctuations can be obtained by fitting the density profile in the vicinity of the domain wall by the function \( P \cdot \text{erf}(x - Q)/|\sigma| + R \) \([12]\), with the parameters \( P, Q, R, \sigma \). We find \( \sigma \) to diverge with a power law dependence on \((\theta - \theta_c)\) as,

\[
\sigma \sim (\theta_c - \theta)^{-\beta},
\]
with \( \beta = 3/4 \) obtained from our MCS studies as shown in Fig. 8. In contrast, at an off-critical point, i.e., for \( \theta \neq 1/2 \), DW fluctuations are finite and vanish in TL \( L \to \infty \) as \( L^{-1/2} \); we have shown this in Fig. 7. For investigating the variation of domain wall width with \( L \) for various values of \( \theta \) we have taken \( L = 32, 64, 128, 256 \) and 512.

V. SUMMARY AND OUTLOOK

Analytical and numerical studies of our model amply illustrate the underlying rich phase behaviour, including a delocalisation transition, unexpected in a system without boundaries. While boundary-induced phase transitions including delocalisation transitions have been observed in several open systems with exclusion processes together with spatially nontrivial steady state densities \([12, 17]\), analogous studies on bulk closed systems are less studied so far. The competition between the diffusive and driven dynamics, and the division of the SEP current into two parallel TASEP currents are crucial to the macroscopic behaviour we obtained. The latter is controlled by a parameter \( \theta \), which is a tuning parameter in the model. The most striking feature in our work vis-a-vis the results in Ref. \([12]\) is the possible existence of a delocalisation transition and correspondingly the formation of DWs in both \( T_A \) and \( T_B \) simultaneously at a special value \( \theta = 1/2 \). In contrast to the DWs formed either in \( T_A \) or \( T_B \) (but not simultaneously in both) for \( \theta \neq 1/2 \), as found in Ref. \([12]\) as well as in the present work, the DWs at \( \theta = 1/2 \) are no longer pinned to a fixed point in the lattice with vanishing fluctuations in the thermodynamic limit. Instead they delocalise and have position fluctuations that do not vanish in the thermodynamic limit. Thus the parameter \( \theta \) in our model appears as a tuning parameter or a switch, which can be used to control the nature of domain wall fluctuations (localised/delocalised). In addition for \( \theta \neq 1/2 \), the value of \( \theta \) can be tuned to make the DW appear or disappear in one of the active channels. There is no analogue of these in the study of Ref. \([12]\). While we have considered only two TASEP channels, many more may be added and studied systematically as above. Recalling protein synthesis by ribosomes along mRNA strands as one of the phenomenological motivation for our model, it may be noted that several mRNAs compete for same resources (ribosomes) in a cell. Thus a systematic study of multiple TASEP channels connected in parallel with a single SEP channel would be useful. The failure of the traditional MFT calls for further analysis by means of more sophisticated analytical techniques, e.g., Bethe ansatz \([17]\) or density matrix renormalisation group \([18]\), which are beyond the scope of the present work. From the point of view of nonequilibrium statistical mechanics, our model belongs to the class of models lacking translation invariance and without boundaries that displays a phase transition (in the form of a delocalisation transition). Our model may be extended in several new directions, e.g., again motivating by ribosome movements along mRNA, one may in our model consider particle exchanges between \( T_A \) and \( T_B \), or between one of the active channels and passive channel (representing ribosome attachments or detachments), allow defects along the active channels (representing defects in the mRNA), introduce a second control parameter at the exit ends of \( T_A \) and \( T_B \) that controls the relative outgoing currents to SEP and unequal hopping rates in \( T_A \) and \( T_B \). These will be considered elsewhere. We close this work with a note of caution: As mentioned in the beginning, despite some similarities our model cannot be directly used for quantitative descriptions of ribosome translocations along mRNA strands due to its limitations. First of all, ribosome diffusion takes place inside a cell, which, although geometrically confined, has a three-dimensional (3d) structure, as opposed to our 1d diffusive model for it. Secondly, the description of a ribosome as a single unit (i.e., a point particle here) is also questionable, for it gets released from an mRNA by falling apart into different subunits, a feature not possible to capture in our simplified description here. Nevertheless, our work provides some clues about the actual biological system, e.g., the crucial role of particle number conservation in determining the nature of the steady states. We expect that more realistic theoretical descriptions of ribosome translocation and detachment should have some of the basic features of our model in-built into it.

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