

Disordered totally asymmetric simple exclusion process: Exact results

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We study the effect of quenched spatial disorder on the current-carrying steady states of a totally asymmetric simple exclusion process with spatially disordered jump rates. Expressions for the steady state weights and the current are derived for this model in one dimension. These solutions are exploited to study analytically the *exact* symmetries of the system. In particular, we confirm the recent numerical observation of Tripathy and Barma [Phys. Rev. E **58**, 1911 (1998)] that the magnitude of the steady state current is left invariant when the direction of all the allowed particle jumps are reversed.

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Driven diffusive systems have been the subject of extensive studies in recent years [1]. A key ingredient that makes the study of these systems interesting is the presence of a driving field due to which the underlying dynamics do not generically obey a detailed balance, leading to steady states with nonvanishing currents. In the absence of a unifying theme that encompasses our understanding of nonequilibrium phenomena, these systems offer a relatively simple framework within which phenomena far from thermal equilibrium may be studied.

These systems further provide the possibility of studying the intriguing interplay of disorder, interaction, and drive for a wide range of parameter values like the degree of disorder, filling, and drive strength [2]. Driven systems in the absence of disorder have been studied extensively, and have revealed basic differences between equilibrium and nonequilibrium systems [1,3,4]. For instance, spontaneous symmetry breaking [5,6] and phase separation have been demonstrated in one-dimensional asymmetric exclusion processes [7]. In contrast it is well known that one-dimensional systems in thermal equilibrium with short range interactions do not exhibit such phenomena [8]. Also, systems with disorder and drive but no interactions between particles have been reasonably well studied and understood [9].

A number of physical situations involving flow in random media require an understanding of disorder driven diffusive systems of interacting particles [10]. Most of the understanding gained in these system was largely based on numerical simulations. In fact, analytical characterizations in terms of exact steady state measures in systems *without* translational invariance have only been found in the case of the disordered drop-push model [11].

An interesting class of models, for which again there exists *no* analytical characterization of the steady state weights or the steady state current, is the disordered totally asymmetric simple exclusion process (DTASEP). Even the single disorder case has not been amenable to an analytic treatment.

Extensive numerical and mean-field studies have been done, and a number of interesting features have been highlighted [11–14].

In this work we derive formally exact solutions for the steady state weights and current for the DTASEP model in one dimension. These solutions are valid for arbitrary disorder and particle fillings. We further show how these solutions can be exploited to study the exact symmetries of the model by studying the transformations that leave the magnitude of the steady state current invariant. In particular we show that the model possesses an exact particle-hole symmetry for any *given* disorder realization, a result that was observed in numerical simulations by Tripathy and Barma [15].

Definition of the model. The DTASEP model is defined on a one-dimensional lattice of length L with periodic boundary conditions. Each site can hold either one particle or zero. Each bond $(i, i+1)$ of the lattice is assigned a quenched random rate α_i chosen independently from some chosen probability distribution. The evolution is governed by random sequential dynamics defined as follows: in a time interval dt the particle attempts to hop, with probability $\alpha_i dt$, to its neighboring site $i+1$. We consider the case in which the jumps are allowed only in one direction (to the right), and are the same for all bonds. In addition, the move is completed if and only if site $i+1$ is unoccupied. The time averaged steady state current J_i in the bond $(i, i+1)$ is given by

$$J_i = \alpha_i \langle n_i (1 - n_{i+1}) \rangle, \quad (1)$$

where n_i counts the number of particles at site i .

Since for every particle hopping to the right, a ‘‘hole’’ hops to the left, this implies that interchanging all the particles for holes (charge conjugation C) and reversing the direction of hopping (time reversal T), leaves the steady state current, up to a sign, the same. Hence the steady state current is symmetric under a combined CT transformation. This symmetry is valid in general: in any dimension; in the presence of disorder; and in the case when the particle can hop along any direction with finite probabilities (DASEP).

In Eq. (1), if all the α_i 's are set equal to the same constant α , then it follows that the steady state current J_0 , which is

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assumed to be the same on each bond and hence $J_0 = L^{-1} \sum_i J_i$, is invariant under $n_i \rightarrow 1 - n_i$ for all i . Hence for the clean totally asymmetric simple exclusion process in one dimension (TASEP), charge conjugation by itself leaves the steady state current invariant. Since CT symmetry always holds, it follows that for the TASEP model in one dimension both charge conjugation (C) and time reversal (T) symmetries hold individually.

Surprisingly, in one dimension, it was shown that charge conjugation symmetry is respected even when disorder is included (the DTASEP model). This symmetry was exposed in numerical simulations carried out by Tripathy and Barma [15]. They studied a system of size $L=6$ with $N=2$ particles, and verified the invariance of the current up to one part in 10^8 for some arbitrarily given disorder realization. Further, studying the steady state weights of all the ${}_6C_2$ particle configurations showed no straightforward correspondence between the two systems related by charge conjugation.

With these observations in mind, for this model we derive a formally exact expression for the steady state probability density and the current J_0 . The validity of these expressions have been confirmed explicitly for small system sizes. They allow us to demonstrate the observed reflection symmetry (T symmetry) in general for all fillings and disorder configuration, which in turn from CT symmetry implies the symmetry of the steady state current under charge conjugation (C symmetry). We then derive an expression relating the two sets of steady state weights after reflection, and explicitly show that their relationship is indeed nontrivial.

For L sites with N particles, the number of configurations $M = {}_L C_N$. Here ${}_L C_N = L! / (L-N)! N!$ is the number of ways N particles can be distributed among L sites, with a maximum of only one particle per site. The dynamics of these configurations, for a given realization of the quenched bond variables $\mathbf{R} = \{\alpha_1, \alpha_2, \dots, \alpha_L\}$, are given by the rate equation

$$\frac{dP_m}{dt} = \sum_n T(n \rightarrow m) P_n - \sum_{n'} T(m \rightarrow n') P_m, \quad (2)$$

where $T(m \rightarrow n)$ gives the transition probability from configuration $m \rightarrow n$. This expression can be conveniently expressed in matrix notation as

$$\frac{d\mathbf{P}(t)}{dt} = \mathbf{W}\mathbf{P}(t), \quad (3)$$

with $W_{mn} = T(n \rightarrow m)$ and $W_{mm} = -\sum_{n'} T(m \rightarrow n')$. Since $\mathbf{1} \cdot \mathbf{P}(t) = \sum_m P_m(t) = 1$ for all time t (normalization), it follows that $\mathbf{1} \cdot \mathbf{W} = 0$. This implies that W has a zero eigenvalue with left eigenvector $\mathbf{1}$. Hence it follows that there also exists a right eigenvector \mathbf{P} such that $\mathbf{W}\mathbf{P} = 0$. This defines the steady state solution of the problem for a given choice of the disorder \mathbf{R} .

The steady state of the problem considered above is characterized by a uniform current J_0 across each bond. Given the solution \mathbf{P} , the current across, say, site i and $i+1$, is given as $\alpha_i \sum P_m = J_0$, where the sum is *only* over the set of configurations with a particle on site i and a hole on site $i+1$ [see Eq. (1)].

The above sum for all sites i can be combined and conveniently written in matrix notation by defining a matrix G such that $G \cdot \mathbf{P} = J_0 (1/\alpha_1, 1/\alpha_2, \dots, 1/\alpha_L)^T \equiv J_0 (1/\alpha)^T$. The entries of G for a given row i (corresponding to site i) has 1 in column m if the m th configuration, which arises with probability P_m in the steady state, has a particle at site i and a hole at site $i+1$, and is 0 otherwise. The order of the G matrix is therefore $L \times M$, since there are L sites and M configurations. The G matrix can be expanded to an $M \times M$ matrix by augmenting an $(M-L) \times M$ zero matrix to G , such that

$$Q \cdot \mathbf{P} \equiv \begin{pmatrix} G_{L \times M} \\ 0_{(M-L) \times M} \end{pmatrix} \cdot \mathbf{P} = J_0 \begin{pmatrix} 1/\alpha \\ 0 \end{pmatrix} \equiv J_0 \mathbf{V}, \quad (4)$$

where, for convenience, we have defined new variables $Q = (G, 0)^T$ and $\mathbf{V} = (1/\alpha, 0)^T$. Hence the three equations that determine the steady state distribution and current are

$$\mathbf{W} \cdot \mathbf{P} = 0, \quad (5a)$$

$$Q \cdot \mathbf{P} = J_0 \mathbf{V}, \quad (5b)$$

$$\mathbf{1} \cdot \mathbf{P} = 1. \quad (5c)$$

If we assume that row rank (W) = $M-1$, and is not less, then there exists a one-parameter solution to Eq. (5a). The most general form of the solution will be of the form $\beta \mathbf{P}$, where β is the arbitrary parameter. The solution when substituted into Eq. (5b) allows the β factor to be absorbed in the definition of J_0 by rescaling $J_0 \rightarrow J_0/\beta$. Hence the most general solution $\mathbf{P} \equiv \mathbf{P}(J_0)$ will have J_0 appearing as the only free parameter. The value of J_0 is fixed by the normalization condition given in Eq. (5c). Hence a unique \mathbf{P} and J_0 solve Eq. (5).

Although a unique solution exists, neither Eq. (5a) nor Eq. (5b) can be inverted to obtain a solution for \mathbf{P} and J_0 as both W and Q are singular matrices. However, except for a few values of η , the sum $Q + \eta W$ is invertible since $\det(Q + \eta W)$ is a polynomial in η . Therefore, multiplying Eq. (5a) by η and adding it to Eq. (5b) gives us

$$(Q + \eta W) \cdot \mathbf{P} = J_0 \mathbf{V}. \quad (6)$$

Now, if η is such that $(Q + \eta W)$ is invertible, then, using Eq. (6), we obtain $\mathbf{P}(J_0) = J_0 (Q + \eta W)^{-1} \cdot \mathbf{V}$. The steady state current J_0 is obtained using the normalization condition in Eq. (5c), giving $1/J_0 = \mathbf{1} \cdot (Q + \eta W)^{-1} \cdot \mathbf{V}$. Hence the final solutions are given as

$$\mathbf{P} = \frac{(Q + \eta W)^{-1} \cdot \mathbf{V}}{\mathbf{1} \cdot (Q + \eta W)^{-1} \cdot \mathbf{V}}, \quad (7a)$$

$$J_0 = \frac{1}{\mathbf{1} \cdot (Q + \eta W)^{-1} \cdot \mathbf{V}}. \quad (7b)$$

It is important to note that, since we have already shown that a unique solution to Eq. (5) exists, the above solutions are independent of η .

Now we consider the system in which the direction of the allowed jumps is reversed. We denote the set of quenched

random bond variables when the particles are allowed to jump to the left as $\bar{\mathbf{R}} = \{\alpha_1, \alpha_2, \dots, \alpha_L\}$. In $\bar{\mathbf{R}}$ the magnitude and ordering of the α_i 's are the same as in \mathbf{R} , although the direction of hopping has been reversed. Let $\bar{\mathbf{P}}$ be the steady state weights and \bar{W} and \bar{Q} the corresponding matrices such that $\bar{W} \cdot \bar{\mathbf{P}} = 0$ and $\bar{Q} \cdot \bar{\mathbf{P}} = \bar{J}_0 \mathbf{V}$. The \mathbf{V} vector in both cases are the same, and \bar{J}_0 is the appropriate current. Following the same procedure as above, we obtain

$$\bar{\mathbf{P}} = \frac{(\bar{Q} + \eta \bar{W})^{-1} \cdot \mathbf{V}}{\mathbf{1} \cdot (\bar{Q} + \eta \bar{W})^{-1} \cdot \mathbf{V}}, \quad (8a)$$

$$\bar{J}_0 = \frac{1}{\mathbf{1} \cdot (\bar{Q} + \eta \bar{W})^{-1} \cdot \mathbf{V}}. \quad (8b)$$

In order to prove the equality of the two currents J_0 and \bar{J}_0 , we proceed by defining a matrix S satisfying the relations

$$Q \cdot S = \bar{Q}, \quad (9a)$$

$$S^{-1} \cdot \mathbf{P} = \bar{\mathbf{P}}. \quad (9b)$$

It follows from Eq. (5b) that the existence of such a matrix S guarantees the equality of the currents under time reversal. We now proceed to derive further constraints that S should satisfy. First, since each row of G contains as many 1's as the number of configurations for which there exists a particle at site i and a hole at site $i+1$, we have $G \cdot \mathbf{1} = {}_{L-2}C_{N-1} \mathbf{1}$. The same is true of \bar{G} , although the exact location of each of the 1's will differ since the direction of hopping has been reversed. Going back to Eq. (9a), we obtain

$$Q \cdot S \begin{pmatrix} \mathbf{1} \\ \mathbf{1} \end{pmatrix} = \bar{Q} \begin{pmatrix} \mathbf{1} \\ \mathbf{1} \end{pmatrix} = {}_{L-2}C_{N-1} \begin{pmatrix} \mathbf{1} \\ \mathbf{0} \end{pmatrix} = Q \begin{pmatrix} \mathbf{1} \\ \mathbf{1} \end{pmatrix}. \quad (10)$$

All the conditions in the above equation can be satisfied if we take $S \cdot \mathbf{1} = \mathbf{1}$. Second, since both \mathbf{P} and $\bar{\mathbf{P}}$ are normalized, from Eq. (9b) we obtain that $\mathbf{1} \cdot \mathbf{P} = \mathbf{1} \cdot S \cdot \bar{\mathbf{P}} = 1$. This equation can be satisfied if we take $\mathbf{1} \cdot S = \mathbf{1} + \mathbf{A}$, with the additional constraint that $\mathbf{A} \cdot \bar{\mathbf{P}} = 0$. We observe that the equation is satisfied only up to a vector \mathbf{A} which is "orthogonal" to $\bar{\mathbf{P}}$.

Acting by W on both sides of Eq. (9b) gives

$$W \cdot \mathbf{P} = WS \cdot \bar{\mathbf{P}} = 0. \quad (11)$$

This equation can be satisfied if we take $WS = -\bar{W}$. The sign is fixed by observing that, since the direction of hopping has

been reversed in $\bar{\mathbf{R}}$, the outgoing configurations with respect to a given initial particle configuration are mapped to the incoming configurations in \mathbf{R} and vice versa, leading to the relation $W \cdot \mathbf{1} = -\bar{W} \cdot \mathbf{1}$ [refer to Eqs. (2) and (3)]. Then, using the property that $S \cdot \mathbf{1} = \mathbf{1}$, it follows that $WS \cdot \mathbf{1} = W \cdot \mathbf{1} = -\bar{W} \cdot \mathbf{1}$.

Thus the two equations that S should satisfy are

$$QS = \bar{Q}, \quad (12a)$$

$$WS = -\bar{W}. \quad (12b)$$

It is interesting to note that it is *not* a similarity transformation that relates the two systems defined by W and \bar{W} .

By multiplying Eq. (12) by an appropriate parameter η , and adding the two equations, we obtain

$$S = (Q + \eta W)^{-1} \cdot (\bar{Q} - \eta \bar{W}). \quad (13)$$

It is now trivial to numerically check that the form of S derived above explicitly solves Eqs. (9), thereby confirming the observation made by Tripathy and Barma [15] in their numerical simulations that the currents under time reversal are equal for all fillings and disorder strength. The nontrivial nature of the S matrix also explains why they did not find a simple relationship between the two steady state weights which we give in Eq. (9b). At this point, one should note that, in contrast to our algebraic approach, Goldstein and Speer [16] recently gave an interesting probabilistic proof of the same observation.

In conclusion, we show how our approach offers a unified way to "search" for other quantities that are also invariant under time reversal. For example, if \mathbf{Z} is some left eigenvector of the matrix S with eigenvalue 1 (i.e., $\mathbf{Z} \cdot S = \mathbf{Z}$), then it follows from Eq. (5b) that $\mathbf{Z} \cdot \mathbf{P} = \mathbf{Z} \cdot \bar{\mathbf{P}}$. This implies that there are as many invariant quantities as the number of such left eigenvectors of S (if only one could find and interpret them). We therefore believe that the algebraic approach we have developed has wider applicability in studying and understanding the symmetries of more general models not amenable to direct analytical studies.

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