Random attraction in the TASEP model

Lars Grüne and Thomas Kriecherbauer and Michael Margaliot

Abstract

The totally asymmetric simple exclusion process (TASEP) is a basic model of statistical mechanics that has found numerous applications. We consider the case of TASEP with a finite chain where particles may enter from the left and leave to the right at prescribed rates. This model can be formulated as a Markov process with a finite number of states. Due to the irreducibility of the process it is well-known that the probability distribution on the states is globally attracted to a unique equilibrium distribution. We extend this result to the more detailed level of individual trajectories. To do so we formulate TASEP as a random dynamical system. Our main result is that the trajectories from all possible initial conditions contract to each other yielding the existence of a random attractor that consists of a single trajectory almost surely. This implies that in the long run TASEP “filters out” any perturbation that changes the state of the particles along the chain.

Keywords. Ribosome flow model; contraction; random dynamical systems; random attractor; synchronization; mRNA translation.

I. Introduction

The totally asymmetric simple exclusion process (TASEP) is a fundamental dynamical model from nonequilibrium statistical mechanics. It was first introduced as a 1D lattice model for the motion of ribosomes along the mRNA strand during translation [17]. TASEP describes particles stochastically hopping along a one-directional 1D chain of sites, where each site can be either empty or contain a single particle. This simple exclusion principle generates an indirect coupling between the particles, as a particle cannot hop to a site that is already occupied by another particle. TASEP is a generic tool that has been used to model and analyze numerous natural and artificial processes including vehicular traffic, the kinetics of molecular motors, and ribosome flow along the mRNA during translation [8], [28], [33]. Although one-dimensional, TASEP exhibits phase transitions between low-density, high-density, and maximum-current phases [5], [15].

The simple exclusion principle allows to model and analyze the evolution of particle “traffic jams”. Indeed, if a particle remains in the same site for a long time then other particles will accumulate in the sites “behind” the occupied site. Traffic jams in the flow of

Research supported in part by research grants from the Israel Science Foundation and the US-Israel Binational Science Foundation.

LG and TK are with the Mathematical Institute, University of Bayreuth, Germany. MM is with the School of Electrical Engineering and the Sagol School of Neuroscience, Tel Aviv University, Israel.
“biological machines” like ribosomes and molecular motors, have important ramifications and are attracting considerable interest (see e.g. [7], [27], [29]).

The ribosome flow model (RFM) [26] is the dynamic mean-field approximation of TASEP. The RFM and its variants have been used extensively to model mRNA translation of both isolated mRNA molecules [31], [32], and networks of mRNAs [21], as well as other important cellular processes like phosphorelay [3].

For a chain of \( n \) sites the RFM can be written as set of \( n \) ODEs:

\[
\begin{align*}
\dot{x}_1 &= \alpha(1 - x_1) - h_1 x_1 (1 - x_2), \\
\dot{x}_2 &= h_1 x_1 (1 - x_2) - h_2 x_2 (1 - x_3), \\
&\vdots \\
\dot{x}_n &= h_{n-1} x_{n-1} (1 - x_n) - \beta x_n,
\end{align*}
\]

where \( x_i(t) \in [0, 1] \) represents the normalized density of particles at site \( i \) along the chain, with \( x_i(t) = 0 \ [x_i(t) = 1] \) representing that this site is almost surely empty [full] at time \( t \). The number \( h_i > 0 \) is the transition rate from site \( i \) to site \( i + 1 \) and \( \alpha, \beta > 0 \) denote the rates at which particles enter the chain from the left or exit to the right, respectively. To explain this model, consider the equation for \( \dot{x}_2 \). This states that the change in the density at site 2 is the flow from site 1 to site 2 minus the flow from site 2 to site 3. The latter is given by \( h_2 x_2 (1 - x_3) \) i.e. it is proportional to the transition rate, the density at site 2 and the “free space” in site 3. This is a “soft” version of simple exclusion. Just like TASEP, the RFM can be used to model and analyze the evolution of traffic jams. For \( a \in [0, 1]^n \), we use \( x(t, a) \) to denote the solution of the RFM at time \( t \geq 0 \) with \( x(0) = a \).

The RFM has been analyzed using various tools from systems and control theory including the theory of cooperative dynamical systems [19], contraction theory [18], continued fractions, the spectral theory of tridiagonal matrices [24], and more.

Recall that a dynamical system

\[
\dot{x} = f(x),
\]  

(I.1)

with \( x(t) \in \mathbb{R}^n \), is called contractive if there exist a vector norm \( \| \cdot \| : \mathbb{R}^n \to \mathbb{R}_+ \) and \( \eta > 0 \) such that for any two initial conditions \( a, b \) in the state-space, we have

\[
|x(t, a) - x(t, b)| \leq \exp(-\eta t)|a - b| \text{ for all } t \geq 0.
\]

Thus, any two solutions approach one another at an exponential rate and in particular the initial conditions are exponentially “forgotten”. It was shown in [18] that the RFM is an (almost) contractive system.

This statement also holds on a more detailed level when one considers the time-evolution of the probability distribution on the \( 2^n \) states. This time-evolution is governed by a linear differential equation that is called Kolmogorov’s forward equation or master
equation in the theory of Markov processes. Since TASEP defines an irreducible Markov process it is well-known that any initial distribution is contracted to a unique equilibrium distribution that only depends on the transition rates $\alpha, \beta, h_1, \ldots, h_{n-1}$. In the special case where all the internal transition rates $h_i$ are equal an extremely useful representation for the equilibrium measure was derived in [10] using the matrix product ansatz, see also [5], [16].

As a side remark we mention that there is also another celebrated result regarding TASEP that concerns a closely related model of an infinite chain with step-like initial conditions and identical transition rates. It was shown in [11] that the fluctuations of the particle current obey the Tracy-Widom limit law from random matrix theory, see e.g. [14] for an elementary description of the result.

In this paper we investigate TASEP from a new perspective. Having observed that densities and probability distributions contract to an equilibrium it is natural to ask: do the trajectories of TASEP also contract? Of course, as the individual trajectories do not converge to an equilibrium it only makes sense to ask whether there is contraction between different trajectories. Note that the mutual contraction of different trajectories is also called synchronization, see e.g. [22, Definition 3.1.1]. In order to investigate such a question one needs to have a model of TASEP that describes the random jumps of particles simultaneously for all $2^n$ states of the system. The usual Markov process associated with TASEP does not provide such information as any realization $\omega$ of randomness defines only a single trajectory. A standard framework for investigating the question of synchronization is given by random dynamical systems (RDS). To the best of our knowledge such an RDS for TASEP is missing in the literature. We fill this gap for finite chains. It is then shown for the resulting model that all trajectories of TASEP indeed contract to one another almost surely, i.e. the system is globally synchronizing. This is also the basis for proving (see Theorem [12] below) that the RDS possesses a random attractor that almost surely consists of a single trajectory.

We would like to point out that this result is not a consequence of the fact that the equilibrium of the master equation description of TASEP is a global attractor in the space of probability distributions. Indeed, we present an example (see Remark [13] (ii) below) of a Markov process for which the equilibrium of the corresponding master equation is a global attractor due to the irreducibility of the process but for which the dynamics preserves the Hamming distances between states implying that trajectories do not contract.

It is known [20] that convergence to a unique probability distribution holds for the TASEP master equation also in the case where the transition rates are time-varying and jointly periodic. The same is true for the convergence of densities for the RFM [18]. These results provide a framework for studying entrainment to periodic excitations like the cell division process at the genetic level. Of course, for both equations the limiting state is
not stationary any more but depends periodically on time. In Section VII we describe briefly how our result may be extended to this more general situation.

Our result for TASEP that random dynamics leads to a synchronization of trajectories has been observed for a number of quite different settings and goes back at least to the work of Baxendale and Stroock [4, Proposition 4.1], see also the discussion in [22, Section 4.1]. One such setting that bears some similarity with our case is the time-discrete dynamics induced by the composition of random maps on the circle. For example, Kleptsyn and Nalskii [13] considered a finite set of orientation-preserving homeomorphisms $T_k$, $k = 1, \ldots, n$, of the circle, and the dynamical system obtained by applying a randomly and independently chosen $T_i$ at each time step. They showed that under certain assumptions on the semigroup generated by the $T_i$s there exists a $C^1$-open set of random dynamical systems for which the distance between the iterates of different points tends to zero as the number of iterations tends to infinity.

A general framework for such noise-induced synchronization (or synchronization by noise) was introduced by Newman [22]. He considered the composition of independent and identically distributed random maps or a memoryless stochastic flow on a compact metric space $X$. He derived conditions for almost-sure mutual convergence of any given pair of trajectories (i.e., global synchronization), namely, synchronization occurs and is “stable” if and only if the following properties hold: (i) there is a smallest non-empty invariant set $K \subset X$; (ii) any two points in $K$ are capable of being moved closer together; and (iii) $K$ admits asymptotically stable trajectories. In our case (i) is satisfied with $K = X$, condition (ii) is verified by Lemma 4 and (iii) is trivially satisfied as our system has a finite number of states. Therefore, our Proposition 7 also follows from [22, Theorem 4.2.1]. However, as [22] uses the more detailed version of an filtered RDS we present a self-contained (and short) proof of Proposition 7 without reference to [22, Theorem 4.2.1]. In addition, we investigate a question that is not addressed in [22], namely, we use our synchronization result for TASEP to prove the existence of two types of random attractors that are central for the description of the long-time behavior of an RDS.

Finally, we would like to mention a set of stochastic differential equations that is not directly related to our results but belongs to the same theme park. These equations consist of a diffusive or contractive deterministic evolution equation that is subjected to stochastic driving. In this realm the question of synchronization has been addressed for Itô stochastic differential equations with a contractive deterministic part in [23]. There two copies of the same deterministic system with different initial conditions and driven by distinct and independent Wiener processes were considered, and a bound for the mean square distance between the solutions was derived. On the side of stochastically driven diffusive systems a celebrated representative is the Kardar-Parisi-Zhang (KPZ) equation of statistical physics. It is conceptually interesting that this equation can be derived as a certain continuum limit of TASEP. In fact, the discovery of the relation between TASEP
and random matrix theory indicated above and the resulting enhanced understanding of TASEP led to a renewed interest in the KPZ equation (see [25] for a recent review on these developments).

The remainder of this paper is organized as follows. The next section reviews the notion of an RDS. Section III carefully formulates TASEP as an RDS. Section IV shows that solutions of TASEP emanating from different initial conditions coincide with arbitrarily large probability after sufficiently long time. Section V recalls two concepts of random attractors for an RDS and shows for our TASEP-RDS that both types of attractors exist and consist of single trajectories almost surely. Our theoretical results are demonstrated using numerical simulations in Section VI. Extensions of our main results to time-periodic transition rates and to the asymmetric simple exclusion process (ASEP) are described in Section VII. The final section summarizes our findings.

II. RANDOM DYNAMICAL SYSTEMS

In order to analyze random attraction in TASEP, we make use of the framework of random dynamical systems (RDS). The definition of RDS goes back at least as far as [2], a comprehensive treatment can be found in the monograph [1]. In the literature, one can find several variants of this definition, which differ in minor technical details. The definition we use in this paper is taken from [9]:

**Definition 1.** A continuous time random dynamical system (RDS) \((\theta, \varphi)\) on a topological space \(X\), equipped with the corresponding Borel sigma algebra, consists of

- an autonomous measurable and measure-preserving dynamical system \(\theta = \{\theta_t\}_{t \in \mathbb{R}}\) acting on a probability space \((\Omega, \mathcal{F}, \mathbb{P})\), i.e.,
  
  (i) \(\theta_0(\omega) = \omega\),
  (ii) \(\theta_{s+t}(\omega) = \theta_s \circ \theta_t(\omega)\)
  (iii) \((t, \omega) \mapsto \theta_t(\omega)\) is measurable

  for all \(\omega \in \Omega\) and all \(s, t \in \mathbb{R}\), such that \(\theta_t \mathbb{P} = \mathbb{P}\) for every \(t \in \mathbb{R}\), where \(\theta_t \mathbb{P}(A) = \mathbb{P}(\theta_t A)\) for all \(A \in \mathcal{F}\)

- a cocycle mapping \(\varphi : \mathbb{R}_0^+ \times X \times \Omega \to X\), i.e.,

  (1) \(\varphi(0, x, \omega) = x\) for all \(x \in X\) and \(\omega \in \Omega\) \hspace{2cm} (initial condition)

  (2) \(\varphi(s + t, x, \omega) = \varphi(s, \varphi(t, x, \omega), \theta_t \omega)\) for all \(s, t \in \mathbb{R}_0^+, \ x \in X\) and \(\omega \in \Omega\) \hspace{2cm} (cocycle property)

  (3) \((t, x, \omega) \mapsto \varphi(t, x, \omega)\) is measurable \hspace{2cm} (measurability)

  (4) \(x \mapsto \varphi(t, x, \omega)\) is continuous for all \((t, \omega) \in \mathbb{R}_0^+ \times \Omega\) \hspace{2cm} (continuity)

The interpretation of the times in this definition is as follows: \(\varphi(\cdot, x_0, \theta_{t_0} \omega)\) denotes the solution path corresponding to \(\omega\) starting at time \(t_0\) in state \(x_0\) and \(\varphi(t, x_0, \theta_{t_0} \omega)\)
denotes the state on this path at time $t + t_0$. This means that the first time argument of $\varphi$ indicates the time that elapsed since the initial time $t_0$, rather than the absolute time.

### III. TASEP as a Random Dynamical System

The **totally asymmetric simple exclusion process** (TASEP) is a Markov process for particles hopping or jumping along a 1D chain. We consider the continuous time version of TASEP here. Moreover, we restrict ourselves to finite lattices with $n \in \mathbb{N}$ sites. Then the Markov process has only a finite number of states. A particle at site $k \in \{1, \ldots, n-1\}$ hops to site $k+1$ (the next site on the right) at a random jump time that is exponentially distributed with rate $h_k$, provided that site $k+1$ is not occupied by another particle. This simple exclusion property generates an indirect coupling between the particles and allows, e.g., to model the formation of traffic jams. Indeed, if a particle “gets stuck” for a long time in the same site then other particles accumulate behind it. At the left end of the chain particles enter with a certain entry rate $\alpha > 0$ and at the right end particles leave with a rate $\beta > 0$. We refer to [16], [28] and the references therein for more information about this model.

In the following subsections we describe how TASEP can be written as a random dynamical system.

**The dynamics of hopping in TASEP**

In order to define the state of the system we define a variable $s_k$ for each site $k \in \{1, \ldots, n\}$. We set $s_k = 1$ if site $k$ is occupied by a particle and $s_k = 0$ if it is not. Hence, the (finite) state space of TASEP is $X = \{0,1\}^n$. Since the state space is finite, we use the discrete topology and its Borel sigma algebra, i.e. all subsets of $X$ are open and measurable.

For defining the dynamics of TASEP, we start with formalizing a single hop via a map $f$ and then a sequence of hops via a map $\tilde{\varphi}$. The map $\varphi$ needed in Definition 1 will then be derived from $\tilde{\varphi}$ in the last subsection of this paragraph, when the stochastic model defining the jump times has been introduced.

A single hop can be defined as follows. We are given a state $x = (s_1, \ldots, s_n) \in X$ and an index $k \in \{0, \ldots, n\}$ of the site at which the particle attempts to hop, where $k = 0$ represents a particle entering the chain. Then we define

$$f(x, k) := \begin{cases} (1, s_2, \ldots, s_n) & \text{if } k = 0 \\ (s_1, \ldots, s_{n-1}, 0) & \text{if } k = n \\ (s_1, \ldots, s_{k-1}, 0, 1, s_{k+2}, \ldots, s_n) & \text{if } k \neq 0, k \neq n, s_k = 1 \text{ and } s_{k+1} = 0 \\ x & \text{otherwise.} \end{cases}$$
Now assume that we have a sequence of jump times \( t_i(\omega) \) with \( t_i(\omega) \in \mathbb{R} \) and \( t_i(\omega) < t_{i+1}(\omega) \) for all \( i \in \mathbb{Z} \) together with indices \( k_i(\omega) \in \{0, \ldots, n\} \) indicating at which site a particle attempts to jump at time \( t_i(\omega) \). The argument \( \omega \) indicates that these (deterministic) sequences are realizations of random sequences \( (t_i) \) and \( (k_i) \). We will specify below how we generate these random sequences in order to meet the exponential distribution requirement. The transition \( \tilde{\varphi} : \mathbb{R}_+^n \times X \times \mathbb{R}_+^n \times \{0, \ldots, n\}^\mathbb{Z} \to X \) mapping the initial value \( x_0 \) at initial time 0 to the state \( \tilde{\varphi}(t, x_0, (t_i(\omega)), (k_i(\omega))) \) at time \( t \), given the jump time and index sequences \( (t_i(\omega))_{i \in \mathbb{Z}} \) and \( (k_i(\omega))_{i \in \mathbb{Z}} \) is then defined by

\[
\tilde{\varphi}(t, x_0, (t_i(\omega)), (k_i(\omega))) := x_0 \text{ if } t_i(\omega) \notin [0, t) \text{ for all } i \in \mathbb{Z}, \text{ otherwise inductively via}
\]

\[
x_{p+1} := f(x_p, k_{p+i_0}) \text{ for } p = 0, \ldots, \Delta i, \quad \tilde{\varphi}(t, x_0, (t_i(\omega)), (k_i(\omega))) := x_{\Delta i+1} \quad (\text{III.1})
\]

where \( i_0 := \inf\{i \in \mathbb{Z} | t_i(\omega) \geq 0\}, \; i_1 := \sup\{i \in \mathbb{Z} | t_i(\omega) < t\} \) and \( \Delta i = i_1 - i_0 \). Here we assume that \( (t_i(\omega)) \) has no accumulation points in \( \mathbb{R} \), which can be done since our specification of \( t_i \), below, will ensure that this indeed holds.

**Assignment of the jump times**

When trying to write TASEP as an RDS, it is not enough to define the “hopping dynamics”. In addition, we face the difficulties described in [1, top of p. 55]: a model that is described in terms of transition probabilities does not define a unique RDS because it only describes the evolution of single or one-point motions. For defining an RDS, however, we need to specify the simultaneous motion of solutions subject to different initial conditions but identical random influence. This specification is in general not unique. We will explain this with an example at the end of this section.

As the random influence in TASEP is entirely determined by the jump times, this requires to specify the relation between the elementary events \( \omega \in \Omega \) and the random jump times. In the usual description of TASEP, the rule specified for the jump times is that once a particle jumped or attempted to jump, the time to the next jump attempt is exponentially distributed. This suggests that to each particle \( p \) we assign a sequence of random jump times \( \tau_{p,i} \) (that we may think of as “random clocks”), such that the increments \( w_{p,i} := \tau_{p,i+1} - \tau_{p,i} \) are independent and exponentially distributed as well as independent of \( \tau_{p,i} \) and of all jump times for all the other particles.

Attaching the random clocks to the particles, however, has the disadvantage that one needs to keep track at which site the particle is, as the expected rate \( h_k \) at which the clock goes off depends on the location \( k \) of the particle. We therefore assign the random clocks to the sites \( k \). That is, we model the jumps using sequences of jump times \( T_{k,j} \) with exponentially distributed and independent increments \( W_{k,j} := T_{k,j+1} - T_{k,j} \), such that \( W_{k,j} \) is independent of \( T_{k,j} \) and of all jump times associated with the other sites. Besides

\footnote{Actually, “jump attempt times” would be the more accurate name, but as it is also more clumsy we prefer the shorter “jump times”.
}
being more convenient for our subsequent analysis, this definition is also quite natural in view of the fact that the jump rates $\alpha$, $\beta$ and $h_k$ in the model are site-dependent and not particle-dependent.

Fortunately, it does not matter for the transition probabilities whether we attach the random clocks to the particles or to the sites. Attaching the jump times to the sites is still consistent with the requirement that the difference between any two consecutive jump times is exponentially distributed, even if the corresponding particle hops, i.e., when it changes its site. This is due to the memorylessness of the exponential distribution and the independence assumption: if a particle attempts to jump at time $T = T_{k,l}$ but cannot jump, then the next jump time is $T_{k,l+1}$, whose difference to $T = T_{k,j}$ is exponentially distributed, because by independence for each $t \geq 0$ we have

$$P(T_{k,j+1} - T \geq t \mid T_{k,l} = T) = P(W_{k,j} \geq t \mid T_{k,j} = T) = P(W_{k,j} \geq t).$$

If the jump at time $T = T_{k,j}$ is successful, then the next jump time for the particle is $T_{k+1,m+1}$, where $m$ is such that $T_{k+1,m} \leq T$ and $T_{k+1,m+1} > T$. In this case, we can exploit the memorylessness, which says that for all $t > s \geq 0$ the identity

$$P(W_{k+1,m} \geq t + s \mid W_{k+1,m} > s) = P(W_{k+1,m} \geq t)$$

holds. Together with the fact that $T_{k+1,m} \leq T$ and $T_{k+1,m+1} > T$ is equivalent to $T_{k+1,m} \leq T$ and $W_{k+1,m} > s$ for $s := T - T_{k+1,m} \geq 0$ and independence of $W_{k+1,m}$ and $T_{k+1,m}$ we obtain

$$P(T_{k+1,m+1} - T \geq t \mid T_{k+1,m} \leq T, T_{k+1,m+1} > T)$$

\[= P(W_{k+1,m} \geq t + s \mid T_{k+1,m} \leq T, T_{k+1,m+1} > T)\]

\[= P(W_{k+1,m} \geq t + s \mid T_{k+1,m} \leq T, W_{k+1,m} > s)\]

\[= P(W_{k+1,m} \geq t + s \mid W_{k+1,m} > s) = P(W_{k+1,m} \geq t)\]

Hence, at time $T$ the next jump time $T_{k+1,m+1}$ is again exponentially distributed.

In the sequel, we attach the jump time sequences to the sites.

\section*{Generation of the jump times}

We now give a precise stochastic definition of the random jump time sequences $(T_{k,j})_{j \in \mathbb{Z}}$. From the requirement that the increments $T_{k,j+1} - T_{k,j}$ are exponentially distributed and stochastically independent of $T_{k,j}$ it follows that the $(T_{k,j})_j$ can be modeled by a Poisson process. Usually it is of no interest on which underlying probability space this process is constructed and it is enough to know that it exists. However, for an RDS one is required by Definition [1] to provide a measure-preserving dynamical system $\{\theta_t\}_{t \in \mathbb{R}}$ acting on the probability space. The role of $\theta_t$ for $t \in \mathbb{R}$ is revealed by the cocycle property (2) in Definition [1]. Associated with $\omega \in \Omega$ and $k \in \{0, \ldots, n\}$ is the sequence of jump times $(T_{k,j}(\omega))_j$ corresponding to the site $k$. Then the sequence $(T_{k,j}(\omega) - t)_j$ should
also be a realization of the Poisson process. Therefore, there should exist an \( \omega' \in \Omega \) and a \( \Delta_j \in \mathbb{Z} \) with \( T_{k,j}(\omega) - t = T_{k,j-\Delta_j}(\omega') \) for all \( j \). This \( \omega' \) is then denoted by \( \theta_t(\omega) \). Note that this construction can only work if the Poisson process is defined on the whole real line and not just on \([0, \infty)\), which suffices to construct TASEP and is usually used there.

We now provide an explicit construction of a generalized Poisson process on the whole real line that allows us to define \( \theta_t \) in the sense just described. For this purpose it is convenient to think of the Poisson process as a point process. We follow the wonderful book of Kingman [12]. From [12, Sections 1.3 and 2.1] we extract the following definition.

**Definition 2.** Let \((\Omega, \mathcal{F}, \mathbb{P})\) be a probability space, \(|\cdot|\) the Lebesgue measure on \(\mathbb{R} \), \(\mathcal{B}(\mathbb{R})\) the set of Borel sets \(A \subset \mathbb{R}, \lambda > 0\), and let \(\mathbb{R}^\infty\) denote the set of all countable subsets of \(\mathbb{R}\). A homogeneous Poisson process on \(\mathbb{R}\) with rate \(\lambda\) is a map \(\Pi : \Omega \to \mathbb{R}^\infty\) satisfying conditions (i)-(iii).

(i) The maps \(N(A) : \Omega \to \mathbb{N} \cup \{\infty\}, \omega \mapsto |(\Pi(\omega) \cap A)|\) are measurable for all \(A \in \mathcal{B}(\mathbb{R})\), i.e. for all \(m \in \mathbb{N} \cup \{\infty\}\) and all \(A \in \mathcal{B}(\mathbb{R})\) we have that the set \(\{\omega \in \Omega \mid \Pi(\omega) \cap A\text{ contains exactly } m \text{ points}\}\) belongs to the sigma algebra \(\mathcal{F}\).

(ii) For any pairwise disjoint sets \(A_1, \ldots, A_p \in \mathcal{B}(\mathbb{R}), p \in \mathbb{N}\), the random variables \(N(A_1), \ldots, N(A_p)\) are independent.

(iii) \(N(A)\) is Pois\((\lambda|A|)\)-distributed for all \(A \in \mathcal{B}(\mathbb{R})\).

Note that for a homogeneous Poisson process \(\Pi\) on \(\mathbb{R}\) with positive rate the set \(\Pi(\omega) \in \mathbb{R}^\infty\) has almost surely no accumulation points in \(\mathbb{R}\), because all \(\omega\) for which \(\Pi(\omega)\) has a finite accumulation point are contained in \(\bigcup_{L \in \mathbb{N}} \{\omega \mid N([-L, L]) = \infty\}\) which is a countable union of sets of zero measure due to condition (iii). In Section 2.5 of [12] an explicit construction for a rather general class of Poisson processes is presented. For our purposes it is more convenient to proceed in a different way that is described in Section 4.1 of [12]: Since \(\Pi_+ := \Pi \cap \mathbb{R}_0^+\) and \(\Pi_- := \Pi \cap \mathbb{R}^-\) are independent homogeneous Poisson processes with rate \(\lambda\) (cf. Restriction Theorem [12, Section 2.2] and condition (ii)) and \(x \mapsto -x\) maps \(\Pi_-\) to a homogeneous Poisson process on \(\mathbb{R}^+\) with rate \(\lambda\) (cf. Mapping Theorem [12, Section 2.3]) the Interval Theorem [12, Section 4.1]) allows us to construct \(\Pi\) using partial sums of two independent iid sequences of exponentially distributed random variables. The observation made above about the almost sure absence of accumulation points allows us to consider divergent series only. We summarize these considerations in a precise way:

**Definition 3.** Let \(\lambda\) be positive and denote by \(\mathcal{W}_0^\lambda := (\Omega_0, \sigma_0, \nu_0^\lambda)\) the probability space on \(\Omega_0 := [0, \infty)\) equipped with the corresponding Borel sigma algebra \(\sigma_0\) and the measure \(\nu_0^\lambda(dx) := \lambda e^{-\lambda x} dx\). For \(i \in \mathbb{Z} \setminus \{0\}\) we denote by \(\mathcal{W}_i^\lambda\) identical probability spaces that are obtained from \(\mathcal{W}_0^\lambda\) by restricting \(\Omega_0\) to the open interval \((0, \infty)\). We set \(\mathcal{W}^\lambda = (\hat{\Omega}, \hat{\mathcal{F}}, \hat{\mathbb{P}}^\lambda)\)
to be the countable product of these spaces
\[ \mathcal{W}^\lambda := \bigotimes_{i=1}^{\infty} \mathcal{W}_{\omega_i}^\lambda \times \mathcal{W}_0^\lambda \times \bigotimes_{i=1}^{\infty} \mathcal{W}_i^\lambda. \]

Any \( \omega \in \hat{\Omega} \) is therefore given by a sequence \((\xi_i)_{i \in \mathbb{Z}}\) with \(\xi_0 \geq 0\) and \(\xi_i > 0\) for all \(i \in \mathbb{Z} \setminus \{0\}\). Then the map \(\Pi: \hat{\Omega} \to \mathbb{R}^\infty\) given by

\[ \Pi(\omega) = \Pi((\xi_i)_i) := \{Y_i \mid i \in \mathbb{Z}\} \quad \text{with} \quad Y_i := \Phi(\omega)_i := \begin{cases} \sum_{j=0}^{l} \xi_j & \text{for } l \geq 0 \\ -\sum_{i=0}^{l} \xi_i & \text{for } l < 0 \end{cases} \]
defines a homogeneous Poisson process on \(\mathbb{R}\) with rate \(\lambda\). Finally, we modify the probability space \(\mathcal{W}^\lambda\) and all related quantities by restricting \(\hat{\Omega}\) to those \(\omega \equiv (\xi_i)_i\) for which \(\sum_{i=0}^{\infty} \xi_i = \infty\) and \(\sum_{i=0}^{\infty} \xi_i = \infty\). As argued above this removes a set of measure 0. Thus the modified version also defines a homogeneous Poisson process on \(\mathbb{R}\) with rate \(\lambda\) and we transfer our notation \(\mathcal{W}^\lambda, \hat{\Omega}, \hat{F}, \mathbb{P}^\lambda, \Pi\) to the modified version.

There is a somewhat confusing aspect about this construction. The distance between neighboring points \(Y_i - Y_{i-1}\) is exponentially distributed except for \(i = 0\), because \(Y_0 - Y_{-1} = \xi_{-1} + \xi_0\) is the sum of two independent exponentially distributed random variables and is therefore not distributed exponentially. However, this does not contradict the fact that for any time \(t \in \mathbb{R}\) the time until the next jump attempt is exponentially distributed. The reason for this is the waiting time paradox and we refer the reader to the end of Section 4.1 in [12] for an explanation.

We now study the question raised at the beginning of this subsection, i.e. to identify the map \(\tilde{\theta}_t\) that is induced on \(\hat{\Omega}\) by shifting the origin of the real axis to \(t\). First we notice that the map \(\Phi: \omega \mapsto (Y_i)_{i \in \mathbb{Z}}\) that is implicit in Definition 3 is a bijection between \(\hat{\Omega}\) and the set of all strictly increasing sequences \((a_i)_{i \in \mathbb{Z}}\) with \(a_{-1} < 0 \leq a_0\) and \(\lim_{t \to \pm \infty} a_t = \pm \infty\). Note that the last property follows from the modification performed at the end of Definition 3. Now fix \(t \in \mathbb{R}\). The translated sequence \((Z_i)_{i \in \mathbb{Z}}\) defined by \(Z_i := Y_i - t\) is again a strictly monotone sequence that is unbounded from above and below and we can therefore find some \(l_0 \in \mathbb{Z}\) with \(Z_{l_0} < 0 \leq Z_{l_0}\). Consequently, the shifted sequence \((b_i)_{i \in \mathbb{Z}}\) with \(b_l := Z_{l+t_0}\) lies in the range of the map \(\Phi\). Defining \(\tilde{\theta}_t(\omega) := \Phi^{-1}((b_i))\) we have that the set \(\Pi(\omega)\) shifted by \(-t\) equals \(\Pi(\tilde{\theta}_t(\omega))\) as desired. Moreover, the just defined family \(\{\tilde{\theta}_t\}_{t \in \mathbb{R}}\) satisfies properties (i)-(iii) of Definition 1 by construction. In order to see that all \(\tilde{\theta}_t\) preserve the measure \(\mathbb{P}^\lambda\) one may proceed as follows: By the Mapping Theorem [12, Section 2.3] the shifted map \(\Pi' := \Pi - \{t\}\) is again a homogeneous Poisson process with rate \(\lambda\). As argued in the paragraph above Definition 3 the corresponding random variables \((\xi_i')_{i \in \mathbb{Z}}\) are again iid and exponentially \(\lambda\)-distributed by the Restriction Theorem and by the Interval Theorem. Hence the distribution of \((\xi_i')_{i \in \mathbb{Z}}\) is again governed by \(\mathbb{P}^\lambda\).

After all these preparatory discussions we are finally ready to define our RDS.
Definition of the TASEP random dynamical system

We begin with the probability space \((\Omega, \mathcal{F}, \mathbb{P})\). It is essentially given by the \((n+1)\)-fold product (cf. Definition \([3]\))

\[
\mathcal{W}^n \times \bigotimes_{k=1}^{n-1} \mathcal{W}^{h_k} \times \mathcal{W}^{\beta}.
\]

Any \(\omega\) then corresponds to \(n+1\) stochastically independent point processes that we may represent by strictly increasing sequences \((T_{k,j}(\omega))_{j \in \mathbb{Z}}\) that are unbounded above and below. Here \(k = 0, \ldots, n\) denotes the lattice site of the random clock where \(k = 0\) represents the clock for particles entering the first site. Since the exponential distribution is absolutely continuous it is not hard to see that the event that there exist \(k \neq k', j, j'\) with \(T_{k,j}(\omega) = T_{k',j'}(\omega)\) has zero probability and we remove this event from our probability space. This completes the definition of \((\Omega, \mathcal{F}, \mathbb{P})\).

By construction all jump times \(T_{k,j}(\omega)\) are pairwise distinct for all \(\omega \in \Omega\). Therefore there exist unique sequences \(k_i = k_i(\omega)\) and \(j_i = j_i(\omega), i \in \mathbb{Z}\), with

\[
T_{k_i,j_i}(\omega) < T_{k_{i+1},j_{i+1}}(\omega), i \in \mathbb{Z}, \quad \text{and} \quad T_{k_{-1},j_{-1}} < 0 \leq T_{k_0,j_0}.
\]

We call the random sequence \((k_i)_{i}\) the jump order sequence with corresponding jump time sequence \(t_i := T_{k_i,j_i}\).

The dynamics \(\theta_t\) is defined by \(\theta_t(\omega) = (\hat{\theta}_t(\omega_0), \ldots, \hat{\theta}_t(\omega_n))\). We noticed above that \(\{\hat{\theta}_t\}_t\) satisfies properties (i)-(iii) of Definition \([1]\) and argued that \(\hat{\theta}_t\) leaves the probability measure invariant. All this carries over to \(\theta_t\) acting on the product space restricted to the event of pairwise distinct jump times. Moreover, it is clear from the construction that for every \(\omega \in \Omega\) and \(t \in \mathbb{R}\) there exists \(\Delta i(\omega, t) \in \mathbb{Z}\) such that the jump time and jump order sequences satisfy

\[
t_{i-\Delta i(\omega, t)}(\hat{\theta}_t(\omega)) = t_i(\omega) - t, \quad \hat{k}_{i-\Delta i(\omega, t)}(\hat{\theta}_t(\omega)) = k_i(\omega) \quad \text{for all} \ i \in \mathbb{Z}.
\]

Finally, we can define the cocycle mapping \(\varphi\) using \(\hat{\varphi}\) of \((III.1)\) and the just defined sequences of jump order \((k_i)\), and jump times \((t_i)\):

\[
\varphi(t, x, \omega) := \hat{\varphi}(t, x, (t_i(\omega), (k_i(\omega)))).
\]

Let us check the requirements of Definition \([1]\). There is nothing to show for condition (4), because the state space is discrete. Condition (3) follows from the construction and (1) holds because \(\hat{\varphi}\) leaves \(x\) unchanged for \(t = 0\) (there is no jump time \(t_i(\omega)\) in \([0, 0) = \emptyset\)). The cocycle property (2) is an immediate consequence of \((III.2)\).

Non-Uniqueness of the TASEP random dynamical system

The construction of the random dynamical system for TASEP we just presented appears to be the most reasonable one from the point of view of physical intuition. This is why
we use it in the remainder of this paper. However, we would like to point out that the RDS is not uniquely determined by the transition probabilities as we illustrate now. For instance, in TASEP with chain length \( n = 3 \), when the clock for site 1 rings at time \( t \) (i.e., when \( T_{1,j}(\omega) = t \) for some \( j \in \mathbb{Z} \)), then this will trigger the transitions

\[
100 \rightarrow 010 \quad \text{and} \quad 101 \rightarrow 011
\]

while the clock at site 2 will trigger the transitions

\[
010 \rightarrow 001 \quad \text{and} \quad 110 \rightarrow 101
\]

(for all other states, nothing will happen). Now, if the rates \( h_1 \) and \( h_2 \) are equal, then one may also define a random dynamical systems in which the ringing of clock number 1 triggers the transitions

\[
100 \rightarrow 010 \quad \text{and} \quad 110 \rightarrow 101
\]

while clock number 2 triggers the transitions

\[
010 \rightarrow 001 \quad \text{and} \quad 101 \rightarrow 011.
\]

Since the rates of the two clocks are the same, this will yield a model with exactly the same state transition statistics as the one constructed above, but the resulting random dynamical systems differ: for the redefined dynamical system there is a positive probability that both \( \varphi(1, 100, \omega) = 010 \) and \( \varphi(1, 110, \omega) = 101 \) hold true, while for the system defined in the previous section such an \( \omega \) does not exist. The latter statement can be verified by checking that there are no two states \( x_1, x_2 \) such that \( x_1 \) goes to or remains at 010 and simultaneously \( x_2 \) goes to or remains at 101 by the ringing of any of the four clocks.

**IV. Finite and infinite time attraction of solutions**

In this section we give an important auxiliary result, which shows that solutions with different initial conditions coincide with arbitrarily large probability after sufficiently long time. The derivation relies on the jump order sequences \((k_i)\), that were introduced in the previous subsection.

Given a bounded interval \( I = [\tau_1, \tau_2] \) of positive length then for all \( \omega \in \Omega \) there exist only finitely many \( i \in \mathbb{Z} \) with \( t_i(\omega) \in I \), because the jump times do not accumulate on the real line by construction. Therefore only finite jump order sequences can be be realized in \( I \). In turn, we now argue that for any prescribed finite tuple of sites \((k_1, \ldots, k_m)\) of any given length \( m \), there is a positive probability that this tuple equals the section of the jump order sequence which corresponds to the jump times in the interval \( I = [\tau_1, \tau_2] \). Indeed, devide \( I \) into \( m \) subintervals \( I_i = (q_{i-1}, q_i) \subset I \), \( \tau_1 = q_0 < q_1 < \ldots < q_m = \tau_2 \) and denote by \( \Pi_k \) the point process that is associated with the probability space \( \mathcal{W}^\mathbb{N} \) that is used in
the construction of $\Omega$ above with $h_0 := \alpha$ and $h_n := \beta$. Since the point processes $\Pi_k$ are independent one can compute from Definition 2 the probability that for each $i = 1, \ldots, m$ we have $N_k(I_i) = N_k(\bar{I}_i) = 1$ and that $N_k(\bar{I}_i) = 0$ for all $k \in \{0, \ldots, n\} \setminus \{k_i\}$ where the random variables $N_k(A) := \#(\Pi_k \cap A)$ are defined according to Definition 2. This probability is a finite product of positive numbers and therefore positive as we have claimed. Due to homogeneity of the Poisson processes, the probability for a particular jump order sequence to occur depends only on the length $\tau_2 - \tau_1$ of the interval $I$ and not on the concrete values of $\tau_1$ and $\tau_2$. Moreover, on two non-overlapping intervals $[\tau_1, \tau_2)$ and $[\tau_3, \tau_4)$, where $\tau_1 < \tau_2 < \tau_3 < \tau_4$, the jump order sequences are stochastically independent; this follows from the fact that $\Pi_k \cap [\tau_1, \tau_2)$ and $\Pi_k' \cap [\tau_3, \tau_4)$ are independent both for $k = k'$ due to condition (ii) of Definition 2 and for $k \neq k'$ which by construction even holds for the unrestricted point processes $\Pi_k$ and $\Pi_k'$.

Based on these observations, we can state the following result for the set

$$\Gamma(t, t_0) := \{\omega \in \Omega | \varphi(t, x, \theta_{t_0} \omega) = \varphi(t, x_2, \theta_{t_0} \omega) \text{ for all } x_1, x_2 \in X\}.$$ 

**Lemma 4.** For any $t > 0$ there exists a $\delta > 0$ such that for all $t_0 \in \mathbb{R}$

$$\mathbb{P}(\Gamma(t, t_0)) = \mathbb{P}(\Gamma(t, 0)) \geq \delta.$$

**Proof.** The independence of $t_0$ follows from the fact that the probability measure is invariant under the action of $\theta_{t_0}$. According to our previous considerations, the probability that on the interval $[0, t]$ the jump order sequence

$$n, \ n-1, n, \ n-2, n-1, n, \ n-3, \ldots, n, \ldots \ 1, 2, \ldots, n$$

occurs is equal to some $\delta > 0$. Now, for all $\omega \in \Omega$ generating this sequence it is easily seen that $\varphi(t, x, \omega) = (0, \ldots, 0)$ for all $x \in X$. This shows the claim. \qed

**Remark 5.** We note that for the subsequent considerations it would be enough that Lemma 4 holds for any $t \geq t^*$, where $t^* > 0$ is some fixed time.

**Remark 6.** The probability bound $\delta > 0$ that follows from the proof of Lemma 4 is clearly not optimal and we will see in our numerical simulations in Section VII that it significantly underestimates the true probability $\mathbb{P}(\Gamma(t, t_0))$. More tight estimates would have to identify the set of all jump order sequences that yield identity. For this task, we conjecture that the observation that the distance between $\varphi(t, x_1, \theta_{t_0} \omega)$ and $\varphi(t, x_2, \theta_{t_0} \omega)$ is monotone decreasing in $t$ might be helpful. Since in this paper we are interested in the long time behaviour, the precise value of $\delta$ is not important. We therefore leave this question to future research.

We now use the bound from Lemma 4 in order to estimate the long time behaviour
of the probability $P(\Gamma(t, t_0))$.

**Proposition 7.** For any $t_0 \in \mathbb{R}$ it holds that
\[
\lim_{t \to \infty} P(\Gamma(t, t_0)) = \lim_{t \to \infty} P(\Gamma(t, t_0 - t)) = 1
\]
and the rate of convergence is independent of $t_0$.

**Proof.** By Lemma 4 it suffices to prove $\lim_{t \to \infty} P(\Gamma(t, t_0)) = 1$. Note first that for each $\omega \in \Omega$ the identity $\varphi(t, x_1, \omega) = \varphi(t, x_2, \omega)$ ensures $\varphi(s, x_1, \omega) = \varphi(s, x_2, \omega)$ for all $s > t$. This property implies
\[
\Gamma(t_3, t_1) \supset \Gamma(t_3, t_2) \cup \Gamma(t_2, t_1)
\]
and thus for the complements $A^C := \Omega \setminus A$:
\[
\Gamma(t_3, t_1)^C \subset \Gamma(t_3, t_2)^C \cap \Gamma(t_2, t_1)^C \quad \text{(IV.1)}
\]
for all $t_1 < t_2 < t_3$. Moreover, the monotonicity of $\Gamma$ implies that $t \mapsto P(\Gamma(t, 0))$ is increasing. Hence, it suffices to prove the assertion for a suitable sequence $t_m \to \infty$.

Fix an arbitrary $\Delta t > 0$ and let $t_m = m \Delta t$. From Lemma 4 it follows that
\[
P(\Gamma(\Delta t, t_m)) \geq \delta > 0,
\]
implying
\[
P(\Gamma(\Delta t, t_m)^C) \leq 1 - \delta < 1.
\]
Clearly, $\delta$ only depends on $\Delta t$ and not on $m$. Since $\Gamma(\Delta t, t_m)$ and thus $\Gamma(\Delta t, t_m)^C$ are entirely determined by the Poisson processes on the non-overlapping intervals $[t_m, t_{m+1})$, they are stochastically independent for different $m$. Thus, using (IV.1) we obtain
\[
P(\Gamma(t_m, 0)^C) \leq \prod_{l=1}^{m} P(\Gamma(\Delta t, t_{l-1})^C) \leq (1 - \delta)^m \to 0
\]
as $m \to \infty$. This shows the claim. \hfill $\square$

As a consequence, we can make a statement about the probability that two solutions with different initial values coincide after sufficiently large time. For its formulation we use
\[
\varphi(t, X, \theta_{t_0} \omega) := \bigcup_{x_0 \in X} \{\varphi(t, x_0, \theta_{t_0} \omega)\}.
\]

**Corollary 8.** All solutions with identical $\omega$ and identical initial time $t_0 \in \mathbb{R}$, i.e., driven by the same jump times, coincide almost surely after sufficiently large time. Formally: for any $t_0 \in \mathbb{R}$ we have
\[
P(\{\omega \in \Omega | \varphi(t, X, \theta_{t_0} \omega) \text{ is a singleton for some } t \geq 0\}) = 1.
\]
The same statement holds for \( t_0 = -t \), i.e.,
\[
P(\{ \omega \in \Omega \mid \varphi(t, X, \theta_{-t}\omega) \text{ is a singleton for some } t \geq 0 \}) = 1.
\]

**Proof.** In order to prove the first statement, assume contrary to the assertion that there are \( \varepsilon > 0 \) and \( t_0 \in \mathbb{R} \) with
\[
P(\{ \omega \in \Omega \mid \varphi(t, X, \theta_{-t_0}\omega) \text{ is a singleton for some } t \geq 0 \}) \leq 1 - \varepsilon.
\]
Since \( \varphi(t, X, \theta_{t_0}\omega) \) is a singleton if and only if \( \varphi(t, x_1, \theta_{t_0}\omega) = \varphi(t, x_2, \theta_{t_0}\omega) \) for all \( x_1, x_2 \in X \), this implies
\[
P(\{ \omega \in \Omega \mid \varphi(t, x_1, \theta_{t_0}\omega) = \varphi(t, x_2, \theta_{t_0}\omega) \text{ for all } x_1, x_2 \in X \}) \leq 1 - \varepsilon
\]
for all \( t \geq 0 \), which contradicts the statement of Proposition 7.

Likewise, violation of the second statement contradicts the statement of Proposition 7 with \( t_0 = 0 \).

**Remark 9.** The almost sure identity does not exclude the existence of non-trivial jump time sequences for which \( \varphi(t, x_1, \theta_{t_0}\omega) \) and \( \varphi(t, x_2, \theta_{t_0}\omega) \) never coincide. Consider TASEP with, e.g., chain length \( n = 3 \) and initial conditions \( x_1 = 110 \) and \( x_2 = 000 \). Any jump time sequence that on \([t_0, \infty)\) generates the periodic jump order sequence \( (k_i(\omega)) = (2, 1, 0, 1, 2, 3; 2, 1, 0, 1, 2, 3; 2, 1, 0, 1, 2, 3; \ldots) \) yields the two solutions

\[
\begin{array}{ccc}
    t & \varphi(t, x_1, \theta_{t_0}\omega) & \varphi(t, x_2, \theta_{t_0}\omega) \\
    t_0 & 110 & 000 \\
    t_1(\omega) & 101 & 000 \\
    t_2(\omega) & 011 & 000 \\
    t_3(\omega) & 111 & 100 \\
    t_4(\omega) & 111 & 010 \\
    t_5(\omega) & 111 & 001 \\
    t_6(\omega) & 110 & 000 \\
\end{array}
\]

that are periodically continued (the table shows the values of the solutions right after the jump times \( t_i(\omega) \), \( i \geq 1 \), which are numbered such that \( t_1(\omega) \) is the first jump time after the initial time \( t_0 \)). Hence, the two solutions never coincide. However, Corollary 8 implies that the set of \( \omega \) corresponding to such jump time sequences must have measure 0.

**V. Random attractors**

In this section we show that TASEP exhibits a global random attractor \( A \) such that almost surely each fiber \( A(\omega) \) consists of a single point, i.e., almost surely \( A(\theta_t\omega), t \in \mathbb{R} \),
is a single trajectory. In other words, the long time behaviour of TASEP is a.s. uniquely
determined by the jump time sequence and does not depend on the initial condition.

We use the following definitions of random attractors in the pullback and in the
forward sense. We refer to [6] for a study of the difference between pullback and forward
attraction. Here we limit ourselves to the definition of global random attractors.

**Definition 10.** A random set $C$ on a probability space $(\Omega, \mathcal{F}, \mathbb{P})$ is a measurable subset
of $X \times \Omega$ with respect to the product $\sigma$-algebra of the Borel $\sigma$-algebra of $X$ and $\mathcal{F}$. The
$\omega$-section of a random set $C$ is for each $\omega \in \Omega$ defined by

$$C(\omega) = \{ x \in X \mid (x, \omega) \in C \}.$$  

The random set is called compact if every $C(\omega)$ is compact.

**Definition 11.** Let $(\theta, \varphi)$ be an RDS on a Polish space $X$. A compact random set
$A \subset X \times \Omega$ that is strictly $\varphi$-invariant, i.e.,

$$\varphi(t, A(\omega), \omega) = A(\theta^t \omega) \text{ for every } t \in \mathbb{R}^+ \text{ a.s.},$$

is called a global random pullback attractor, if

$$\lim_{t \to \infty} \text{dist} \left( \varphi(t, X, \theta^{-t} \omega), A(\omega) \right) = 0 \text{ a.s.}.$$  

It is called a random forward attractor if

$$\lim_{t \to \infty} \text{dist} \left( \varphi(t, X, \omega), A(\theta^t \omega) \right) = 0 \text{ a.s.}.$$  

Here $\text{dist}(A, B) = \sup_{a \in A} \inf_{b \in B} d(a, b)$.

In our case the finite state space $X$ is equipped with the discrete topology and we
may therefore use the distance defined by $d(x_1, x_2) = 1$ if $x_1 \neq x_2$ and $d(x_1, x_2) = 0$ if
$x_1 = x_2$. This implies for subsets $A, B \subset X$ that $d(A, B) = 0$ if $A \subset B$ and $d(A, B) = 1$,
otherwise. For the construction of the attractor, we use that for each $s > 0$ the cocycle
property implies

$$\varphi(t + s, X, \theta^{-s} \omega) = \varphi(t, \varphi(s, X, \theta^{-s} \omega), \theta^{-t} \omega) \subseteq \varphi(t, X, \theta^{-t} \omega)$$

implying that the set $\varphi(t, X, \theta^{-t} \omega)$ is decreasing in $t$ w.r.t. set inclusion. Hence, we can
define its set valued limit via

$$A(\omega) := \bigcap_{t \geq 0} \varphi(t, X, \theta^{-t} \omega).$$  

**Theorem 12.** The random set $A$ from (V.1) is a random pullback attractor and a random
forward attractor. Moreover, almost surely the set $A(\omega)$ is a singleton.

**Proof.** The fact that a.s. the set $A(\omega)$ is a singleton follows from the definition of $A(\omega)$
together with the second statement of Corollary 8. It remains to show that $A$ is a random attractor in both senses. To this end, we use that $\varphi(t, X, \theta_{-t}\omega)$ is a finite set and decreasing in $t$ w.r.t. set inclusion. This implies

for each $\omega \in \Omega$ there is $T > 0$ with $\varphi(t, X, \theta_{-t}\omega) = \varphi(T, X, \theta_{-T}\omega)$ for all $t \geq T$, \quad (V.2)

hence $\varphi(T, X, \theta_{-T}\omega) \subseteq \varphi(t, X, \theta_{-t}\omega)$ for all $t \geq T$, and thus

$$
\varphi\left(s, \bigcap_{t \geq 0} \varphi(t, X, \theta_{-t}\omega), \omega\right) = \bigcap_{t \geq 0} \varphi(s, \varphi(t, X, \theta_{-t}\omega), \omega).
$$

Using the cocycle property we then have that

$$
\varphi(s, A(\omega), \omega) = \varphi\left(s, \bigcap_{t \geq 0} \varphi(t, X, \theta_{-t}\omega), \omega\right) = \bigcap_{t \geq 0} \varphi(s, \varphi(t, X, \theta_{-t}\omega), \omega) = \bigcap_{t \geq 0} \varphi(t + s, X, \theta_{-t-s}\theta_{s}\omega) = A(\theta_s\omega)
$$

and thus $\varphi$-invariance of $A$.

In order to prove pullback attraction, observe that (V.2) implies $A(\omega) = \varphi(t, X, \theta_{-t}\omega)$ for all $t \geq T$, and thus pullback attraction.

For proving forward attraction, consider those $\omega$ for which $A(\omega) = \{x(\omega)\}$ is a singleton (which is a set of measure 1). By invariance of $A$ we obtain $x(\theta_t\omega) = \varphi(t, x(\omega), \omega)$ for all $t \geq 0$. Now the first statement of Corollary 8 implies that almost surely there exists $t_\omega > 0$ such that

$$
\varphi(t, x, \omega) = \varphi(t, x(\omega), \omega) = x(\theta_t\omega)
$$

for all $x \in X$ and all $t \geq t_\omega$. This implies

$$
\varphi(t, X, \omega) = A(\theta_t\omega)
$$

for all $t \geq t_\omega$ and thus yields forward convergence

$$
\lim_{t \to \infty} \text{dist}\left(\varphi(t, X, \omega), A(\theta_t\omega)\right) = 0.
$$

Since the set of $\omega$ for which this property holds has measure 1, we obtain the desired almost sure forward convergence.

\textbf{Remark 13.} (i) We note that the finite state space of TASEP simplifies some of the arguments in this paper, but it is not the decisive property for the existence of a random attractor that consists of single trajectories a.s. In fact, it is easy to write down RDS with a finite state space $X$ that do not have this property, cf. part (ii) of this remark.

(ii) Likewise, one may conjecture that the irreducibility of TASEP, i.e., the fact that
every state is reachable from every other state with positive probability, is the decisive property, but this is also not true: Consider for example a variant of TASEP in which particles do not hop but where the states $s_k$ simply change from 0 to 1 and vice versa at each jump time $T_{k,j}$. It is easily seen that this system is irreducible, too, but that two solutions starting from different initial conditions will never coincide, regardless of the jump times, because the Hamming distance between any two solutions is constant. Conversely, a finite state continuous time Markov process in which there is a single absorbing state $x^*$ will have a random attractor with $A(\omega) = \{x^*\}$ a.s. despite the fact that it need not be irreducible, at all. Hence, irreducibility is neither necessary nor sufficient for the existence of a random attractor consisting of trajectories a.s.

VI. Numerical simulations

We demonstrate the random attraction using numerical simulations. To this end, we have simulated three random jump time sequences. Each of it was used to simulate two TASEP trajectories with different initial conditions. The resulting trajectories are shown in Figure 1, where each column corresponds to one of the jump time sequences and the states of the two trajectories with different initial conditions are shown on top of each other for times $t = 0, 10, \ldots, 100$. The parameters were chosen as $n = 20$ sites and $\alpha = \beta = h_k = 1$ for all rates.

One clearly sees random attraction to a single trajectory at $t = 40$ in the left column, at $t = 100$ in the middle and at $t = 50$ in the right column. These numbers are quite small when compared to the expected number of jumps that are needed to see the particular jump sequence (of length 210) for the first time that was used to prove Lemma 4. This number is an integer with 278 digits.

We have also conducted some Monte-Carlo simulations to investigate the dependence of the synchronization time on the length of the chain. Using the initial conditions displayed in Figure 1 i.e. the first trajectory starts with all sites empty, except for the first one, and the second trajectory starts with all sites occupied, we performed 5000 runs for each chain where the number of sites was varied from $N = 10$ to $N = 200$ at steps of 10. We found that the average number of jump attempts needed for synchronization is well described by $CN^\gamma$ with constant $C \approx 0.73$ and exponent $\gamma \approx 2.56$. For $N = 20$ this formula gives approximately 1560 jump attempts which is very close to the actual average of about 1550 attempts. Since there are 21 clocks ringing, each at rate 1, this translates to an average synchronization time of approximately 74 units. Preliminary further investigations for different pairs of initial conditions indicate that such a power law always holds but that the constant $C$ and the exponent $\gamma$ both depend on the pair of initial conditions.
VII. Extensions

The reasoning used in this paper can be extended or adapted to various other models. One example where this is possible is the asymmetric simple exclusion process (ASEP). ASEP follows the same rules as TASEP except that the particles can hop in both directions, see, e.g., [30]. One can model ASEP as an RDS either via two Poisson processes for each site, one for jump attempts to the left and one to the right, or via an additional sequence of random variables $d_i(\omega) \in \{-1, 1\}$, where $-1$ denotes a hop to the left and $1$ to the right. In both cases, we need to add a Poisson process for modelling particles that enter the chain from the right.

Fig. 1. Six trajectories of TASEP with three different random jump time sequences (left to right) and two different initial conditions (depicted on top of each other for each $t$)
The decisive consequence this extension of the model has on our formalism is that the jump order sequences \((k_i)_{i \in \mathbb{Z}}\) now take values in \((-n - 1, \ldots, -1, 0, 1, \ldots, n)\). Here, \(k = 1, \ldots, n\) represents particles hopping from site \(k\) to the right, \(k = -1, \ldots, -n\) represents particles hopping from site \(-k\) to the left and \(k = 0\) and \(k = -n - 1\) represent particles entering from the left or from the right, respectively, into the chain. As before, on a finite interval each finite jump order sequence occurs with positive probability that only depends on the length of the interval. Hence, Lemma \([4]\) remains valid (although the probability \(\delta\) for the sequence constructed in the proof becomes smaller). Since all subsequent results in this paper build solely upon Lemma \([4]\) they thus remain valid if TASEP is replaced by ASEP.

Another modification would be to consider TASEP with time-periodic and, say, continuous transition rates. Then the construction of the RDS needs to be modified as the Poisson processes are not homogeneous any more and have no representation as partial sums of exponentially distributed variables. For such a construction the method described in \([12, \text{Section 2.5}]\) appears to be useful. The proof of the central Lemma \([4]\) however, can be adapted easily as it only requires that there is a positive lower bound on each transition rate. Even in the case that transition rates are temporarily zero (but not identically equal to zero) one may prove Lemma \([4]\) in the periodic case for times \(t\) large enough (cf. Remark \([5]\) as one might need to wait for several periods to realize the jump sequence prescribed in the proof of Lemma \([4]\)
VIII. CONCLUSION

In this paper we have shown that random attraction to a single trajectory occurs almost surely in the TASEP model with finite chain length. This implies the existence of a random attractor that almost surely consists of single trajectories.

For the many dynamical systems and processes that were modeled using TASEP, ranging from mRNA translation to vehicular traffic, this implies that in the long run these systems are insensitive to the initial conditions. Alternatively, this may be interpreted as saying that a perturbation of the state of the system is filtered out.

In order to rigorously prove our main result we first reformulated TASEP as a random dynamical system (RDS), which is a contribution of independent interest. Our construction of an RDS relies on the definition of jump times generated via generalized Poisson processes that are attached to the sites of the chain. This modelling is consistent with the fact that the exponential transition rates in TASEP are usually chosen site dependent. We have, moreover, shown, that neither the finiteness of the state space nor the irreducibility of TASEP are the decisive factors for the proven attraction. Rather, it is the fact that there exists a sequence of clock ticks, with non zero probability, that transfers the system to the same final state from any initial state.

Acknowledgment: We thank Melanie Birke and Walter Olbricht for making us aware of the literature on generalized Poisson processes. We also thank Peter Kloeden for discussing the construction of the TASEP-RDS with us.

REFERENCES

[1] L. Arnold, Random Dynamical Systems. Springer-Verlag, Heidelberg, 1998.
[2] L. Arnold and H. Crauel, “Random dynamical systems,” in Lyapunov exponents. Proceedings of the Second Conference held in Oberwolfach, May 28–June 2, 1990, ser. Lecture Notes in Mathematics, L. Arnold, H. Crauel, and J.-P. Eckmann, Eds., vol. 1486. Berlin: Springer-Verlag, 1991, pp. 1–22.
[3] E. Bar-Shalom, A. Ovseevich, and M. Margaliot, “Ribosome flow model with different site sizes,” SIAM J. Applied Dynamical Systems, 2019, to appear. [Online]. Available: http://arxiv.org/abs/1903.05141
[4] P. H. Baxendale and D. W. Stroock, “Large deviations and stochastic flows of diffeomorphisms,” Probab. Theory Related Fields, vol. 80, no. 2, pp. 169–215, 1988.
[5] R. A. Blythe and M. R. Evans, “Nonequilibrium steady states of matrix-product form: a solver’s guide,” J. Phys. A: Math. Gen., vol. 40, no. 46, pp. R333–R441, 2007.
[6] D. N. Cheban, P. E. Kloeden, and B. Schmalfuß, “The relationship between pullback, forward and global attractors of nonautonomous dynamical systems,” Nonlinear Dyn. Syst. Theory, vol. 2, no. 2, pp. 125–144, 2002.
[7] D. Chowdhury, A. Schadschneider, and K. Nishinari, “Physics of transport and traffic phenomena in biology: from molecular motors and cells to organisms,” Physics of Life Reviews, vol. 2, no. 4, pp. 318–352, 2005.
[8] L. Ciandrini, M. C. Romano, and A. Parmeggiani, “Stepping and crowding of molecular motors: Statistical kinetics from an exclusion process perspective,” Biophysical J., vol. 107, pp. 1176–1184, 2014.
[9] H. Crauel and P. E. Kloeden, “Nonautonomous and random attractors,” Jahresber. Disch. Math.-Ver., vol. 117, no. 3, pp. 173–206, 2015.
[10] B. Derrida, M. R. Evans, V. Hakim, and V. Pasquier, “Exact solution of a 1D asymmetric exclusion model using a matrix formulation,” J. Phys. A, vol. 26, no. 7, pp. 1493–1517, 1993.
[11] K. Johansson, “Shape fluctuations and random matrices,” Comm. Math. Phys., vol. 209, no. 2, pp. 437–476, 2000.
[12] J. F. C. Kingman, *Poisson Processes*, ser. Oxford Studies in Probability. The Clarendon Press, Oxford University Press, New York, 1993, vol. 3.

[13] V. A. Kleptsyn and M. B. Nalskii, “Contraction of orbits in random dynamical systems on the circle,” *Functional Analysis and Its Applications*, vol. 38, pp. 267–282, 2004.

[14] T. Kriecherbauer and J. Krug, “A pedestrian’s view on interacting particle systems, KPZ universality and random matrices,” *J. Phys. A*, vol. 43, no. 40, p. 403001.

[15] J. Krug, “Boundary-induced phase transitions in driven diffusive systems,” *Phys. Rev. Lett.*, vol. 67, pp. 1882–1885, 1991.

[16] J. Krug, “Nonequilibrium stationary states as products of matrices,” *J. Phys. A: Math. Theor.*, vol. 49, p. 421002, 2016.

[17] C. T. MacDonald, J. H. Gibbs, and A. C. Pipkin, “Kinetics of biopolymerization on nucleic acid templates,” *Biopolymers*, vol. 6, pp. 1–25, 1968.

[18] M. Margaliot, E. D. Sontag, and T. Tuller, “Entrainment to periodic initiation and transition rates in a computational model for gene translation,” *PLoS ONE*, vol. 9, no. 5, p. e96039, 2014.

[19] M. Margaliot and T. Tuller, “Stability analysis of the ribosome flow model,” *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 9, pp. 1545–1552, 2012.

[20] M. Margaliot, L. Grüne, and T. Kriecherbauer, “Entrainment in the master equation,” *Royal Society Open Science*, vol. 5, no. 4, p. 172157, 2018. [Online]. Available: https://royalsocietypublishing.org/doi/abs/10.1098/rsos.172157

[21] I. Nanikashvili, Y. Zarai, A. Ovseevich, T. Tuller, and M. Margaliot, “Networks of ribosome flow models for modeling and analyzing intracellular traffic,” *Sci. Rep.*, vol. 9, no. 1, 2019.

[22] J. Newman, “Necessary and sufficient conditions for stable synchronization in random dynamical systems,” *Ergodic Theory and Dynamical Systems*, vol. 38, no. 5, pp. 1857–1875, 2018.

[23] Q.-C. Pham, N. Tabareau, and J.-J. Slotine, “A contraction theory approach to stochastic incremental stability,” *IEEE Trans. Automat. Control*, vol. 54, pp. 816–820, 2009.

[24] G. Poker, Y. Zarai, M. Margaliot, and T. Tuller, “Maximizing protein translation rate in the non-homogeneous ribosome flow model: a convex optimization approach,” *J. Royal Society Interface*, vol. 11, no. 100, p. 20140713, 2014. [Online]. Available: https://royalsocietypublishing.org/doi/abs/10.1098/rsif.2014.0713

[25] J. Quastel and H. Spohn, “The one-dimensional KPZ equation and its universality class,” *J. Stat. Phys.*, vol. 160, no. 4, pp. 965–984, 2015.

[26] S. Reuveni, I. Meilijson, M. Kupiec, E. Ruppin, and T. Tuller, “Genome-scale analysis of translation elongation with a ribosome flow model,” *PLoS Computational Biology*, vol. 7, p. e1002127, 2011.

[27] J. L. Ross, “The impacts of molecular motor traffic jams,” *Proceedings of the National Academy of Sciences*, vol. 109, no. 16, pp. 5911–5912, 2012.

[28] A. Schadschneider, D. Chowdhury, and K. Nishinari, *Stochastic Transport in Complex Systems: From Molecules to Vehicles*. Elsevier, 2011.

[29] C. L. Simms, L. L. Yan, J. K. Qiu, and H. S. Zaher, “Ribosome collisions result in +1 frameshifting in the absence of no-go decay,” *Cell Reports*, vol. 28, no. 7, pp. 1679–1689.e4, 2019.

[30] C. A. Tracy and H. Widom, “Integral formulas for the asymmetric simple exclusion process,” *Comm. Math. Phys.*, vol. 279, no. 3, pp. 815–844, 2008.

[31] Y. Zarai, M. Margaliot, and T. Tuller, “Modeling and analyzing the flow of molecular machines in gene expression,” in *Systems Biology*, N. Rajewsky, S. Jurga, and J. Barciszewski, Eds. Springer, 2018, pp. 275–300.

[32] Y. Zarai, M. Margaliot, and T. Tuller, “Ribosome flow model with extended objects,” *J. Royal Society Interface*, vol. 14, no. 135, p. 20170128, 2017. [Online]. Available: https://royalsocietypublishing.org/doi/abs/10.1098/rsif.2017.0128

[33] R. Zia, J. Dong, and B. Schmittmann, “Modeling translation in protein synthesis with TASEP: A tutorial and recent developments,” *J. Statistical Physics*, vol. 144, pp. 405–428, 2011.