

# SPATIAL MODELS: STOCHASTIC AND DETERMINISTIC

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## Abstract

Theoretical studies of biological populations via analysis and/or simulation of deterministic and stochastic systems sometimes end up drawing conflicting conclusions. Papers purporting to investigate the same dynamics, albeit through different methods, often cannot agree on essential properties of the system being modeled. This problem often arises when trying to compare results that were obtained from different kinds of mathematical models, say those based on differential equations and individual-based stochastic models. While such models can successfully represent or characterize different views of the same phenomena, it is important to know when two different approaches are comparable, as well as any limitations that may be inherent in such a comparison. This survey paper is directed primarily to mathematical biologists whose primary mode of operation is partial differential equations. More generally, we seek to illuminate connections between the two main realms of spatial modeling. We begin by presenting a quick introduction to a class of stochastic spatial models, known as interacting particle systems, which are readily applicable to biological (and many other) systems. We then give examples of how various scaled limits of these models give rise to reaction-diffusion equations and integro-differential equations. The first case falls under the heading of hydrodynamic limits and the second case is an example of a mean-field limit theorem.

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## 1 Introduction

In mathematical biology, modeling typically begins in a nonspatial deterministic (mean field) setting, the models taking the form of ODE's or difference equations. The next level of complexity involves incorporating spatial structure either via deterministic continuum models (PDE's) or, closer still to the

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real dynamics, via continuous-time discrete-space stochastic models (interacting particle systems). These different approaches amount to viewing the dynamics on various length and time scales. In some cases an analysis of a model in one setting suggests something about the behavior of an analogous model in a more complicated setting. For example, the existence of threshold phenomena in epidemiological models, in the form of a basic reproductive ratio  $R_0$ , is most easily derived from the mean field ODE's. This suggests similar phenomena in analogous PDE and interacting particle system (IPS) models. It is also possible for different approaches to yield strikingly different behavior. Thus determining the correct level of detail for the model (spatial/nonspatial, discrete/continuum, deterministic/stochastic) constitutes one of the most important steps in the study of complex biological systems.

The comparison that seems to lead to the most confusion in the literature is the one between spatial models that are on the one hand discrete and stochastic (IPS), and on the other, continuous and deterministic (PDE). Our main goal in this paper is to make clear the connection between these two approaches via well-established mathematical ideas from the subject of hydrodynamic limits. When comparing behavior (simulations or analytical results) in the discrete and continuous settings, this approach gives the correct way to interpret the results. Having such connections between two classes of models can give some justification for comparing results derived in each case and can help one avoid some of the pitfalls that are all too often encountered when trying to draw conclusions by patching together different studies. For example, one might do simulations of a stochastic spatial model and want to see how the results compare to those of a related PDE model. Choosing the parameters and structure of the PDE so that the resulting equation arises as a hydrodynamic limit of an appropriately scaled version of the stochastic model means that these different models can be thought of as two views of the same phenomena. To simply compare the stochastic model to a reasonable-looking, but otherwise arbitrarily chosen, PDE is to invite confusion.

There is a growing literature on hydrodynamic limits, found mostly in mathematics and physics journals, as well as in a few texts. While interest in spatial models is at an all-time high in subjects like ecology and epidemiology, the material on hydrodynamic limits is quite technical and hence remains inaccessible to most biologists and to many mathematicians who are not specialists in the area. Nevertheless, these ideas can provide much insight and should be understood, at least at an intuitive level, by those interested in spatially explicit models. We endeavor to present an overview of the basic ideas in this subject in a way that will firstly provide an intuitive understanding to researchers who do not have the background or time to assimilate the technical literature, and secondly to serve as a starting point for those who decide to delve more deeply into the mathematics of this beautiful subject.

We begin with an introduction to the collection of stochastic spatial models known as *interacting particle systems*. These are continuous-time stochastic processes whose state at a given time is some configuration of "particles" on the  $d$ -dimensional integer lattice (or some other graph). One can usually think

of a site on the lattice as being either vacant or occupied by a particle of one or more possible types. In some cases, the particles do not move, but sites on the lattice change types according to the configuration at nearby sites. In other cases, there is some kind of particle movement.

Once we are familiar with a few basic particle systems, we show how certain reaction-diffusion equations can be obtained as *hydrodynamic limits* of these models. Roughly, this means that we construct a “type-changing” particle system on a lattice with small spacing and then add some fast (local) particle motion which serves to “stir” things up. In an appropriately scaled limit, in which the lattice spacing goes to zero and the speed of stirring goes to infinity, the densities of the different types of particles converge to continuous densities which are solutions of a reaction-diffusion equation. The reaction term arises from the type-changing mechanism, while the diffusion term comes from the particle motion. Thus we can think of the reaction-diffusion equation as giving a “macroscopic” description of the system and the particle system as giving a corresponding “microscopic” description.

Finally, we discuss another kind of particle system in which types can change due to long-range interaction. An appropriately scaled limit gives rise to a system of integro-differential equations.

## 2 Interacting Particle Systems

Interacting particle systems provide a natural framework for modeling stochastic phenomena that have a (discrete) spatial component. The key requirement is that a given sites change its state due to interactions that are determined by the types in some local neighborhood of the site. Such processes have found application in areas like biology and physics, where often it is relatively easy to describe such local interactions. Our goal in this section is to introduce the reader to some of the ideas and results of interacting particle systems via a few basic examples. For a more detailed account of this subject, the reader can consult [1], [2], and [3]. For an overview of such models in a biological setting and their relationships to other types of models, we recommend [4].

Let  $\mathbb{Z}^d$  denote the  $d$ -dimensional integer lattice. The set of types is usually given by some finite set  $F = \{0, 1, \dots, \kappa\}$ . A site in state 0 is often thought of as being vacant and a site in state  $i > 0$  can be thought of as being occupied by a particle of type  $i$ . When we are only interested in whether or not a site is “occupied,” the set of types will be  $F = \{0, 1\}$ , whereas when we want to distinguish between several types of particles, we will employ a larger collection of types. Of course, the interpretation of “particle” depends on the application. For example, in an epidemic model, one might use 1 to denote a susceptible individual, 2 for an infective, and 0 for dead or removed. In general, an interacting particle system will be a continuous-time Markov process whose state at time  $t$  is some configuration  $\xi_t \in F^{\mathbb{Z}^d}$ ; i.e., the state of site  $x \in \mathbb{Z}^d$  at time  $t$  is  $\xi_t(x) \in F$ .

To define the dynamics of an interacting particle system, we must specify

the rates at which any site changes its state. In general, this will depend on the current state of the site and the configuration in some neighborhood about that site. Interest typically focuses on two types of transitions. In the first, single sites change their types, one at a time, while the other sites remain (temporarily) as they were. We refer to this as *particle flip dynamics*, sometimes called Glauber dynamics in the physics literature. The second type of transition involves two (or more) particles exchanging sites, and includes as a special case a particle moving to a vacant site (for example, a 0 and a 1 exchange positions). This stirring of particles is referred to as *particle exchange dynamics*, or Kawasaki dynamics in the physics literature.

When describing a particle system with flip dynamics, we write  $c_{ij}(x, \xi)$  for the rate at which site  $x \in \mathbb{Z}^d$  flips to state  $j$  when it is in state  $i$  and the current configuration is given by  $\xi \in F^{\mathbb{Z}^d}$ . We assume that this flip rate only depends on  $\xi$  through the states in some finite neighborhood of sites  $\mathcal{N}(x)$  about  $x$ . Without much loss in generality, we will assume that the neighborhood has the form

$$\mathcal{N}(x) = \{y \in \mathbb{Z}^d : 0 < \|y - x\|_p \leq r\}. \quad (1)$$

Here,  $r \geq 1$  gives the range of interaction, while  $\|x\|_p = (x_1^p + \dots + x_d^p)^{1/p}$  when  $1 \leq p < \infty$ , and  $\|x\|_\infty = \max_i |x_i|$  give the usual  $\ell^p$  norms. For example,  $\mathcal{N}(x)$  is the  $2d$  nearest neighbors of  $x$  when  $p = 1$  and  $r = 1$ . We will refer to this as nearest neighbor interaction. If we use  $p = \infty$ , the neighborhoods are box-shaped. For many qualitative results, the shape of the neighborhood is of no consequence. The range, on the other hand, can have a strong effect. In most cases, we will suppress the dependence on  $p$  and  $r$  to keep the notation simple. When describing flip rates, it will often be helpful to let

$$n_i(x, \xi) = |\{y \in \mathcal{N}(x) : \xi(y) = i\}| \quad (2)$$

denote the number of neighbors of  $x$  in state  $i$  when the configuration is  $\xi$ .

A *stationary measure* (or invariant measure) for a particle system is a probability measure  $\mu$  on the configuration space  $F^{\mathbb{Z}^d}$  which satisfies  $\mu P_t = \mu$  for all  $t \geq 0$ . Here,  $\{P_t : t \geq 0\}$ , denotes the semigroup for the process and is defined by  $P_t f(\xi) = \mathbb{E}_\xi f(\xi_t)$ , for all continuous functions  $f$  on configuration space. (Throughout this paper, we use  $\mathbb{P}$  to denote the probability law for a process and  $\mathbb{E}$  for the corresponding expectation. Subscripts on these specify the initial configuration.) For general a probability measure  $\mu$  specifying the distribution of the initial configuration, the measure  $\mu P_t$  is the distribution of the process at time  $t$ . The stationary measures give the possible equilibrium distributions of the process.

## 2.1 Examples with particle flip dynamics.

**Example 2.1 (Richardson's growth model)** In this simple model, occupied sites remain occupied forever and each occupied site tries to give birth at rate  $\lambda$ . (Throughout this paper, saying an event occurs at rate  $\lambda$  means that

the time until the event is an exponential random variable with rate  $\lambda$ ; i.e., mean  $1/\lambda$ .) The new particle is sent to a neighboring site chosen at random. If a birth event is attempted and the receiving site is vacant, it accepts the birth and changes to state 1; if the receiving site is already in state 1, the birth is suppressed. Thus we allow at most one particle per site. So we have  $F = \{0, 1\}$  and the dynamics are completely described by the birth rate onto vacant sites:

$$c_{01}(x, \xi) = \lambda n_1(x, \xi). \quad (3)$$

If you watch a simulation of Richardson's model starting with a single occupied site, the most obvious thing you will notice about its behavior is that it spreads at a linear rate and has a (convex) asymptotic shape. This is stated more carefully in following theorem.

**Theorem 2.2 (Shape Theorem)** *Let  $\xi_t^0$  denote the set of occupied sites at time  $t$  when initially only the origin is occupied. Then there is a convex set  $A$  such that, for any  $\varepsilon > 0$ ,*

$$\mathbb{P}((1 - \varepsilon)tA \subset \xi_t^0 \subset (1 + \varepsilon)tA) \rightarrow 1, \quad \text{as } t \rightarrow \infty. \quad (4)$$

Of course, the above sets are restricted to  $\mathbb{Z}^d$ . The reader can find a proof of this shape theorem in [1].

**Example 2.3 (Contact process)** This model arises if we add spontaneous deaths to Richardson's model. Thus a site in state 1 changes to state 0 at a rate  $\delta$  that does not depend on the types of the other sites. By changing the time scale if necessary, there is no harm in assuming  $\delta = 1$ . Now  $F = \{0, 1\}$  and the flip rates are given by

$$\begin{aligned} c_{01}(x, \xi) &= \lambda n_1(x, \xi), \\ c_{10}(x, \xi) &= 1. \end{aligned} \quad (5)$$

Later it will be convenient to express these transition rates for a given particle system by the *generator*  $G$  of the process.  $G$  is an operator defined by its action on a sufficiently large collection of "test functions." For example, if our particle system has  $F = \{0, 1\}$ , then the generator would be written in the form

$$Gf(\xi) = \sum_{\xi(x)=1} c_{10}(x, \xi)(f(\xi - \delta_x) - f(\xi)) + \sum_{\xi(x)=0} c_{01}(x, \xi)(f(\xi + \delta_x) - f(\xi)), \quad (6)$$

where  $\xi - \delta_x$  is the configuration obtained from  $\xi$  by removing the particle from site  $x$  and leaving all other sites unchanged, and  $\xi + \delta_x$  is the configuration we get by adding a particle at  $x$ . This looks complicated, but it's just a way to express the transition rates at each site. To read this, just think of the first sum as saying: if a site  $x$  is currently in state 1 and the overall configuration is given by  $\xi$ , then at rate  $c_{10}(x, \xi)$  we remove the 1 at  $x$ . Thus the configuration goes from  $\xi$  to  $\xi - \delta_x$ ; this is encoded in the expression  $(f(\xi - \delta_x) - f(\xi))$ . Remember

that  $f$  is just a test function, so you ignore it when “reading” the rates in the generator. The second sum is interpreted similarly, giving the rate at which a site currently in state 0 turns into a 1, and hence the configuration going from  $\xi$  to  $\xi + \delta_x$ .

When doing calculations with generators, it is sometimes helpful to begin with test functions on configuration space that have a very simple form. Consider, first of all, the following “evaluation” test functions:

$$f_x(\xi) = \xi(x).$$

Applying the above generator, we get

$$\begin{aligned} Gf_x(\xi) &= (0 - 1)c_{10}(x, \xi)1(\xi(x) = 1) + c_{01}(x, \xi)(1 - 0)1(\xi(x) = 0) \\ &= \begin{cases} -c_{10}(x, \xi), & \text{if } \xi(x) = 1 \\ c_{01}(x, \xi), & \text{if } \xi(x) = 0. \end{cases} \end{aligned}$$

Armed with this observation, it is then easy to compute  $Gf(\xi)$  for test functions of the form

$$f(\xi) = \sum_y \phi(y)\xi(y) = \sum_y \phi(y)f_y(\xi). \quad (7)$$

In this case,

$$\begin{aligned} Gf(\xi) &= \sum_y \phi(y)Gf_y(\xi) \\ &= \sum_y \phi(y)[c_{01}(x, \xi)(1 - \xi(y)) - c_{10}(x, \xi)\xi(y)]. \end{aligned}$$

For example, the generator for the contact process is given by

$$Gf(\xi) = \sum_{\xi(x)=1} (f(\xi - \delta_x) - f(\xi)) + \lambda \sum_{\xi(x)=0} n_1(x, \xi)(f(\xi + \delta_x) - f(\xi)). \quad (8)$$

For functions of the form (7), this becomes

$$Gf(\xi) = \sum_y \phi(y)[- \xi(y) + \lambda n_1(y, \xi)(1 - \xi(y))].$$

The generator for Richardson’s model is similar to (8) but does not have the first sum since there are no deaths.

The most important result for the contact process is that there exists a critical birth rate  $\lambda_c = \lambda_c(d, r) < \infty$  such that, starting with a single occupied site, the process dies (i.e., hits the absorbing configuration of all 0’s) with probability 1 when  $\lambda \leq \lambda_c$ , and survives forever with positive probability when  $\lambda > \lambda_c$ . There is also a shape theorem which says, when the process survives, it spreads at a linear rate and has an asymptotic shape. This is very much like what happens in Richardson’s model except that spontaneous deaths give rise to a

twinkling effect as occupied sites in the interior of the growing blob are killed and then become occupied again and again. A coupling argument also shows that an equilibrium is reached inside the blob in the sense that, away from the boundary, the behavior is indistinguishable from that of the contact process starting with all sites occupied. See [1] for a careful statement of these results.

In the above models, the flip rates were asymmetric. For example, in the contact process  $0 \rightarrow 1$  transitions depend on the number of 1's in the neighborhood, whereas  $1 \rightarrow 0$  transitions occur spontaneously. The next model is symmetric in the dynamics for 0's and 1's.

**Example 2.4 (Voter model)** This can be thought of as a model of two competing species in a spatial setting, with neither species having a competitive advantage. In population genetics, it corresponds to a neutral model with spatial structure. In fact, if one replaces the integer lattice  $\mathbb{Z}^d$  with a complete graph on a finite number  $N$  of vertices (i.e., no spatial structure), then one obtains the classical Moran model for a population of size  $N$ . There is also a biased version of the voter model, in which one type has an advantage, that can be used to model competitive advantage or natural selection.

We will describe the model in terms that are closer in spirit to its name. Think of 0 and 1 as giving two possible opinions (instead of their usual meanings as vacant and occupied). The voter model can be regarded as a simple-minded model of peer pressure in which a site changes its opinion at a rate equal to the number of neighbors with the opposite opinion. So  $F = \{0, 1\}$  and the flip rates are given by

$$\begin{aligned} c_{01}(x, \xi) &= n_1(x, \xi), \\ c_{10}(x, \xi) &= n_0(x, \xi). \end{aligned} \tag{9}$$

The signature results for the voter model with nearest-neighbor interactions involve the ideas of clustering and coexistence. When  $d \leq 2$ , clustering occurs. This means, for any translation-invariant initial distribution with positive densities of both 0's and 1's,

$$\mathbb{P}(\xi_t(x) \neq \xi_t(y)) \rightarrow 0, \quad \text{as } t \rightarrow \infty, \tag{10}$$

holds for any pair of sites  $x, y$ . Intuitively, this says that sites tend toward consensus (even though the same global densities of 0's and 1's are maintained). Otherwise put, clusters appear on longer and longer length scales as time increases. One can also describe the sizes of typical clusters. In dimension one, for example, it can be shown that the mean cluster size grows like the square root of time (cf. [3]). When  $d \geq 3$ , coexistence can occur. Roughly, this means that the types approach a well-mixed state.

These results are determined by the behavior of the “dual process,” which describes the “ancestry” of the sites. Using a “graphical construction” of the process (cf. [1]), it is not hard to see that at any time in the past a given site

has a unique ancestral site from which it obtains its type. For the voter model, the dual process is given by a system of coalescing random walks. Clustering occurs precisely because two independent symmetric random walks eventually meet with probability one if and only if  $d \leq 2$ . Although dual processes are at the heart of much of the work on particle systems, we will not treat them here since that would take us too far from our stated goal. We recommend [1] for a first look at dual processes for particle systems.

Up to now, all our examples had type space  $F = \{0, 1\}$ . With the exception of the voter model, this was interpreted as meaning that there was one type of particle and sites were either occupied (1) or vacant (0). We now introduce several multi-type particle systems.

**Example 2.5 (Multi-type contact process)** This is a model in which two types of particles (1 and 2) compete for open space, and both types die (change to state 0) at the same rate. Now  $F = \{0, 1, 2\}$  and the flip rates are given by

$$\begin{aligned} c_{01}(x, \xi) &= \lambda_1 n_1(x, \xi), \\ c_{02}(x, \xi) &= \lambda_2 n_2(x, \xi), \\ c_{10}(x, \xi) &= c_{20}(x, \xi) = 1. \end{aligned} \tag{11}$$

This model was studied by Neuhauser [5].

In the case where both types have the same dispersal range and one of the birth rates is higher, say  $\lambda_2 > \lambda_1$ , the type with the higher rate takes over. More precisely, if the process starts with an initial distribution that is translation invariant with a positive density of 2's, then the process converges to the stationary distribution of the contact process with states 0 and 2.

When  $\lambda_1 = \lambda_2$ , the process behaves more like a voter model. That is, in the case  $d \leq 2$ , clustering occurs; when  $d \geq 3$ , there is a one-parameter family of stationary measures including both types of particles.

**Example 2.6 (2-stage contact process)** This is a generalization of the contact process in which occupied sites come in two types, young (1) and adult (2). Only adults can give birth and new individuals are young. Young individuals become adults at constant rate  $\gamma$ . The death rate for adults is 1 and for young is  $1 + \delta$ , where  $\delta \geq 0$  represents an added “infant mortality” rate. The rate at which adults give birth to young is  $\lambda$ . Again  $F = \{0, 1, 2\}$ , and the flip rates are now given by

$$\begin{aligned} c_{01}(x, \xi) &= \lambda n_2(x, \xi), \\ c_{12}(x, \xi) &= \gamma, \\ c_{10}(x, \xi) &= 1 + \delta, \\ c_{20}(x, \xi) &= 1. \end{aligned} \tag{12}$$

This model was introduced by Krone [6]. Unlike the above models, this process has a multi-type dual process. Also note that one type of particle (2) gives birth to a different type (1). Results are obtained on the structure of the survival region in parameter space. Modulo certain adjustments, this process behaves qualitatively much like the contact process. In fact, in the extreme case where  $\gamma = \infty$ , one recovers the contact process with states  $\{0, 2\}$ .

**Example 2.7 (Epidemic model)** Next, we consider a stochastic spatial version of the classical SIR models of mathematical epidemiology. Here one thinks of a population of individuals, some of which are dead or otherwise “removed” (0), some healthy and hence “susceptible” (1) to the disease, and some “infected” (2). So  $F = \{0, 1, 2\}$  and the flip rates are

$$\begin{aligned} c_{01}(x, \xi) &= \alpha, \\ c_{12}(x, \xi) &= \lambda n_2(x, \xi), \\ c_{20}(x, \xi) &= \delta. \end{aligned} \tag{13}$$

Here,  $\alpha \geq 0$  represents the rate of a spontaneous “regrowth” at a dead site; this might correspond to a birth or the arrival of an immigrant from outside the population. The infection rate for the disease is  $\lambda$  and the infection spreads by “contact.” Finally,  $\delta$  is the death rate for infected individuals.

The case of no regrowth ( $\alpha = 0$ ) was studied by Cox and Durrett [7]. They showed, in the 2-dimensional setting, that there is a critical infection rate  $\lambda_c(r)$  depending on the dispersal range  $r$  of the disease such that, if we start with a single infected site and all the others in state 1, the infection will die out with probability one when  $\lambda < \lambda_c(r)$ , and has positive probability of surviving forever when  $\lambda > \lambda_c(r)$ . Here, survival is equivalent to coexistence of healthy and infected individuals in the sense that there exists a stationary distribution concentrating on configurations with positive densities of both 1’s and 2’s.

The case with positive regrowth rate was studied in Durrett and Neuhauser [8]. They proved in the 2-dimensional, nearest-neighbor case, that coexistence can occur if  $\alpha$  is any positive constant and  $\lambda > \lambda_c(1)$ , the same critical value for the model with no regrowth. This amounts to showing that the 2’s can survive since all other transitions are spontaneous. Many other stochastic spatial epidemic models have been studied. These attempt to add other features that are present in real epidemics. For example, Schinazi [9] treats a process that can be interpreted as a model for an epidemic in which two strains of the pathogen are allowed to co-infect the host. In section 4, we will discuss an epidemic model that characterizes plant/disease interactions in which plants and disease both spread by contact and have different dispersal ranges.

## 2.2 Examples with exchange dynamics.

Let  $p(x, y)$ ,  $x, y \in \mathbb{Z}^d$ , be a finite-range, translation-invariant, irreducible transition probability function. We will sometimes restrict to the *symmetric nearest-*

*neighbor* case in which

$$p(x, y) = \begin{cases} \frac{1}{2d}, & \text{if } \|y - x\|_1 = 1, \\ 0, & \text{otherwise.} \end{cases} \quad (14)$$

When writing generators for exchange dynamics, we will use the letter  $L$  to distinguish it from generators for flip dynamics. This will be useful when we combine the two types of dynamics later.

**Example 2.8 (Exclusion process)** In this model, a particle at  $x$  tries to jump to another site  $y$  chosen according to the probability distribution  $p(x, y)$ . If site  $y$  is already occupied by a particle, the jump is suppressed. There is only one type of particle and we can have at most one particle per site, so  $F = \{0, 1\}$ . The generator for this process is given by

$$Lf(\xi) = \sum_{\substack{\xi(x)=1 \\ \xi(y)=0}} p(x, y)(f(\xi^{x,y}) - f(\xi)), \quad (15)$$

where  $\xi^{x,y}$  is the configuration obtained from  $\xi$  by exchanging the states at sites  $x$  and  $y$ ; i.e.,

$$\xi^{x,y}(z) = \begin{cases} \xi(z), & \text{if } z \neq x, y, \\ \xi(y), & \text{if } z = x, \\ \xi(x), & \text{if } z = y. \end{cases} \quad (16)$$

Notice that if sites  $x$  and  $y$  have the same state, then  $\xi^{x,y} = \xi$  and hence the above sum could be taken over all sites  $x, y \in \mathbb{Z}^d$ ; i.e., such a transition would not change anything since all particles are identical. Of course, since  $p(x, y)$  is a finite range transition probability function, the sum over  $y$  is really only over “neighboring” sites.

Note that, in the symmetric nearest-neighbor case, the above generator applied to an evaluation test function yields

$$Lf_x(\xi) = \begin{cases} n_1(x, \xi)/2d, & \text{if } \xi(x) = 0 \\ -n_0(x, \xi)/2d, & \text{if } \xi(x) = 1. \end{cases}$$

It is perhaps instructive to write the generator for the exclusion process in a slightly different form for later comparisons:

$$Lf(\xi) = \sum_{\substack{\xi(x)=1 \\ \xi(y)=0}} p(x, y)(f(\xi^{x \rightarrow y}) - f(\xi)), \quad (17)$$

where  $\xi^{x \rightarrow y}$  is the configuration obtained from  $\xi$  by moving the particle at site  $x$  to site  $y$ . In other words, when  $\xi(x) = 1$  and  $\xi(y) = 0$ ,

$$\xi^{x \rightarrow y}(z) = \begin{cases} \xi(z), & \text{if } z \neq x, y, \\ \xi(x) - 1, & \text{if } z = x, \\ \xi(y) + 1, & \text{if } z = y. \end{cases} \quad (18)$$

Here it matters that the sum in (17) is restricted to pairs  $x, y$  satisfying  $\xi(x) = 1$  and  $\xi(y) = 0$ . The sums in (15) and (17) are the same simply because exchanging the states at a pair of sites holding a 1 and a 0 is equivalent to moving the 1 to the vacant site.

In the exclusion process, particles try to move around like a continuous-time Markov process with jumps determined by the transition function  $p(x, y)$ , but are inhibited by the presence of other particles. This is equivalent to exchanging the states at any pair of sites at rate  $p(x, y)$ . If the two sites are in the same state (i.e., have the same occupancy number), then there is no net change in the configuration. Note that the global density of particles is preserved by the dynamics.

The symmetric nearest-neighbor exclusion process has a one-parameter family of stationary measures  $\{\nu_\alpha : \alpha \in [0, 1]\}$ . Here  $\nu_\alpha$  is a Bernoulli product measure with particle density  $\mathbb{E}_{\nu_\alpha}[\xi(x)] = \nu_\alpha\{\xi : \xi(x) = 1\} = \alpha$ . This stationary distribution corresponds to assigning the types of the sites independently with probability  $\alpha$  of type 1. The existence of invariant product measures is helpful in deriving hydrodynamic limits, as we will discuss later.

**Example 2.9 (Stirring process)** The exclusion process can be thought of as a special case of the following model. Here, we allow more than one *type* of particle, say  $F = \{0, 1, \dots, \kappa\}$ , but still at most one particle per site. Now any two sites  $x, y$  will exchange their types at rate  $p(x, y)$ , whatever the types may be. The generator is thus given by

$$Lf(\xi) = \sum_{x,y} p(x, y) (f(\xi^{x,y}) - f(\xi)), \quad (19)$$

where  $\xi^{x,y}$  is defined by (16). Since there is either one particle or no particles at any given site, this is unambiguous. As with the exclusion process, exchanges between sites with the same state have no effect. This process does allow, however, for the exchange of (different types of) particles. Thus, even if the lattice were fully occupied, this process allows movement of particles via exchange of different types. As for the above models of exchange dynamics, the stirring process has invariant product measures.

**Example 2.10 (Zero-range process)** In this process, there is no restriction on the number of particles per site, but there is only one type of particle; thus,  $F = \mathbb{Z}_+ \equiv \{0, 1, 2, \dots\}$ , with  $\xi_t(x) \in \mathbb{Z}_+$  representing the number of particles at site  $x$  at time  $t$ . Particles leave a site at a rate that depends on the number currently at that site. Let  $g : \mathbb{Z}_+ \rightarrow \mathbb{R}_+$  be a function satisfying  $g(0) = 0$ , and let  $p(x, y)$ ,  $x, y \in \mathbb{Z}^d$ , be a finite-range, translation-invariant, irreducible transition probability function. If there are currently  $k$  particles at site  $x$ , then,

independent of everything else, at rate  $g(k)p(x, y)$  one of the particles at  $x$  jumps to site  $y$ . The generator for this process is

$$Lf(\xi) = \sum_x \sum_y g(\xi(x))p(x, y)(f(\xi^{x \rightarrow y}) - f(\xi)). \quad (20)$$

Here,  $\xi^{x \rightarrow y}$  is defined by (18); we emphasize that only one particle is moved from  $x$  to  $y$  during such a transition. Under mild conditions, the zero-range process has a one-parameter family of invariant measures  $\{\nu_\alpha : \alpha \geq 0\}$ . Here  $\nu_\alpha$  is a product measure with particle density  $\mathbb{E}_{\nu_\alpha}[\xi(x)] = \alpha$ .

### 3 Hydrodynamic Limits of Particle Systems

In this section, we show how certain reaction-diffusion equations can be thought of as approximations of particle systems with a combination of flip and exchange dynamics, suitably scaled. We will view the dynamics in three different landscapes. The first is the integer lattice  $\mathbb{Z}^d$  with lattice spacing 1, on which our particle systems are defined. Next, we view the particle systems on a “squeezed lattice”

$$\mathbb{Z}_N^d = \{x/N : x \in \mathbb{Z}^d\}$$

with lattice spacing  $1/N$ . Here,  $N$  will operate as a parameter and when it tends to infinity  $\mathbb{Z}_N^d$  will become our third landscape, the continuum  $\mathbb{R}^d$ .

When defining the particle flip dynamics on the scaled lattice  $\mathbb{Z}_N^d$ , we use neighborhoods

$$\mathcal{N}_N(x) = \{y \in \mathbb{Z}_N^d : 0 < \|y - x\| \leq r/N\}.$$

Notice that the number of neighbors of a site,  $v_r^{(N)} = v_r$ , is independent of  $N$ . Let

$$n_{N,i}(x, \xi) = |\{y \in \mathcal{N}_N(x) : \xi(y) = i\}|$$

denote the number of neighbors of  $x \in \mathbb{Z}_N^d$  in state  $i$  when the configuration is  $\xi$ . With these adjustments, we define the flip rates  $c_{ij}(x, \xi)$  as before.

If the original process has particle flip dynamics described by generator  $G$ , we write  $G_N$  for the generator for the corresponding process with particle flip dynamics on  $\mathbb{Z}_N^d$ . This does not change how the sites interact with their neighbors; it just moves all the sites closer together. To visualize this, imagine watching a simulation of the process. Moving the process to the squeezed lattice  $\mathbb{Z}_N^d$  is like moving further away from the computer screen; the sites appear to be closer to each other. Next, we add some “fast stirring” to the system on the squeezed lattice. Roughly, this means that we exchange nearest-neighbor particles at rate  $N^2$ . The fact that spatial jumps are of order  $1/N$  and time is scaled like  $N^2$  suggests that this should lead to a diffusion term in the limit. The type of diffusion

will depend on the specific form of the exchange dynamics used. If the exchange dynamics used to do the stirring is given by a generator  $L$  on  $\mathbb{Z}^d$ , then we let  $L_N$  denote the corresponding generator when we move to  $\mathbb{Z}_N^d$ . Then  $N^2 L_N$  is the generator for the speeded up exchange dynamics; i.e., the exchange jumps are run at a rate that is  $N^2$  times faster than those in  $L_N$ . This is the usual “diffusion scaling.” For example, it takes a symmetric random walk roughly  $N^2$  jumps to move distance  $N$ , and on our squeezed lattice  $\mathbb{Z}_N^d$  a distance of  $N$  sites corresponds to one unit of distance in  $\mathbb{R}^d$ .

Since we are only speeding up the exchange dynamics, the generator of the resulting composite process  $(\xi_t^N)$  on  $\mathbb{Z}_N^d$  is of the form

$$\mathcal{L}_N = G_N + N^2 L_N. \quad (21)$$

The goal is to obtain a deterministic limit, as  $N \rightarrow \infty$ , that describes the macroscopic behavior of the particle density and is characterized by a reaction-diffusion equation.

Hydrodynamic limits are typically proved for the setting in which the particle exchange dynamics has a family of invariant measures which are product measures, and hence correspond to independent sites. The basic idea behind this is fairly simple. Let’s consider the case of a single particle type. We start the approximating particle system  $\xi_t^N$  on  $\mathbb{Z}_N^d$  with initial distribution given by a product measure with local density  $\mathbb{P}(\xi_0^N(x) = 1) = g(x)$ , where  $g(x)$  is continuous and hence is approximately constant in a small macroscopic region. This corresponds to a large number (order  $N^d$ ) of sites near  $x$  in  $\mathbb{Z}_N^d$  being distributed (approximately) according to the invariant measure with constant density  $g(x)$  at time 0; i.e., the process starts in a state which is locally at some equilibrium. This local equilibrium can change (smoothly) as we move around in space. In each macroscopically small region, we thus have the law of large numbers forcing convergence to a deterministic limit. For positive times, this equilibrium can be maintained because of the fact that the exchange dynamics are operating much faster (due to the factor  $N^2$ ) than the flip dynamics, giving the exchange dynamics plenty of time to equilibrate between flip events. Filling in the details to prove convergence to the appropriate limit can be quite involved and is outside the scope of this paper. For a careful mathematical treatment of hydrodynamic limits, we suggest [10] and [11]. Two standard references with a more physical flavor are [12] and [13]. In the special case where the exchange dynamics is given by symmetric nearest-neighbor stirring, De Masi, Ferrari, and Lebowitz [14] (see also Durrett and Neuhauser [8]) were able to use a relatively simple dual process to avoid some of the technical issues that must be faced in other cases.

To describe the convergence involved in a hydrodynamic limit, we begin by defining the *empirical measure*

$$\pi_t^N = N^{-d} \sum_{x \in \mathbb{Z}_N^d} \xi_t^N(x) \delta_x \quad (22)$$

of the scaled process  $\xi_t^N$  (i.e., the process defined on  $\mathbb{Z}_N^d$  via a generator of the form (21)). Here,  $\delta_x$  denotes a point mass at site  $x$ . To see that  $N^{-d}$  is the

right scaling, note that there are  $N^d$  sites per unit volume in  $\mathbb{Z}_N^d$ . Consider the case of a particle system with only one type of particle. Then, for any set  $A$ ,

$$\pi_t^N(A) = N^{-d} \sum_{x \in \mathbb{Z}_N^d \cap A} \xi_t^N(x) \quad (23)$$

gives the proportion of occupied sites in  $A$  at time  $t$ . (When there is more than one type of particle to keep track of,  $\pi_t^N$  is actually a vector of measures  $\pi_t^N = (\pi_t^{N,0}, \dots, \pi_t^{N,\kappa})$ , one for each state.)

The empirical measure is determined by its integrals against functions in  $C_c^\infty(\mathbb{R}^d)$ , the infinitely differentiable functions with compact support. Thus, for the case of a single particle type, we define the so-called *density field* by

$$\pi_t^N(\phi) = N^{-d} \sum_{x \in \mathbb{Z}_N^d} \xi_t^N(x) \phi(x), \quad \phi \in C_c^\infty(\mathbb{R}^d). \quad (24)$$

When there are different types of particles, this must be done for each particle type  $i$ , and the appropriate sum is

$$\pi_t^{N,i}(\phi) = N^{-d} \sum_{x \in \mathbb{Z}_N^d} \phi(x) \mathbf{1}(\xi_t^N(x) = i). \quad (25)$$

We say that a function  $u(x, t)$  is the *hydrodynamic limit* for a family  $\{(\xi_t^N) : N \geq 1\}$  of scaled processes determined by generators of the form (21) if, for each  $\phi \in C_c^\infty(\mathbb{R}^d)$  and  $t \geq 0$ ,

$$N^{-d} \sum_{y \in \mathbb{Z}_N^d} \phi(y) \xi_t^N(y) \xrightarrow{P} \int \phi(y) u(y, t) dy, \quad \text{as } N \rightarrow \infty, \quad (26)$$

where  $\xrightarrow{P}$  denotes convergence in probability. In other words,

$$\mathbb{P}\left(\left|\pi_t^N(\phi) - \int \phi(y) u(y, t) dy\right| > \epsilon\right) \rightarrow 0, \quad \text{for all } \epsilon > 0. \quad (27)$$

Thus, for each fixed  $t$ , the empirical measure converges to an absolutely continuous measure with density function  $x \mapsto u(x, t)$ . Intuitively, for large  $N$ , in the scaled particle system on the squeezed lattice, the density of particles becomes more and more “blurred” and is approximated by a continuous density function. When there are multiple particle types, say  $F = \{0, 1, \dots, \kappa\}$ , the appropriate limits are

$$N^{-d} \sum_{y \in \mathbb{Z}_N^d} \phi(y) \mathbf{1}(\xi_t^N(y) = i) \xrightarrow{P} \int \phi(y) u_i(y, t) dy, \quad i = 0, \dots, \kappa, \quad (28)$$

with one density function  $u_i(x, t)$  for each state.

It should be noted that there are a number of variations and refinements in the literature concerning the type of convergence. In some cases, weak convergence of the entire path-valued process is proven, rather than convergence in

probability at each fixed time  $t$ . Under certain conditions, the limiting density satisfies a PDE in the classical sense, while in other cases it is only a weak solution. We refer the reader to the references for detailed statements and proofs. For our purposes it is enough to realize that, under certain conditions, a microscopic particle picture when viewed (scaled) in an appropriate way “evolves like” a deterministic mass distribution governed by a PDE. Roughly speaking, the randomness acting at the microscopic level averages out to yield deterministic behavior at the macroscopic level.

### 3.1 A warm-up example

Let’s do a back-of-the-envelope calculation to see what the hydrodynamic limit should be in a simple example, assuming we know it exists and ignoring all technical difficulties. This calculation contains some of the basic ideas in the general approach (cf. [10]) to deriving hydrodynamic limits. In practice, however, accounting for various assumptions on initial configurations, proving existence of a limit, existence and uniqueness of solutions of the appropriate PDE, etc., can be technically demanding and often requires new approaches.

To keep things as simple as possible, we consider a one-dimensional process with flip dynamics given by Richardson’s growth model and stirring given by nearest-neighbor exclusion dynamics. Let  $\xi_t^N$  be the scaled particle system on  $\mathbb{Z}_N^1$  with generator  $\mathcal{L}_N = G_N + N^2 L_N$ . The calculation begins by using a standard result connecting Markov processes and their generators to martingales. Loosely speaking, a martingale is a stochastic process,  $M_t$ , that on average stays the same. These processes have many useful properties and are ideal for doing certain kinds of calculations (cf. [15]). Here’s the connection: for any nice function  $f$ , there is a martingale  $M_t^{N,f}$  such that

$$f(\xi_t^N) = f(\xi_0^N) + \int_0^t \mathcal{L}_N f(\xi_s^N) ds + M_t^{N,f} \quad (29)$$

holds for all  $t \geq 0$  (cf. [15]). We apply this to the function

$$f(\xi^N) = \frac{1}{N} \sum_{y \in \mathbb{Z}_N^1} \xi^N(y) \phi(y),$$

where  $\phi$  is a given test function. Note that plugging the process into this  $f$  gives  $f(\xi_t^N) = \pi_t^N(\phi)$ , the density field.

For this function, our generator in the one-dimensional setting becomes

$$\begin{aligned} \mathcal{L}_N f(\xi^N) &= \frac{1}{N} \sum_{y \in \mathbb{Z}_N^1} [G_N \xi^N(y) + N^2 L_N \xi^N(y)] \phi(y) \\ &= \frac{1}{N} \sum_{y \in \mathbb{Z}_N^1} \left\{ \lambda \cdot \left( \xi^N(y - 1/N) + \xi^N(y + 1/N) \right) (1 - \xi^N(y)) \phi(y) \right. \\ &\quad \left. + \frac{N^2}{2} \left( \xi^N(y - 1/N) - \xi^N(y) + \xi^N(y + 1/N) - \xi^N(y) \right) \phi(y) \right\} \end{aligned}$$

$$\begin{aligned}
&= \frac{1}{N} \sum_{y \in \mathbb{Z}_N^1} \left\{ \lambda \cdot \left( \xi^N(y-1/N) + \xi^N(y+1/N) \right) (1 - \xi^N(y)) \phi(y) \right. \\
&\quad \left. + \frac{\xi^N(y)}{2} \left( \frac{\phi(y-1/N) + \phi(y+1/N) - 2\phi(y)}{1/N^2} \right) \right\},
\end{aligned}$$

where the last equality follows from two applications of summation by parts. The ratio involving  $\phi$  in the last term is just the discrete approximation to the second derivative, i.e., the discrete one-dimensional Laplacian, which we write as  $\Delta_N \phi$ .

If we use this representation of the generator in (29) for the special function  $f$  we have chosen, we get

$$\begin{aligned}
\pi_t^N(\phi) &= \pi_0^N(\phi) + M_t^{N,f} + \int_0^t \left\{ \pi_s^N \left( \frac{1}{2} \Delta_N \phi \right) \right. \\
&\quad \left. + \frac{\lambda}{N} \sum_{y \in \mathbb{Z}_N^1} \left( \xi_s^N(y-1/N) + \xi_s^N(y+1/N) \right) (1 - \xi_s^N(y)) \phi(y) \right\} ds.
\end{aligned} \tag{30}$$

Now let  $N \rightarrow \infty$  in (30) and assume that there is a smooth limit density  $u(x, t)$  such that  $\lim_{N \rightarrow \infty} \pi_t^N(\phi) \equiv \pi_t(\phi) = \int_{\mathbb{R}} u(x, t) \phi(x) dx$ . We then obtain the equation

$$\pi_t(\phi) = \pi_0(\phi) + M_t + \int_0^t \left\{ \pi_s \left( \frac{1}{2} \Delta \phi \right) + 2\lambda \int_{\mathbb{R}} u(x, s) (1 - u(x, s)) \phi(x) dx \right\} ds, \tag{31}$$

where  $M_t$  is a martingale. (The martingale property is preserved under certain kinds of limits.) The martingale  $M_t$  has mean 0 and a second moment argument can be used to show that the martingale itself is identically 0. Thus, if the initial density can be approximated by a continuous function  $g$ , (31) is just the weak form of the reaction-diffusion equation

$$\begin{cases} \frac{\partial u}{\partial t} = \frac{1}{2} \Delta u + 2\lambda u(1 - u), \\ u(x, 0) = g(x). \end{cases} \tag{32}$$

This is a special case of *Fisher's equation*. Note that the density-dependent (logistic) growth term is built in because of the restriction of one particle per site in Richardson's model. Fisher's equation is the simplest nonlinear reaction-diffusion equation and is known to have traveling wave solutions. These traveling waves provide a macroscopic manifestation of the shape theorem mentioned earlier.

We remark that the Laplacian term,  $\frac{1}{2} \Delta u$  in the above differential equation, is the generator of Brownian motion. The convergence  $\frac{1}{2} \Delta_N \phi \rightarrow \frac{1}{2} \Delta \phi$  is just a statement of the fact that the symmetric nearest-neighbor random walk, when appropriately scaled, converges to Brownian motion. This is another way to understand how the diffusion term arises from fast exchange dynamics. One often sees hydrodynamic limits with  $\Delta$  in place of  $\frac{1}{2} \Delta$ . This is what arises when

we speed up the exclusion dynamics by a factor of  $2N^2$  instead of  $N^2$ ; i.e., we get Brownian motion run at twice the usual speed. Since this factor of  $1/2$  is easy to account for, we will leave it out of the hydrodynamic limit equations for the rest of this paper.

### 3.2 Examples with linear diffusion

A linear diffusion term arises in the hydrodynamic limit PDE when the exchange dynamics produces something like simple symmetric random walk behavior; see the above example. We now present an easy-to-use theorem that can be found in [14], [8], or [2], and which contains the previous example as a special case. (The methods outlined in the previous subsection, however, are applicable in a much broader setting.) This result furnishes reaction-diffusion equations corresponding to a large class of particle systems which allow at most one particle per site and have exchange dynamics given by symmetric nearest-neighbor stirring. The proof, which will not be given here, rests on the fact that the dual process for the scaled interacting particle system in the theorem is essentially a system of independent branching random walks.

**Theorem 3.1** *Suppose the particle flip dynamics on  $\mathbb{Z}^d$  are translation invariant, of finite range, and  $F = \{0, 1, \dots, \kappa\}$  with  $\kappa \geq 1$ . Let the exchange dynamics be given by symmetric nearest-neighbor stirring as in (19) and (14). Then the scaled process  $\xi_t^N$  with generator of the form (21) and initial configuration distributed according to product measure with  $\mathbb{P}(\xi_0^N(x) = i) = g_i(x)$ ,  $i = 0, \dots, \kappa$ , has hydrodynamic limit  $\mathbf{u}(x, t) = (u_0(x, t), \dots, u_\kappa(x, t))$ , where  $u_i(x, t)$  is the bounded solution of*

$$\begin{cases} \frac{\partial u_i}{\partial t} = \Delta u_i + f_i(\mathbf{u}), \\ u_i(x, 0) = g_i(x). \end{cases} \quad (33)$$

The reaction term is given by

$$f_i(\mathbf{u}) = \sum_{j \neq i} \langle c_{ji}(0, \xi) \mathbf{1}(\xi(0) = j) \rangle_{\mathbf{u}} - \sum_{j \neq i} \langle c_{ij}(0, \xi) \mathbf{1}(\xi(0) = i) \rangle_{\mathbf{u}}. \quad (34)$$

Here,  $\mathbf{u} = (u_0, \dots, u_\kappa)$  and  $\langle \dots \rangle_{\mathbf{u}}$  denotes expected value under product measure (i.e., independent sites) in which state  $j$  has density  $u_j$ .

In this theorem, it is assumed that the  $g_i$ 's are continuous. The convergence is as in (28). To understand the form of the reaction term, note that the first sum can be thought of as the rate at which a given site (say 0) changes to state  $i$  if it is currently of another type. This is averaged according to the current (local) fractions of sites in each state. The second sum has a similar interpretation and basically gives the ‘‘flow’’ out of state  $i$ . Finally, we remind the reader that in the scaled process,  $\xi_t^N$ , the stirring rate is  $N^2$  and we only exchange sites  $x, y \in \mathbb{Z}_N^d$  with  $\|y - x\|_1 = 1/N$ .

The next three examples are special cases of the above theorem. In all three, we will let  $v_r = |\mathcal{N}(x)|$  denote the number of sites within range  $r$  of site  $x$  (cf. (1)), where we recall that  $r$  is the generic *dispersal range* of a particle trying to give birth. We write

$$\beta_r \equiv v_r \lambda$$

for the maximum birth rate onto a site.

**Example 3.2 (Richardson's growth model with fast stirring)** For simplicity, let  $u(x, t) = u_1(x, t)$  be the density of 1's. (No equation is needed for  $u_0(x, t) = 1 - u_1(x, t)$ .) The fast-stirring limit equation for Richardson's model is

$$\frac{\partial u}{\partial t} = \Delta u + \beta_r u(1 - u),$$

in agreement with the result in the previous subsection where we assumed  $d = 1$  and  $r = 1$  (and hence  $v_r = 2$ ). Note that, if we were to change Richardson's model so that a vacant site becomes occupied at rate  $\lambda$  times the *fraction*  $n_1(x, \xi)/v_r$  of occupied neighboring sites (instead of the *number* of occupied neighbors), the hydrodynamic limit PDE would have  $\lambda$  in place of  $\beta_r$ .

**Example 3.3 (Contact process with fast stirring)** This model has births as in Richardson's model, and has the added feature of spontaneous deaths of particles. The fast-stirring limit equation is

$$\frac{\partial u}{\partial t} = \Delta u - u + \beta_r u(1 - u).$$

Note that this can also be written as a Fisher-type equation. We remark that the hydrodynamic limit is sometimes used to help guess the behavior of the process. For example, the spatially homogeneous equation (ODE) has a nontrivial equilibrium  $\bar{u} = 1 - 1/\beta_r > 0$  if and only if  $\beta_r > 1$ . This gives the equilibrium density of occupied sites under fast stirring and suggests, for example, that there might be some sort of threshold phenomenon in the contact process itself; cf. the critical birth rate in Example 2.3. We remark that the numerical value of the critical birth rate for survival in the deterministic model (ODE or PDE) is different than that in the corresponding particle system (although their difference does go to zero in the limit); the qualitative result that guarantees the existence of a threshold is what carries over from one model to the other. One must always be careful when comparing numerical values that are obtained with different models.

Since the above two models have only one type of particle, stirring is the same as symmetric nearest-neighbor exclusion dynamics. See [10] for this approach to the hydrodynamic limit.

**Example 3.4 (2-stage contact process with fast stirring)** In this example we have two types of particles, so we must keep track of two densities. Since there are two types, the exchange mechanism is stirring and cannot be thought of as exclusion dynamics. Theorem (3.1) yields hydrodynamic equations

$$\begin{cases} \frac{\partial u_1}{\partial t} = \Delta u_1 - (1 + \delta + \gamma)u_1 + \beta_r u_2(1 - u_1 - u_2), \\ \frac{\partial u_2}{\partial t} = \Delta u_2 + \gamma u_1 - u_2, \end{cases} \quad (35)$$

where  $\beta_r = v_r \lambda$ .

### 3.3 Nonlinear diffusion

In the above examples, fast stirring (exclusion dynamics) led to linear diffusion terms. To get nonlinear diffusion, we replace stirring/exclusion with some type of density-dependent particle movement. Such motion is quite prevalent in biological populations, especially in the context of resource-limited growth. We will keep these examples short and point the reader to the relevant literature for a more elaborate development.

**Example 3.5 (1-dimensional nondegenerate diffusion)** This is a one-dimensional model. The particle exchange rate on  $\mathbb{Z}_N^1$  is

$$N^2 \mathbf{1}(\xi(x) \neq \xi(x + 1/N)) [1 + \alpha \{\xi(x - 1/N) + \xi(x + 2/N)\}].$$

Here, there is a maximum of one particle per site and the rate at which a given particle moves to a vacant adjacent site is 1 plus  $\alpha$  times the number of particles bordering this pair of sites. Roughly speaking, the more crowded a particle feels, the more it wants to jump to an adjacent vacant site. The limiting density of occupied sites satisfies

$$\frac{\partial u}{\partial t} = \frac{\partial}{\partial x} \left( D(u) \frac{\partial u}{\partial x} \right),$$

where the diffusion coefficient is given by

$$D(u) = 1 + 2\alpha u.$$

This example is treated in [13].

**Example 3.6 (Zero-range exchange dynamics)** Here we allow more than one particle per site. If there are currently  $k$  particles at  $x$ , one of them jumps at rate  $g(k)$  to a nearest-neighbor site chosen at random according to the transition

probability  $p(x, y)$ . Speeding up this jumping by a factor  $N^2$  as before and taking the limit as  $N \rightarrow \infty$ , the limiting density satisfies

$$u_t = \Delta(\Phi(u)),$$

where

$$\Phi(u) = \mathbb{E}_{\nu_u} g(\xi(x))$$

is the expected jump rate under product measure with density  $u$ . This example is discussed in [10].

**Example 3.7 (Multi-particle migration)** In the above particle systems, we allow only one particle to jump from a site. Ekhaus and Seppäläinen [11] obtain the porous medium equation

$$u_t = \Delta(u^2) \tag{36}$$

as the hydrodynamic limit for a class of particle systems which allow more than one particle to jump from a site at a given moment. We refer the reader to [11] for a full discussion of this model and a few related models.

**Remark 3.8** By adding particle flip dynamics as in earlier examples, one can get reaction-diffusion equations with nonlinear diffusion. For example, if we combine the contact process (Example 2.3) and fast zero-range dynamics (Example 3.6), we get a hydrodynamic equation of the form

$$u_t = \Delta(\Phi(u)) - u + \beta_r u(1 - u).$$

## 4 A Mean-Field Limit

In this final section, we briefly discuss a different kind of scaling limit for a model introduced by Krone and Neuhauser [16]. Our underlying particle system is a one-dimensional epidemic model in which both disease and susceptibles spread by contact, unlike Example 2.7. Moreover, the dispersal ranges are different. There are three states: vacant or dead (0), healthy plant (1), and infected plant (2).

For each  $\varepsilon > 0$ , we build a process  $\xi_t^\varepsilon$  on  $\varepsilon\mathbb{Z}$  as follows. (We will use the letter  $\varepsilon$  in place of  $1/N$  to describe the scaling so as not to confuse this with the hydrodynamic scaling used earlier.) A 1 at site  $x$  tries to give birth at rate  $\lambda_1$ . The offspring is sent to a site  $y$  chosen at random according to a probability kernel  $k_R^\varepsilon(y - x)$ . If site  $y$  is not in state 0, the birth is suppressed. Similarly, a 2 at site  $x$  tries to give birth at rate  $\lambda_2$ . The offspring is sent to a site  $y$  chosen at random according to a probability kernel  $k_M^\varepsilon(y - x)$ . If site  $y$  is not in state 1, the birth is suppressed. Finally, 2's die at rate 1. The subscripts  $R$  and  $M$

on the kernels correspond to dispersal ranges. Fairly general dispersal kernels can be used, but to keep things simple, let's assume we have uniform kernels of the form

$$k_r^\varepsilon(x) = \frac{\varepsilon}{2r} \mathbf{1}_{[-r,r]}(x), \quad x \in \varepsilon\mathbb{Z}, \quad (37)$$

i.e.,  $k_r^\varepsilon(x) = \varepsilon/2r$  if  $x \in \varepsilon\mathbb{Z} \cap [-r, r]$ .

In this case, the dynamics can be defined as follows. Let

$$\mathcal{N}_r^\varepsilon(x) = \{y \in \varepsilon\mathbb{Z} : 0 < |y - x| \leq r\} \quad (38)$$

and

$$n_i^{r,\varepsilon}(x) = n_i^{r,\varepsilon}(x, \xi) = \#\{y \in \mathcal{N}_r^\varepsilon(x) : \xi(y) = i\}, \quad i = 1, 2. \quad (39)$$

If the current configuration is  $\xi$ , then we have the following transition rates at  $x$ :

$$\begin{aligned} 0 \rightarrow 1 & : \text{rate } \lambda_1 n_1^{R,\varepsilon}(x) / v_R^\varepsilon \\ 1 \rightarrow 2 & : \text{rate } \lambda_2 n_2^{M,\varepsilon}(x) / v_M^\varepsilon \\ 2 \rightarrow 0 & : \text{rate } 1, \end{aligned} \quad (40)$$

where  $v_r^\varepsilon = 2r/\varepsilon$  denotes the number of sites within range  $r$  of  $x$ . Notice that the macroscopic dispersal range  $r$  of a given type is the same for each  $\varepsilon$ ; the number of sites within range  $r$ , however, increases as  $\varepsilon \rightarrow 0$ . This results in a ‘‘high density’’ limit.

Let  $u_\varepsilon(x, t) = \mathbb{P}(\xi_t^\varepsilon(x) = 1)$  and  $v_\varepsilon(x, t) = \mathbb{P}(\xi_t^\varepsilon(x) = 2)$ ,  $t \geq 0$ ,  $x \in \varepsilon\mathbb{Z}$ . In addition, let

$$k_r(x) = \frac{1}{2r} \mathbf{1}_{[-r,r]}(x), \quad x \in \mathbb{R}, \quad (41)$$

be the continuum dispersal kernel corresponding to the discrete kernel of (37). The following mean-field limit theorem can be found in [16]. It gives a system of integro-differential equations for the densities of 1's and 2's.

**Theorem 4.1** *Let  $\xi_t^\varepsilon$  be the above epidemic model defined by (40), and assume  $\{\xi_0^\varepsilon(x), x \in \varepsilon\mathbb{Z}\}$  are independent with  $\mathbb{P}(\xi_0^\varepsilon(x) = 1) = g_1(x)$  and  $\mathbb{P}(\xi_0^\varepsilon(x) = 2) = g_2(x)$ ,  $g_1$  and  $g_2$  being continuous functions with  $0 \leq g_1(x) + g_2(x) \leq 1$ . Then, as  $\varepsilon \rightarrow 0$ ,*

$$u_\varepsilon(x, t) \rightarrow u(x, t) \quad \text{and} \quad v_\varepsilon(x, t) \rightarrow v(x, t), \quad (42)$$

where  $u(x, t)$  and  $v(x, t)$  are the bounded nonnegative solutions of

$$\begin{aligned} \frac{\partial u}{\partial t} &= -\lambda_2 u k_M * v + \lambda_1 (1 - u - v) k_R * u \\ \frac{\partial v}{\partial t} &= -v + \lambda_2 u k_M * v, \end{aligned} \quad (43)$$

with initial conditions  $u(x, 0) = g_1(x)$ ,  $v(x, 0) = g_2(x)$ , where  $*$  denotes convolution.

The convergence in the above theorem is uniform on compact subsets of  $\mathbb{R} \times \mathbb{R}_+$ . We remark that in this theorem there is no stirring. The convergence comes about because of the averaging effect caused by a large number of sites in a small macroscopic region. Krone and Neuhauser [16] show that the solution of (43) exhibits spatial pattern formation (Turing instabilities). This is used to help explain the temporary waves of susceptibles and infectives that are observed in simulations.

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