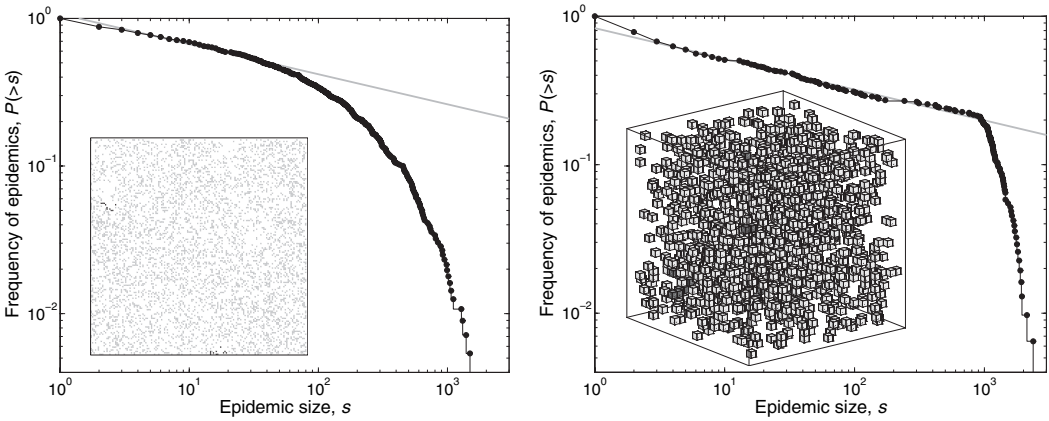

Figure 7.12. Distribution of epidemic sizes and examples of the lattice configuration for 2D and 3D versions of the Rhodes and Anderson model. In the lattice example, gray sites are susceptible, black are infectious, and empty sites are recovered. For both models, the best power-law fit to the distribution of epidemic sizes ($\mathbb{P}(\text{epidemic} \geq s) = s^{-\alpha}$) is calculated to be $\alpha \approx 0.2$. ($\tau = 5$, $\gamma = 0.1$, $\nu = 4 \times 10^{-5}$, imports $\varepsilon = 3.3 \times 10^{-6}$, movement rate $m = 0.1$. $N \approx 25000$.)

7.4. CONTINUOUS-SPACE CONTINUOUS-POPULATION MODELS

One major disadvantage of the lattice-based models is the discretization of space that is introduced by the lattice structure. In consequence, the resolution at which we know an individual's position is limited by the scale of each grid cell. An alternative formulation is to treat both space and the population as continuous, therefore specifying a density of individuals at all locations. We can think of this as the limit of a lattice model as the grid size becomes infinitely fine scale.

The natural way to describe the dynamics of continuous populations in continuous space is using partial differential equations (PDE), or integro-differential equations (IDE). The mathematics behind these formalisms is complex and often highly technical; the details of this approach are excellently described by Murray (2003), so here we review the salient epidemiological implications. Although some notable examples of continuous space models are being used for applied modeling purposes (Noble 1974; Murray et al. 1986; Caraco et al. 2002), such models are generally used to provide theoretical predictions and a generic understanding of the spatial spread of infection (Lopez et al. 1999; Beardmore and Beardmore 2003; Reluga 2004). The main theoretical advantage is the deterministic and tractable nature of the continuous-space models, whereas the assumption of continuous-population levels tends to be a disadvantage in many applied situations. We now focus on the two forms of models, PDEs and IDEs, to illustrate how they are derived from simple nonspatial models (Chapter 2).

7.4.1. Reaction-Diffusion Equations

The standard PDE models are derived from the assumption that infectious individuals transmit the disease only to susceptibles at their current location, and that all individuals are free to move at random (or diffuse) through the landscape. We first show an example of a PDE model, before explaining the individual terms and how such a model is formulated.

A typical PDE model for a disease with SIR-type dynamics would be:

$$\begin{aligned}\frac{\partial X}{\partial t} &= \nu - \beta XY/N - \mu X + D_X \nabla^2 X,\\ \frac{\partial Y}{\partial t} &= \beta XY/N - \gamma Y - \mu Y + D_Y \nabla^2 Y,\\ \frac{\partial Z}{\partial t} &= \gamma Y - \mu Z + D_Z \nabla^2 Z,\end{aligned} \tag{7.17}$$

where X, Y, and Z are functions of both space and time, and represent the local density of susceptible, infectious, and recovered individuals, and as always $N = X + Y + Z$. Hence, if we're dealing with a two-dimensional landscape, $X(x, y, t)$ is the density of susceptibles at location (x, y) at time t. We now have to specify the rates of change with partial derivatives (e.g. $\frac{\partial}{\partial t}$), because our variables are now multi-dimensional, being functions of both space and time—this, however, is a technicality and does not change our understanding of what these derivatives mean.

The term ∇^2 is introduced to model the local diffusion of individuals through space. ∇ is shorthand for the rate of change of the quantity across space, so ∇^2 is the change in the rate of change. In two dimensions, the diffusion term for susceptibles becomes:

$$\nabla^2 X = \frac{\partial^2 X}{\partial x^2} + \frac{\partial^2 X}{\partial y^2}.$$

The inclusion of these spatial derivatives mimics the diffusion of individuals across the environment. For greater generality, susceptible, infectious, and recovered individuals are assumed to diffuse at different rates (D_X, D_Y, and D_Z), reflecting the fact that sick individuals may be less likely to move.

We can understand the role of diffusion in such PDE models, by considering the diffusion of a group of susceptibles initially piled at a single point (0,0). Ignoring demography, our equation will be:

$$\frac{\partial X}{\partial t} = D_X \nabla^2 X.$$

This has the solution:

$$X(x, y, t) \propto \frac{1}{2\pi D_X t} \exp\left(-\frac{(x^2 + y^2)}{2 D_X t}\right),$$

which is an ever-expanding bell-shaped (Gaussian) distribution, with the total density of individuals remaining constant. The diffusion parameter D_X governs the speed at which the variance of the Gaussian grows. We can therefore see that diffusion away from a point source leads to Gaussian-like distributions of individuals.

Reaction-diffusion models, which use a PDE formulism, assume local transmission of infection and rely on spatial diffusion of hosts to spread the infection.

Very few PDE models have an exact analytical solution and therefore numerical methods are required for their simulation. Although PDEs are formulated as continuous space models, determining their solution by computer necessitates discretizing space, usually into a regular grid (see Box 7.1). Therefore, for the vast majority of situations, PDE models are approximated by coupled lattice models with a very fine resolution lattice.

Box 7.1 Solving Diffusion PDEs

Although PDE models are formulated in continuous space, numerical solution of the equations often requires us to discretize space in some manner. The most common method of achieving this is to subdivide space into a regular grid, therefore we are again dealing with a lattice-based model. Here we explain how to translate the differential terms into a lattice formulation.

We impose a lattice structure onto our space, where adjacent lattice points are separated by a distance d; we therefore want the lattice solution $X_{i,j}(t)$ to approximate the PDE solution $X(i \times d, j \times d, t)$. We are familiar with ways to treat temporal derivatives (e.g., $\frac{d}{dt}$), integrating forward in time using methods such as forward Euler or Runge-Kutta. However, the PDE model also contains spatial derivatives and these need to be expressed in terms of the lattice structure. Considering the x spatial second derivative for the number of susceptibles:

$$\frac{\partial^2 X_{i,j}}{\partial x^2} \approx \frac{\frac{\partial X_{i+\frac{1}{2},j}}{\partial x} - \frac{\partial X_{i-\frac{1}{2},j}}{\partial x}}{d}.$$

In words, this means the second derivative can be approximated as the change in the first derivative of X between $(i+\frac{1}{2}, j)$ and $(i-\frac{1}{2}, j)$ divided by the distance, d, between $(i+\frac{1}{2}, j)$ and $(i-\frac{1}{2}, j)$. We now perform a similar approximation for the first derivatives in this term:

$$\begin{aligned}\frac{\partial^2 X_{i,j}}{\partial x^2} &\approx \frac{\left(\frac{X_{i+1,j}-X_{i,j}}{d}\right) - \left(\frac{X_{i,j}-X_{i-1,j}}{d}\right)}{d}, \\ &\approx \frac{X_{i+1,j} - 2X_{i,j} + X_{i-1,j}}{d^2}.\end{aligned}$$

Therefore, if we consider the full diffusion term:

$$\begin{aligned}D_X \nabla^2 X_{i,j} &= D_X \frac{\partial^2 X_{i,j}}{\partial x^2} + D_X \frac{\partial^2 X_{i,j}}{\partial y^2}, \\ &\approx \frac{D_X}{d^2}\left(X_{i+1,j} + X_{i-1,j} + X_{i,j+1} + X_{i,j-1} - 4X_{i,j}\right).\end{aligned}$$

This spatial approximation can now be substituted in the PDE equations to give an ODE equation for each lattice point, which we can solve in the usual manner. Diffusion therefore acts like the movement of individuals between the four nearest-neighbor lattice sites. The rate of this movement (or coupling) is $\frac{D_X}{d^2}$, such that it is proportional to the diffusion coefficient but increases quadratically with the number of lattice sites that represent one unit length. It is therefore clear that PDEs can be approximated by very fine scale lattices, with very high levels of movement between neighboring sites.

Figure 7.13 gives an example of the types of spatio-temporal dynamics that can be observed using a PDE model for the spread of an SIR-type infection. Starting at a point source, infection spreads as an expanding epidemic wave, leaving secondary oscillations around the endemic equilibrium in its wake. The left-hand graph of Figure 7.13 shows a snapshot of this circular wave front. However, the right-hand graph provides a more intuitive understanding of the spatial pattern, plotting disease prevalence as a function of the distance from the initial source (black solid line). This is compared to the solution of the standard (nonspatial) SIR model (gray dashed line); clearly there is good agreement between these two, although due to the movement of susceptibles into infected regions, the PDE shows a slightly slower decay of the epidemic because diffusion of susceptibles is playing a comparable role to births, allowing infection to persist locally.

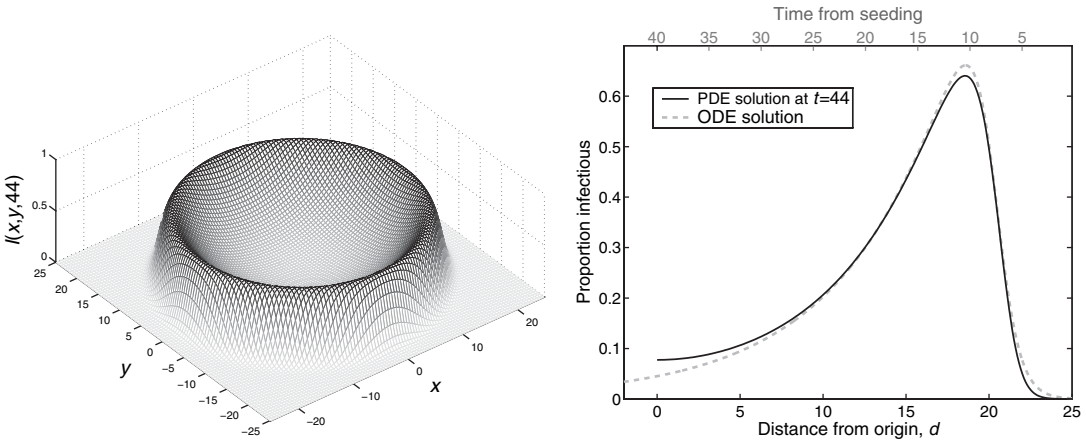

Figure 7.13. Results from the SIR-type PDE model equation (7.18). The left-hand figure is a snapshot, at time $t = 44$, of the density of infecteds in the PDE model. The right-hand figure compares the distribution of infection (at time $t = 44$) as a function of distance from the initial source, with the results from a standard (nonspatial) SIR model with the same basic parameters. For the nonspatial model the x-axis represents the time from the start of the simulation, whereas for the PDE model the x-axis represents the distance from the initial point of infection. The values on the x-axis have been scaled by the wave speed so that the two curves coincide. (The PDE was simulated using a 501×501 lattice, $N = 1$, $\nu = \mu = 10^{-3}$, $\gamma = 0.1$, $\beta = 1$, $D_X = D_Y = D_Z = 0.1$.)

The comparison between the diffusion-based PDE and the nonspatial SIR model hints at a deeper relationship. Involved mathematical calculation shows that, once transient dynamics have died away, the PDE leads to a traveling wave with constant velocity, c (Box 7.2). All such traveling waves (initiated at the origin) can be written as:

$$Y(x, y, t) = \widehat{Y}(r - ct), \qquad \text{where } r = \sqrt{x^2 + y^2}.$$

Therefore, if we stand in one place and record the wave moving past us, we observe the same profile as looking at the spatial wave form at a given time.

For PDE models (in two dimensions), infection spreads as a growing circular wave of near constant velocity.

7.4.2. Integro-Differential Equations

Integro-differential equations (IDEs) share the continuous-space and continuous-population assumptions of the PDE models, but provide far greater flexibility in the way in which infection is transmitted. The PDE model was concerned with the very localized spread of infection and the movement (diffusion) of individuals; in contrast, the IDE models focus on longer-range transmission from static individuals—although this latter constraint is not always true. Although a wide variety of model forms exist, the following

Box 7.2 Speed of Infection Wave

Calculating the invading epidemic wave speed analytically for a given set of diffusion-based PDEs is a complex procedure, which is covered comprehensively and in great detail by Murray (2003). Here we give a brief outline of the concept for the simple epidemic (with no births or deaths) in a two-dimensional population. We start with the basic equations together with host diffusion:

$$\begin{aligned}\frac{\partial X}{\partial t} &= -\beta XY/N + D\nabla^2 X,\\ \frac{\partial Y}{\partial t} &= \beta XY/N - \gamma Y + D\nabla^2 Y.\end{aligned}$$

We now assume that the number of susceptibles and infecteds are circularly distributed ($X(x, y, t) = \hat{X}(r, t)$, $Y(x, y, t) = \hat{Y}(r, t)$ where $r^2 = x^2 + y^2$); this changes the equations to:

$$\begin{aligned}\frac{\partial \hat{X}}{\partial t} &= -\beta \hat{X}\hat{Y}/N + D\frac{1}{r}\frac{\partial}{\partial r}\left(r\frac{\partial \hat{X}}{\partial r}\right),\\ \frac{\partial \hat{Y}}{\partial t} &= \beta \hat{X}\hat{Y}/N - \gamma \hat{Y} + D\frac{1}{r}\frac{\partial}{\partial r}\left(r\frac{\partial \hat{Y}}{\partial r}\right).\end{aligned}$$

Next, we assume that the dynamics can be written as a traveling wave solution with velocity c ($\hat{X}(r, t) = \tilde{X}(z)$, $\hat{Y}(r, t) = \tilde{Y}(z)$ where $z = r - ct$):

$$\begin{aligned}-c\frac{d\tilde{X}}{dz} &= -\beta \tilde{X}\tilde{Y}/N + \frac{D}{r}\frac{d\tilde{X}}{dz} + D\frac{d^2\tilde{X}}{dz^2},\\ -c\frac{d\tilde{Y}}{dz} &= \beta \tilde{X}\tilde{Y}/N - \gamma \tilde{Y} + \frac{D}{r}\frac{d\tilde{Y}}{dz} + D\frac{d^2\tilde{Y}}{dz^2}.\end{aligned}$$

Looking at the $\tilde{Y}$ equation, and assuming that r is large so that we are looking for the long-term large-radius dynamics:

$$D\frac{d^2\tilde{Y}}{dz^2} + c\frac{d\tilde{Y}}{dz} + \frac{\beta \tilde{X}\tilde{Y}}{N} - \gamma \tilde{Y} = 0$$

At invasion, when $X = N$, this differential equation only has wavelike solutions when $Ds^2 + cs + (\beta - \gamma) = 0$ has real solutions for s. This provides a lower bound for c; this lower bound is the observed wave speed:

$$c = 2\sqrt{D(\beta - \gamma)} = 2\sqrt{D(R_0 - 1)\gamma}.$$

Therefore, the wave speed is proportional to the square root of the diffusion coefficients, the square root of $(R_0 - 1)$, and the square root of the rate of recovery. This is an *asymptotic* wave speed, which only holds at large radii and once an invading wave front has fully developed.

relatively simple example illustrates the salient points of integro-differential equations:

$$\begin{aligned}\frac{dX(x,t)}{dt} &= \nu(x) - \lambda(x,t)X(x,t) - \mu(x)X(x,t),\\ \frac{dY(x,t)}{dt} &= \lambda(x,t)X(x,t) - \gamma Y(x,t) - \mu(x)Y(x,t),\\ \text{where } \lambda(x,t) &= \beta\int Y(y,t)K(x-y)dy,\end{aligned} \tag{7.18}$$

where the dependence on location, x (which could be in one, two, or more dimensions), and time, t, have been explicitly stated, and the demographic parameters are allowed to vary between locations. The equation for the number of susceptible and infectious individuals is the same as in Chapter 2; it is only through the force of infection, λ, that spatial interactions enter the dynamics.

The force of infection, $\lambda(x,t)$, models the transmission of infection from all points in space (labeled y in the integral) to the point x that we are considering. The transmission rate is assumed to vary with the distance between the susceptible and infectious individual $(x-y)$, and is described by a transmission kernel, K. In simple terms, K defines how infectivity decreases with distance. Clearly, this gives far greater flexibility than achieved by the PDE model; rather than transmission being a local event, it can now occur over a variety of scales. Equation (7.18) models transmission as a density-dependent process; making transmission frequency dependent is more complex because it depends on how we expect the transmission to operate. Two possible alternatives are:

$$\lambda_1(x,t) = \beta \int \frac{Y(y,t)}{N(y,t)} K(x-y)dy, \qquad \lambda_2(x,t) = \beta \frac{\int Y(y,t)K(x-y)dy}{\int N(y,t)K(x-y)dy}.$$

In the first formulation, it is the local proportion infectious at each point that is important, which most closely mimics the situation where interactions at each point y take place sequentially, so that transmission is based on the point frequency. In contrast, the second formulation corresponds to simultaneous interaction with individuals from a range of points, such that it is the averaged proportion infectious that is important.

With integro-differential equations, the spatial spread of infection is via a transmission kernel that defines how transmission risk decays with distance.

Various properties can now be defined for this type of model. Here we will assume that demographic and epidemiological parameters are invariant across space and that space is infinite and two-dimensional, but this does not necessarily have to be the case. To simplify the calculations we rescale the parameters such that the population density at each point is one, $N=1$. First, we consider R_0, which again will predict the likely success of an epidemic.

$$R_0 = \beta \int_{\mathbb{R}^2} K(y)dy = 2\pi\beta \int_0^\infty rK(r)dr.$$

Therefore, for the basic reproductive ratio to be finite we require that the kernel, $K(r)$, eventually decreases faster than r^{-2}. If the kernel decays more slowly (has a "fat tail"), then the integral is infinite; it is difficult to envisage situations where this is a reasonable assumption. In a similar manner, the average dispersal distance, D, is given by:

$$D = \frac{\beta \int_{\mathbb{R}^2} \|y\| K(y)dy}{\beta \int_{\mathbb{R}^2} K(y)dy} = \frac{2\pi\beta}{R_0} \int_0^\infty r^2 K(r)dr,$$

and for this to be finite requires that the tail of $K(r)$ decays faster than r^{-3}. Finally, when the variance of the dispersal distance $var(D)(= \frac{2\pi\beta}{R_0} \int_0^\infty r^3 K(r)dr - D^2)$ is also finite ($K(r)$ decreases faster than r^{-4}), we observe a wave of infection that moves with a constant speed. However, if the variance is infinite but the average is finite ($K(r)$ decays slower than r^{-4} but faster than r^{-3}), the wave front accelerates indefinitely (Diekmann 1978; van den Bosch et al. 1990; Mollison 1991; Shaw 1995). Therefore, Gaussian and