Epidemic Thresholds and Vaccination in a Lattice Model of Disease Spread

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Received December 1, 1995

We use a lattice-based epidemic model to study the spatial and temporal rates of disease spread in a spatially distributed host population. The prevalence of the disease in the population is studied as well as the spread of infection about a point source of infection. In particular, two distinct critical population densities are identified. The first relates to the minimum population density for an epidemic to occur, whilst the second is the minimum population density for long-term persistence to occur. Vaccination regimes are introduced that are used to measure the impact of spatially and nonspatially dependent intervention strategies. Specifically we show how a ring of vaccinated susceptibles, of sufficient thickness, can halt the spread of infection across space.

1. INTRODUCTION

Recently there has been renewed interest in the effect of spatial heterogeneity in modelling dynamic processes in ecology, epidemiology, and evolutionary biology. Due to increases in computational power this important feature of most real interacting populations can be addressed using a diverse variety of techniques.

The first point of departure for many epidemiological studies is a set of deterministic mass-action-based differential equations incorporating the major epidemiological features of the disease in question (Anderson and May, 1991; Bailey, 1975). An early investigation of the likely impact of spatial heterogeneity on the vaccination requirement for the eradication of a canonical infectious disease is by May and Anderson (1984). They considered a host population that predominantly inhabited one large city with the remaining fraction evenly distributed amongst a number of small villages. With the reasonable assumption that intragroup transmission is higher than intergroup transmission, an optimally applied immunisation program to eradicate the infection can result in fewer individuals being vaccinated than would be estimated by assuming the population mixes homogeneously. The corollary to this is that a uniformly applied immunisation schedule will require more vaccinations than the homogeneous case.

One of the most thoroughly studied diseases is measles virus infection in humans. The basic SEIR equations which are often used in quantitative discussions of measles infection can be enhanced by the addition of more important realistic features such as age-structured transmission rates (Schenzle, 1984). Corresponding stochastic implementations of this program of work, using Monte Carlo simulation techniques, have also been extensively studied (Grenfell, 1992; Olsen et al, 1988; Olsen and Schaffer, 1990). Generalisation of both the deterministic and stochastic models to allow for spatial heterogeneity result in meta-population models. The population is divided amongst a number of distinct sites with a conventional SEIR process within each site, as well as a coupling term allowing influence proportional to the magnitude of infection at the other sites (Bolker and Grenfell, 1995). Most of this corpus of work has been aimed at reconciling observed persistence and temporal dynamic patterns as observed in real measles data sets. However, the conventional mass-action assumption is retained for the within-patch dynamics and there is as yet
no a-priori way of assigning the coupling magnitudes between patches.

A second widely used method to account for a spatially dispersed population is the diffusive approach. Population movement is accounted for by the addition of diffusion terms to the conventional coupled differential equation systems. Such models have been used to study likely spread of rabies in the U.K. (Murray et al., 1986) and the actual spread of the Black Death (Noble, 1974) across medieval Europe. Any likely impact of demographic stochasticity cannot be assessed as these are continuum models.

A more recent trend in modelling spatial effects has been the use of lattice methods. In these systems the spatial distribution of the population is explicitly represented by the use of a discrete set of (usually square) lattice points. A set of rules then defines the range of possible interactions between the individuals on the lattice and their range of movement, if any. Pacala, Hassell, and May (1990) and Hassell, Commins, and May (1991) used this approach to investigate spatial host–parasitoid interactions. The resulting dynamical behaviour is very rich, with the spontaneous emergence of ordered phases, consisting of spiral waves and regular “crystal” arrangements, as well as chaotic patterns. From a population biology perspective the important conclusion that can be drawn is that the combination of a spatially heterogeneous environment and local dispersion can stabilise otherwise unstable host–parasite arrangements. A related study is that of Rand et al. (1995) on a generic host–pathogen dies out and, if mutation of the transmissibility is allowed, evolution of transmissibility towards this critical value occurs. This appears to be a novel consequence of using a spatially extended host population.

In the area of evolutionary biology Nowak and May (1992) introduced a lattice implementation of the Prisoner’s Dilemma approach, conventionally used to study the emergence of cooperative behaviour. As in the other lattice methods the appearance of spatially ordered structures or chaos is a feature.

More general spatial models in epidemiology and ecology, using interacting particle systems, were studied initially by Mollison (1977, 1991) in order to introduce the stochasticity and nonlinearity inherent in dynamical processes occurring in the natural world. More recently this approach has been developed by Cox and Durrett (1988), Durrett and Neuhauser (1991, 1994), and Durrett and Levin (1994a, 1994b). These models are similar in spirit to our approach and additionally they are able to obtain some analytic results for spatial contact processes in some instances. Durrett and Levin (1994a) compare the use of mean field approaches (i.e., coupled ordinary differential equations), patch models, reaction diffusion models, and interacting particle models, as applied to three examples of spatially distributed interacting populations, and make thorough and illuminating comparisons between the results obtained for each of the different methods. Durrett (1995) has recently provided the most up-to-date summary of spatial contact processes as applied to the spread of epidemics and this is the individual-based system about which most is now known.

In this paper we discuss results obtained using a lattice implementation of a simple epidemic process in a uniform, spatially distributed, and mobile population. Particularly, we are interested in the conditions for an epidemic to occur and the impact of a variety of vaccination schedules on the endemic fixed point. Previously we have studied similar lattice models and their relation to mean-field formulations (Rhodes and Anderson, 1996a, and 1996b). As discussed below, the lattice approach provides a model for epidemic spread where the host population exists in integral units and each individual interacts with those other individuals in its immediate neighbourhood. Individuals may be susceptible, infective, or recovered and birth/death processes can take place with the desired frequency. Disease transmission occurs by the stochastic infection of a susceptible by a neighbouring infective, and spread takes place when infectives mix by diffusion amongst susceptibles. These are all features of disease spread that are in tune with our intuitive understanding of how epidemics of simple communicable diseases occur in the real world and are what gives lattice models their appeal as a method for studying epidemiological dynamics.

2. THE MODEL

In the lattice epidemic model the host population inhabits a square ($L \times L$) grid of points usually taken to be of dimension $100 \times 100$. During a given time-step each individual is free to move from its current node to any of the eight nearest neighbour nodes which happen to be uninhabited, or it can remain where it is. Each of the possible movements, or the possibility of remaining stationary, occurs with equal probability. A set of transition rules then determines the nature of the interaction of susceptible individuals with any other infective individuals who may be at any of the four nearest neighbour lattice points. We have in mind the modelling of a simple nonfatal communicable disease in a population which remains constant in size.
The probability that a susceptible becomes infective when adjacent to an infective is a variable, $p$, set at the start of a simulation (in more sophisticated models this transmission parameter can be made to vary in a time-dependent way, but we do not consider that possibility here). The population density, $C$, is kept low ($\approx 0.2$) to order that overcrowding and the inability of individuals to make a move does not start to affect the dynamics. To mirror the epidemiological situation we wish to model, each member of the host population is either susceptible, infective, or recovered. The susceptibles remain in the susceptible class until such a time as they become infected. Once in the infected class individuals may recover from infection with a probability $p_s$; thus they spend an average time span of $1/p_s$ as an infective. From the infective phase the individuals move into the recovered phase. After recovery, individuals can move back into the susceptible phase with probability $p_x$, where $p_x < p_s$. This is a simple device to simulate birth–death processes whilst keeping the population density constant. In our simulations we have set $p_x = 0.1$ and $p_s = 0.05$; so the life-time of the individuals on the lattice is longer than the time spent as an infective, but not so long as to make the simulation times unmanageably time-consuming and it allows us to see the effect of replenishment of the susceptible class. It is a straightforward matter to include an exposed class of individual in the model, namely those who have been infected with the disease but who are not yet capable of transmitting the disease to other susceptibles. Although the inclusion of an exposed class would add a measure of epidemiological realism to our model, we do not do so here as it introduces another parameter (an average incubation period) and increases stochastic effects for a given population size (as the total population would be divided amongst four, as opposed to three, classes).

In overall structure the model is similar to that of Boccara and Cheong (1992) who used a lattice approach to show the importance of population mixing in disease spread. A related epidemic model, using a static host population, is discussed in Johansen (1994, 1996). Periodic boundary conditions are imposed on the lattice and at each time step the numbers of susceptibles, infectives, and recovereds are recorded. This lattice formulation does not impose any fragmentation of the population into patches and at each time-step every individual is interacting with only its local neighbourhood of individuals. The infection process generates a spatially localised increase in disease correlation which is dissipated over time by the motion of the infectives. Propagation of the disease relies on the physical mixing of infectives into regions of susceptible density.

Additionally, the model has a straightforward mean-field limit. Following Boccara and Cheong (1992) the mean-field equations are

$$ \dot{S}(t+1) = \dot{S}(t) - \dot{S}(t)\{1 - (1 - p)\rho(t)^4\} + b\dot{R}(t) $$

$$ \dot{I}(t+1) = \dot{I}(t) + \dot{S}(t)\{1 - (1 - p)\rho(t)^4\} - a\dot{I}(t) $$

$$ \dot{R}(t+1) = \dot{R}(t) + a\dot{I}(t) - b\dot{R}(t), $$

where

$$ \dot{S}(t) = \Sigma_{i,j} S_{i,j}(t)/L^2 $$

$$ \dot{I}(t) = \Sigma_{i,j} I_{i,j}(t)/L^2 $$

$$ \dot{R}(t) = \Sigma_{i,j} R_{i,j}(t)/L^2 $$

and $a^{-1} = p_s, b^{-1} = p_x$.

At equilibrium

$$ \dot{S}(t+1) = \dot{S}(t) = \dot{S}^* $$

$$ \dot{I}(t+1) = \dot{I}(t) = \dot{I}^* $$

$$ \dot{R}(t+1) = \dot{R}(t) = \dot{R}^*. $$

Solving for $\dot{I}^*$ (for $\dot{I}$ small) we find

$$ \dot{S}^* = \frac{a}{np} $$

$$ \dot{I}^* = \frac{C - a^2p}{(1 + a/b)} $$

$$ \dot{R}^* = \frac{a(C - a(np))}{a + b}. $$

In the simulation we can recover agreement with these equations by randomly redistributing the entire population over the lattice after each time-step, as this effectively destroys any build up of localised clustering of infection.

Expanding about the fixed point $\dot{S}(t) = \dot{S}^*(t) + \delta(t)$ and $\dot{I}(t) = \dot{I}^*(t) + \eta(t)$, we can establish the stability of the fixed point $\dot{S}^* = C$ and $\dot{I}^* = 0$. We are led to the characteristic equation

$$(\lambda_1 + b)(npC - a - \lambda_2) = 0. $$

Therefore the eigenvalues are $\lambda_1 = -b$ and $\lambda_2 = npC - a$. Stability requires that $C < anp$; otherwise, above this critical population density a saddle point results in an endemic level of infection with $\dot{I}^* \neq 0$. We have shown how by gradually increasing the hopping range of the population on the lattice (Rhodes and Anderson, 1966b)
it is possible to smoothly interpolate from the fixed point of a simulation to the fixed point of the mean-field equations, clearly demonstrating the effect of increased mixing and spatial heterogeneity on the prevalence of disease in a population.

At the start of a conventional simulation a number of susceptibles are randomly scattered over the lattice nodes. A single Infective "seed" is then placed at the centre of the lattice to initiate the course of infection in the population. We can monitor the total number of infectives as a function of time as well as the spatial distribution of the infectives.

3. EPIDEMIC TIME SERIES

Because of the stochastic nature of the simulation process each realisation of an infectious time-series will be different. Consequently we take the mean and variance of a large number of simulations and see how these quantities stabilise as the ensemble of simulations increases in number. At each time step we have a mean number of infectives on the lattice and an associated variance. In Fig. 1 a typical time-series for the mean number of infectives is shown. The population density is 0.1. An average over 100, 250, 400, and 500 separate simulations was taken to obtain the four profiles in the figure. Above 400 simulations the mean has stabilised and increasing the number of runs any further does very little to add any increase in the numerical accuracy of the result. Figure 2 shows the associated square-root of the variance as a function of time for each of the graphs in Fig. 1. Again, this quantity stabilises to a well defined limit above 400 simulations. Whilst we cannot predict the outcome of an individual realisation of a simulation, the mean and variance at least give us statistical estimators of the likely infective population size as a function of time. From this approach we can begin to investigate whether a given host population density is likely to maintain the disease in an endemic state. From this we infer that the population density of 0.1 is below the critical population threshold. As when using any stochastic model it is necessary to bear in mind the expected size of variance of the infective population when estimating quantities such as the time-to-extinction or the critical community size.

**FIG. 1.** Time series of the mean number of Infectives in a lattice epidemic simulation. We use $p = 0.5$, $p_i = 0.1$, and $p_s = 0.05$ and a lattice size $L = 100$. The population density $C = 0.1$. Ensemble averages over 100, 250, 400, and 500 simulations are shown. All subsequent simulations, the results of which are shown in the figures below, use these same parameters for ease of comparison.
FIG. 2. The square root of the variance for the simulations in Fig. 1.

FIG. 3. The coefficient of variation as a function of time obtained from Fig. 1 and Fig. 2.
FIG. 4. The mean number of infectives as a function of time for a population density $C = 0.2$.

FIG. 5. The coefficient of variation relating to Fig. 4.
As the magnitude of the variance is related to the infective population size it is useful to look at the coefficient of variation, that is $CV(t) = \sqrt{\text{Var}(t)}/\text{Ave}(t)$. In Fig. 3 $CV(t)$ as a function of $t$ is plotted. Clearly this quantity diverges and is $>1 \forall t > 70$. After 70 time-steps the standard deviation is greater than the mean which implies that some realisation are dying out. The implication of this is that we will see fade-out of the infection in the population.

In Fig. 1 the disease is unable to maintain itself in the host population. If we increase the population density on the lattice above a certain threshold the disease becomes endemic. Figure 4 represents this situation and as before we plot the mean of the infective population as a function of time for ensembles of up to 500 simulations. The host density on this case is 0.2, corresponding to 2000 individuals. The disease appears to maintain itself in the population, with $CV(t) < 1$ $\forall t$, as is clearly shown in Fig. 5.

This simple spatial model of epidemic spread is capable of reproducing the intuitively understood idea that as a population increases in density it is more capable of sustaining endemic infection. A criterion for persistence would appear to be $CV(t) < 1$ $\forall t$. For the parameters used in the above simulations this occurs for a host population density of 0.14.

It is possible to generate a rough estimate of this population threshold from the rate of decline of infectives in the subendemic situation. From the stability analysis above we know that perturbations decay at a rate

$$\delta(t) \approx \delta(0)e^{-(a-npC)t},$$

so if $t_{1/2}$ is the time taken for the number of infectives to decline by a factor of 2, we can estimate the “effective” number of neighbours, $n_{\text{eff}}$, as a phenomenological parameter,

$$n_{\text{eff}} = n \approx \frac{a}{pc} \frac{\ln 2}{pCt_{1/2}}$$

and the threshold for persistence will be given by

$$C = \frac{a}{pn_{\text{eff}}}.$$  

From Fig. 1 the estimated $t_{1/2}$ is around 50 days which gives $n_{\text{eff}} = 1.72$, implying that the threshold for

![FIG. 6. Phase space plot for the lattice epidemic model showing the evolution to the endemic fixed point and the extinct fixed point.](image_url)
persistence is a population of approximately 1200 individuals. Clearly this calculation, relying as it does on $n_{\text{crit}}$ being weakly dependent on $C$, provides only a rough estimate of the critical population threshold. In the next section we will discuss population thresholds in more detail.

Our results can be compared with those obtained in the lattice model of Johansen (1994, 1996), where infection is introduced into a stationary spatially distributed host population. There oscillation in the numbers of infectives is seen, resulting from the emergence of organised coherent motion of fronts across the lattice, followed by regrowth of susceptibles after the fronts have passed. In our case, movement of the population across the lattice would appear to destroy any tendency to oscillation, resulting in a stable fixed point rather than a noisy limit cycle as Johansen observes. In the limit of infinite lattice size the oscillations observed by Johansen disappear. At most animal and human populations are mobile lattice simulations suggest that any oscillations that are observed in disease incidence probably arise from seasonal effects or other forms of host heterogeneity.

Figure 6 is a phase-space plot for three population densities showing the emergence of the endemic fixed point. It is a fixed point in the sense that for any given set of model parameters, $L, p, p_s, p_x$, and $S_x$, the system will evolve to the same endemic level, regardless of the number of infectives, $I_s$, initially present on the lattice at the start of the simulation. Each trajectory is made up of a sequence of plots of the mean infective and susceptible populations after 500 simulations. We have to bear in mind that each of the points along each of the trajectories should be surrounded by an “error ellipse” whose major and minor axes correspond to the variances of the infective and susceptible populations.

4. EPIDEMIC SPREAD

In models that utilise a spatially distributed population the formation of wave-fronts can occur under the right conditions. For example, the model of a rabies epidemic in the event of a U.K. outbreak by Murray et al. (1986) demonstrates the propagation of an epizootic front through the susceptible fox population. Recent data for the spread of rabies across continental Europe (Anderson et al., 1981) shows a frontlike progress, where propagation is faster in regions of higher fox density. Clearly such spatially explicit models have great scope for investigating the effect of various intervention strategies, be that involving culling or vaccination. Similarly, in the model of Noble (1974) for the spread of plague in human populations, the rate of progress of the disease can be estimated from epidemiologically derived parameters yielding acceptable agreement with the historic record of the epidemic’s progress after its introduction into southern Europe in 1347. The epidemic simulation model we have used is rather less directly applicable than the coupled differential equation approach in that, at present, estimations of epidemiological parameters and their relation to variables in the simulation has not been solved uniquely. However, the model does show many of the expected properties of epidemic spread through a spatially distributed population and we are nevertheless able to gain some insight.

The formation of wave-fronts in the various classes of cellular automata is itself a matter of some general interest (Schonfisch, 1995), although here we confine our discussion to disease spread.

In the above section we concluded that there is a certain threshold density of host population above which an infection can remain endemic. To investigate how this arises it is necessary to look at the spatial dynamics of the infection. If we place a seed of infection at the centre of a lattice populated wholly by susceptible hosts then, broadly speaking, three possible outcomes may arise for the time-course of the disease. The simplest outcome is that the disease in incapable of spreading into the bulk of the population and, over a time-scale of the average duration of infection for a host, the seed of infection simply fades out. Alternatively, the population density might be high enough for the seed of infection to generate a positive number of secondary infectives, so at some time $t > 0$ we have $I > I_s$. This is generally what is meant by an epidemic threshold. However, it is possible that these secondaries are unable to sustain the chain of infection and these, too, will ultimately fade out, even though the infection may have spread out some distance into the population. A third possibility is that the population density is sufficient to maintain the chain of infection and a “front” of infection appears to move out concentrically from the source of infection at the centre of the lattice. It continues to move radially outwards until it reaches the edge of the lattice. What happens at this stage is very much dependent on the choice of boundary conditions. For simplicity we have used periodic boundary conditions where opposite sides of the lattice are mapped onto each other.

In Fig. 7 we show the time series for the infection where the density of population, 0.05, is too low for the epidemic to occur and $I < I_s$, for $t > t_e$. Figure 8 shows the radial density of infectives on the lattice for $t = 30$, $t = 50$, and $t = 70$ time-steps. The abscissa is the radial
FIG. 7. Time series of number of infectives for a population density of $C = 0.05$ (i.e., $<S_{c1}$). The dots indicate the three times at which the radial distribution of infectives are measured. An ensemble average over 500 simulations is shown.

FIG. 8. The radial density distribution of infectives for a population density of $C = 0.05$ (i.e., $<S_{c1}$). Three times-steps, corresponding to the radial distribution of Infectives at $t = 30$, $t = 50$, and $t = 70$, are shown.
FIG. 9. Time series of number of infectives for a population density of $C = 0.08$ (i.e., $> S_1$). An ensemble average over 500 simulations is shown.

FIG. 10. The radial density distribution of infectives for a population density of $C = 0.08$ (i.e., $> S_1$). Three time-steps are shown.
FIG. 11. Time series of number of infectives for a population density of $C = 0.2$ (i.e., $> S_c$). An ensemble average over 500 simulations is shown.

FIG. 12. The radial density distribution of infectives for a population density of $C = 0.2$ (i.e., $> S_c$). Three times-steps are shown.
5. VACCINATION STRATEGIES

One of the central motivations for developing models of epidemic disease is so that an estimate of the likely impact of any vaccination strategy can be assessed. In our model, as we are not considering age-dependent or seasonal effects, it is sufficient to determine some critical fraction of susceptibles to be vaccinated in order to eradicate the infection. Due to the spatial nature of the model we can look at the spatial distribution of vaccination coverage. Vaccination involves moving a chosen susceptible directly into the recovered class. We are primarily interested in studying the reduction of the endemic disease intensity by vaccination as would be applied to human populations and to some animal populations. The simplistic mixing patterns that occur in our model due to movement of individuals on the lattice means that our vaccination schedules and conclusions should not be interpreted as directly addressing disease eradication programmes in human communities. Much greater social and spatial heterogeneity would be required in the model in order to do this. As in any computational simulation study of this sort there are myriad epidemiological scenarios that can be considered, so inevitably we must select a subset of cases for examination. Also, our investigation is circumscribed by the fact that we do not, as yet, have a comprehensive working phenomenology for the spatial dynamics of the model.

As noted above, the model can be used in two regimes. First (Case 1), we can consider the endemic state to represent a fixed point of the dynamics of the disease model and thus determine the fraction of susceptible hosts who have to be instantaneously vaccinated at every time-step in order for complete eradication to occur. An alternative strategy is to adopt a "pulsed" vaccination campaign. At temporally space intervals a predetermined proportion of the susceptible population is vaccinated. In neither the continuous nor the pulsed vaccination schedule is the spatial dependence of the susceptibles taken into account when vaccination is administered; our only concern is the proportion of susceptibles to be vaccinated.

Second (Case 2), we can consider a point source of infection appearing at the centre of the lattice which sets up a propagating front of infection which moves radially outwards to the boundary. A sensible approach in this instance is to vaccinate only those (or a proportion of those) susceptibles found within an annulus centered on the source of the outbreak, creating a ring-like region of suppressed susceptible density. This forms a "fire-break," the purpose of which is to dissipate the "energy" of the infective wave-front so that it cannot propagate into the
susceptible population beyond. In this case the spatial location of susceptibles as well as the proportion to be vaccinated are of concern here. Note also that the vaccinated ring is not a static entity; it begins to disperse due to the intrinsic mixing effect due to the motion of the individuals that made it up at the time of formation. From the time the vaccinated ring is constituted to the time the front reaches it, the density of recovereds in the ring will have reduced slightly. One can imagine for extreme choices of parameters a situation where the density of the ring has reduced to such an extent as to render it ineffective at epidemic control when the front is finally incident upon it. If we were to model a real epidemic containment scenario, where resources are finite, we might have to consider the effect of using a second or perhaps a third concentric vaccination ring, where each ring reduces the intensity of the epidemic. Because of computational limitations we have not attempted to model such a strategy yet. Instead, we maintain the density of vaccination ring by repeatedly vaccinating a proportion of the susceptibles found in the ring at that time. This avoids any complications due to ring dispersal or depletion.

Case 1. Figure 13 shows the number of infectives as a function of time for a population density of 0.2. A vaccination regime is introduced at \( t = 250 \). At each subsequent time-step a proportion of the available susceptibles currently on the lattice are vaccinated. Three schedules are shown, 1%, 3%, and 5% of available susceptibles are vaccinated at each time-step. For 1% vaccination the model simply moves to a lower endemic fixed point. On the other hand, vaccination of 5% of available susceptibles eliminates the infection. Simulations show that the threshold proportion of vaccinations to eliminate the disease is approximately 3%. This number will vary as other parameters in the simulation are changed, but most interestingly, as the population density is increased (keeping the epidemiological parameters constant) simulations show that the vaccination proportion for the elimination of infection must be increased. Greater population crowding makes for easier disease spread, hence, the greater the proportion to be vaccinated.

As discussed above, a pulsed vaccination strategy can also be considered. Figure 14 illustrates the time-series of infectives when such a regime is introduced. There are numerous combinations of time-interval and vaccination

![Graph showing vaccination of population density with 1%, 3%, and 5% of susceptibles vaccinated every time-step.](image-url)

**FIG. 13.** Vaccination of population density of \( C = 0.2 \) with 1%, 3%, and 5% of susceptibles vaccinated every time-step. Ensemble averages over 500 simulations is shown.
proportions that could be tried in such an experiment. The illustration shows 50% and 100% of susceptibles being vaccinated every 25 time-steps. Extensive simulations show that the threshold for elimination is such that approximately 90% of susceptibles should be vaccinated in each pulse. Interestingly, for our parameters chosen here, it would seem that there is an upper critical time interval (of the order of 30 time-steps) for vaccination to lead to eradication. Vaccinating 100% of susceptibles every 40 time-steps could never lead to elimination of infection. As the population density increases this critical time interval gets shorter. Also, the closer in time the pulses of vaccination occur the less the proportion of susceptibles who have to be vaccinated.

Case 2. A single infective is placed at the centre of a lattice with a host population density of 0.2. Without vaccination we would expect a front of infective density to move outwards to the edge of the lattice as illustrated in Fig. 12. The vaccination strategy this time involves maintaining over time a vaccinated proportion of the susceptibles which are found in a circular ring about the focus of infection from the moment the infection takes hold at the centre of the lattice. In our vaccination scenario we confine out attention to the simplest possible case; assuming we can vaccinate all the susceptibles in the ring, is the ring sufficient to halt the spread of the disease across the lattice, and what is the minimum thickness of the ring required to do this? A population of 2000 individuals are placed on the lattice and an infected index case is introduced at the centre. A vaccination ring is set up with inner radius of 15 lattice spacings and the outer radius can be set as required. Figure 15 shows the ring of vaccinated cases around the focus of infection with an inner radius of 15 and an outer radius of 25 at the beginning and towards the end of a typical simulation. This clearly illustrates how the ring of vaccination seeks to isolate those susceptibles outside the ring from the infectives within. We have performed a series of simulations for vaccination rings of increasing thickness, and the radial density of infectives as a function of time are shown in Fig. 16. For thin rings the front is able to move relatively unimpeded across the lattice and it is possible to transfer infective density into the pool of susceptibles beyond the ring. As the thickness increases it becomes increasingly difficult for infectives to cross the barrier in any number and eventually there reaches a critical minimum width of the order of 10 lattice spacings above.
FIG. 15. A pictorial representation of the lattice. Susceptibles are indicated by crosses, infectives by squares, and the recovereds by circles. The top panel shows the location of the ring of vaccinated individuals soon after formation and the lower panel shows the situation some 60 time-steps into a typical simulation. Note that all the infectives are contained within the ring of vaccination.

FIG. 16. Radial density of infectives at time $t = 30$, $t = 50$, and $t = 70$ timesteps. Vaccination rings of increasing thickness are used. The position of the inner and outer limit of the rings are shown by the vertical lines on the radial axis. The top panel has a vaccination ring of width-2 lattice spacings; the middle panel has a width-5 lattice spacings and the bottom panel has a vaccination ring of width-10 lattice springs. In contrast, Fig. 12 shows what happens when the spread is unimpeded by any zone of vaccination.
which there is no further progress of the front of infection once it hits the ring. For vaccination rings greater than 10 lattice spacings all the infective density is confined to the space within the region that has been vaccinated for as long as the ring is maintained.

These simulations suggest that ring vaccination around known foci of infection can be an effective method for reducing disease incidence when we have a mobile spatially distributed population. Providing the ring is maintained at sufficient density, the mobility of the infectives is no guarantee that the epidemic front can transcend the barrier. Clearly, though, in human communities, particularly in the developed world, individuals can be highly mobile and ring vaccination is not likely to work well, because a vaccination ring of enormous width would be required, effectively resulting in a mass-vaccination policy. In the past, most studies of spatial vaccination strategies have used continuum-based epidemiological models with additional diffusion terms. Although it is sometimes possible to obtain analytical results for the required width of vaccination zones, there is a problem with the appearance of unfeasibly small residual regions of infective density which can generate further epizootics long after the initial wave has passed, which can lead to erroneous interpretations of observed dynamics. Our approach can be seen to eliminate this problem. By developing the individual-based lattice model it should be possible to circumvent problems of this sort and investigate vaccination strategies within a framework that allows for spatial distribution of the host population and its ability to move through mixing.

6. DISCUSSION

We have used a lattice-based SIR epidemic model to study the spatio-temporal evolution of infection in a spatially distributed host population. It is one amongst a number of different models introduced recently that tries to account for the effect of spatial heterogeneity on epidemic spread. As yet we have no a-priori method for calculating this threshold in the lattice model. Also, as the model is stochastic, we have presented means and variances of an ensemble of simulations, giving an idea of the number required to obtain a stable mean and variance for a given population density. Empirical investigation of the model indicates that that persistence is possible when \( CV(t) < 1 \forall t \). The simulations above are the simplest representation of the epidemic process. Development of the model, by adding further refinements, such as age-structured contact rates, subgroups with different mobilities, inhomogeneously distributed population (the list could go on, reflecting whatever epidemiological situation we wished to model) would greatly add to the appeal of this approach. Before these additions are made, however, an understanding of the basic processes at work in this class of model is required.

To investigate the spatial dynamics of the model we tested the response of the model to a point source of infection placed at the centre of the lattice. For sufficiently high population densities, a front of infection could be seen moving radially outward from the source of infection. To the accuracy obtainable in the simulations the velocity of the front appears to be constant. For lower host population densities the the front of infectives dissipates before reaching the boundaries of the lattice. Two distinct regimes of behaviour are evident in the model. In the first, a front of infection can be seen to propagate radially outward from a point source of infection at the centre of the lattice. For low population densities the propagation dissipates before reaching the edge of the lattice. For sufficiently high densities the front reaches the edge of the lattice and long-term persistence ensues. For the interval of time before the front reaches the lattice edge a coherent spatial distribution of infectives can be seen. The uniform preepidemic density of susceptibles exists ahead of the front and suppressed susceptible population density is evident behind it. In the second, long term persistence occurs by virtue of the fact that we have periodic boundary conditions and a replenishment of fresh susceptibles at a suitable rate. There is no overall spatial organisation relating to this state.

A natural extension of the model is to include vaccination of susceptibles. There exist clear thresholds for the proportion of susceptibles that have to be vaccinated in both continuous and pulsed vaccination strategies. A spatially explicit ring-vaccination strategy showed the effect of the front of infection impinging upon a region of low susceptible density and how this obstructs the movement of infective density into regions beyond the ring. In this model complete protection of the susceptible population beyond the ring seems to be afforded.

The simulations show many of the aspects associated with disease spread, although we have got no further on the issue of parameter estimation. Clearly, if better parameter estimation becomes available for spatial disease processes then incorporating those parameters into this kind of lattice model might prove useful in assessing the usefulness of the sort of vaccination strategies considered above. Also, as stressed by Durrett and Levin (1994b), despite the fact that a lattice model of interacting individuals naturally incorporates spatial distribution and population discreteness effects, quantitative
predictions are, on the whole, impossible to obtain. We can only really expect to see the emergence of a qualitative understanding of the role of each of the variables in the model. Although still at an early stage in its development, spatial interacting particle models show much promise as an approach to studying the dynamics of disease in spatially distributed host populations. However, using a related lattice-based approach we have recently been able to account for the dynamics of measles epidemics in small isolated populations (Rhodes and Anderson, 1996c).

The lattice epidemic model is quite general and flexible and could be applied to a variety of animal epizootics too. For rabies would be probably be a suitable case to model as the animals tend to remain within home ranges and good spatial and temporal data is available for U.K. urban foxes (Smith and Harris, 1991). A good model of spread would be required in the event of outbreak in the U.K. in order to quantify the effect of various containment strategies. In that case we are likely to see a front of infection spreading out from the focus of infection (probably in a large urban centre), with a requirement for culling/vaccination intervention in a circle outside the wave-front. As understanding of the lattice and interacting particle system approaches increases this epizootic systems might be a useful place to investigate realistic parameterisation. Additionally, using our model framework, it would be straightforward (if it were found to be necessary) to introduce animal motion parameterised by Levy statistics as has recently been observed in radio-tracking experiments (Viswanathan et al., 1996). The presence of such patterns of motion would have a significant impact on the spread of communicable disease in those animal communities where it was observed.

ACKNOWLEDGMENTS

The authors thank the Wellcome Trust for kindly providing research support. We also thank Dr. C. Neuhauser of the Department of Ecology and Evolutionary Biology, Princeton University, for useful discussions and the referees for many helpful comments.

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