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DEPENDENCE OF EPIDEMIC AND POPULATION VELOCITIES ON BASIC PARAMETERS

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ABSTRACT

This paper describes the use of linear deterministic models for examining the spread of population processes, discussing their advantages and limitations. Their main advantages are that their assumptions are relatively transparent and that they are easy to analyse, yet they generally give the same velocity as more complex linear stochastic and nonlinear deterministic models.

Their simplicity, especially if we use the elegant reproduction and dispersal kernel formulation of Diekmann (1978) and van den Bosch *et al* (1990), allows us greater freedom to choose a biologically realistic model, and greatly facilitates examination of the dependence of conclusions on model components and of how these are incorporated into the model and fitted from data. This is illustrated by consideration of a range of examples, including both diffusion and dispersal models and by discussion of their application to both epidemic and population dynamic problems.

A general limitation on fitting models results from the poor accuracy of most ecological data, especially on dispersal distances. Confirmation of a model is thus rarely as convincing as those cases where we can clearly reject one (see §4.1, §4.4).

We also need to be aware that linear models only provide an upper bound for the velocity of more realistic nonlinear stochastic models, and are almost wholly inadequate when it comes to modelling more complex aspects such as the transition to endemicity and endemic patterns. These limitations, which will be discussed in §§4.5-7, are, however, to a great extent shared by linear stochastic and nonlinear deterministic models.

1 INTRODUCTION

1.1 Basic model components

Many potentially useful conclusions from models for spatial spread are sensitive to the assumptions made in formulating and fitting them, and it is therefore essential that they be formulated in a way that presents such assumptions clearly and encourages their discussion by both theorists and applied workers. It is usually most helpful if models are framed as far as possible in terms of basic ecological parameters that are readily understood and (as far as possible) can be estimated from data.

In this subsection we introduce the main ecological components involved in the spatial spread of epidemics and populations. In the next (§1.2) we shall illustrate their use in a simple example, a spatial *epidemic with recovery.*

The *basic reproductive ratio* R_0 is the mean number of contacts made by an infective (or in the population context, the mean number of offspring). R_0 plays a crucial part in determining whether an epidemic outbreak can occur.

The time T of a typical infection relative to that of its 'parent' infective we call the *generation gap*, and its relative location in space X the *dispersal distance* (strictly this should be the dispersal *vector*). We call the distribution of T the *reproduction kernel* B, and that of X the *dispersal* or *contact* distribution V.

Note that T is not the same as the *lifetime* T', defined for an epidemic as the time from infection of an individual to the end of that individual's infectious period. In the population context, T is the age of the parent at the birth of a typical offspring, and T' is the lifetime of an individual. While for any individual T is, of course, less than its parent's T', the fact that individuals with large values of T' tend to have more offspring means that the average value of T is not necessarily less than that of T'. Confusingly, T and T' have exactly the same distribution in the case where contacts are made at a constant rate (i.e. in a Poisson process) during an exponentially distributed infectious period; this is one of a number of simple 'paradoxes' associated with the Poisson process.

We shall use K to denote the (maximum) population density, or *carrying capacity*; assumptions as to how R_0 depends on K will be of importance in applications (see §4.3). Where an epidemic depletes the population significantly, or where we are interested in a long time scale, the (re)growth rate of the population and its dependence on population density will also be important. However, we shall not include this aspect in our introductory example, which follows.

1.2 Example: a spatial epidemic with recovery

Suppose we have a population of density K (carrying capacity), divided into *susceptibles* $S(x,t)$ and *infectives* $I(x,t)$; here x denotes space and t time. Suppose that infectives remain in that state for an infectious period distributed exponentially with mean τ, and that during this period they make contacts at constant rate β; then, as explained in §1.1, T is also exponentially distributed with mean τ, and $R_0 = \beta\tau$.

We shall consider the case where the (vector) distance from an infective to one of its contacts, X, is independent of the generation gap T, and assume that the individuals contacted are chosen randomly, so that the probability that a contact is successful in causing a new infection is equal to the proportion of susceptibles at the chosen site. The dynamics of the process can thus be summed up by specifying the transition rates for a recovery at x at time t as I/τ [i.e. the probability of a recovery in time dt is $(I/\tau)dt$], and the transition rate for an infection as $(R_0/\tau)\bar{I}S/K$, where $\bar{I}(x,t)$ denotes the convolution of I with V, $= \int I(x-y,t)dV(y)$; $\bar{I}$ can be thought of as describing the infectious pressure at x due to all current infectives.

This kind of infection rate term has traditionally been written as $\beta'\bar{I}S$, where $\beta' = R_0/K\tau$. Although mathematically convenient, this has had the unfortunate consequence that there has been a tendency to treat β' as though it were a constant for any one disease, with the dubious implication that $R_0 \propto K$ (see Mollison 1984, 1985). This kind of unthinking assumption is much easier to fall into when dealing with a compound parameter such as β' [which has units of $(\textit{population} \times \textit{time})^{-1}$], because neither mathematician nor ecologist can be expected to have any feel for what its value should be or whether it should indeed be constant.

Eschewing β' then, we have for our model that $I = K - S$, so that the infection rate is $(R_0/\tau)\bar{I}(1 - I/K)$. Where I is small, as for instance at the front of advance of the epidemic, it is of interest to consider the linear approximation in which we ignore the probability I/K that an attempted infection will fail. In the present instance this linear stochastic model is simply a spatial birth-and-death process with birth rate $(R_0/\tau)\bar{I}(x,t)$ and death rate $(1/\tau)I(x,t)$.

We can define deterministic versions of both linear and nonlinear models by writing down differential equations using the form of the stochastic transition rates, that is,

$$\dot{I} = (R_0/\tau)\bar{I}(1 - I/K) - I/\tau$$

for the nonlinear model, and

$$\dot{I} = (R_0/\tau)\bar{I} - I/\tau$$

for the linearisation. The relations between these four models will be discussed in the next subsection.

1.3 The connections between deterministic and linear models

We can cross-classify models for spatial population dynamics as stochastic/deterministic and linear/nonlinear. There are known and conjectured close connections between the behaviour of three of these classes – the exception unfortunately being the most realistic case, *stochastic nonlinear* models.

First, in the linear case there is a close connection between stochastic and deterministic models, namely that the expected numbers of the former satisfy the latter. Thus the expected numbers of the linear stochastic model of the last subsection, the spatial birth-and-death process, satisfy the linear deterministic equation $\dot{I} = (R_0/\tau)\bar{I} - I/\tau$.

Note that the linear differential equation here depends only on the difference between the rate terms. Thus the same deterministic linear model can correspond to a wide variety of stochastic models, for instance including one which cannot die out and others with arbitrarily small probability of survival. Possibly the simplest example of this is the non-spatial birth process with rate β, compared with the birth-and-death process with rates $\beta + \mu$ and μ, μ large.

The connection relative to mean numbers does not carry over in general to nonlinear models. For instance, for the epidemic with recovery where the transition rates include a second-order term $I\bar{I}$, the equation for expected numbers will differ from the 'deterministic version' by a term representing the difference between its mean $\mathbf{E}[I\bar{I}]$ and $\mathbf{E}[I]\mathbf{E}[\bar{I}]$, namely the covariance of I and $\bar{I}$.

Further, quite different nonlinear models can have the same linearisation. For instance, our epidemic with recovery has the same linearisation as the *epidemic with removal* with removal rate I/τ and infection rate $(R_0/\tau)\bar{I}S/K$. (These formulae are the same as for the former model, though with different interpretation; removals now form a separate class instead of being returned to the susceptible class, so we can no longer replace S by $K - I$.)

Secondly, it is strongly conjectured that nonlinear differential equations for population spread will always have the same velocity as their linear approximation. This *Linear Conjecture*, developed from many instances over more than fifty years (see §3.1), is stated explicitly by van den Bosch *et al* (1990) as likely to hold under two conditions:

(i) The average rate of reproduction of an individual experiencing throughout its life (infectious period) an environment 'occupied' by a certain (possibly varying) population is always smaller than the rate of reproduction in a 'virgin' environment (i.e., in particular, there are no Allee-like effects).
(ii) the influence of an individual on the environment very far from its (present) position is negligible.

The second condition does not refer to long distance dispersals – we can allow arbitrary dispersal distributions, though if these do not have exponentially bounded tails linear and nonlinear velocities will both be infinite (Mollison 1972b) – but rather to nonlocal nonlinearities such as in

$$\dot{n} = Dn'' + rEn$$

where the 'environment' $E, \equiv 1 - \int_{\mathcal{R}} n(x,t)dx$, 'deteriorates everywhere' as soon as the total population nears 1, so that no wave can develop (Hans Metz, *personal communication*).

It is not surprising that the nonlinear model should be bounded by its linearisation, and therefore have at most the same velocity, provided a condition such as (i) holds. The converse is perhaps surprising, and depends crucially on the fact that the set of possible velocities for linear models turns out to be of the form $\{c \geq c_\beta\}$ and that for bounded initial conditions the minimal velocity c_β is what matters (see §2.1). Now the nonlinear model may be expected to behave like the linear one at its front where numbers are small, provided (ii) holds. Therefore its set of possible velocities must be a subset of those of the linear model; but this implies that its velocity must be at least c_β.

Combining the above known and conjectured relations, linear stochastic and nonlinear deterministic models can be expected to have the same velocity as the simpler linear deterministic case. It also turns out that for some of the most basic models there is a much stronger direct connection: namely that the nonlinear differential equation gives the distribution of the furthest forward individual in the linear stochastic process. Two of these cases are given by McKean (1975) and Mollison & Daniels (1977). A third, which generalises the second, is the linear example of §1.2, the dispersal birth-and-death process. (McKean's example can be similarly generalised to a diffusion birth-and-death process.)

For the dispersal birth-and-death process we find (using the same, backwards, approach as McKean and Mollison & Daniels) that, if S_t denotes the position of the furthest forward individual, then $y(x,t) = Prob(S_t > s)$ satisfies $\dot{y} = (R_0/\tau)\bar{y}(1-y) - y/\tau$, which is the nonlinear differential equation of §1.2 with $y = I/K$. Results on the convergence of nonlinear waves for such equations (e.g., Bramson 1983) can then be interpreted as showing how the front S_t of the birth and death process has unrealistically small

stochastic variability; this can also be understood as a consequence of the independence of descendants of different individuals in the (exponentially growing) population of the linear stochastic process.

There are no such close relations between the basic nonlinear stochastic epidemic and the other three models, except that the linear stochastic model provides an upper bound [in general presumably subject to a condition such as (i)]. There do exist general results on the convergence of nonlinear stochastic processes to deterministic versions (see e.g. Kurtz 1980), as some indicator of population size, here K, tends to infinity. However, such results generally only hold over a fixed time interval, whereas velocities are defined asymptotically over time; and we are often interested in relatively small values of K, here interpreted as a measure of the number of others with whom an individual interacts. Certainly, the conditions for finite velocity can be quite different (Mollison 1972b).

1.4 Advantages of linear models

We have seen that linear deterministic models for spatial spread have close connections with both linear stochastic and nonlinear deterministic models. Thus, at least if the Linear Conjecture holds, there is no advantage to using nonlinear deterministic or linear stochastic models for the calculation of velocities. Indeed there is a strong reason for preferring linear models, namely that the complexity of nonlinear models, and the difficulties of analysing them, distract attention from discussion of the assumptions that go into them, and the difficult and delicate matter of assessing what ecological conclusions can safely be drawn from mathematical results (see Section 4).

The considerable effort that still goes into analysing nonlinear models, each time providing one more example supporting the Linear Conjecture, would be much more usefully devoted to proving it rigorously or finding a counter-example.

A further advantage of linear models is that they can be described simply in terms of their reproduction and dispersal kernel (essentially a combination of R_0 and the joint distribution of X and T; the details will be presented in Section 2), in a way that reflects their structure, in particular their basic ecological components, much more clearly than a traditional differential or difference equation presentation.

Surprisingly complex sets of equations (for example, the rabies model of §3.2) can be dealt with through a single kernel. The historic and continuing prevalence of diffusion rather than dispersal models is largely due to the greater difficulties of analysing the latter. The Linear Conjecture sets us free to study a reproduction and dispersal kernel chosen on biological rather than mathematical grounds.

1.5 Limitations of linear and deterministic models

As already noted in §1.3, quite distinct models may share the same linear approximation and thus have the same velocity, though for nonlinear stochastic versions these will not be equal.

For instance, consider Harris (1974)'s *Contact Process*, which is our epidemic with recovery in the case where individuals live at integer sites, with recovery rate $\mu = 1/\tau = 1$ and infection rate λ for each neighbour. This one-dimensional Contact Process can survive if $\lambda > \lambda_c \approx 1.65$ and then has velocity between $\lambda - \lambda_c$ and $\lambda - 1$ (Liggett 1985). However the corresponding epidemic with removal becomes extinct with probability one, provided only that the removal rate μ is nonzero (Kelly, in discussion of Mollison 1977; this result holds more generally, for any dispersal distribution of finite mean).

A second fault of linear models – though one which simplifies their analysis greatly – is that for them dimensionality is trivial. Thus if we have a linear model in any number of spatial dimensions, its projections into one dimension can be analysed as one-dimensional processes. Through the Linear Conjecture, nonlinear deterministic models to a large extent share this fault.

In contrast, the behaviour of nonlinear stochastic models can change radically with dimension. For instance, in two dimensions the epidemic with removal *can* survive, provided $\lambda_0 > \lambda_c \approx 1.13$ (Kuulasmaa 1982). [Note that we need to be careful when extending the definition of R_0 to stochastic nonlinear models. For consistency with linear models, we should take R_0 to be the mean number of contacts by an individual, here equal to 4λ (giving $R_c \approx 4.5$), whereas the mean number of different individuals contacted $= 4\lambda/(1 + \lambda)$ (giving $R_c \approx 2.12$, Mollison & Kuulasmaa 1985).] For the Contact Process in two dimensions, $\lambda_c \approx 0.41$ (Brower *et al* 1978).

As an example of how velocities can change with dimension, the simple epidemic (i.e. the epidemic with removal/recovery in the case where $\mu = 0$) with nearest-neighbour dispersal distribution has velocity 0.5 in one dimension, ≈ 0.84 in two (see §4.5, and Figure 3), although its linearisation has velocity ≈ 1.5 in both one and two dimensions (Mollison 1986).

When using linear models for velocities, we need to appreciate that they give upper bounds, the closeness of which is likely to depend on features such as the number with whom an individual interacts and the shape of the dispersal distribution (see §4.5). Thus a conclusion that a linear model gives a velocity too low to be consistent with data is safe, whereas if it were too high, further consideration of the likely difference from the nonlinear stochastic model would be required.

Lastly, nonlinear models are clearly necessary when considering endemic equilibrium, and the transition to it. However the evidence is that present deterministic nonlinear models, at least in the spatial context, are inadequate for this (see §4.6).

We conclude that for problems of spatial epidemic and population spread there is good reason to prefer linear deterministic to nonlinear deterministic (and linear stochastic) models, because they are much simpler and more transparent, while differing little if at all in their limitations. Because they are not exact, and in any case exact fitting from data is usually far from possible, they are best used in an exploratory way, ideally paralleled by simulations of nonlinear stochastic models.

2 CALCULATION OF VELOCITIES FOR LINEAR MODELS

In this section we shall look at two basic types of model, diffusion and dispersal. Dispersal models, in which the dispersal vector X and generation gap T are treated as independent, are particularly suitable where individuals have a home base (e.g. a range or territory). Where individuals are nomadic we may expect the magnitude of X to be positively correlated with T; diffusion models offer an example of this, though they have less flexibility, in that for them the conditional distribution of X given T is fixed as being Normal.

For each of these types of model we shall show how velocities can be calculated in the linear case, and examine how they depend on basic components such as R_0, and the distributions of X (the *dispersal* or *contact* distribution V) and T (the *reproduction kernel* B).

There are two major advantages of the reproduction and dispersal kernel technique we shall use (see §2.1). First, it allows a general relationship between X and T. Secondly, it can naturally be expressed in terms of the basic ecological components; in contrast, these are often quite difficult to recognise in a traditional description such as a differential equation (see, e.g., §3.2).

Because the effect of dimension for linear models is trivial (see §1.4), we shall restrict this exposition to one dimension. For two dimensions, especially the case of asymmetric dispersal distribution, see van den Bosch *et al* (1990).

2.1 Introduction

The basic technique of looking for exponential travelling wave solutions of linear models of the form $A\,e^{-\theta(x-ct)}$, goes back at least to Kolmogoroff *et al* (1937) and Fisher (1937) for the diffusion case, Mollison (1972b) and Atkinson & Reuter (1975) for the dispersal case. Both these cases are covered by a general framework in terms of a reproduction and dispersal kernel, introduced by Diekmann (1978) and van den Bosch *et al* 1990).

The *reproduction and dispersal ('R&D') kernel* $\beta(x,t)$ specifies the distribution in space and time (both measured relative to the parent) of the mean numbers of contacts of an infective individual (or, in the population context, offspring of an individual). Provided the total mean number R_0 is finite, it is convenient to write $\beta(x,t) = R_0\beta_0(x,t)$, where β_0 is a probability kernel describing the joint distribution of X and T. For notational simplicity we shall always write β_0 as a probability density function, though the theory applies equally to general probability kernels, for instance with either space or time discrete rather than continuous.

We shall use B, with density $b(t)$ and mean τ, to denote the marginal distribution of T (the reproduction kernel); and V, with density $v(x)$ and root mean square d, to denote the marginal distribution of X (the dispersal or contact distribution; we shall often concentrate on the symmetric case, when V has mean zero and standard deviation d). We can generally regard d and τ as scaling parameters, and it is thus often convenient to express a velocity c as $(d/\tau)c_0$.

For consistency with van den Bosch *et al*, and because it allows more felicitous phrasing in a number of places, we shall mostly use the terminology of population growth rather than of epidemics, speaking of parents and offspring rather than infectives and their contacts. Nevertheless, these models in one respect fit the epidemic case more naturally: the population interpretation is in terms of reproduction by single individuals.

Note that the R&D kernel only depends on mean numbers. Thus we have families of distinct models sharing the same kernel, and therefore the same velocity, although they may differ in important ways, for instance (see §1.3, §3.4) in their probability of extinction. Also, in the epidemic context, note that movement of susceptibles does not matter; the linear model implicitly assumes an inexhaustible supply.

These facts simplify analysis. For instance, a set of differential equations will often have a range of consistent probabilistic interpretations; when we need to calculate the corresponding kernel, we can choose whichever of these seems simplest (see example of §3.2). (Exceptionally, §3.4 provides an example in the other direction, where by changing the definition of what constitutes an individual we relate what is essentially the same stochastic model to two different kernels.)

However it is clearly a drawback from the modelling point of view that features that presumably do matter in a full nonlinear stochastic model should have no effect. Intuitively, the explanation of the insensitivity to correlation between the sites of the offspring of any one individual is that the advance of a linear process is governed by the behaviour of the very large numbers in its exponentially growing population.

For a population with R&D kernel β it is immediate that the mean density of births a satisfies the spatial renewal equation

$$a(x,t) = \int_0^\infty \int_{\mathcal{R}} a(x-y, t-u)\beta(y,u)dy\,du$$

(van den Bosch *et al* 1990). If we then look for an exponential travelling wave of velocity c for the right hand edge of the population, we find that this is possible for any c for which there is a $\theta > 0$ such that $L(c,\theta) = 1$, where

$$L(c,\theta) \equiv \int_0^\infty \int_{\mathcal{R}} \beta(x,t)e^{\theta(x-ct)}\,dx\,dt.$$

Note that L is the expectation of a product of random variables,

$$L(c,\theta) = R_0\mathbf{E}[e^{\theta X}\,e^{-\theta cT}],$$

since $\beta = R_0\beta_0$, where β_0 is the probability kernel describing the joint distribution of X and T.

Thus for the dispersal model, where X and T are independent,

$$L(c,\theta) = R_0 M_B(-c\theta)M_V(\theta),$$

where M_V and M_B are the respective moment generating functions of the dispersal distribution and the generation gap (e.g. $M_V(\theta) \equiv \mathbf{E}[e^{\theta X)}]$).

The set of possible velocities turns out to be of the form $\{c \geq c_\beta\}$. Now for any such c, the population will be bounded, for all time, by the wave solution $Ae^{-\theta(x-ct)}$ provided this bounds it at time zero. For realistic conditions in which the initial population is only nonzero on some bounded set, we can always use the wave of minimal velocity, c_β, which is therefore an upper bound for the velocity of the process.

It has been proved that the asymptotic velocity actually is c_β in a number of cases, even when non-linearities are incorporated (see van den Bosch *et al* 1990, Section 4, for references), confirming that this is the only velocity of practical importance. We shall therefore henceforth refer to c_β as *the* velocity of the linear model with R&D kernel β.

Thinking of stochastic models, the velocities we are talking about here refer to the expected numbers that satisfy our linear differential equation. For certain special cases

in which the position of the furthest forward individual S_t is given by a well-known *nonlinear* differential equation (see §1.3), results on the latter confirm the importance of c_β: S_t asymptotically travels at velocity c_β with very little stochastic variability.

It is often convenient to characterise c_β as the solution of $L(c,\theta) = 1$ together with $L'(c,\theta) = 0$ (where the prime denotes differentiation with respect to θ).

Note that c_β can be negative, but only in the case of asymmetric dispersal kernel, with $\mathbf{E}(X) < 0$. The condition for $c_\beta < 0$ is that $L(0,\theta) < 1$ for some $\theta > 0$. Now $L(0,\theta) = R_0 M_V(\theta)$, which is ≥ 1 for all $\theta > 0$ provided that (a) $R_0 \geq 1$ (the condition for the population to survive) and (b) $\mathbf{E}(X) = M_V'(0) \geq 0$.

The interpretation of L as the expectation of a product of random variables allows a simple proof that positive association between X and T tends to decrease the velocity. To be precise, if $e^{\theta X}$ and $e^{-c\theta T}$ are negatively correlated, then

$$L(c,\theta) = R_0 \mathbf{E}[e^{\theta X} e^{-c\theta T}] < \mathbf{E}[e^{\theta X}]\mathbf{E}[e^{-c\theta T}] = R_0 M_B(-c\theta) M_V(\theta).$$

Thus L is smaller than in the dispersal case where X and T (and hence $e^{\theta X}$ and $e^{-c\theta T}$) are independent, and consequently the minimal velocity is lower.

This explains why diffusion models and Ball's dynamic epidemic (see §3.4) have lower velocities than the dispersal models with the same marginal distributions of X and T. In both these cases the conditional distribution of X given T has increasing dispersion in the sense that $M_{X|T=t}(\theta)$ is an increasing function of t for all θ, from which it is easy to show that $e^{\theta X}$ and $e^{-\theta cT}$ are negatively correlated (for $c > 0$).

2.2 Diffusion models

Suppose that individuals have reproduction kernel $b(t)$ and throughout their reproductive life move in Brownian motion with diffusion coefficient D, so that their position at age t has Normal distribution $N(0, 2Dt)$, with probability density function $\phi_t(s)$ say. Offspring start off at their parent's site, subsequently moving similarly in Brownian motion.

First note that the r.m.s. distance d of offspring from their parent is given by

$$d^2 = \int_0^\infty (2Dt) b(t) dt = 2D\tau$$

Now the R&D kernel $\beta(x,t) = R_0 \phi_t(x) b(t)$, so that

$$\begin{aligned} L(c,\theta) &= R_0 \int_0^\infty \int_{\mathcal{R}} b(t) e^{-\theta ct} \phi_t(x) e^{\theta x} dx dt \\ &= R_0 \int_0^\infty e^{-t(c\theta - D\theta^2)} b(t) dt \end{aligned}$$

since $\int_{\mathcal{R}} \phi_t(x)e^{\theta x}dx$ is equal to the moment-generating function of $N(0,2Dt), = e^{Dt\theta^2}$.

Comparing this expression for $L(c,\theta)$ with the definition of a population's intrinsic rate of natural increase r (Keyfitz 1968, Roughgarden 1979),

$$\int_0^\infty \beta(t)e^{-rt}dt = 1,$$

where here $\beta(t) = R_0 b(t)$, we see that $L(c,\theta) = 1$ is equivalent to $c\theta - D\theta^2 = r$. Our second condition for c, $L'(c,\theta) = 0$, then gives $(c - 2D\theta)L(c,\theta) = 0$, that is, $\theta = c/2D$. Hence $c = 2\sqrt{rD}$ (van den Bosch *et al* 1990), and substituting $D = d^2/2\tau$ we find that $c = (d/\tau)c_0$, where

$$c_0 = \sqrt{2r\tau}.$$

Thus the velocity depends more directly on $r\tau$, which can be interpreted as the population increase per generation on a logarithmic scale, than on the 'mean family size' R_0.

For given r and τ, R_0 is minimised when the reproduction kernel is Constant, that is, when $b(t)$ is the delta function at τ. In this case $r\tau = \ln(R_0)$, and the standardised velocity c_0 is therefore $\sqrt{2\ln(R_0)}$.

At the other extreme, it is possible to make r, and thus the velocity, infinite by assigning sufficient probability to reproduction at age zero. Just about the most extreme case of practical interest (because of the large probability it attributes to small values of T) is the Exponential distribution, which arises where individuals throughout their lives reproduce at a constant rate and are also subject to a constant death rate. This case has received perhaps excessive attention because of its mathematical simplicity: it arises naturally in Markov process and differential equation models. In this case $r\tau = R_0 - 1$, and so $c_0 = \sqrt{2(R_0 - 1)}$.

An intermediate case that is often considered is where individuals go through two exponentially distributed stages: first a non-reproductive ('latent') stage of mean τ_L, then a reproductive ('infectious') stage of mean τ_I during which they reproduce at constant rate. Perhaps counter-intuitively, this gives a reproduction kernel which is symmetric with respect to τ_L and τ_I. Thus, for example, we get the same Exponential kernel as in the previous case when individuals have an exponential latent period followed by an instantaneous reproductive period producing a family of average size R_0. The explanation lies in the Poisson paradox of §1.1, which tells us that in each case the generation gap T has the same distribution as the lifetime T'; and the lifetime distributions for the two cases are obviously equal, being the sum of independent Exponentials of means τ_L and τ_I; thus the reproduction kernel in either case is

$$b(t) = (e^{-t/\tau_I} - e^{-t/\tau_L})/(\tau_I - \tau_L).$$

For the same reason the mean generation gap is in each case simply the sum of the two parameters, $\tau = \tau_I + \tau_L$.

For this two-stage model, let $p \equiv \tau_L/\tau$, $a \equiv 1/p + 1/(1-p)$. Then we find in general that

$$r\tau = (a/2)(\sqrt{1 + [4(R_0 - 1)/a]} - 1),$$

and hence that $c_0 (= \sqrt{2r\tau})$, takes its minimum value of $2\sqrt{\sqrt{R_0} - 1}$ when $p = 1/2$, i.e. when the two stages have the same distribution, and its maximum, $\sqrt{2(R_0 - 1)}$ when $p = 0$ or 1, that is in the cases in which one stage is instantaneous. The difference between maximum and minimum is small except when R_0 is very large, for instance it reaches 2:1 only when $R_0 = 49$, although the asymptotic behaviour varies ($R_0^{1/2}$ and $R_0^{1/4}$ respectively).

We may note further that for R_0 close to 1, the velocity $\approx \sqrt{2(R_0 - 1)}$ for any reproduction kernel B and that for values of R_0 up to about 10, velocities vary by less than 2:1 for kernels ranging from Constant to Exponential.

We shall return to diffusion models in the examples of §3.2 (a two-stage model in which individuals only diffuse during the second stage, so that the result $c_0 = \sqrt{2r\tau}$ does not hold) and §3.5 (an extension to two competing populations).

2.3 Dispersal models

We here consider the case in which the spatial location X of an individual relative to its parent is independent of the parent's age at its birth, T. Then, as pointed out in §2.1,

$$L(c, \theta) = R_0 M_B(-c\theta) M_V(\theta)$$

where M_B and M_V denote the respective moment generating functions of the distributions of T and X.

Note that, since M_B is a monotone increasing function and M_V is convex, there is a partial ordering on velocities: if $M_V \leq M_{V'}$ (indicating that V' is more dispersed), then $c \leq c'$ for the corresponding velocities. In particular, for symmetric V with fixed standard deviation d, the minimum possible velocity is when V is concentrated on $\pm d$ (Mollison 1972b).

Note also that if V does not have exponentially bounded tails then $M_V(\theta) = \infty$ (except at $\theta = 0$), so that the velocity is infinite regardless of B. Therefore the most extreme dispersal distribution we shall consider here is the Double Exponential, with density $v(x) = (1/d\sqrt{2})e^{-x\sqrt{2}/d}$. (In contrast, at least a wide class of *nonlinear stochastic*

models in one dimension – those bounded by the simple epidemic – will have finite velocity provided only that d is finite (Mollison 1972b, see §4.5).) Note that the Double Exponential arises naturally as the marginal density when juveniles disperse through diffusion for an Exponential period (van den Bosch *et al* 1990, Section 5).

We shall survey values of the velocity, and its dependence on R_0, for a range of distributions of T and X, starting in each case with the most concentrated distribution.

Suppose first that T is constant, $= \tau$. If V is concentrated on $\pm d$, it is immediate that the velocity cannot exceed d/τ ($c_0 = 1$), no matter how large R_0 is; and it is not difficult to show that this bound is attained for $R_0 \geq 2$. More generally if T is bounded below by τ' and X is bounded above by d', the velocity will have a bound d'/τ' independent of R_0.

Continuing with T constant, if X has a Normal distribution we have the unique case where the dispersal and diffusion models coincide (note that for the diffusion model X and T can only be independent if T is constant), so (from §2.2) $c_0 = \sqrt{2\ln(R_0)}$. For X with Double Exponential distribution (see above), $c_0 \propto \ln(R_0)$ for large R_0.

In contrast, if T has an Exponential distribution, c_0 is approximately proportional to R_0. Here $M_B(\theta) = (1-\tau\theta)^{-1}$. Let V' denote the distribution V scaled to have standard deviation $= 1$. Then $c = (d/\tau)c_0(V)$, where

$$c_0 = \min_{\theta>0} \frac{R_0 M_{V'}(\theta) - 1}{\theta}.$$

Then it is not difficult to show that c_0 is greater than a 'diffusion approximation' (N.B. *not* diffusion model) value of $R_0\sqrt{2(1-1/R_0)}$ for all V and R_0, and $\approx c_V R_0$ for large R_0, where $c_V = \min M_{V'}(\theta)/\theta$. Values of c_V range from a minimum ≈ 1.51 when V is concentrated on $\pm d$, through $\sqrt{e} \approx 1.65$ for V Normal to ≈ 1.85 for V Double Exponential.

An example intermediate between T constant and T Exponential arises where individuals go through two exponentially distributed stages, with reproduction only in the second of these. For instance, when V is Normal, this gives velocity approximately proportional to $\sqrt{R_0}$ for large R_0.

The strongly increasing dependence of the velocity on R_0 as the generation gap's distribution B ranges from Constant through the two-stage case to Exponential is associated, *pace* van den Bosch *et al*, not so much with increasing dispersion of B as with the possibility of very short generation gaps (i.e. very small values of T). Thus the Constant distribution has minimal value equal to its mean, in contrast to the Exponential distribution which has its maximum density at 0. It is easily shown that, if the generation

gap has a minimal value > 0, the asymptotic dependence of the velocity on R_0 will be as for the case of constant T.

Van den Bosch *et al* give an expression for the velocity as an expansion in terms of the bivariate cumulants κ_{ij} of the R&D kernel $\beta_0(x,t)$, arguing that, at least for R_0 near 1, the velocity will usually be close to that for the case where B is Constant and V Normal (the case where diffusion and dispersal models coincide), that is that $c_0 \approx \sqrt{2\ln(R_0)}$.

More exactly, their expansion approximation is

$$c_0 = \sqrt{2\ln(R_0)}(1 + \alpha \ln(R_0)),$$

where $\alpha = var(T)/\tau^2 - \kappa_{21}/(d^2\tau) + (1/12)\kappa_{40}/d^4$ (note that $\kappa_{21} = 0$ in the dispersal case because X and T are then independent).

While it may be useful in many practical cases, the cumulant expansion does rather obscure the crucial role in determining velocities played by the behaviour of B near 0, and by the tail behaviour of V. An admittedly somewhat artificial example illustrating the importance of the behaviour of B near 0 is the case where it actually has an atom at 0, for instance, where B is concentrated on 0, with $\text{Prob}\{T = 0\} = q > 0$, and on $\tau', = \tau/(1-q)$. This distribution is well behaved in terms of moments, yet its velocity becomes infinite when R_0 reaches $1/q$.

The dependence of the behaviour of the velocity on the tails of the dispersal distribution is of more practical importance; this will be discussed further in §4.5. For well-behaved kernels, meaning that the probabilities of short generation gaps and long dispersals are both low, a very rough 'rule of thumb' which may nevertheless be sufficiently accurate relative to the quality of data usually available is that c_0 rises from zero at $R_0 = 1$ to $c_0 = 1 - 2$ at $R_0 = 2$, and $c_0 = 2 - 4$ at $R_0 = 10$.

3 EXAMPLES

This section demonstrates the use of the R&D kernel technique in providing a unified treatment of a wide range of models, including the 'dynamic epidemic' (§3.4) and a model for two competing populations (§3.5).

For the reasons presented in §1.4, in each case we concentrate on extracting the R&D kernel, throwing away the nonlinear details.

The kernel technique yields clear and simple analyses which provide a good basis for discussion of questions of applied importance, as with the contrasted rabies models of §3.2 and §3.3. The significance of the differences between these two models will be discussed later (§4.3).

3.1 Early diffusion models

The earliest calculations of velocity were those of Kolmogoroff, Petrovsky and Piscounoff (1937) ('KPP') and Fisher (1937), who by slightly different routes both derived the *KPP/Fisher equation*

$$\dot{y} = Dy'' + ry(1-y)$$

for the advance of an advantageous gene.

For the linearisation of this,

$$\dot{y} = Dy'' + ry,$$

the straightforward choice of kernel (others are possible) is $\beta(s,t) = r\phi_t(s)$, where $\phi_t(s)$ is the probability density function of the Normal distribution $N(0, 2Dt)$. From the diffusion case theory of §2.2 we therefore have that the velocity $c = 2\sqrt{rD}$. (Note that in this case we cannot express the velocity in terms of d, τ or R_0 because these are all infinite.)

Fisher, in an attempt to resolve the ambiguity of velocity, considered a linear stochastic model for which the distribution of the mean numbers at time t can be found, and with the same velocity, $2\sqrt{rD}$. This 'confirmation' in fact rests on two lucky coincidences – or perhaps we should say the intuition of genius – for Fisher's second model is actually a dispersal model, with T constant and V Normal. Firstly, this is the *only* dispersal model with the same velocity as its diffusion equivalent (see §2.3); and secondly, even then it can be considered to give the same velocity only if we match the models through their values of r, as Fisher indeed did.

Skellam (1951) later applied Fisher's discrete-time model, for instance to the reinvasion of northern Europe by oaks (see §4.4).

3.2 The rabies diffusion model of Murray *et al*

This model will be compared with that of van den Bosch *et al* (§3.3) in Section 4. It seems worth giving the details for a number of reasons. It does not yield to the simple result for diffusion models, $c_0 = \sqrt{2r\tau}$ (§2.2), because of the authors' assumption that infected individuals do not move during their latent period. Nevertheless, it provides a good illustration of the kernel technique, giving a simple expression for the epidemic threshold, and a derivation of an equation for the linear velocity which is more straightforward than that of the authors. This allows us to plot the relation between the velocity and the basic parameters R_0 and $p = \tau_I/\tau$, which greatly facilitates comparison with the alternative model of §3.3, and discussion of the model in relation to data (§4.3).

The rabies model of Murray *et al* (1986) can be written as follows:

$$\begin{aligned}
\dot{S} &= (a-b)(1-N/K)S - \beta SI \\
\dot{L} &= \beta SI - \sigma' L - [b + (a-b)N/K]L \\
\dot{I} &= \sigma' L - \alpha' I - [b + (a-b)N/K]I + DI''
\end{aligned}$$

where S, L and I are the respective densities of susceptible, latent and infectious individuals, $N = S + L + I$, and K as before is the carrying capacity, that is the population density in the absence of the disease.

For the linearisation we take L, I small, $S \approx K$; then

$$\begin{aligned}
\dot{L} &= \beta KI - \sigma L \\
\dot{I} &= p_i \sigma L - \alpha I + DI''
\end{aligned}$$

where $\sigma = \sigma' + a$, $\alpha = \alpha' + a$, and $p_i = \sigma'/\sigma$ (= the probability that a latent individual will reach the infected state).

A corresponding kernel can then be defined as follows. Individuals go through an exponentially distributed latent period of mean $\tau_L = 1/\sigma$, followed with probability $1 - p_i$ by death, otherwise by an exponentially distributed infectious period of mean $\tau_I = 1/\alpha$, during which they infect at rate βK and diffuse with coefficient D. (Note that this stochastic description is not unique, but it is easily checked that its expected numbers satisfy the linearisation equations and that it therefore gives a correct kernel.)

Hence $R_0 = \beta K p_i \tau_I$ ($R_0 > 1$ then gives the threshold condition for the epidemic), and the kernel is

$$\beta K p_i \int_0^t \sigma e^{\sigma(t-z)} e^{-\alpha z} \phi_t(z) dz,$$

where $\phi_t(z)$ is the probability density function of $N(0, 2Dz)$. Multiplying by $e^{-\theta(ct-s)}$ and integrating over first s (from $-\infty$ to ∞) and then t (from 0 to ∞), we obtain

$$\begin{aligned} L(c,\theta) &= \alpha\sigma R_0 \int_0^\infty e^{-(\sigma+\theta c)t} \int_0^t e^{(\sigma-\alpha)z} e^{D\theta^2 z} dz dt \\ &= \alpha\sigma R_0 \frac{1}{(\sigma+\theta c)(\alpha+\theta c - D\theta^2)} \end{aligned}$$

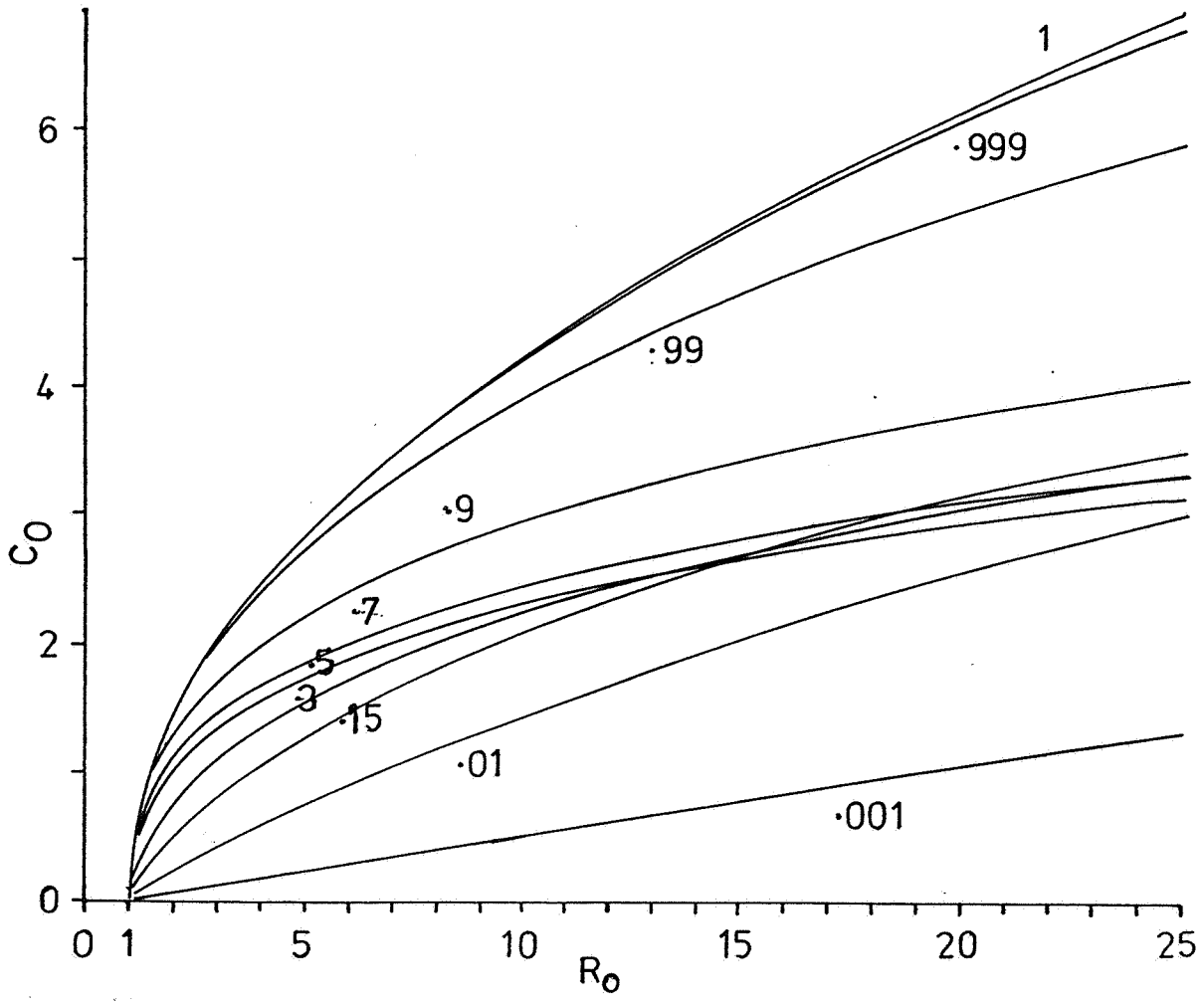

Figure 1 : Murray *et al*'s rabies model. Standardised velocity c_0 as a function of the basic reproductive ratio R_0 for a range of values of $p = \tau_I/\tau$ [$p \approx 0.15$ for the data quoted in Murray *et al* (1990)].

Setting this equal to 1 gives a cubic for θ. If we let $\tau = \tau_L + \tau_I$, $d = \sqrt{2D\tau}$, and substitute

$$y = c\tau\theta, \quad k = c\tau/D, \quad p = \tau_I/\tau, \quad q = \tau_L/\tau = 1 - p,$$

we obtain

$$\frac{y^3}{2k^2} + (\frac{1}{2qk^2} - 1)y^2 - \frac{1}{pq}y + \frac{1}{pq}(R_0 - 1) = 0.$$

This cubic has positive roots iff $k \geq c_0$, where c_0, p and R_0 are related by

$$R_0 = 1 + \frac{2(a^2 + 3b)^{1.5} - 2a^3 - 9ab}{27b},$$

where

$$a = \frac{1}{q} - 2c_0^2, \quad b = 2c_0^2/pq \quad \text{(remember } q = 1 - p\text{)}.$$

This explicit expression for R_0 as a function of c_0 and p allows us to plot the standardised velocity c_0 as a function of R_0 for various fixed values of p (Figure 1). Note how the shape changes as p varies. At $p = 1$ we have the diffusion model of §2.2 with B Exponential, for which $c_0 = \sqrt{2(R_0 - 1)}$. At $p = 5/33 \approx 0.15$, the data value used by Murray *et al*, c_0 is close to half this value over the range of values plotted. The limit as $p \to 0$ is a dispersal model with V Normal, again with B Exponential, so that the velocity grows approximately linearly with R_0.

3.3 The rabies model of van den Bosch *et al*

Van den Bosch *et al* (1990) criticise some of the assumptions of Murray *et al* (1986), suggesting that what is known about fox rabies (Andral *et al* 1982) supports a dispersal model rather than a diffusion model and that the movements of rabid foxes do not differ significantly from those of normal ones. To illustrate this they take a dispersal model with a less variable reproduction kernel, based on estimates of Berger (1976), whose standard deviation v is small compared with τ (4.94 and 33.44 days respectively). They take a Normal dispersal distribution, for which $\kappa_{40} = 0$. Then the parameter α in their expansion approximation for c_0 (see §2.3) is simply v^2/τ^2, ≈ 0.02, sufficiently small to neglect (except for very large R_0). They thus conclude that $c_0 \approx \sqrt{2\ln(R_0)}$.

While this has different behaviour from Murray *et al*'s c_0, it is quite similar over the range $R_0 = 1$ to 10 (see Figure 2(a), page 27). The large differences in their conclusions, which will be discussed in §4.3, are thus almost wholly due to the way they fit their models to data for d (or D) and R_0, especially the dependence of the former on population density.

3.4 Ball's dynamic epidemic model

Ball (1991) describes a dynamic epidemic model in which infective individuals migrate between integer sites, able to infect only at their current site; and, among other results, gives calculations for the velocity of the linear version of this model based on the kernel technique. He conjectures on the basis of numerical calculations that the dynamic epidemic always has a lower velocity than what he calls the *corresponding* dispersal model, namely the one with the same marginal distributions of X and T (this has a general explanation; see last paragraph of §2.1). I show here that there is another dispersal model whose kernel can be matched exactly to the dynamic epidemic; it therefore *(inter alia)* has exactly the same velocity as the dynamic epidemic.

While it is pleasing thus to extend the dispersal case analysis to a wider class of models, this also illustrates the caution with which linear models need to be treated, by providing an example of two models with the same kernel but with different correlation structure and probability of extinction.

The linearised version of Ball's dynamic epidemic is a birth, death and migration process with birth rate β, death rate γ, migration rate α and migration distribution U. It can be viewed as a discrete-time version of the diffusion model of §2.2, the Brownian motion being replaced by a continuous-time simple random walk with rate α, and migration distribution U.

For quite general B and U, the R&D kernel is

$$\beta(x,t) = R_0 \psi_t(x) b(t)$$

where $\psi_t(x)$ is the probability kernel for the simple random walk at time t, which has moment-generating function $e^{\alpha t(M_U(\theta)-1)}$. In the basic Markovian case the reproduction kernel B is Exponential with mean $1/\gamma$ [B has density $b(t) = \gamma e^{-\gamma t}$] and $R_0 = \beta/\gamma$.

Continuing for general B and U, we have

$$\begin{aligned} L(c,\theta) &= R_0 \int_0^\infty b(t) e^{-t(c\theta - \alpha(M_U(\theta)-1))}\, dt \\ &= R_0 M_B(\alpha(M_U(\theta)-1) - c\theta). \end{aligned}$$

Just as for the diffusion model in §2.2, we may compare the first expression for L here with the definition of the intrinsic growth rate r. We obtain $c\theta - \alpha(M_U(\theta)-1) = r$, whence the velocity is

$$c = \min_{\theta>0} \frac{\alpha(M_U(\theta)-1) + r}{\theta}.$$

For the basic case where B is Exponential and U is the nearest-neighbour distribution, giving equal probabilities $\frac{1}{2}$ each to ± 1, we have $r = \beta - \gamma$ and $M_U(\theta) = \cosh(\theta)$, so that

$$c = \min_{\theta>0} \frac{\alpha(\cosh(\theta) - 1) + \beta - \gamma}{\theta}$$

as found by Ball (1991).

We now turn to an alternative way of looking at the dynamic epidemic, in which it has the *same* kernel as a dispersal model. We need to restrict ourselves to the Markovian case of age-independent rates α, β and γ, but can allow a general migration distribution U.

Then we observe that we can treat a migration from s to u as the combination of a death at s plus birth of an offspring at u. This has the same kernel as if these deaths and births were independent, that is those of the birth-and-death process with respective rates $\beta + \alpha$ and $\gamma + \alpha$, and dispersal distribution $V' = q\Delta + pU$, where Δ denotes the distribution concentrated at 0 and $p = \alpha/(\beta + \alpha)$, $q = 1 - p$. This is a dispersal model whose reproduction kernel B' is Exponential with mean $\tau' = 1/(\gamma+\alpha)$ and so is covered by the theory of §2.3.

We thus obtain the alternative kernel

$$\beta(x,t) = R_0'(q + pu(x))b'(t)$$

for which

$$L(c,\theta) = R_0'(q + pM_U(\theta))M_{B'}(-c\theta)$$

where R_0' is the basic reproductive ratio for the Birth and Death process, $= (\beta+\alpha)/(\gamma+\alpha)$. Hence the velocity is

$$c = \frac{1}{\tau'}\min_{\theta>0} \frac{R_0'(q + pM_U(\theta)) - 1}{\theta}.$$

Substituting for R_0', τ', p and q, we find that

$$c = \min_{\theta>0} \frac{\beta + \alpha M_U(\theta) - (\gamma + \alpha)}{\theta},$$

the same value as was found above using the original kernel.

Note that although they share a kernel, the Birth and Death process and the linear dynamic epidemic have different probabilities of extinction, $R_0'^{-n_0} = [(\gamma+\alpha)/(\beta+\alpha)]^{-n_0}$ and $R_0^{-n_0} = (\gamma/\beta)^{-n_0}$ respectively, when $\beta > \gamma$ (both are certain to die out when $\beta \leq \gamma$).

As already remarked, the dynamic epidemic can be viewed as a discrete-time version of the diffusion model. Indeed, if we go through the usual limiting argument, taking

smaller quicker steps – that is replacing α by $2D/\delta^2$, θ by $\theta\delta$, and letting $\delta \to 0$ – then the kernel tends to that of the diffusion case. [In particular, note that $\alpha M_U(\theta) \to \theta^2 D$, so that the velocity tends to the diffusion model value of $2\sqrt{rD}$.]

3.5 Okubo *et al*'s two population model

Okubo *et al* (1989) introduce a two population diffusion model in the context of competition between red and grey squirrels. They only consider parameter values for which one population (grey) drives out the other. Indeed, when they come to their particular application (see §4.4), they argue from circumstantial data that the effect of the red squirrels in impeding the advance of the greys is negligible, so they do not really use their new model at all; their calculations are essentially for the single population diffusion model of §2.2 (see §4.4).

We here show, for the linearisation of their two population model, how the velocity of advance can be obtained by the kernel technique, and point out that for other parameter values different behaviour may be expected. In particular, it is possible that each population may advance into the other's territory.

Okubo *et al*'s equations, for the one-dimensional case, can be rewritten as

$$\dot{G} = D_G G'' + r_G G(1 - G/K_G - R/\hat{K}_R)$$

and similarly for $\dot{R}$, interchanging R and G. Here K_G denotes the carrying capacity for grey squirrels, and $\hat{K}_R$ the population level of red squirrels sufficient (if sustained) to drive the greys to extinction. The linearisation when considering the advance of the greys is given by G small, $R \approx K_R$:

$$\dot{G} = D_G G'' + \hat{r}_G G$$

where $\hat{r}_G$ denotes $r_G(1 - K_R/\hat{K}_R)$, the intrinsic growth rate for a small population of greys in a population of reds at carrying capacity. From the theory of §2.2 we know that this equation has minimum velocity

$$c = 2\sqrt{\hat{r}_G D_G} \quad [= (d_G/\tau_G)\sqrt{2\hat{r}_G \tau_G} \text{ if } D_G = d_G^2/2\tau_G].$$

Note that this can yield waves of negative velocity if $\gamma_R = K_R/\hat{K}_R$ is > 1. These, however, would require arbitrarily large populations to their rear to be sustained and are therefore presumably of no practical relevance.

Okubo *et al*, on the basis of circumstantial evidence for their case of interest, restrict attention to the case where in equilibrium there are only grey squirrels, that is, when

γ_R is < 1 and the similarly defined γ_G is > 1. Then they make a generalisation of the usual nonlinear conjecture, supported by analysis of one special case, that the greys will advance at their linear velocity, driving the reds to extinction.

In general there are two other cases of interest. If γ_R and γ_G are both greater than 1, then either population can (at least in the non-spatial version of the model) drive out a small number of the other, so that if we start with spatially segregated populations we would expect them to be stable against invasions by each other and therefore to remain segregated.

On the other hand, if γ_R and γ_G are both less than 1, an equilibrium of coexistence is possible, given by

$$G/K_G + R/\hat{K}_R = 1 = R/K_R + G/\hat{K}_G.$$

This corresponds precisely to the case in which each in its linearisation has a positive velocity, so we may conjecture that in this case spatially segregated populations are unstable and that (in the nonlinear deterministic model) each will advance at its linearised velocity among the other, propagating the equilibrium of coexistence.

4 APPLICATIONS AND DISCUSSION

For a variety of linear spatial models, we have seen how the velocity depends on basic components and the way these are incorporated into the model. We now turn to the problems of choosing models, and of fitting them to data.

There are many examples in the literature of the fitting of models such as we have surveyed here, especially the basic diffusion model of Kolmogoroff *et al* (1937) and Fisher (1937), first applied by Skellam in 1951. Because of the imprecision of data, especially on dispersal distances, it is often very easy to obtain a reasonable 'fit', but equally difficult to come to firm conclusions as to the most appropriate model or to make reliable predictions based on the fitted model.

We shall deliberately restrict attention to thorough discussion of a small number of examples. For a wider range, with applied aspects well discussed, see Hengeveld (1989); and for further examples Elton (1958), Mollison (1986), van den Bosch *et al* (1988, 1991).

After considering the use of linear/deterministic models in a variety of applications (§§4.1-4), we shall discuss their limitations in relation to velocities (§4.5), and (more severely) endemicity (§4.6).

4.1 Fitting and falsifying

Many authors have regarded the aim of modelling spatial spread as to obtain 'good agreement with data'. In the context of the linear and deterministic models we have presented here, this essentially means that spread should be at a steady velocity, with value as calculated from the preferred model. Unfortunately, uncertainty over parameters, especially d and R_0, means that such agreement is often all too easy to obtain.

On the other hand, a wide range of linear models gives broadly similar velocities, rising from 0 at $R_0 = 1$ to a small multiple of d/τ at $R_0 = 10$ (see §2.3), so that it is not at all easy to discriminate between alternative models. Thus broad agreement of a model with data does not provide a safe basis for extrapolation or prediction; cases where we can actually reject our model may be much more informative.

As to parameter values, τ may be known fairly accurately, but in many cases d (or its diffusion coefficient equivalent, $\sqrt{2D\tau}$) is known only to within a factor of 2. The basic reproductive ratio is often even more difficult to estimate: indeed it is common to argue that $R_0 > 1$ from the fact that the population does spread. Thus it may be better to view the model as allowing us to estimate d, and perhaps R_0, from data on velocities rather than as allowing us to test the model.

Given such problems with data, it is not surprising if it is found to be difficult to discriminate between quite different models (see §4.2), or quite different assumptions about how (for instance) R_0 and d vary with population density (see §4.3). Some of the most useful analyses, therefore, are those where comparison with data leads us to reject a model as false, because this will typically have interesting – and relatively clear-cut – implications (see §4.4).

4.2 Problems of fitting

Here we discuss the general problems of estimating the components of the R&D kernel, namely the reproduction kernel B and dispersal distribution V, the relation between them, and the basic reproductive ratio R_0. Examples of estimation of these components from data will be given later.

The mean τ of the reproduction kernel B is usually the easiest parameter to estimate, with reasonably accurate data often available. The shape of B is more problematic; however, from the analysis of Section 2 we know that the aspect that has the most important effect on the velocity is whether it effectively has a minimum possible value, when its behaviour will be similar to that of the Constant distribution ($T = \tau$ with probability 1), or whether values small compared with τ have appreciable probability, which will give a stronger dependence of the velocity on R_0.

Compared with τ, any spatial scale parameter such as, for symmetric V, the r.m.s. dispersal distance d is much more difficult to estimate with any accuracy, as is the diffusion constant D for diffusion models.

When using data on dispersal distances we need to be careful to distinguish between the two-dimensional r.m.s. dispersal distance, d_2 say, and the one-dimensional marginal value d; for rotationally symmetric V, $d_2 = d\sqrt{2}$, and the corresponding diffusion constant $D = d^2/2\tau = d_2^2/4\tau$.

For diffusion models, we have no choice as to the shape of the dispersal distribution V, only the question as to whether this type of model is appropriate. While there will certainly be circumstances in which a model with correlation between B and V is appropriate, for instance where we have nomadic rather than home-based individuals, and others where the difference between diffusion and dispersal models is negligible (B near Constant, V near Normal), diffusion models quite often seem to be used as a mathematically simpler substitute for a preferable dispersal model; a restriction which the R&D kernel approach (together with the Linear Conjecture) suggests is unnecessary. Certainly, estimates for the diffusion coefficient D are often obtained by considering the r.m.s. dispersal distance in a corresponding dispersal model (e.g. Okubo *et al* 1989, see below).

As to the shape of V for dispersal models, it is the probability of *large* values that matters most. If the reproduction kernel B is near Constant, the shape of V is important if R_0 is large; if R_0 is small we have the expansion approximation of van den Bosch *et al* (§2.3), with first-order term giving $c_0 \approx \sqrt{2\ln(R_0)}$. At the other extreme, if B attaches large probability to small values, the shape of V matters much less, but c_0 then depends much more strongly on R_0, approximately proportionally in the case of Exponential B.

All this assumes that V has exponentially bounded tails; if not, the velocities of the linear models considered here are all infinite (see §4.5).

Lastly, it is seldom possible to estimate R_0 at all accurately, still less the form of its dependence on variables such as the carrying capacity K It is commonly (though dubiously, see §2.1) assumed that $R_0 \propto K$, and hence that $R_0 = K/K_0$ where K_0 is the minimal density at which the disease can propagate. That such a threshold density usually exists is supported by data, but it is not easy to estimate its value (for an example see §4.3; for an elegant experimental estimation of a threshold density see van den Bosch *et al* 1990a).

Nor is it easy to estimate the value of R_0 at other densities. We could try to use the formula $R_0 = K/K_*$, where K_* is the equilibrium density of susceptibles, which holds for homogeneously mixing models and for nonlinear deterministic spatial models such as that of Murray *et al* (§3.2); but unfortunately it does not hold for nonlinear stochastic spatial models (Mollison & Kuulasmaa 1985; note that the definition of R_0 in this reference is slightly different from that used here (see §1.5)).

4.3 Comparison of fits

Here we use the two rabies models of Murray *et al* (1986) and van den Bosch *et al* (1990) to illustrate the problems of fitting models from data, especially if we wish to use them predictively.

Both papers use very similar values for the mean τ of the generation gap T: Murray *et al* 33 days, van den Bosch *et al* 33.44 days. As to its distribution, the main difference is that Murray *et al*'s combination of two exponentials allows small values of T, which means that c_0 will grow faster with R_0 (see Figure 2(a)).

For the r.m.s. dispersal distance d, van den Bosch *et al* take a one-dimensional value of 2.3 kilometres for the position of individual foxes, when living at a density of one fox per square kilometre (Lambinet *et al* 1978); arguing that contacts arise between two individuals with independent movements, this gives $d = 2.3\sqrt{2} \approx 3.25$, equivalent to $D = d^2/2\tau \approx 58$ km^2/year.

Murray *et al*, via data on dispersal distances at various times (Andral *et al* 1982), estimate D as being in the range $65 - 320$ km^2/yr, with preferred value $D = 200$ (this is for foxes at an unspecified density, though an average territorial size of 5 km^2 is quoted in part of their argument). The equivalent r.m.s. dispersal distance, defined by $d^2 = 2D\tau$ as in §3.2, is then $d = 6.01$ km. (The actual r.m.s. dispersal distance, taking into account

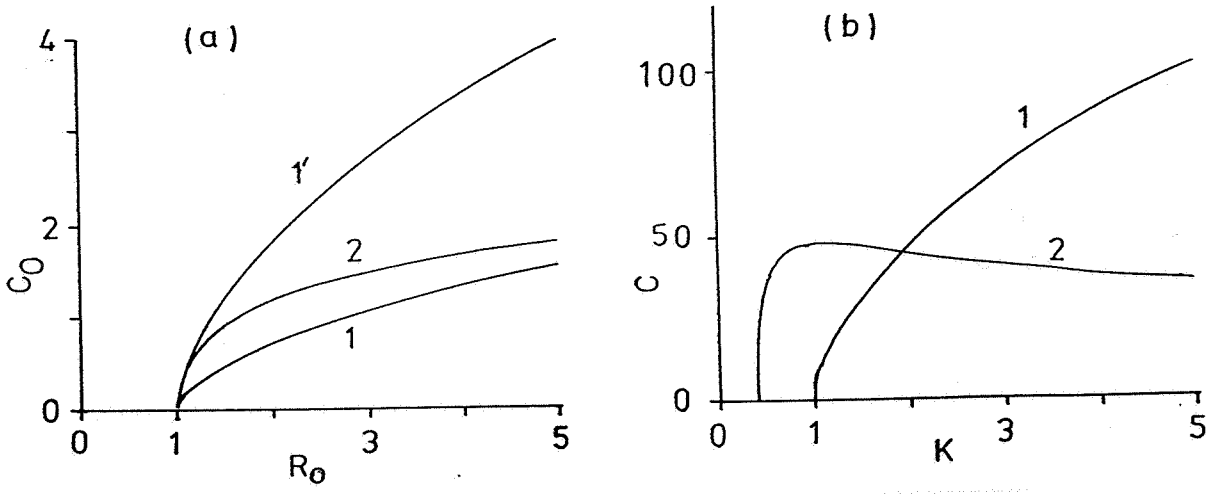

Figure 2 : Comparison of the fitting of the fox rabies models of (1) Murray *et al* (1986) and (2) van den Bosch *et al* (1990).

(a) Plots of the standardised velocity c_0 against R_0 ($1'$ shows an alternative standardisation, $c_0' = (d/d')c_0$, for Murray *et al*'s model (see text for definition of d')).

(b) Plots of velocity $c = (\frac{d}{\tau})c_0$ (in km/year) against carrying capacity K foxes/km^2).

that this model allows diffusion only during the infectious period, is $d' = d\sqrt{\tau_I/\tau} = 2.34$ km.)

Thus far, there is fairly close agreement between the two models, as shown in the plots of $c = (d/\tau)c_0$ against R_0 in Figure 2(a). Major differences enter when we turn to estimates of R_0, and to the dependence of R_0 and d on the carrying capacity K.

Both papers make the dubious assumption that $R_0 = K/K_0$, and quote similar ranges of estimates of K_0 from the applied literature (Murray *et al* 0.2 – 1.0 or 1.2, van den Bosch *et al* 0.25 – 1.0 foxes/km^2); though the estimates they prefer, at least for illustration, differ widely, 1.0 and 0.4 respectively.

However the most interesting difference is in their assumptions about the dependence of d on K. Murray *et al* treat d as independent of K, but van den Bosch *et al* suggest that because of the territorial behaviour of foxes d should be inversely proportional to $\sqrt{K}$. This turns their already slower growth of c_0 with R_0 into an actual velocity $c, \propto \sqrt{\ln(K/K_0)/K}$, which has a maximum (at $R_0 = K/K_0 = e$), beyond which it is a slowly *decreasing* function of K (see Figure 2(b)). They claim that this is in rough agreement with observations (Bögel and Moegle 1980) which suggest that the velocity is roughly independent of K once K is appreciably above threshold.

The argument that d should decrease as K increases is interesting and plausible. However van den Bosch *et al* do not seem to recognise that in the strong form they adopt, where the number of individuals living within a given multiple of d is independent of K (since $d \propto 1/\sqrt{K}$), it would be more consistent to take R_0 independent of K rather than the traditional assumption they adhere to, that $R_0 \propto K$. (There are, though, a variety of plausible models for fox behaviour that lead to intermediate dependence of R_0 on K.)

To take R_0 independent of K would be to deny the existence of a threshold population density. Probably it would be more realistic to have R_0 increasing with K, but more slowly than linearly (Mollison 1985); and d decreasing as K increases, but more slowly than $\propto 1/\sqrt{K}$. One might model the dispersal density as a mixture of local contacts, affected by territorial scale and thus $\propto 1/\sqrt{K}$, and of long distance contacts independent of K; note that the long distance contacts would then be of relatively greater significance at high densities. (Both papers assume well-behaved dispersal distributions, and thus implicitly that long distance contacts are of small importance – but see §4.5.)

4.4 Examples of falsifying

Skellam (1951) considered the recolonisation of Britain by oak trees following the last Ice Age, using Fisher (1937)'s models to argue that the observed velocity was too high to be explained by local dispersal, i.e. simply by the seeds (acorns) falling and rolling from their parent trees. Oaks only begin to produce acorns at a substantial age ($\tau_0 \sim 50$ years) and then produce very large numbers ($R_0 \sim 9,000,000$), so a dispersal model with constant generation gap τ_0 should be reasonably accurate. Skellam, following Fisher, assumed a Normal dispersal distribution, so that $c_0 = \sqrt{2\ln(R_0)}$ (see §3.1).

Because of the very large value of R_0, the shape of the dispersal distribution has an appreciable effect on the velocity: varying V over the range from Constant to Exponential can change the velocity by a factor of $\approx \sqrt{\ln(R_0)} \approx 4$ in either direction (Mollison 1977). However even this is not enough to alter Skellam's conclusion, that the observed velocity of about 0.3 km/year is far too high to be explained by local dispersal (assuming Normal V, this would require $d \sim 3$ km).

A similar argument has been presented for the spread of Dutch elm disease within Britain in the 1960s and 70s, inferring from observed velocities which are too high to be explained by movement of the disease-carrying beetles from tree to tree that some other mechanism, probably transport of infected timber, must be responsible.

Grey squirrels (not the red who are among the principal suspects in the oaks case) provide our third example. As described in §3.5, Okubo *et al* (1989) set up a competition

model for the advance of grey squirrels at the expense of red, but when it comes to estimation treat the effect of the latter as negligible ($\gamma_R \approx 0, \Rightarrow \hat{r}_G \approx r_G$), so that we are essentially back with the single population diffusion model of §2.2, with velocity $2\sqrt{r_G D_G}$.

They first use data on individual squirrel movements to estimate the diffusion rate $D \equiv D_G = 0.63$ km^2/year, but find that this gives too low a velocity by a factor of more than 5 (1.4 as opposed to 7.7 km/year).

The clear inference, as for the oaks, is that the assumed local dispersal is insufficient to explain the velocity of spread. We can go further and estimate what scale of dispersal is required to fit the observed velocity. This is essentially what Okubo *et al* go on to do, though it is unfortunately presented, with 'good agreement with data' being claimed for their revised model when it has just been fitted from the same data !

Their revised model is based on dispersal of subpopulations between neighbouring woods spaced d_2 apart. It seems a pity that this model is not formulated fully (the authors describe it as 'speculative and tentative'), because it is a nearest-neighbour square lattice model and a fair amount is known about such processes (Mollison & Kuulasmaa 1985, Cox & Durrett 1988). Okubo *et al* only use this dispersal model to estimate a value for τ (= 1.4 years), so that they can use a rescaled version of their original model with revised diffusion constant $D = d_2^2/4\tau$. They find that a plausible r.m.s. inter-woodland distance of $d_2 = 10$ km ($D = 17.9$ km^2/year) will match the observed velocity of 7.7 km/year.

4.5 Velocities of nonlinear stochastic models

What the examples of the previous subsection have in common is that in each case the observed velocity is much too high compared with the estimate assuming a local dispersal mechanism. It is fortunate that examples where the observed velocity is too low seem to be comparatively rare. Since the linear model velocities we are using are only an upper bound for the velocity of a more accurate nonlinear stochastic model, the inference would be less clear in such cases.

Because there is no known way of calculating the velocities of any but the simplest nonlinear stochastic models, we cannot generalise authoritatively as to how much lower they are than the velocities we have studied here for linear and deterministic models, using the R&D technique. We summarise here what is known or conjectured, largely on the basis of simulations.

First, it has actually been proved for the basic case of the nearest-neighbour epidemic with removal on a square lattice that it does have an asymptotic velocity, in a strong law sense (Cox & Durrett 1988). Simulations of Mollison *et al* (1991) confirm that the velocity, c_0' say, is significantly lower than the velocity c_0 for its linearisation, the nearest-neighbour birth-and-death process (Figure 3).

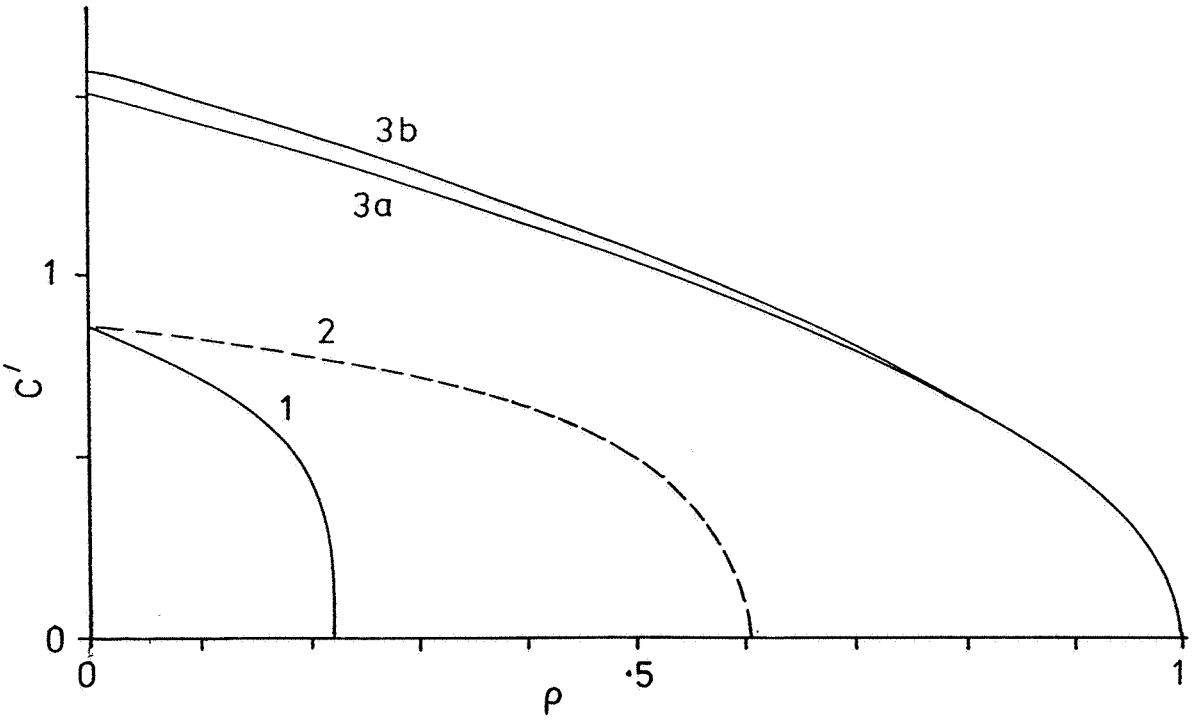

Figure 3 : Velocities of nearest-neighbour processes on the square lattice.
In each case the velocity shown is $c' = c/d$, where c is the velocity of the process with infection rate 1 and removal/recovery rate $\rho, = 1/\tau$. [We do not use the usual standardised velocity, $c_0 = c\tau/d = c'/\rho$, because it is infinite in the basic Simple Epidemic and Birth & Death Process cases ($\rho = 0$).]
Note that $d = 1/\sqrt{2}$ for any 1-dimensional projection of the 2-dimensional nearest-neighbour distribution.

1 Epidemic with removal (critical value is $\rho_c \approx 1/4.55 \approx 0.22$, see §1.5).

2 Epidemic with recovery, i.e. Contact Process with $\lambda = 1/\rho$. (Approximate, only the end points are known with any precision; $\rho_c = 1/4\lambda_c \approx 0.61$.)

3 Birth and death process, the linearisation of (1) and (2): velocity in (a) 45° and (b) axial directions.

Other nonlinear stochastic epidemic models for which velocities have been found by simulation (e.g. Mollison 1972b, Ball 1991) may be divided according to whether c_0 is finite. When c_0 is finite, simulations show well-behaved advance, with c_0' getting closer to c_0 as the number with whom an individual interacts increases. Typically, except where that number is very small (as in the models of Figure 3), the ratio seems to be closer than 1:2, a difference that is likely to be difficult to distinguish in practice, because of the difficulty of estimating d (and R_0) reliably. For instance, Mollison (1987) on the basis of nonlinear stochastic models suggests a velocity for fox rabies of the order of 25-50 km/year, or rather higher allowing for long-distance dispersals; this is in reasonable agreement with the estimates from both of the linear models discussed above (see Figure 2(b)), and from data (Macdonald & Voigt 1985, Ball 1985b).

When V has exponentially unbounded tails c_0 is infinite, and it is possible, at least in one dimension, for nonlinear stochastic models to have much more irregular patterns of spread (Mollison 1972b) even when the velocity c_0' is finite.

The borderline case is intriguing, in that such data as exist on dispersal distances suggest that a distribution with approximately exponential tails is not uncommon (see, e.g., data for muskrats in van den Bosch *et al* 1990, for the collared dove in Hengeveld 1989, and for two plant diseases transmitted by airborne spores in van den Bosch *et al* 1988).

Windborne diseases in particular show irregular patterns of spread (e.g. foot-and-mouth disease, Smith 1982), suggesting that their dispersal distributions are not exponentially bounded. Although linear models cannot deal directly with such cases, it may be possible to approximate their behaviour using separate models for local and long-distance spread (Zadoks 1989).

4.6 Endemicity and the atto-fox

We here explain briefly why nonlinear stochastic models are needed to model endemic patterns and the transition to endemicity.

First, the threshold value of R_0 is generally greater than the linear/deterministic value of 1 (Mollison & Kuulasmaa 1985).

As to mean densities of each type of individual in the endemic state, deterministic models generally give the same values as for homogeneously mixing, non-spatial, models, whereas simulations suggest that this is far from the case. For instance, Mollison & Kuulasmaa cite an example where the proportion of susceptibles is 80% of the carrying capacity when homogeneous mixing would have suggested 25%.

The explanation is that stochastic equilibrium does not look at all like homogeneous mixing, but rather has a random 'patchy' nature, with wandering foci of infection (for simulations see Mollison & Kuulasmaa, for data analysis Sayers *et al* 1985). The oscillations predicted by many deterministic models are thus almost certainly spurious; approximate periodicity shown by some data can be explained as a turnover period (Mollison 1987).

A striking example showing the inability of nonlinear deterministic models to handle the transition to endemicity is given by Murray *et al* (1986) in their prediction of how fox rabies might invade a new country (Britain). They predict a roughly circular expanding wave of advance, followed after a quiet phase of about 7 years by another wave originating from the same starting point.

This is incredible on two counts. As regards the first advancing wave, the weight of evidence from fox rabies in Europe suggests that after a short while it would manage to 'break back' across the devastated territory immediately behind it and induce an endemic equilibrium as described above. The deterministic model's inability to describe this is not surprising because it is an essentially stochastic phenomenon.

As to the second wave, close inspection shows that the explanation lies, not so much in the determinism of the model, as in its modelling of the population as continuous rather than discrete and its associated inability to let population variables reach the value zero. Thus the density of infected at the place of origin of the epidemic never becomes zero, it only declines to a minimum of around one atto-fox (10^{-18} of a fox, Hughes 1960) per square kilometre. The model then allows this atto-fox to start the second wave as soon as the susceptible population has regrown sufficiently.

Similar problems arise in attempts to model control zones deterministically. Unless the control zone is assumed totally impervious, atto-foxes will be found on the other side. We need stochastic models (e.g. Ball 1985a), and we need to consider the tail of the dispersal distribution (Mollison 1987).

Lastly, it is important to avoid simplistic assumptions about how parameters, particularly R_0, will change as conditions vary (Mollison 1984, 1985). For instance, to follow a simple model in assuming that R_0 will change proportionately as the density of susceptibles changes, whether that change is natural or due to vaccination or to culling, is to allow models to become a substitute for thought.

5 CONCLUSIONS

In this paper I have tried to show how useful simple linear models can be for investigating velocities of epidemic and population spread. The R&D kernel formulation due to Diekmann (1978) and van den Bosch *et al* (1990) allows us to deal straightforwardly with a quite general generation gap T and dispersal distance X (and any correlation between them).

Their strong advantage over nonlinear deterministic models is that, while they generally have the same velocity, they are far simpler, and their natural formulation in terms of basic ecological components such as R_0, T and X greatly facilitates discussion of the crucial and difficult questions concerning how we relate models to necessarily imprecise data.

In using linear models we need to be cautious in three respects: first as to the probabilities attributed to small values of T and large values of X, because these are particularly influential in determining the velocity (see §2.2 and §2.3).

Secondly, we need to remain aware that they only give upper bounds for the velocity of the more realistic nonlinear stochastic case, which is likely to be appreciably less at least when the number with whom an individual interacts is small.

Thirdly, if the dispersal distribution does not have exponentially bounded tail the velocity of the linear model will be infinite, though that of the nonlinear stochastic model may still be finite, so we certainly need to consider the latter. In any of these cases, computer simulations of the nonlinear stochastic model can be useful in exploring the accuracy of the linear model.

Because of the limitations of linear models, and the imprecision of data, they are most useful as an exploratory tool, clarifying – and possibly falsifying – hypotheses, rather than fitting or extrapolating from data.

From the applied point of view, there is scope for much closer discussion of the right form of R&D kernel for particular species or diseases; of how it may be expected to change with circumstances, for instance as the carrying capacity changes; and of how it can be estimated from or tested against data. Data on dispersal distributions, particularly looking at the probability of long distance dispersal, would also be helpful.

On the theoretical side, there is the challenge of clearing up the exact conditions under which the Linear Conjecture holds. It might also be possible to develop alternative deterministic nonlinear population models that avoid some of the drawbacks of present ones, for instance models in which densities can fall to zero in finite time.

The ultimate goal remains a better understanding of nonlinear stochastic models. There has been significant progress on this in recent years (see §4.5 and §4.6). The linear models reviewed here, together with computer simulations, can complement this progress, revealing patterns to be explained and raising conjectures to prove or disprove.

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