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ON AN EPIDEMIC IN A STRATIFIED POPULATION

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Abstract

Most epidemic models previously studied have assumed a homogeneously mixing population. Instead of making this assumption, a population divided into classes is considered; and it is assumed that the degree of mixing between classes is less than that within classes. The stochastic model in this form is intractable and approximations are made, yielding results in reasonable agreement with simulation trials.

STOCHASTIC EPIDEMIC MODEL; NONHOMOGENEOUS MIXING; DETERMINISTIC APPROXIMATION; STOCHASTIC APPROXIMATION; SIMULATION

1. Introduction

Of the assumptions commonly used in continuous infection models, the least likely to be even approximately true in large populations, is that of homogeneous mixing. In this paper, we investigate a model for the spread of infection amongst a population which is divided into classes, such that the individuals of each class mix homogeneously amongst themselves, but mix to a lesser degree with individuals of other classes. A class could be thought of either as a group of friends or associates, or as a collection of individuals in a certain region of the community.

An assumption of this kind appears to be a quite realistic substitute for the homogeneous mixing assumption. That such a model is appropriate is also suggested by observed epidemic behaviour. It is known that epidemics in large populations can often be broken down into smaller outbreaks which are in general not in phase, and which interact with each other to some extent, as envisaged in the present model.

Simple models of this kind have been put forward by Haskey (1957), who studied the case of a simple epidemic (i.e., no removal) in two classes, and Rushton and Mautner (1955) who studied the case of a deterministic simple epidemic in m equivalent classes. Also, Bailey (1957) made mention of the possibility of

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such a model, and Bartlett (1957) simulated a recurrent epidemic model using a similar assumption.

Although the primary purpose of this model is to provide an alternative to the homogeneous mixing assumption, non-homogeneous behaviour with respect to the infection may also be taken into account. Thus, for example, this may be useful in dealing with the case of a community which includes a region, such as a slum area, the individuals of which, for some reason or other, are more prone to infection.

Further, by suitable amendment of the interpretation given to the parameters, the model can be used to describe another important situation: that of a population consisting of a number of distinct types of individuals exhibiting differing susceptibility and rates of recovery. The division of the population into age groups is a possible classification for which the model is applicable.

As is perhaps to be expected, the resulting stochastic model presents as yet insurmountable difficulties, but nevertheless, some useful results can be obtained by means of approximating processes.

2. Definition of the model

We consider a population of size N, divided into m distinct classes or subpopulations, C_r of size N_r $(1 \leqq r \leqq m)$. The essential features of the process insofar as infection and removal are concerned are the same as for the general stochastic epidemic. We make the following definitions:

X_r = number of susceptibles in C_r, $X = \sum X_r$;
Y_r = number of infectives in C_r, $Y = \sum Y_r$;
Z_r = number of removed cases in C_r, $Z = \sum Z_r$;
β_{rs} = infection rate in C_r due to infectives in C_s, $(1 \leqq r, s \leqq m)$;
γ_r = removal rate in C_r, $(1 \leqq r \leqq m)$.

The process is then defined by the transition rates:

rate of infection in C_r $(X_r \to X_r - 1,\ Y_r \to Y_r + 1) = X_r \sum_{s=1}^{m} \beta_{rs} Y_s$;
rate of removal in C_r $(Y_r \to Y_r - 1,\ Z_r \to Z_r + 1) = \gamma_r Y_r$.

The initial conditions are

$$(X_r, Y_r, Z_r) = (n_r, a_r, 0); \tag{1}$$

and it is usually assumed that the outbreak is started in one class, C_1 say, so that only a_1 is non-zero. The final state of the process is given by

$$(X_r, Y_r, Z_r) = (n_r - \zeta_r, 0, \zeta_r + a_r),$$

with $\sigma_r = \zeta_r / n_r$ = the severity of the outbreak in C_r.

In the case of a population subdivided into a number of classes such that the members of each class mix homogeneously amongst themselves, but to a

lesser degree with individuals of other classes, the β_{rs} can be expressed in terms of more meaningful parameters as follows:

$$\beta_{rs} = \beta_r p_{rs} N_r / N_s ,$$

where

β_r = infection rate in C_r, and

p_{rs} = degree of mixing between C_r and C_s.

There are certain constraints on the p_{rs} inherent in their meaning:

$$p_{sr} = p_{rs}, \; p_{rr} = 1, \; 0 \leqq p_{rs} \leqq 1 .$$

It should be noted that $p_{rs} = 1$ gives homogeneous mixing, while $p_{rs} = 0$ gives m completely separate populations. Thus, the process under consideration is bounded by these two known extremes.

We will consider in some detail the case of equivalent classes, for which we have

$$N_r = N_0, \; \gamma_r = \gamma, \; \beta_{rs} = \begin{cases} \beta & (r = s), \\ q\beta & (r \neq s), \end{cases} \tag{2}$$

where $0 \leqq q \leqq 1$. This model corresponds to the general stochastic epidemic except in regard to the homogeneous mixing assumption—we have a uniform population divided into m classes.

3. Deterministic approximation for the severity

The deterministic approximations are obtained as the solutions of the differential equations which result when the second moments are neglected from the equations satisfied by the stochastic means. They do not reflect the detailed behaviour of the process, particularly in regard to extinctions, and are best regarded as approximations to the means. The deterministic approximations then, which we denote by (X_{rd}, Y_{rd}, Z_{rd}) satisfy the following equations:

$$\frac{dX_{rd}}{dt} = -X_{rd} \sum_{s=1}^{m} \beta_{rs} Y_{sd}, \tag{3}$$

$$\frac{dY_{rd}}{dt} = -X_{rd} \sum_{s=1}^{m} \beta_{rs} Y_{sd} - \gamma_r Y_{rd}, \tag{4}$$

$$\frac{dZ_{rd}}{dt} = \gamma_r Y_{rd}, \tag{5}$$

with initial conditions (1), and final state

$$(X_{rd}, Y_{rd}, Z_{rd}) = (n_r - \zeta_{rd}, 0, \zeta_{rd} + a_r);$$

with $\sigma_{rd} = \zeta_{rd}/n_r$ = the deterministic approximation to the severity of the outbreak in C_r.

We now derive equations for the σ_{rd}. From (5) we obtain

$$\frac{d}{dt}\left\{\sum_{s=1}^{m}\frac{\beta_{rs}}{\gamma_s}Z_{sd}\right\} = \sum_{s=1}^{m}\beta_{rs}Y_{sd}. \tag{6}$$

Then, we derive from (3) and (6), using initial conditions (1),

$$X_{rd} = n_r \exp\left\{-\sum_{s=1}^{m}\frac{\beta_{rs}}{\gamma_s}Z_{sd}\right\}. \tag{7}$$

So, letting $t \to \infty$ in (7) we are led to

$$\log(1-\sigma_{rd}) + \sum_{s=1}^{m}\frac{n_s\beta_{rs}}{\gamma_s}\sigma_{sd} + \sum_{s=1}^{m}\frac{a_s\beta_{rs}}{\gamma_s} = 0. \tag{8}$$

Thus, we have a set of m equations in m unknowns for the σ_{rd}. No explicit solution is available, but in any particular case, solutions may be found by an iterative procedure. For example, if $\sigma_{rd}^{(i)}$ is the estimate of σ_{rd} after the ith iteration, then we define

$$\sigma_{rd}^{(i+1)} = 1 - \exp\left\{-\sum_{s=1}^{r-1}\frac{n_s\beta_{rs}}{\gamma_s}\sigma_{sd}^{(i+1)} - \sum_{s=r}^{m}\frac{n_s\beta_{rs}}{\gamma_s}\sigma_{sd}^{(i)} - \sum_{s=1}^{m}\frac{a_s\beta_{rs}}{\gamma_s}\right\},$$

with $\sigma_{rd}^{(0)} = 1$, say. Such a method is easily programmed, and high accuracy can be obtained quite quickly—for example, with $m = 50$, four decimal accuracy is obtained in less than ten seconds on an IBM 7044 machine.

In the case of equivalent classes, the Equations (8) for the σ_{rd} become

$$\log(1-\sigma_{rd}) + \beta\gamma^{-1}(N_0 - a_r)\left[\sigma_{rd} + q\sum_{s\neq r}\sigma_{sd}\right] + \beta\gamma^{-1}\left[a_r + q\sum_{s\neq r}a_s\right] = 0.$$

If we neglect the a_r, then $\sigma_{rd} = \sigma_d$, where σ_d satisfies

$$\log(1-\sigma_d) + QN_0\beta\gamma^{-1}\sigma_d = 0, \tag{9}$$

with $Q = 1 + (m-1)q$.

4. The equivalent classes model

For this model, defined by (2), since $X_r \leqq N_0$, we have

$$\Pr\{Y \to Y+1 \text{ in } (t, t+\Delta t)\} = \sum_{r=1}^{m}\sum_{s=1}^{m}\beta_{rs}X_rY_s\Delta t + o(\Delta t) \leqq Q\beta N_0 Y\Delta t + o(\Delta t),$$

$$\Pr\{Y \to Y-1 \text{ in } (t, t+\Delta t)\} = \sum_{r=1}^{m}\gamma_r Y_r\Delta t + o(\Delta t) = \gamma Y\Delta t + o(\Delta t).$$

So, the linear birth and death process, $Y_u(t)$, having birth rate $Q\beta N_0$ and death rate γ, is an upper bounding process which approximates $Y(t)$ in the early stages.

It is known, e.g., Karlin ((1966), ch. 7), that $Y_u(t)$ becomes extinct with probability equal to $P_0 = \min\{1, (\gamma/\beta Q N_0)^{Y_u(0)}\}$; and this corresponds to early extinction of $Y(t)$, i.e., a minor outbreak. Otherwise, $Y_u(t)$ explodes, corresponding to a major outbreak.

Thus, as might be expected from (9), we find a threshold such that a major outbreak is possible only if $\beta Q N_0 > \gamma$. But, the nature of this outbreak has yet to be specified. It is to be expected that if q is large, the outbreak will include a majority of the classes, while if q is small, only a few of the classes will be affected; assuming the outbreak to be initiated from only one of the classes. So, we now envisage three types of outbreak:

localized outbreak — minor outbreak in initially infected class;

restricted outbreak — major outbreak in a few classes;

generalized outbreak — major outbreak in most classes.

Which one of these types of outbreak will be exhibited is dependent on the parameters of the model. Figure 1 indicates the probability of the three types of outbreak, as a function of $\theta = \beta N_0/\gamma$.

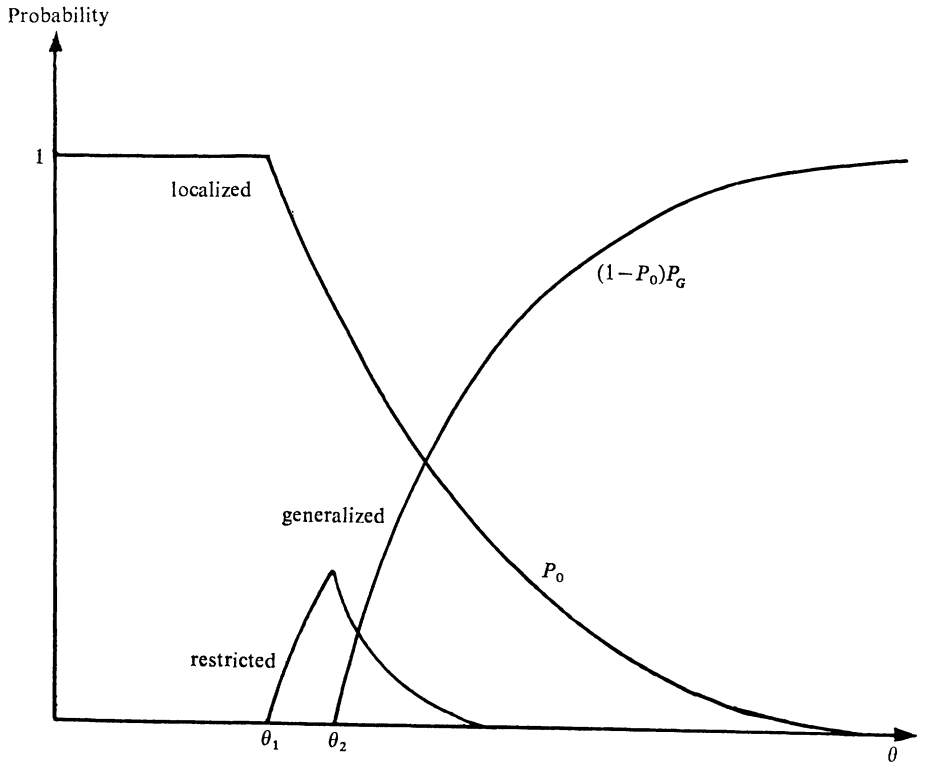

Figure 1

The probabilities of the three types of outbreak, as functions of $\theta = \beta N_0/\gamma$

Here, θ_1 and θ_2 are functions of m, q. From the expression for P_0, we see that

$$\theta_1(m,q) = 1/Q = 1/(1 + q(m-1)).$$

Further we expect that $\theta_2 \simeq \theta_1$, $P_G \simeq 1$ except when q is small. We approximate to P_G, θ_2 in this case below.

The class to class spread of infection, when q is small, may be approximated by a model similar to one considered by Daley (1967). This model may be described as follows. A class, once infected, remains infective for a random positive time, at the end of which the infection is transmitted to a number of other classes, each of which have a probability p of being contacted. A susceptible class becomes infective with probability π after contact, while any infective or removed class contacted is unaffected.

Here, we apply the following interpretations.

(i) One class contacts another if an infective in the one infects at least one susceptible in the other.

(ii) A class is susceptible if there has been no major outbreak in the class.

(iii) A class is infected if a major outbreak occurs in the class.

(iv) A class is removed if a major outbreak has occurred in the class.

Corresponding to the original model, it is assumed that initially there is only one infective, in class C_1 say.

For this model, Daley's results are modified to the following.

(i) *Threshold.* A generalized outbreak is possible only if

$$(m-1)p\pi > 1.$$

(ii) *Severity.* If there is a generalized outbreak the number of classes affected is approximated by $\zeta_G = 1 + (m-1)\sigma_G$, where σ_G satisfies

$$\log(1-\sigma_G) + (m-1)p\pi\sigma_G = 0.$$

(iii) *Probability of generalized outbreak.* The probability of generalized outbreak is $(1-P_0)P_G$, where P_G is the larger solution of

$$1-x = 1 - p\pi x^{m-1}, \qquad 0 \leqq x \leqq 1;$$

and $P_0 = \min\{1, \gamma/\beta N_0\}$.

All that is required then, is to find expressions for π, p in terms of the parameters of the model. Exact expressions have not been derived, but reasonable and simple approximations are easily found for the case when q is small, and m moderately large, (say $m \geqq 10$), so that distinction between restricted and generalized outbreaks is possible.

If L is the number of individuals in a given class infected from another infected class, then, assuming q sufficiently small, L has a distribution which is approximately negative binomial. Thus, if L^* is such that

$$\Pr\{L^* = j\} = \binom{-\zeta}{j} \left(1 + q\beta N_0 \gamma^{-1}\right)^{-\zeta} \left(\frac{-q\beta N_0 \gamma^{-1}}{1+q\beta N_0 \gamma^{-1}}\right)^j, (j \geqq 0),$$

where ζ is the size of the outbreak in the infected class; then L^* is an upper approximation for L. If, instead of the random variable ζ, we use the deterministic approximation ζ_d, the solution of the equation

$$\log(1 - (\zeta_d/N_0)) + Q\beta\zeta_d\gamma^{-1} = 0,$$

then we find the following approximations:

$$p = \Pr\{L > 0\} \simeq 1 - (1 + q\beta N_0 \gamma^{-1})^{-\zeta_d}$$

$$\pi = \Pr\{\text{major outbreak} \mid L > 0\} \simeq p^{-1}\{1 - (1 - qQ^{-1} + q\beta N_0 \gamma^{-1})^{-\zeta_d}\}.$$

Note that θ_2 is determined as the solution of

$$(m - 1)p(\theta)\pi(\theta) = 1,$$

which gives, using the above approximations

$$\theta_2 \simeq \theta_1 + q^{-1}\{(1 + 1/(m-2))^{1/\zeta_d} - 1\}.$$

Two numerical examples are given in Tables 1 and 2 to illustrate the variation of p, π, ζ_G, P_G with q.

TABLE 1

$m = 10$, $N_0 = 100$, $\gamma = 0.06$, $\beta = 0.001$

q	ζ_d	p	π	ζ_G	P_G
0.100	95	1.00	1.00	10.0	1.00
0.050	88	1.00	0.99	10.0	1.00
0.010	74	0.71	0.60	9.9	0.99
0.006	72	0.51	0.52	9.2	0.92
0.005	71	0.44	0.50	8.7	0.85
0.004	70	0.37	0.48	7.8	0.70
0.003	70	0.29	0.46	6.0	0.36
0.0025	69	0.25	0.45	4.7	0.09
0.002	69	0.21	0.44	3.3	0.00
0.001	68	0.11	0.42	1.6	0.00

TABLE 2

$m = 50$, $N_0 = 50$, $\gamma = 0.03$. $\beta = 0.001$

q	ζ_d	p	π	ζ_G	P_G
0.1000	50	1.00	1.00	50.0	1.00
0.0100	45	0.52	0.68	50.0	1.00
0.0050	41	0.29	0.56	50.0	1.00
0.0020	37	0.12	0.47	46.0	0.92
0.0015	36	0.09	0.45	39.7	0.79
0.0012	36	0.07	0.44	31.1	0.59
0.0010	36	0.06	0.44	21.2	0.35
0.0008	35	0.05	0.43	8.8	0.04
0.0006	35	0.03	0.42	3.2	0.00
0.0003	34	0.02	0.41	1.5	0.00

Further, a series of simulations of the epidemic process has been done for populations of size 1000 and 2500 with various values of m, N_0, q, and $\rho = \gamma/\beta$; and the results obtained are in reasonable agreement with the theoretical predictions. Details of the simulation series may be obtained on application to the author.

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