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STRONG APPROXIMATIONS FOR MOBILE POPULATION EPIDEMIC MODELS

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We consider a stochastic model for the spread of an epidemic in a population split into m groups in which both infective and susceptible individuals are able to move between groups. Using a coupling argument similar to those applied to various other epidemic models by previous authors, we show that as the initial susceptible population becomes large, the process of infectives in this epidemic model converges to a multitype birth-and-death process with time-dependent birth rates. The behavior of this limiting process is then considered, in particular, the conditions under which extinction is almost certain.

1. Introduction. In stochastic epidemic modeling, it is common to approximate the model of interest by an appropriate branching process. This is useful since epidemic models are generally nonlinear and the linear branching process approximation is likely to be rather more tractable. The method goes back to the comments of Bartlett (1955) and Kendall (1956), who pointed out that in the case of the general stochastic epidemic model [see, for example, Bailey (1975)] when the population is large, the process of infectives approximately follows a linear birth-and-death process. This idea was made more precise by Ball (1983), who used a coupling argument similar to that of Metz (1978); the results also were extended to cover an epidemic model in which the population is split into several groups. In this model, individuals were not able to move between groups, but infection from one group to another could occur. Ball (1991) pointed out that if infectives are allowed to move between groups, then essentially the same argument can still be applied. The technique has been extended by Ball and Donnelly (1995) and Ball and O'Neill (1994) to cover a very wide class of epidemic models. In each case details were given only for the single group case, but the methods used clearly apply to multigroup models as long as susceptibles are not able to move between groups. For a simple model in which both infectives and susceptibles are able to move between groups, Clancy (1995) argued heuristically to conclude that the process of infectives can be approximated by a multitype birth-and-death process with time-dependent birth rates. In this paper, this result is made rigorous using an argument similar to that of O'Neill (1996). We also look at possible extensions of the model and at the behavior of the limiting process.

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2. Construction of the epidemic process and the main convergence result. Our basic epidemic model is defined as follows. We consider a closed population divided into m groups, such that at time t, group i contains $X_i(t)$ susceptibles and $Y_i(t)$ infectives. Initially, we have $X_i(0) = N_i$ and $Y_i(0) = a_i$, and we define $N = N_1 + N_2 + \cdots + N_m$ to be the total number of susceptibles in the population at time $t = 0$. Each susceptible individual moves between groups according to a Markov process on $\{1, 2, \ldots, m\}$ with transition rate matrix R and each infective moves according to a Markov process with transition rate matrix Q. When an individual becomes infected, it remains so for a time which is exponentially distributed with mean γ^{-1} (independent of its movement process) and is then removed. Each pair of individuals in group i makes contact at the points of a Poisson process of rate $\beta m / N$, the contacts between distinct pairs of individuals being mutually independent, and contact between an infective and a susceptible results in the infection of the susceptible. The infectious periods and movement processes of distinct individuals are mutually independent.

We are interested in the behavior of our epidemic process when the initial number of susceptibles is large. Thus defining $\pi_i = N_i/N$ $(i = 1, 2, \ldots, m)$, we consider a sequence of epidemics indexed by n such that as $n \to \infty$, $N^{(n)} \to \infty$ and $\pi_i^{(n)} \to \pi_i > 0$ for each i. We suppose that $a_1, a_2, \ldots, a_m$ are independent of n, as are the parameters β, γ, R and Q. Up to any finite time t, the number of initial susceptibles which have been infected will be negligible compared to the number of uninfected susceptibles. Also, since the number of susceptibles is very large, their movement can be well approximated by a deterministic process. Thus for $0 \le s \le t$, the process of susceptibles $\boldsymbol{X}(s) = (X_1(s), X_2(s), \ldots, X_m(s))$ can be approximated by $N\boldsymbol{\pi}\exp(Rs)$, where $\boldsymbol{\pi} = (\pi_1, \pi_2, \ldots, \pi_m)$. Now since infections occur in group i at rate $\beta m X_i Y_i / N$, this implies that the process of infectives $\boldsymbol{Y}(s) = (Y_1(s), Y_2(s), \ldots, Y_m(s))$ in $[0, t]$ can be approximated by a multitype birth-and-death process in which each individual lives for a time which is exponentially distributed with mean γ^{-1}, during which time it moves between groups according to a Markov process with transition rate matrix Q, and while in group i produces offspring in group i at rate $\beta m(\boldsymbol{\pi}\exp(Rs))_i$.

In order to prove this, we first of all give a construction of the limiting birth-and-death process and then show how the nth epidemic process can be constructed from this process. The process of infectives in the epidemic can differ from the birth-and-death process in two ways—a birth can occur with no corresponding infection or vice versa. An individual born into the birth-and-death process with no corresponding infection in the epidemic process will be called a "ghost," following Mollison (1977), while an infection with no corresponding birth will be called a shadow infection, following O'Neill (1996). Infectives which do not result from a shadow infection will be referred to as natural infectives. The proof that the process of infectives converges to the birth-and-death process then consists of showing that given any fixed time t, if n is sufficiently large, then there will be no ghosts and no shadow infections in the interval $[0, t]$.

The birth-and-death process is constructed as follows. We have a closed population divided into m groups, group i initially consisting of a_i individuals. The initial group i individuals are labelled (i, r) for $r = -(a_i - 1), -(a_i - 2), \ldots, 0$ and for $r = 1, 2, \ldots$, the rth individual to be born in group i is labelled (i, r). Individual (i, r) has "life history" $(I^{(i,r)}, \chi^{(i,r)}, P^{(i,r)})$, where $I^{(i,r)}$ is an exponentially distributed random variable with mean γ^{-1}, $\chi^{(i,r)}$ is a Markov process on $\{1, 2, \ldots, m\}$, starting from i, with transition rate matrix Q, and $P^{(i,r)}$ is a homogeneous Poisson process of rate 1. For any particular individual (i, r), the components of its life history $I^{(i,r)}$, $\chi^{(i,r)}$, and $P^{(i,r)}$ are independent of one another, and the life histories of distinct individuals are all mutually independent. If individual (i, r) is born at time τ, then it lives until time $\tau + I^{(i,r)}$. For $0 \le s \le I^{(i,r)}$, the group which this individual is in at time $\tau + s$ is given by $\chi^{(i,r)}(s)$. Finally, defining

$$\tilde{\beta}_j(s) = \beta m(\boldsymbol{\pi} \exp(Rs))_j \qquad (j = 1, 2, \ldots, m),$$

$$V^{(i,r)}(s) = \int_0^s \tilde{\beta}_{\chi^{(i,r)}(u)}(\tau + u)\, du,$$

then individual (i, r) gives birth at those times $\tau + s$ $(0 \le s \le I^{(i,r)})$ such that $V^{(i,r)}(s)$ is a point of $P^{(i,r)}$, the birth producing a new individual in group $\chi^{(i,r)}(s)$.

In order to construct our epidemic process, we suppose that for each (i, r) such that $i = 1, 2, \ldots, m$ and $r = 1, 2, \ldots$, we have defined on the same probability space as our birth-and-death process the following additional ingredients:

1. A Markov process $\xi^{(i,r)}$ on $\{1, 2, \ldots, m\}$, starting from state i and with transition rate matrix R.
2. A random variable $U^{(i,r)}$ uniformly distributed on $[0, 1]$.
3. A homogeneous Poisson process $\tilde{P}^{(i,r)}$ of rate 1.
4. A life history $(I_*^{(i,r)}, \chi_*^{(i,r)}, P_*^{(i,r)})$ having the same distribution as the life history of an individual born into group i of the birth-and-death process.

These additional random variables and processes are all supposed independent of one another and of our birth-and-death process.

For $n = 1, 2, \ldots$, we now construct the epidemic process indexed by n as follows. Initially, group i consists of $N_i^{(n)}$ susceptibles and a_i infectives. The initial group i individuals are each given a label (i, r), where the initial infectives have $r = -(a_i - 1), -(a_i - 2), \ldots, 0$ and the initial susceptibles have $r = 1, 2, \ldots, N_i$. Each initial infective (i, r) is associated with the initial individual (i, r) in the birth-and-death process. It moves between groups according to $\chi^{(i,r)}$ until time $I^{(i,r)}$, when it is removed. The initial susceptible (i, r) moves according to the process $\xi^{(i,r)}$ until it becomes infected (which may never happen).

Suppose that the rth group i birth in the birth-and-death process occurs at time τ. If this birth is the offspring of a ghost, then it is ignored in the construction of the epidemic process and the offspring is also a ghost. If the

parent is not a ghost, then if

$$U^{(i,r)} > \frac{X_i(\tau-)}{N(\boldsymbol{\pi}\exp(R\tau))_i},$$

the offspring is again treated as a ghost and ignored, together with all its subsequent offspring. Otherwise, an infection occurs in the epidemic at time τ. The susceptible (i', r') to be infected is chosen uniformly at random from those in group i at time $\tau-$ and associated with the individual (i, r) born into the birth-and-death process. This individual now moves between groups according to $\chi^{(i,r)}$ [so at time $\tau + s$ it is in group $\chi^{(i,r)}(s)$], rather than its original movement process $\xi^{(i',r')}$, until time $\tau + I^{(i,r)}$, when it is removed.

The infective which is associated with individual (i, r) in the birth-and-death process also has associated with it the Poisson process $\bar{P}^{(i,r)}$, governing the times at which shadow infections occur. If this individual is born at time τ and is not a ghost, then defining

$$\bar{\beta}_j(s) = \frac{\beta m X_j(s)}{N} \qquad (j = 1, 2, \ldots, m),$$

$$\bar{V}^{(i,r)}(s) = \int_0^s \max\left\{0, \bar{\beta}_{\chi^{(i,r)}(u)}(\tau+u) - \tilde{\beta}_{\chi^{(i,r)}(u)}(\tau+u)\right\} du,$$

the associated infective causes shadow infections at those times $\tau + s$ $(0 \le s \le I^{(i,r)})$ such that $\bar{V}^{(i,r)}(s)$ is a point of $\bar{P}^{(i,r)}$. (There is a slight technical problem here in that if $\bar{V}^{(i,r)}$ remains constant on the interval $[s, s+\delta)$ for some $\delta > 0$, then we would have shadow infections occurring at every point of this interval. However, we simply need to observe that the probability of this problem arising is zero.) A susceptible is chosen uniformly at random from those currently in the same group as the infective (i, r), and this susceptible becomes a shadow infective. The rth shadow infective to be created in group i has associated with it the life history $(I_*^{(i,r)}, \chi_*^{(i,r)}, P_*^{(i,r)})$. If shadow infective (i, r) becomes infected at time τ, then it moves between groups according to $\chi_*^{(i,r)}$ until it is removed at time $\tau + I_*^{(i,r)}$. Defining

$$V_*^{(i,r)}(s) = \int_0^s \bar{\beta}_{\chi_*^{(i,r)}(u)}(\tau+u)\, du,$$

then at those times $\tau + s$ $(0 \le s \le I_*^{(i,r)})$ such that $V_*^{(i,r)}(s)$ is a point of $P_*^{(i,r)}$, the shadow infective infects a susceptible chosen uniformly at random from those in its current group, and this individual itself becomes a shadow infective.

In a similar way to O'Neill (1996), we can easily verify that the above construction does indeed give the required epidemic model by checking that the rates of infection, removal and movement are all correct. We now need to show that for any fixed time interval $[0, t]$, if n is sufficiently large, then no ghosts or shadow infectives will appear in $[0, t]$. Thus the epidemic process on $[0, t]$ converges in the discrete topology to the corresponding birth-and-death process.

THEOREM 2.1. *Writing $Z_i(s)$ for the number of individuals in group i of our birth-and-death process at time s and $\mathbf{Z} = (Z_1, Z_2, \ldots, Z_m)$, then for any fixed $t > 0$,*

$$\lim_{n\to\infty} \sup_{0\le s\le t} \left|\mathbf{Y}^{(n)}(s) - \mathbf{Z}(s)\right| = 0 \quad \textit{almost surely},$$

where for $\boldsymbol{u}, \boldsymbol{v} \in \mathbb{R}^m$, $|\boldsymbol{u} - \boldsymbol{v}| = \max_{i=1,2,\ldots,m} |u_i - v_i|$.

PROOF. Fix $t > 0$ and writing $1_{\{\cdot\}}$ for the indicator function of the event $\{\cdot\}$, define

$$\tilde{X}_j(s) = \sum_{i=1}^{m} \sum_{r=1}^{N_i} 1_{\{\xi^{(i,r)}(s)=j\}} \qquad (j = 1, 2, \ldots, m), \tag{2.1}$$

so $\tilde{X}_j(s)$ is the number of susceptibles which would be in group j at time s if no infection took place. Writing $\tilde{\mathbf{X}} = (\tilde{X}_1, \tilde{X}_2, \ldots, \tilde{X}_m)$, then Theorem 2.1 of Ethier and Kurtz [(1986), Chapter 11] states that

$$\lim_{n\to\infty} \sup_{0\le s\le t} \left| \frac{1}{N}\tilde{\mathbf{X}}^{(n)}(s) - \boldsymbol{\pi}\exp(Rs)\right| = 0 \quad \text{almost surely.}$$

Let W be the total number of births in $[0, t]$ in the birth-and-death process, which is almost surely finite. Then at most $a + W$ natural infectives can exist during the interval $[0, t]$, each of which produces shadow infectives at times governed by the Poisson process $\bar{P}^{(i,r)}$ for some (i, r). Thus there almost surely exists some time t_0 such that for all these $a + W$ values of (i, r), $\bar{P}^{(i,r)}$ has no points in $[0, t_0]$. Now given any $\varepsilon > 0$, there almost surely exists some n_1 such that for $n \ge n_1$,

$$\sup_{0\le s\le t} \left| \frac{1}{N}\tilde{\mathbf{X}}^{(n)}(s) - \boldsymbol{\pi}\exp(Rs)\right| < \varepsilon.$$

Clearly $\mathbf{X}(s) \le \tilde{\mathbf{X}}(s)$, so in $[0, t]$, for each $i = 1, 2, \ldots, m$, we have that for $n \ge n_1$,

$$\frac{1}{N}X_i(s) - (\boldsymbol{\pi}\exp(Rs))_i < \varepsilon,$$

which implies that

$$\bar{\beta}_i(s) - \tilde{\beta}_i(s) < \beta m\varepsilon$$

and hence

$$\bar{V}^{(i,r)}(s) < \beta m\varepsilon t.$$

Choosing ε so that $\beta m\varepsilon t < t_0$, then for $n \ge n_1$ no shadow infectives will be produced by natural infectives in $[0, t]$ and so no shadow infectives will appear at all.

The first ghost appears when an individual (i, r) is born at time τ with

$$U^{(i,r)} > \frac{X_i(\tau-)}{N(\boldsymbol{\pi}\exp(R\tau))_i}. \tag{2.2}$$

Since the number of individuals W born in $[0, t]$ is almost surely finite, there is almost surely some $u_0 < 1$ such that for each of these W individuals, $U^{(i,r)} \leq u_0$. Now for $n \geq n_1$, since no shadow infectives appear in $[0, t]$, we have for $i = 1, 2, \ldots, m$ that in $[0, t]$,

$$\begin{aligned} X_i(s) &\geq \tilde{X}_i(s) - W \\ &> N((\boldsymbol{\pi}\exp(Rs))_i - \varepsilon) - W. \end{aligned}$$

Defining $\delta_i = \inf_{0\leq s\leq t}(\boldsymbol{\pi}\exp(Rs))_i$, then $\delta_i > 0$ (since the components of $\boldsymbol{\pi}$ are all strictly positive) and for $0 \leq s \leq t$,

$$\frac{X_i(s)}{N(\boldsymbol{\pi}\exp(Rs))_i} > 1 - \frac{\varepsilon}{\delta_i} - \frac{W}{N\delta_i}.$$

Thus if we take $\varepsilon < \frac{1}{2}\delta_i(1 - u_0)$ for $i = 1, 2, \ldots, m$ and n_2 sufficiently large that for $n \geq n_2$, $W < \frac{1}{2}\delta_i N^{(n)}(1 - u_0)$ $(i = 1, 2, \ldots, m)$, then for $n \geq n_3 = \max\{n_1, n_2\}$ we have

$$\frac{X_i(s)}{N(\boldsymbol{\pi}\exp(Rs))_i} > u_0 \qquad (i = 1, 2, \ldots, m),$$

which contradicts (2.2) and so no ghosts can appear in $[0, t]$.

We have shown that we can almost surely find some n_3 such that for $n \geq n_3$, neither shadow infectives nor ghosts appear in $[0, t]$, and so up to time t we have $\boldsymbol{Y}^{(n)} = \boldsymbol{Z}$ and the result follows. □

COROLLARY 2.1. *Defining T_i to be the total number of births ever to occur in group i in the birth-and-death process and $T_i^{(n)}$ to be the total number of infections to occur in group i of the nth epidemic process, then as $n \to \infty$,*

$$\boldsymbol{T}^{(n)} \to \boldsymbol{T} \quad \textit{almost surely},$$

where $\boldsymbol{T} = (T_1, T_2, \ldots, T_m)$ and $\boldsymbol{T}^{(n)} = (T_1^{(n)}, T_2^{(n)}, \ldots, T_m^{(n)})$.

PROOF. First choose a particular group i. If $T_i < \infty$, then the birth-and-death process becomes extinct at some finite time t and so from the proof of Theorem 2.1 we have $T_i^{(n)} = T_i$ for n sufficiently large.

If $T_i = \infty$, then for any $M > 0$ there exists t such that the birth-and-death process has more than M births in group i before time t. Again from the proof of Theorem 2.1, there are more than M infections in group i of the nth epidemic process by time t for n sufficiently large, so $T_i^{(n)} > M$ and so since M is arbitrary, $T_i^{(n)} \to \infty$ as $n \to \infty$.

Thus for each i, $T_i^{(n)} \to T_i$ almost surely as $n \to \infty$. □

3. Extensions of the model. The relatively simple model of Section 2 can easily be extended in several directions, the proof of Theorem 2.1 remaining essentially unchanged.

First of all, we could allow contact between group i infectives and group j susceptibles at rate $\beta_{ij}m/N$, no longer insisting that $\beta_{ij} = \beta\delta_{ij}$. In the limiting birth-and-death process, individuals in group i can now produce offspring in any group j, the birth rate depending upon both i and j as well as upon time. It does not seem possible to relax the assumption that infection times are governed by a Poisson process, since otherwise it is not clear how shadow infections should be generated.

We can also allow infectives to move between groups according to an arbitrarily distributed random process on $\{1, 2, \ldots, m\}$, not necessarily Markovian. Similarly, infectious periods need not be exponentially distributed nor independent of the individual's movement process. Thus each individual infected while in group i now has life history distributed as $(I^{(i)}, \chi^{(i)}, P)$, where $I^{(i)}$ is some nonnegative random variable giving the infectious lifetime of the individual, $\chi^{(i)}$, is some random process on $\{1, 2, \ldots, m\}$ with $\chi^{(i)}(0) = i$ almost surely and P is a homogeneous Poisson process of rate 1, independent of $I^{(i)}$ and $\chi^{(i)}$. We still insist that the life histories of distinct infectives are mutually independent and identically distributed.

Generalizing the way in which susceptibles move between groups is a little more complicated. If initial susceptible (i, r) moves between groups according to the process $\xi^{(i,r)}$ until it is infected, the movement processes of distinct susceptibles being mutually independent, then we require that for some deterministic function $\boldsymbol{x}(s) = (x_1(s), x_2(s), \ldots, x_m(s))$ from $[0, \infty)$ to $\mathbb{R}^m$,

$$\lim_{n\to\infty} \sup_{0\le s\le t} \left| \frac{1}{N}\tilde{\boldsymbol{X}}^{(n)}(s) - \boldsymbol{x}(s) \right| = 0 \quad \text{almost surely} \tag{3.1}$$

for each $t > 0$, the components $\tilde{X}_j$ of $\tilde{\boldsymbol{X}}$ being defined by (2.1). We further require that $x_i(s) > 0$ for all $s \ge 0$, $i = 1, 2, \ldots, m$, so that at all times there will be a large number of susceptibles in every group.

For $i, j = 1, 2, \ldots, m$, defining

$$\tilde{X}_j^{(i)}(s) = \sum_{r=1}^{N_i} 1_{\{\xi^{(i,r)}(s)=j\}},$$

$$p_{ij}(s) = \Pr(\xi^{(i,r)}(s) = j),$$

then the strong law of large numbers tells us that for any fixed s,

$$\lim_{n\to\infty} \left| \frac{1}{N_i}\tilde{X}_j^{(i)}(s) - p_{ij}(s) \right| = 0 \quad \text{almost surely.}$$

Denoting by $P(s)$ the matrix with entries p_{ij}, then if we let $\boldsymbol{x}(s) = \boldsymbol{\pi}P(s)$, we have that for each s,

$$\lim_{n\to\infty} \left| \frac{1}{N}\tilde{\boldsymbol{X}}^{(n)}(s) - \boldsymbol{x}(s) \right| = 0 \quad \text{almost surely.}$$

Thus if (3.1) is to hold, we expect the function $\boldsymbol{x}(s)$ to be given by $\boldsymbol{x}(s) = \boldsymbol{\pi}P(s)$. In the limiting process $\boldsymbol{Z}(s)$, the rate at which individuals in group i give birth to offspring in group j at time s will then be $\tilde{\beta}_{ij}(s) = m\beta_{ij}x_j(s)$. Unfortunately, for general processes $\xi^{(i,r)}$, simple conditions which would ensure that (3.1) holds do not appear to be available.

4. The limiting process.

4.1. *Susceptible population in equilibrium.* Most commonly, we think of a small amount of infection being introduced into a large, stable population of susceptibles. In this case, it is natural to suppose that the susceptible population is initially in equilibrium, so that $\boldsymbol{x}(s) = \boldsymbol{\pi}$ for all s. As well as being the most interesting case from an epidemic modeling point of view, this is also the simplest case mathematically, since now the birth rates in our limiting process do not change with time. The limiting process is the same as that for a multigroup epidemic model in which susceptibles do not move between groups, and results given by Ball and Clancy (1993) for such a model (in the case of a small outbreak of infection) can be applied.

Thus for our most general model, the limiting process $\boldsymbol{Z}(s)$ is a branching random walk in which individuals born in group i have lifetimes distributed as $I^{(i)}$, move between groups according to the law of $\chi^{(i)}$ and when in group k give birth in group j at the points of a Poisson process of rate $m\beta_{kj}\pi_j$. The total size vector $\boldsymbol{T}$ of this limiting process is the same as that of an embedded m-type Galton–Watson process, initiated by $\boldsymbol{a} = (a_1, a_2, \ldots, a_m)$ ancestors. If we define $I_j^{(i)}$ to be the time spent in group j by a typical group i infective during its infectious lifetime, that is,

$$I_j^{(i)} = \int_0^{I^{(i)}} 1_{\{\chi^{(i)}(s)=j\}}\, ds,$$

then writing $G_j^{(i)}$ for the number of type j offspring produced during its lifetime by a typical type i individual in the embedded Galton–Watson process, the joint probability generating function of $\boldsymbol{G}^{(i)} = (G_1^{(i)}, G_2^{(i)}, \ldots, G_m^{(i)})$ is given by

$$\begin{aligned} f_i(\boldsymbol{\pi}) &= \mathrm{E}\left[\prod_{j=1}^{m} \theta_j^{G_j^{(i)}}\right] \\ &= \mathrm{E}\left[\exp\left\{-\sum_{j=1}^{m}\sum_{k=1}^{m} mI_k^{(i)}\beta_{kj}\pi_j(1-\theta_j)\right\}\right] \end{aligned}$$

for $\boldsymbol{\pi} = (\theta_1, \theta_2, \ldots, \theta_m)$.

Defining the matrices L and Λ with entries $\{l_{ij}\}$ and $\{\lambda_{ij}\}$ by

$$\begin{aligned} l_{ij} &= \mathrm{E}[I_j^{(i)}], \\ \lambda_{ij} &= \sum_{k=1}^{m} ml_{ik}\beta_{kj}\pi_j, \end{aligned}$$

then λ_{ij} is the mean number of type j offspring produced by each type i individual in the Galton–Watson process.

In the case where the infectious lifetime of each individual is exponentially distributed with mean γ^{-1}, during which time the infective moves between groups according to a Markov process with transition rate matrix Q, its movement being independent of its infectious period, we have from Ball (1991) that $L = (\gamma I - Q)^{-1}$. Similarly, the probability generating functions $f_i(\boldsymbol{\pi})$ can be found in terms of the parameters β_{ij}, π_j, γ and Q as in Ball and Clancy [(1993), Section 5.2].

Suppose that the matrix Λ is irreducible and let R be its Perron–Frobenius eigenvalue. Then by standard branching process theory [e.g., Mode (1971)], if $R \leq 1$, the total number of progeny produced by the branching process is almost surely finite. In this case, the epidemic is said to be below threshold. Alternatively, if $R > 1$, then the epidemic is above threshold and there is a positive probability that the Galton–Watson process produces an infinite number of progeny. This probability is given by $1 - \prod_{i=1}^{m} q_i^{a_i}$, where $\boldsymbol{q} = (q_1, q_2, \ldots, q_m)$ is the unique solution with $0 \leq q_i < 1$ of the equations $q_i = f_i(\boldsymbol{q})$ for $i = 1, 2, \ldots, m$.

4.2. *No movement of infectives.* If we now suppose that only susceptibles move between groups, while infectives do not, and also that infectives are only able to contact susceptibles in their own group, then our limiting process consists of m independent single-group branching processes, with time-dependent birth rates. In the case when each group i infective lives for an exponentially distributed time with mean γ_i, each of these single-group processes is an example of the generalized birth-and-death process studied by Kendall (1948). Thus if we write $\beta_i m / N$ for the infection rate in group i and define

$$\rho_i(s) = \gamma_i s - \beta_i m \int_0^s x_i(u)\, du,$$

then the probability that the process in group i has gone extinct by time t is given by $q_i(t)^{a_i}$, where

$$q_i(t) = \frac{\int_0^t \exp\{\rho_i(s)\}\, ds}{\gamma_i^{-1} + \int_0^t \exp\{\rho_i(s)\}\, ds}.$$

The probability that the process goes extinct eventually in group i is given by $q_i(\infty)^{a_i}$. Thus the whole process will almost surely go extinct eventually, producing only a finite number of progeny (i.e., the epidemic will be below threshold) if

$$\int_0^\infty \exp\{\rho_i(s)\}\, ds \tag{4.1}$$

is divergent for each i such that $a_i > 0$.

Now suppose that $\boldsymbol{x}(s) \to \boldsymbol{\nu}$ as $s \to \infty$ for some $\boldsymbol{\nu} = (\nu_1, \nu_2, \ldots, \nu_m)$. For instance, if each susceptible moves between groups according to a Markov

process with transition rate matrix R, then $\boldsymbol{\nu}$ will be a stationary distribution of R. It is easy to show that the integral (4.1) diverges if $\gamma_i / \beta_i > m\nu_i$ and does not diverge if $\gamma_i / \beta_i < m\nu_i$. (The case $\gamma_i / \beta_i = m\nu_i$ is less clear.) If the infection and removal rates do not differ from group to group, so $\beta_i = \beta$ and $\gamma_i = \gamma$ for $i = 1, 2, \ldots, m$, then assuming that $a_i > 0$ for $i = 1, 2, \ldots, m$, the process is below threshold if

$$\frac{\gamma}{\beta} > \max_{i=1,2,\ldots,m} \{m\nu_i\}. \tag{4.2}$$

The right-hand side of (4.2) is minimized when $\nu_i = 1/m$ for $i = 1, 2, \ldots, m$, which means that as time progresses the susceptibles tend to spread themselves as evenly as possible between groups. In this case, the epidemic threshold occurs when $\gamma = \beta$. If the limiting distribution $\boldsymbol{\nu}$ of the susceptible population is not uniform, then the right-hand side of (4.2) is greater than 1 and so when $\gamma = \beta$, the epidemic will be above threshold. This suggests that heterogeneity in the susceptible population tends to increase the spread of infection.

4.3. *Other special cases.* Before moving on to the general case, we mention two more special cases of our limiting process which have been considered by previous authors. In both cases it is assumed that individuals move between groups according to a Markov process with transition rate matrix Q and produce offspring only in their own group, so that $\beta_{ij} = \beta_i \delta_{ij}$. It is also assumed that for an individual in group i at time s, the probability of being removed in the interval $[s, s + \delta s)$ is given by $\gamma_i s + o(\delta s)$. Thus unless $\gamma_1 = \gamma_2 = \cdots = \gamma_m$, the length of an individual's life is not independent of its movement process.

Raman and Chiang (1973) make the further assumption that $q_{ij} = 0$ for $i > j$; then our limiting process is their Model II. They write down a partial differential equation satisfied by the probability generating function of $\boldsymbol{Z}(s)$, the state of the process at time s, and outline a successive method for the solution of this differential equation involving the solution of a system of Riccati equations. However, no explicit solution is available.

Puri (1968), on the other hand, assumes that $q_{ij} = 0$ for $|i - j| > 1$. Again a partial differential equation is given which is satisfied by the probability generating function of $\boldsymbol{Z}(s)$, but now a recursive method is described for finding an approximation to this generating function. As far as finding the generating function exactly is concerned, the relevant differential equation was found to be intractable.

4.4. *The general case.* Now suppose that both infectives and susceptibles move between groups and that $\boldsymbol{x}(s) \to \boldsymbol{\nu}$ as $s \to \infty$. Then so far as the threshold behavior of the epidemic is concerned, since this depends only on the behavior of the process as $s \to \infty$, it seems likely that the epidemic will be above threshold precisely when a modified version of the process, with $\boldsymbol{x}(s) = \boldsymbol{\nu}$ for all s, is above threshold.

In order to prove this, for $i,\ j = 1, 2, \ldots, m$, define

$$\beta_{ij}^0 = m\beta_{ij}\nu_j,$$

$$\tilde{\lambda}_{ij}(s) = \sum_{k=1}^{m} l_{ik}\tilde{\beta}_{kj}(s),$$

$$\lambda_{ij}^0 = \sum_{k=1}^{m} l_{ik}\beta_{kj}^0$$

and also

$$\hat{\lambda}_{ij} = \sum_{k=1}^{m} l_{ik}\hat{\beta}_{kj}$$

for general $\{\hat{\beta}_{ij}\}$.

Suppose that the matrix Λ^0 with entries $\{\lambda_{ij}^0\}$ is irreducible, with Perron–Frobenius eigenvalue $R < 1$. Then since R is a continuous function of each of the $\{\lambda_{ij}^0\}$, which are themselves continuous functions of the $\{\beta_{ij}^0\}$, there exists some $\varepsilon > 0$ such that if $\hat{\beta}_{ij} = \beta_{ij}^0 + \varepsilon$ for $i,\ j = 1, 2, \ldots, m$, then the matrix $\hat{\Lambda}_{ij}$ with entries $\{\hat{\lambda}_{ij}\}$ is irreducible with Perron–Frobenius eigenvalue less than 1. However, $\tilde{\beta}_{ij}(s) \to \beta_{ij}^0$ as $s \to \infty$ and so we can choose t such that for $s \geq t$, $\tilde{\beta}_{ij}(s) < \beta_{ij}^0 + \varepsilon$ for $i,\ j = 1, 2, \ldots, m$. Now suppose that our limiting process has not already died out by time t. Then by time t, only a finite number of progeny will have been produced in total (almost surely), and from time t onward, the number of births in our process with birth rates $\tilde{\beta}_{ij}(s)$ will be less than in the modified process started at time t with the same number of individuals alive at this time as in the original process, but with birth rates $\beta_{ij}^0 + \varepsilon$. (To be precise, we can couple together our limiting process with this modified version in much the same way as the epidemic was coupled with the limiting birth-and-death process in order to prove the main result of the paper.) This modified process almost surely becomes extinct eventually, having produced only a finite number of progeny in total, and hence so does our process of interest.

A similar argument shows that if Λ^0 is irreducible with Perron–Frobenius eigenvalue $R > 1$, then there is a positive probability that our limiting process will never become extinct. How one might evaluate this probability seems unclear.

Now from Seneta [(1973), Theorem 1.5] we have that

$$\min_{i=1,2,\ldots,m}\left\{\sum_{j=1}^{m}\lambda_{ij}^0\right\} \leq R \leq \max_{i=1,2,\ldots,m}\left\{\sum_{j=1}^{m}\lambda_{ij}^0\right\}. \tag{4.3}$$

In the case when $\beta_{ij} = \beta\delta_{ij}$ and $\mathrm{E}[I^{(i)}] = \gamma^{-1}$ for each i, then we have that $\lambda_{ij}^0 = \beta m l_{ij}\nu_j$ and $\sum_{j=1}^{m} l_{ij} = \gamma^{-1}$, so that (4.3) implies

$$\frac{\beta}{\gamma}\min_{i=1,2,\ldots,m}\{m\nu_i\} \leq R \leq \frac{\beta}{\gamma}\max_{i=1,2,\ldots,m}\{m\nu_i\}.$$

Comparing this with the situation when only susceptibles move, we see that if the condition for an epidemic in which infectives do not move to be below threshold [i.e., the condition (4.2)] is satisfied, then the epidemic is certainly below threshold, whether or not infectives move. Movement of infectives appears to decrease the spread of infection. This may be explained by the observation that even if $\gamma/\beta < m\nu_i$ for some group i, movement of individuals away from this group may bring the process below threshold. On the other hand, if $\gamma/\beta > m\nu_i$ for every i, then individuals moving into the groups where ν_i is large cannot push the process above threshold, since the number of individuals which do so will always remain finite.

5. Concluding comments. We have shown that a quite general multigroup epidemic model incorporating population mobility can be approximated over finite time intervals by an appropriate branching random walk with time-dependent birth rates. Possible further results are suggested by previous work on related problems by various authors.

In the single group case, Ball and Donnelly (1995) considered convergence of various functionals of the epidemic process, such as the duration of the epidemic, or the maximum number of infectives present at any time. These results could easily be extended to our current model. Bounds were also given for the total variation distance between the epidemic process and the approximating branching process, although these bounds were found to be often rather poor.

By looking only at convergence over finite time intervals $[0, t]$, we have in effect restricted ourselves to the early stages of the epidemic. Both Ball and Donnelly (1995) and Ball and O'Neill (1994), looking at different classes of single-group models, were able to improve on this by considering intervals of the form $[0, t_n]$, where $t_n \to \infty$ as $n \to \infty$. The details are quite technical, and whether their methods could be applied to our current model seems unclear. In the case of a major outbreak of infection, Ball and Clancy (1993) were able to show that for a multigroup model in which only infectives move, the total size of the epidemic has an asymptotically Gaussian distribution with mean equal to the total size of a corresponding deterministic epidemic model. When susceptibles are able to move, their arguments [based on those of Scalia-Tomba (1985, 1990)] appear inapplicable.

Finally, our model does not explicitly allow for immigration to or emigration from the population. However, this is easily incorporated following O'Neill (1996).

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