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THE DISTRIBUTION OF GENERAL FINAL STATE RANDOM VARIABLES FOR STOCHASTIC EPIDEMIC MODELS

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Abstract

In this paper we introduce the notion of general final state random variables for generalized epidemic models. These random variables are defined as sums over all ultimately infected individuals of random quantities of interest associated with an individual; examples include final severity. By exploiting a construction originally due to Sellke (1983), exact results concerning the final size and general final state random variables are obtained in terms of Gontcharoff polynomials. In particular, our approach highlights the way in which these polynomials arise via simple probabilistic arguments. For ease of exposition we focus initially upon the single-population case before extending our arguments to multi-population epidemics and other variants of our basic model.

Keywords: Epidemic; final size; final severity; Gontcharoff polynomial

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1. Introduction

The final size of an epidemic model is defined to be the number of initially susceptible individuals who ultimately become infected. In the case of stochastic epidemics, the distribution of final size has received considerable attention in the literature; see Lefèvre (1990) for a review of work prior to 1990. A related statistic of interest is the severity of an epidemic, defined as the total area under the trajectory of infectives. This quantity is equal to the total number of personal time units of infection, and can thus be thought of as representing the cost of the epidemic in a certain sense; see, for example, Gani and Jerwood (1972). In this paper we shall extend the notion of final severity by considering quantities that are associated with each individual infected by the epidemic. Examples include the time that the individual is absent from work, the cost of the epidemic for the individual, and so on. In particular, such quantities are assumed to be dependent upon the individual's own infectious period, and we assume further that summing together such quantities over all ultimately infected individuals gives some interesting or useful measure associated with the epidemic.

The study of final size and severity can be facilitated by the use of a non-standard class of polynomials attributed to Gontcharoff. Although these polynomials were first introduced in the context of epidemic modelling by Daniels (1967), it is only recently that they have become more widely exploited in the analysis of a number of epidemic models. In particular, the

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joint probability generating function and Laplace transform of final size and severity of a wide variety of models has been expressed in terms of Gontcharoff polynomials; see Lefèvre and Picard (1990) and Picard and Lefèvre (1990). Many of these results have been obtained using martingale methods, and may be generalized to multi-group models.

In this paper we begin by considering a generalized single-population epidemic model. The construction of our model leads naturally to exact expressions concerning the distributions of final size, severity and other final state random variables without recourse to martingale methods. By similar arguments we are then able to deduce corresponding results for a generalized multi-group model, in which infective individuals are able to move between groups.

The methods that we employ highlight the connection between the final size distribution and the usual recursive definition of Gontcharoff polynomials. In the single-population case, we are also able to deduce our results by using a particular integral representation of Gontcharoff polynomials. Lefèvre and Picard (1990) comment that this representation is not easily generalized for multi-type Gontcharoff polynomials, and we are able to shed some light onto why this is so by considering the connections between such polynomials and the final outcome of an epidemic.

The paper is organized as follows. In Section 2 we recall the definition and some useful properties of Gontcharoff polynomials and give a technical lemma that will be needed in the sequel. For ease of exposition, we then consider single-population epidemics in Sections 3 and 4, delaying our treatment of the general multi-group model until Section 5. Some extensions of our basic model, to incorporate multiple contacts, outside infection and communities of households, are described in Section 6.

2. Gontcharoff polynomials

We start with some notation. For any integers $i < j$ let $[i; j]$ denote the set $\{i, i+1, \ldots, j\}$. For $m \geq 1$ we shall denote any m-dimensional row vector $(y_1, y_2, \ldots, y_m)$ by $\boldsymbol{y}$. Additionally, we define the following quantities:

$$\boldsymbol{y}^{\boldsymbol{j}} = \prod_{i=1}^{m} y_i^{j_i},$$

$$\boldsymbol{y}! = \prod_{i=1}^{m} y_i!,$$

$$\binom{\boldsymbol{y}}{\boldsymbol{r}} = \prod_{i=1}^{m} \binom{y_i}{r_i}.$$

We define vector inequalities in the following manner. First, we write $\boldsymbol{x} \leq \boldsymbol{y}$ if and only if $x_i \leq y_i$ for all $i \in [1; m]$. However, we shall say that $\boldsymbol{x} < \boldsymbol{y}$ if and only if $\boldsymbol{x} \leq \boldsymbol{y}$ and $x_i < y_i$ for at least one $i \in [1; m]$. For vector summations we adopt the convention that $\sum_{\boldsymbol{r}=\boldsymbol{u}}^{\boldsymbol{v}}$ denotes $\sum_{r_1=u_1}^{v_1} \cdots \sum_{r_m=u_m}^{v_m}$. We define $\mathbf{0}$ to be the vector of zeros and $\mathbf{1}$ to be the vector of 1's. Finally, for m-dimensional row vectors of integers $\boldsymbol{i} < \boldsymbol{j}$, let $[\boldsymbol{i}; \boldsymbol{j}]$ denote the set $\{\boldsymbol{k} : \boldsymbol{i} \leq \boldsymbol{k} \leq \boldsymbol{j}\}$.

We now recall the definition of multi-type Gontcharoff polynomials (e.g. Lefèvre and Picard (1990), Section 4). For $m \geq 1$ and for $j \in [1; m]$ let $U^{(j)} = \{u_{\boldsymbol{i}}^{(j)} : \boldsymbol{i} \in (\mathbb{Z}^+)^m\}$ be a specified collection of real numbers, and let $\boldsymbol{u_i} = (u_{\boldsymbol{i}}^{(1)}, \ldots, u_{\boldsymbol{i}}^{(m)})$. Then associated with $\boldsymbol{U} = (U^{(1)}, \ldots, U^{(m)})$ is a family of polynomials $G_{\boldsymbol{r}}(\boldsymbol{x} \mid \boldsymbol{U})$ of degree r_1 in $x_1, \ldots, r_m$ in x_m, defined recursively by

$$G_{\mathbf{0}}(\boldsymbol{x} \mid \boldsymbol{U}) = 1,$$

and when $\boldsymbol{r} > \mathbf{0}$,

$$G_{\boldsymbol{r}}(\boldsymbol{x} \mid \boldsymbol{U}) = \frac{\boldsymbol{x}^{\boldsymbol{r}}}{\boldsymbol{r}!} - \sum_{\mathbf{0} \le \boldsymbol{j} < \boldsymbol{r}} \frac{\boldsymbol{u}_{\boldsymbol{j}}^{\boldsymbol{r}-\boldsymbol{j}}}{(\boldsymbol{r}-\boldsymbol{j})!} G_{\boldsymbol{j}}(\boldsymbol{x} \mid \boldsymbol{U}). \tag{2.1}$$

For $\boldsymbol{i} \ge \mathbf{0}$, we define $G_{\boldsymbol{j}}^{\boldsymbol{i}}(\boldsymbol{x} \mid \boldsymbol{U})$ as the partial derivative of $G_{\boldsymbol{j}}(\boldsymbol{x} \mid \boldsymbol{U})$ of orders i_1 in $x_1, \ldots, i_m$ in x_m; note that if $\boldsymbol{i} > \boldsymbol{j}$, then $G_{\boldsymbol{j}}^{\boldsymbol{i}}(\boldsymbol{x} \mid \boldsymbol{U}) = 0$. We also define, for $\boldsymbol{r} \ge \mathbf{0}$, $E^{\boldsymbol{r}}\boldsymbol{U} = (E^{\boldsymbol{r}}U^{(1)}, \ldots, E^{\boldsymbol{r}}U^{(m)})$ where, for $i \in [1; m]$, $E^{\boldsymbol{r}}U^{(i)} = \{u_{\boldsymbol{r}+\boldsymbol{k}}^{(i)} : \boldsymbol{k} \in (\mathbb{Z}^+)^m\}$.

In the single-type case, so that $m = 1$, the definition of a Gontcharoff polynomial reduces to

$$\begin{cases} G_0(x \mid U) = 1, \\ G_k(x \mid U) = \dfrac{x^k}{k!} - \displaystyle\sum_{j=0}^{k-1} \frac{u_j^{k-j}}{(k-j)!} G_j(x \mid U) \quad (k = 1, 2, \ldots), \end{cases} \tag{2.2}$$

where U is a real sequence $u_0, u_1, \ldots$. Note that for $k = 1, 2, \ldots$, $G_k(x \mid U)$ depends only upon $u_0, u_1, \ldots, u_{k-1}$, and

$$G_k(x \mid U) = \int_{\xi_0=u_0}^{x} \int_{\xi_1=u_1}^{\xi_0} \cdots \int_{\xi_{k-1}=u_{k-1}}^{\xi_{k-2}} \mathrm{d}\xi_0 \mathrm{d}\xi_1 \ldots \mathrm{d}\xi_{k-1}; \tag{2.3}$$

see Lefèvre and Picard (1990), equation (2.5).

A few other properties of Gontcharoff polynomials that we shall require are listed below. For $0 \le i \le k$,

$$G_k^i(x \mid U) = G_{k-i}(x \mid E^i U), \tag{2.4}$$

see Lefèvre and Picard (1990), equation (2.7). We also have (Lefèvre and Picard (1990), equation (2.8)) that for $a, b \in \mathbb{R}$,

$$G_k(ax + b \mid aU + b) = a^k G_k(x \mid U) \quad (k = 0, 1, \ldots), \tag{2.5}$$

where $aU + b$ is the sequence $\{au_i + b : i \in \mathbb{Z}^+\}$. Note that $G_k(x \mid U)$ admits the Maclaurin expansion

$$G_k(x \mid U) = \sum_{i=0}^{k} G_k^{(k-i)}(0 \mid U) x^{k-i}/(k-i)! \tag{2.6}$$

(Lefèvre and Picard (1990), equation (2.11)). Lemma 2.1, which will be required later, gives an alternative form for the constant term in the Maclaurin expansion of $G_k(x \mid U)$. We treat the multi-type case. Multi-type versions of (2.4) and (2.5) can be found in Lefèvre and Picard (1990), equations (4.6) and (4.7), respectively.

Lemma 2.1. *For* $\boldsymbol{r} > \mathbf{0}$,

$$G_{\boldsymbol{r}}(\boldsymbol{x} \mid \boldsymbol{U}) = \sum_{\mathbf{0} < \boldsymbol{i} \le \boldsymbol{r}} \frac{\boldsymbol{x}^{\boldsymbol{i}} - \boldsymbol{u}_{\mathbf{0}}^{\boldsymbol{i}}}{\boldsymbol{i}!} G_{\boldsymbol{r}}^{\boldsymbol{i}}(\mathbf{0} \mid \boldsymbol{U}). \tag{2.7}$$

Proof. We proceed by induction on $\boldsymbol{r}$. First, for $l \in [1; m]$ define $\Delta(l) = (\delta_{1l}, \delta_{2l}, \ldots, \delta_{ml})$, where δ_{ij} is the Kronecker delta. Then setting $\boldsymbol{r} = \Delta(l)$, the right-hand side of (2.7) becomes

$$\begin{aligned}(\boldsymbol{x}^{\Delta(l)} - \boldsymbol{u}_{\boldsymbol{0}}^{\Delta(l)}) G_{\Delta(l)}^{\Delta(l)}(\boldsymbol{0} \mid \boldsymbol{U}) &= x_l - u_{\boldsymbol{0}}^{(l)} \\ &= G_{\Delta(l)}(\boldsymbol{x} \mid \boldsymbol{U}),\end{aligned}$$

by (2.1) with $\boldsymbol{r} = \Delta(l)$, as required. Assume for induction that (2.7) holds for each $\boldsymbol{i}$ such that $\boldsymbol{0} < \boldsymbol{i} < \boldsymbol{r}$. Then by (2.1),

$$\begin{aligned}G_{\boldsymbol{r}}(\boldsymbol{x} \mid \boldsymbol{U}) &= \frac{\boldsymbol{x}^{\boldsymbol{r}}}{\boldsymbol{r}!} - \sum_{\boldsymbol{0} \le \boldsymbol{k} < \boldsymbol{r}} \frac{(\boldsymbol{u}_{\boldsymbol{k}})^{\boldsymbol{r}-\boldsymbol{k}}}{(\boldsymbol{r}-\boldsymbol{k})!} G_{\boldsymbol{k}}(\boldsymbol{x} \mid \boldsymbol{U}) \\ &= \frac{\boldsymbol{x}^{\boldsymbol{r}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{r}}}{\boldsymbol{r}!} - \sum_{\boldsymbol{0} < \boldsymbol{k} < \boldsymbol{r}} \frac{(\boldsymbol{u}_{\boldsymbol{k}})^{\boldsymbol{r}-\boldsymbol{k}}}{(\boldsymbol{r}-\boldsymbol{k})!} \sum_{\boldsymbol{0} < \boldsymbol{i} \le \boldsymbol{k}} \frac{\boldsymbol{x}^{\boldsymbol{i}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{i}}}{\boldsymbol{i}!} G_{\boldsymbol{k}}^{\boldsymbol{i}}(\boldsymbol{0} \mid \boldsymbol{U}) \\ &= \frac{\boldsymbol{x}^{\boldsymbol{r}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{r}}}{\boldsymbol{r}!} - \sum_{\boldsymbol{0} < \boldsymbol{i} < \boldsymbol{r}} \frac{\boldsymbol{x}^{\boldsymbol{i}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{i}}}{\boldsymbol{i}!} \sum_{\boldsymbol{i} \le \boldsymbol{k} < \boldsymbol{r}} \frac{(\boldsymbol{u}_{\boldsymbol{k}})^{\boldsymbol{r}-\boldsymbol{k}}}{(\boldsymbol{r}-\boldsymbol{k})!} G_{\boldsymbol{k}}^{\boldsymbol{i}}(\boldsymbol{0} \mid \boldsymbol{U}) \\ &= \frac{\boldsymbol{x}^{\boldsymbol{r}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{r}}}{\boldsymbol{r}!} + \sum_{\boldsymbol{0} < \boldsymbol{i} < \boldsymbol{r}} \frac{\boldsymbol{x}^{\boldsymbol{i}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{i}}}{\boldsymbol{k}!} G_{\boldsymbol{r}}^{\boldsymbol{i}}(\boldsymbol{0} \mid \boldsymbol{U}),\end{aligned}$$

where the last line follows by differentiating (2.1) and setting $\boldsymbol{x} = \boldsymbol{0}$. Since $G_{\boldsymbol{r}}^{\boldsymbol{r}}(\boldsymbol{0} \mid \boldsymbol{U}) = 1$, it follows that

$$G_{\boldsymbol{r}}(\boldsymbol{x} \mid \boldsymbol{U}) = \sum_{\boldsymbol{0} < \boldsymbol{i} \le \boldsymbol{r}} \frac{\boldsymbol{x}^{\boldsymbol{i}} - \boldsymbol{u}_{\boldsymbol{0}}^{\boldsymbol{i}}}{\boldsymbol{i}!} G_{\boldsymbol{r}}^{\boldsymbol{i}}(\boldsymbol{0} \mid \boldsymbol{U}),$$

as required.

3. Single population epidemics

3.1. Definition of the model

We begin by defining our epidemic model using a construction due to Sellke (1983). Consider a closed, homogeneously mixing population consisting initially of a infectives, labelled $-(a-1), -(a-2), \ldots, 0$, and N susceptible individuals, labelled $1, 2, \ldots, N$. For $j \in [-(a-1); 0]$ define R_j as the infectious period of the jth initial infective, while for $j \in [1; N]$ define R_j to be the infectious period of the jth susceptible to become infected. Here, each R_j is distributed according to a non-negative random variable with distribution function F_j. The R_j are assumed to be independent of one another, although they need not be identically distributed. This latter feature allows the infectious periods of the initial infectives to differ from those of susceptibles that become infected as in, for example, Downton's (1968) carrier-borne epidemic model. For $j \in [1; N]$ let Q_j denote the infection tolerance of susceptible j, where the Q_j are independent copies of some continuous non-negative random variable Q.

The epidemic now proceeds as follows. Each susceptible individual absorbs exposure to infection at a rate equal to the number of infectives currently present in the population. Susceptible j becomes infected when its total absorbed exposure reaches Q_j. For $j \in [-(a-1); 0]$ initial infective j remains so for a time R_j, while for $j = 1, 2, \ldots$ the jth

infected susceptible remains infective for a time R_j. Once an individual stops infecting, it is removed in the sense that it plays no further part in the epidemic. The epidemic ceases as soon as no more infectives are left in the population.

3.2. Final size

Let $Q_{(1)} \leq Q_{(2)} \leq \cdots \leq Q_{(N)}$ be the order statistics of $Q_1, Q_2, \ldots Q_N$. For $i \in [0; N]$ define

$$\chi_i = \sum_{j=-(a-1)}^{i} R_j,$$

and denote by S the survivor function of Q, so that for $x \geq 0$, $S(x) = \Pr(Q > x)$. Let T denote the final size of the epidemic, so that we have $T = \min\{i \in [0; N] : \chi_i < Q_{(i+1)}\}$, where $Q_{(N+1)} = \infty$. Then for $k \in [1; N]$,

$$\{T \geq k\} = \{Q_{(i)} \leq \chi_{i-1} \text{ for } i \in [1; k]\}$$

and thus

$$\{T \geq k\} = \{S(Q_{(i)}) \geq S(\chi_{i-1}) \text{ for } i \in [1; k]\}. \tag{3.1}$$

For $i \in [1; N]$ define $V_i = S(Q_i)$ and let $V_{(1)} \leq V_{(2)} \leq \ldots V_{(N)}$ be the order statistics of $V_1, V_2, \ldots, V_N$. If follows that the V_i form an independent and identically distributed set of uniform [0, 1] random variables, and for $i \in [1; N]$ we have $S(Q_{(i)}) = V_{(N+1-i)}$. Next, for $i \in [0; N]$ define $W_i = S(\chi_i)$, so that from (3.1),

$$\{T \geq k\} = \{V_{(N+1-i)} \geq W_{i-1}, i \in [1; k]\} \quad (k \in [1; N]).$$

In the following argument, we condition upon the value of $\boldsymbol{R} = (R_{-(a-1)}, R_{-(a-2)}, \ldots, R_N)$ being known, from which it follows that $(W_0, W_1, \ldots, W_N)$ is also known. First note that $(V_{(1)}, V_{(2)}, \ldots, V_{(N)})$ has joint probability density function

$$f(v_1, v_2, \ldots, v_N) = \begin{cases} N! & \text{if } 0 < v_1 < v_2 < \cdots < v_N < 1, \\ 0 & \text{otherwise.} \end{cases}$$

Thus, for $k \in [1; N]$,

$$\Pr(T \geq k) = \Pr(V_{(N)} \geq W_0, V_{(N-1)} \geq W_1, \ldots, V_{(N+1-k)} \geq W_{k-1}),$$

whence

$$\begin{aligned} &\Pr(T \geq k) \\ &= N! \int_{v_N=W_0}^{1} \int_{v_{N-1}=W_1}^{v_N} \cdots \int_{v_{N-k+1}=W_{k-1}}^{v_{N-k+2}} \int_{v_{N-k}=0}^{v_{N-k+1}} \int_{v_{N-k-1}=0}^{v_{N-k}} \cdots \int_{v_1=0}^{v_2} \mathrm{d}v_1 \mathrm{d}v_2 \ldots \mathrm{d}v_N. \end{aligned} \tag{3.2}$$

It follows at once from (2.3) and (3.2) that for $k \in [1; N]$,

$$\Pr(T \geq k) = N!\, G_N(1 \mid U^{(k)}), \tag{3.3}$$

where $U^{(k)}$ is the sequence

$$\{W_0, W_1, \ldots, W_{k-1}, 0, 0, \ldots\}.$$

Let U be the sequence

$$\{W_0, W_1, \ldots, W_N, 0, 0, \ldots\}.$$

Then it follows from (2.2) that

$$G_N(1 \mid U^{(k)}) = \frac{1}{N!} - \sum_{j=0}^{k-1} \frac{W_j^{N-j}}{(N-j)!} G_j(1 \mid U) \quad (k \in [1; N]),$$

whence we obtain

$$\Pr(T \leq k) = \sum_{j=0}^{k} \frac{N!}{(N-j)!} W_j^{N-j} G_j(1 \mid U) \quad (k \in [0; N]),$$

and thus

$$\Pr(T = k) = \frac{N!}{(N-k)!} W_k^{N-k} G_k(1 \mid U) \quad (k \in [0; N]). \tag{3.4}$$

Now removing the conditioning on $\boldsymbol{R}$ in (3.4) yields that for $k \in [0; N]$,

$$\Pr(T = k) = \frac{N!}{(N-k)!} \mathbb{E}_{\boldsymbol{R}}[S(\chi_k)^{N-k} G_k(1 \mid U)]. \tag{3.5}$$

3.3. The joint generating function Laplace transform of final size and general final state variables

We now consider taking account of quantities of interest other than the final size. Specifically, associate a random vector $(A_i^{(1)}, \ldots, A_i^{(p)})$ with the ith individual to become infected. It is supposed that the components of this vector represent quantities of interest associated with the individual and related to the individual's infectious period R_i. Examples include the time that the individual is incapacitated due to the disease, the cost of the epidemic for the individual, and so on. Then we may typically be interested in the quantities

$$A^{(j)}(T) = \sum_{i=-(a-1)}^{T} A_i^{(j)};$$

we refer to such sums as general final state random variables. For example, if $A_i^{(j)} = R_i$ then $A^{(j)}(T)$ is simply the final severity of the epidemic. We shall assume that

$$\{(R_i, A_i^{(1)}, \ldots, A_i^{(p)}) : i \in [-(a-1); N]\}$$

is an independent set of random vectors.

Let $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_p)$ be a vector of real numbers. We define the joint generating Laplace transform of the final size and general final state random variables as

$$\phi(x, \boldsymbol{\theta}) = \mathbb{E}\left[x^{N-T} \exp\left(-\sum_{i=1}^{p} A^{(i)}(T)\theta_i\right)\right], \quad (x \in \mathbb{R}, \boldsymbol{\theta} \in \mathbb{R}^p).$$

It follows at once from (3.4) and (3.5) that

$$\phi(x,\boldsymbol{\theta}) = \sum_{k=0}^{N} \frac{N!}{(N-k)!}\, x^{N-k}\mathbb{E}_{\boldsymbol{R}}\left[S(\chi_k)^{N-k}\mathbb{E}\left[\exp\left(-\sum_{i=1}^{p} A^{(i)}(k)\theta_i\right) \mid \boldsymbol{R}\right] G_k(1 \mid U)\right].$$

By exploiting the independence of different individuals, it is straightforward to deduce that

$$\phi(x,\boldsymbol{\theta}) = \sum_{k=0}^{N} \frac{N!}{(N-k)!}\, x^{N-k}\mathbb{E}_{\boldsymbol{R}}\left[S(\chi_k)^{N-k}\left(\prod_{j=-(a-1)}^{k} h(\boldsymbol{\theta}, R_j)\right) G_k(1 \mid U)\right], \tag{3.6}$$

where $h(\boldsymbol{\theta}, R_j) = \mathbb{E}[\exp(-\sum_{i=1}^{p} A_j^{(i)}\theta_i) \mid R_j]$.

4. Exponential tolerances

We now turn our attention to the situation where the underlying tolerance random variable Q has a negative exponential distribution. Under this assumption our model reduces to a standard SIR model with a Markovian infection mechanism which includes as special cases the Reed–Frost model and the general stochastic epidemic. As we shall see, for such models it is possible to simplify equation (3.5), and in doing so we obtain a generalization of Proposition 3.3 of Picard and Lefèvre (1990).

4.1. Reed–Frost model

The Reed–Frost model is a chain-binomial epidemic model which has received considerable attention in the literature (e.g. Bailey (1975, p. 157) and Lefèvre (1990)). It is a discrete-time model defined recursively in the following manner. Let X_t and Y_t denote respectively the numbers of susceptibles and infectives present at time t, where $t = 0, 1, 2, \ldots$, and let $(X_0, Y_0) = (N, a)$. For $t = 0, 1, 2, \ldots$, draw X_{t+1} from the binomial distribution with parameters (X_t, q^{Y_t}), where $q \in (0, 1)$ is known as the avoidance probability, and set $Y_{t+1} = X_t - X_{t+1}$. The model may be interpreted by observing that at every time step $t = 1, 2, \ldots$ each remaining susceptible avoids infection from each given infective with probability q, independently of other susceptibles, while each infective lives for one time unit before being removed.

In order to use our model to analyse the final size and severity distributions of the Reed–Frost model, we proceed as follows. First, set the infectious periods to be a constant length, which without loss of generality we may assume to be one unit of time. Second, set the infection tolerances to be drawn from a negative exponential distribution of mean $(\log q^{-1})^{-1}$. It is now straightforward to show that the numbers of susceptibles and infectives in the population at time $t = 0, 1, 2, \ldots$ have the same distribution as the numbers of susceptibles and infectives in the Reed–Frost model described in the preceding paragraph.

It follows directly from (3.4) that for $k \in [0; N]$,

$$\Pr(T = k) = \frac{N!}{(N-k)!}\, q^{(a+k)(N-k)} G_k(1 \mid U),$$

where U is the sequence $\{q^a, q^{a+1}, \ldots, q^{a+N}, 0, 0, \ldots\}$, in agreement with Lefèvre and Picard (1990, equation (3.10)). We can immediately obtain the probability generating function for $N-T$, i.e. for the number of susceptibles remaining at the end of the epidemic. Specifically, for $x \geq 0$,

$$\mathbb{E}[x^{N-T}] = \sum_{k=0}^{N} x^k \frac{N!}{k!} q^{k(N+a-k)} G_{N-k}(1 \mid U). \tag{4.1}$$

Notice that (4.1) is an alternative form for the probability generating function given in Lefèvre and Picard (1990, equation (3.8)); the two can be shown to be equivalent via Theorem 4.2 in the next section. Finally, note that since the infectious periods are of unit length, the severity of the Reed–Frost model is equal to $T + a$.

4.2. General results

In this section we shall suppose that Q has an exponential distribution with mean β^{-1}, so that for $x \geq 0$, $S(x) = \exp(-\beta x)$. It will also be assumed that the infectious periods $R_{-(a-1)}, \ldots, R_N$ are identically distributed, so that R_j has the same distribution as some non-negative random variable R, say. Note that if R also has an exponential distribution then the model becomes the general stochastic epidemic (see, for example, Bailey (1975, p. 88)). We begin with a technical lemma, the proof of which is to be found in the appendix.

Lemma 4.1. *For $k \in [0; N]$ and $r \in [0; N-k]$,*

$$\mathbb{E}_{\boldsymbol{R}}\left[\exp\left(-\beta(N-k-r)\sum_{j=k+1}^{k+r} R_j\right)\left(\prod_{i=k+1}^{k+r} h(\boldsymbol{\theta}, R_i)\right) G_r(0 \mid \tilde{U}^{(k)})\right] = G_r(0 \mid E^{(N-k-r)}\tilde{U}^*), \tag{4.2}$$

where $\tilde{U}^{(k)}$ is the sequence $\{1, \exp(-\beta R_{k+1}), \exp(-\beta(R_{k+1} + R_{k+2})), \ldots\}$ and $\tilde{U}^*$ is the sequence $\{\tilde{u}_i^*\}$, where $\tilde{u}_i^* = \mathbb{E}[\exp(-i\beta R)h(\boldsymbol{\theta}, R)]$ $(i = 0, 1, 2, \ldots)$.

We are now ready to state our main result.

Theorem 4.2.

$$\phi(x, \boldsymbol{\theta}) = \sum_{k=0}^{N} \frac{N!}{(N-k)!} (\mathbb{E}[\exp(-\beta k R)h(\boldsymbol{\theta}, R)])^{N-k+a} G_k(x \mid \tilde{U}^*), \tag{4.3}$$

where $\tilde{U}^*$ is defined as in Lemma 4.1.

Proof. From (3.6) we deduce that, since Q is exponential with mean β^{-1},

$$\begin{aligned}
&\phi(x, \boldsymbol{\theta}) \\
&= \sum_{k=0}^{N} x^{N-k} \frac{N!}{(N-k)!} \mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k)\chi_k)\left(\prod_{j=-(a-1)}^{k} h(\boldsymbol{\theta}, R_j)\right) G_k(1 \mid U)\right] \\
&= \sum_{k=0}^{N} x^{N-k} \frac{N!}{(N-k)!} \mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k)\chi_k)\left(\prod_{j=-(a-1)}^{k} h(\boldsymbol{\theta}, R_j)\right) \sum_{r=0}^{k} \frac{G_r(0 \mid E^{k-r}U)}{(k-r)!}\right],
\end{aligned}$$

via (2.6) and (2.4). Using the summation identity

$$\sum_{k=0}^{N} f(k) \sum_{r=0}^{k} g(k, r) = \sum_{k=0}^{N} \sum_{r=0}^{N-k} f(k+r)g(k+r, r),$$

we thus obtain

$$\begin{aligned}
&\phi(x,\boldsymbol{\theta}) \\
&\quad=\sum_{k=0}^{N}\sum_{r=0}^{N-k} x^{N-r-k}\frac{N!}{(N-r-k)!} \\
&\qquad\times \mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-r-k)\chi_{r+k})\Bigg(\prod_{j=-(a-1)}^{k+r} h(\boldsymbol{\theta},R_j)\Bigg)\frac{G_r(0\mid E^kU)}{k!}\right] \\
&\quad=\sum_{k=0}^{N}\sum_{r=0}^{N-k} \frac{x^{N-r-k}}{(N-r-k)!}\,\frac{N!}{k!} \\
&\qquad\times \mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k-r)\chi_{k+r}-\beta r\chi_k)\Bigg(\prod_{j=-(a-1)}^{k+r} h(\boldsymbol{\theta},R_j)\Bigg)G_r(0\mid \tilde{U}^{(k)})\right],
\end{aligned}$$

where $\tilde{U}^{(k)}$ is defined as in Lemma 4.1, using (2.5) with $a=\exp(-\chi_k)$ and $b=0$. Thus

$$\begin{aligned}
\phi(x,\boldsymbol{\theta}) &= \sum_{k=0}^{N}\sum_{r=0}^{N-k} \frac{x^{N-r-k}}{(N-r-k)!}\,\frac{N!}{k!} \\
&\qquad\times \mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k)\chi_k)\exp\Bigg(-\beta(N-k-r)\sum_{j=k+1}^{k+r}R_j\Bigg)\right. \\
&\qquad\left.\times\Bigg(\prod_{j=-(a-1)}^{k+r} h(\boldsymbol{\theta},R_j)\Bigg)G_r(0\mid\tilde{U}^{(k)})\right] \\
&=\sum_{k=0}^{N}\frac{N!}{k!}\,\mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k)\chi_k)\prod_{j=-(a-1)}^{k} h(\boldsymbol{\theta},R_j)\right]\sum_{r=0}^{N-k}\frac{x^{N-r-k}}{(N-r-k)!} \\
&\qquad\times \mathbb{E}_{\boldsymbol{R}}\left[\exp\Bigg(-\beta(N-k-r)\sum_{j=k+1}^{k+r}R_j\Bigg)\Bigg(\prod_{j=k+1}^{k+r} h(\boldsymbol{\theta},R_j)\Bigg)G_r(0\mid\tilde{U}^{(k)})\right],
\end{aligned}$$

using the independence of the $R_j's$. Thus by Lemma 4.1,

$$\begin{aligned}
\phi(x,\boldsymbol{\theta}) &= \sum_{k=0}^{N}\frac{N!}{k!}\,\mathbb{E}_{\boldsymbol{R}}\left[\exp(-\beta(N-k)\chi_k)\prod_{j=-(a-1)}^{k} h(\boldsymbol{\theta},R_j)\right] \\
&\qquad\times\sum_{r=0}^{N-k}\frac{x^{N-r-k}}{(N-r-k)!}\,G_r(0\mid E^{(N-k-r)}\tilde{U}^*), \\
&=\sum_{k=0}^{N}\frac{N!}{k!}(\mathbb{E}_R[\exp(-\beta(N-k)R)h(\boldsymbol{\theta},R)])^{k+a}\,G_{N-k}(x\mid\tilde{U}^*),
\end{aligned} \tag{4.4}$$

using independence again for the first sum in (4.4), and equations (2.6) and (2.4) for the second. The result now follows via the substitution $k\to N-k$.

The following corollary, a Wald's identity for epidemics, is a generalization of a result first proved in Ball (1986).

Corollary 4.3. *For any* $\boldsymbol{\theta} \in \mathbb{R}^p$ *such that* $\psi(\boldsymbol{\theta}) = \mathbb{E}[h(\boldsymbol{\theta}, R)]$ *is finite,*

$$\mathbb{E}\left[\exp\left(-\sum_{i=1}^{p} A^{(i)}(T)\theta_i\right)\Big/\psi(\boldsymbol{\theta})^{T+a}\right] = 1. \tag{4.5}$$

Proof. Note that $\tilde{u}_0^* = \psi(\boldsymbol{\theta})$. Thus,

$$\mathbb{E}\left[\exp\left(-\sum_{i=1}^{p} A^{(i)}(T)\theta_i\right)\psi(\boldsymbol{\theta})^{N-T}\right] = \phi(\tilde{u}_0^*, \boldsymbol{\theta})$$

$$= \sum_{k=0}^{N} \frac{N!}{(N-k)!}(\tilde{u}_k^*)^{N-k+a} G_k(\tilde{u}_0^* \mid \tilde{U}^*),$$

using Theorem 4.2. By Lemma 2.1, $G_k(\tilde{u}_0^* \mid \tilde{U}^*) = 0\ (k > 0)$, so

$$\mathbb{E}\left[\exp\left(-\sum_{i=1}^{p} A^{(i)}(T)\theta_i\right)\psi(\boldsymbol{\theta})^{N-T}\right] = (\tilde{u}_0^*)^{N+a},$$

and (4.5) follows on dividing through by $(\tilde{u}_0^*)^{N+a}$.

Differentiation of (4.5) leads immediately to the following corollary, which is a generalization of a result first proved by Downton (1972) for the severity of the general stochastic epidemic.

Corollary 4.4. *For* $i = 1, 2, \ldots, p$,

$$\mathbb{E}[A^{(i)}(T)] = (\mathbb{E}[T] + a)\mathbb{E}[A^{(i)}], \tag{4.6}$$

where $A^{(i)}$ *is a random variable whose distribution is the common distribution of*

$$A_j^{(i)}\ (j \in [-(a-1); N]).$$

Let $\mu_{N,a} = \mathbb{E}[T]$ denote the mean final size of the epidemic. Then differentiating (4.3) with respect to x, setting $x = 1$ and $\boldsymbol{\theta} = \mathbf{0}$, and using (2.4), yields

$$\mu_{N,a} = N - \sum_{k=1}^{N} \frac{N!}{(N-k)!}\xi(\beta k)^{N+a-k} G_{k-1}(1 \mid E^1 V), \tag{4.7}$$

where V is the sequence $\{v_i\}$, with $v_i = \xi(i\beta)$, and $\xi(\theta) = \mathbb{E}[\exp(-\theta R)]$ $(\theta \geq 0)$ is the moment generating function of R; cf. Ball (1986), equation (2.25). Expressions for higher order factorial moments of $N - T$ can be obtained in a similar fashion, see Lefèvre and Picard (1990), equation (3.11) for the Reed–Frost case.

An explicit expression for the final size distribution is also easily obtained from Theorem 4.2. Setting $\boldsymbol{\theta} = \mathbf{0}$ in (4.3) and differentiating $N - k$ times with respect to x and using (2.4) yields, for $k \in [0; N]$,

$$\Pr(T = k) = \binom{N}{k} \sum_{i=0}^{k} \frac{k!}{(k-i)!}\xi(\beta(N-k+i))^{a+k-i} G_i(0 \mid E^{N-k} V). \tag{4.8}$$

We close this section by using Theorem 4.2 to derive a triangular system of linear equations which determines $\Pr(T = k)$ $(k \in [0; N])$.

Corollary 4.5. *For $n \in [0; N]$,*

$$\sum_{k=0}^{n} \binom{N-k}{n-k} \Pr(T = k)/\xi(\beta(N-n))^{a+k} = \binom{N}{n}. \tag{4.9}$$

Proof. For $n \in [0; N]$, using (3.5) and the form of $S(\chi_k)$,

$$\begin{aligned}
&\sum_{k=0}^{n} \binom{N-k}{n-k} \Pr(T = k)\xi(\beta(N-n))^{n-k} \\
&\quad = \binom{N}{n} \sum_{k=0}^{n} \frac{n!}{(n-k)!} \mathbb{E}_{\boldsymbol{R}}\left[\exp\left(-\beta(N-k) \sum_{i=-(a-1)}^{k} R_i\right) G_k(1 \mid U)\right] \xi(\beta(N-n))^{n-k} \\
&\quad = \binom{N}{n} \sum_{k=0}^{n} \frac{n!}{(n-k)!} \mathbb{E}_{\boldsymbol{R}}\left[\exp\left(-\beta(n-k)\chi_k\right)\right. \\
&\qquad\qquad \left. \times \left(\prod_{j=-(a-1)}^{k} \tilde{h}(\beta(N-n), R_j)\right) G_k(1 \mid U)\right] \xi(\beta(N-n))^{n-k},
\end{aligned}$$

where $\tilde{h}(\theta, R_j) = \exp(-\theta R_j)$. Thus, from the first equation in the proof of Theorem 4.2,

$$\sum_{k=0}^{n} \binom{N-k}{n-k} \Pr(T = k)\xi(\beta(N-n))^{n-k} = \binom{N}{n} \phi_n(x, \beta(N-n)),$$

where $x = \xi(\beta(N-n))$ and $\phi_n(x, \theta) = \mathbb{E}[x^{n-T} \exp(-\theta \sum_{i=-(a-1)}^{T} R_i)]$ for an epidemic with initially n susceptibles and a infectives. By Theorem 4.2, and recalling the form for $\tilde{h}(\theta, R)$,

$$\phi_n(x, \beta(N-n)) = \sum_{k=0}^{n} \frac{n!}{(n-k)!} \mathbb{E}[\exp(-\beta(k+N-n)R)]^{n-k+a} G_k(x \mid \tilde{U}^*),$$

where $\tilde{U}^* = \{\tilde{u}_k^*\}$, with $\tilde{u}_k^* = \mathbb{E}[\exp(-\beta(k+N-n))R]$. Note that $\tilde{u}_0^* = \xi(\beta(N-n)) = x$. But by Lemma 2.1, $G_k(x \mid \tilde{U}^*) = 0$ for $k \geq 1$, and thus $\phi_n(x, \beta(N-n)) = \xi(\beta(N-n))^{n+a}$. Hence

$$\sum_{k=0}^{n} \binom{N-k}{n-k} \Pr(T = k)\xi(\beta(N-n))^{n-k} = \binom{N}{n} \xi(\beta(N-n))^{n+a},$$

and (4.9) follows.

Equation (4.9) was first obtained for the general stochastic epidemic by Whittle (1955), using an algebraic argument. It has been derived previously for the present model by a number of authors, but always using, either explicitly or implicitly, the optional stopping theorem for a suitable martingale.

5. Generalized multi-group case

In this section we extend our existing results to cater for a multi-group model in which infective individuals are permitted to move between groups. The model is itself a slight generalization of that described in Ball and Clancy (1993), the difference being that we no longer assume that the infection mechanism is Markovian.

The model is defined as follows. There are m groups, labelled $1, 2, \ldots, m$. For $i \in [1; m]$ the initial numbers of infectives and susceptibles in the ith group are a_i and N_i, respectively, and we define $\boldsymbol{a} = (a_1, \ldots, a_m)$ and $\boldsymbol{N} = (N_1, \ldots, N_m)$. Each infective individual can move between groups during its infectious lifetime, so for $r \in [-(a_i - 1); N_i]$ and $i, j \in [1; m]$ define $R^{(j)}_{(i,r)}$ to be the time spent in group j by the rth infected individual from group i. We assume that for $r \in [-(a_i - 1); N_i]$, $R^{(j)}_{(i,r)}$ is distributed according to some underlying random variable $R^{(j)}_{(i)}$. Note that the infectious period of individual (i, r) is $\sum_{j=1}^{m} R^{(j)}_{(i,r)}$.

While in group j, an infective from group i contributes to the total infective pressure acting upon remaining susceptibles in group k at rate $\alpha^{(j,k)}_{(i)}$. The jth susceptible in group i has a tolerance level $Q^{(i)}_j$, where for $i \in [1; m]$ the $Q^{(i)}_j$ are distributed according to some random variable $Q^{(i)}$. As soon as the total infective pressure in its group exceeds its own tolerance level, a susceptible becomes infected. Individuals are all assumed to behave independently of each other, and the epidemic ends as soon as there are no more infectives remaining in the population.

Let $\chi^{(i)}_{\boldsymbol{j}}$ denote the total infective pressure in group i given $\boldsymbol{j} = (j_1, \ldots, j_m)$ infections (i.e. j_1 infections in group 1, etc.), so that

$$\chi^{(i)}_{\boldsymbol{j}} = \sum_{k=1}^{m} \sum_{l=-(a_k-1)}^{j_k} \sum_{r=1}^{m} R^{(r)}_{(k,l)} \alpha^{(r,i)}_{(k)}.$$

We define $\boldsymbol{T_N}$ to be the vector of final sizes $(T_1, \ldots, T_m)$, conditional upon there being initially $\boldsymbol{N}$ susceptibles. For $i \in [1; m]$ and $\boldsymbol{k} \in [\boldsymbol{0}; \boldsymbol{N}]$ define $W^{(i)}_{\boldsymbol{k}} = S^{(i)}(\chi^{(i)}_{\boldsymbol{k}})$, where $S^{(i)}$ is the survivor function of $Q^{(i)}$. In the following, we shall condition upon the values of $W^{(i)}_{\boldsymbol{k}}$ being known. However, we shall proceed by adopting a different approach to that described for the single group case in Section 3.1, which will no longer be applicable.

First, consider an epidemic in which $\boldsymbol{k} \geq \boldsymbol{0}$ susceptibles become infected. Then what has essentially occurred is that a particular subset of $\boldsymbol{k}$ initial susceptibles has been infected by the initial infectives, and these new infectives then fail to transmit the disease to any of the remaining $\boldsymbol{N} - \boldsymbol{k}$ susceptibles. Since this subset of $\boldsymbol{k}$ initial susceptibles can be chosen in

$$\binom{\boldsymbol{N}}{\boldsymbol{k}}$$

ways, it follows at once from the construction of the epidemic that

$$\Pr(\boldsymbol{T_N} = \boldsymbol{k}) = \binom{\boldsymbol{N}}{\boldsymbol{k}} \prod_{i=1}^{m} (W^{(i)}_{\boldsymbol{k}})^{N_i - k_i} \Pr(\boldsymbol{T_k} = \boldsymbol{k}),$$

as the probability that a given remaining susceptible in group i avoids infection from the $\boldsymbol{a}$ initial infectives and the $\boldsymbol{k}$ new infectives is $S^{(i)}(\chi^{(i)}_{\boldsymbol{k}}) = W^{(i)}_{\boldsymbol{k}}$, and all individuals are behaving independently.

Define $H_{\boldsymbol{k}} = (1/\boldsymbol{k}!)\Pr(\boldsymbol{T}_{\boldsymbol{k}} = \boldsymbol{k})$. Then since $\Pr(\boldsymbol{T}_{\boldsymbol{k}} = \boldsymbol{k}) = 1 - \Pr(\boldsymbol{T}_{\boldsymbol{k}} < \boldsymbol{k})$ it follows that

$$H_{\boldsymbol{k}} = \frac{1}{\boldsymbol{k}!}\left[1 - \sum_{\boldsymbol{0}\le\boldsymbol{j}<\boldsymbol{k}} \binom{\boldsymbol{k}}{\boldsymbol{j}} \prod_{i=1}^{m} (W_j^{(i)})^{k_i - j_i} \Pr(\boldsymbol{T}_{\boldsymbol{j}} = \boldsymbol{j})\right]$$
$$= \frac{1}{\boldsymbol{k}!} - \sum_{\boldsymbol{0}\le\boldsymbol{j}<\boldsymbol{k}} \frac{1}{(\boldsymbol{k}-\boldsymbol{j})!} \prod_{i=1}^{m} (W_j^{(i)})^{k_i - j_i} H_{\boldsymbol{j}}.$$

It follows at once from (2.1) that $H_{\boldsymbol{k}} = G_{\boldsymbol{k}}(\boldsymbol{1} \mid \boldsymbol{U})$, where $\boldsymbol{U} = (U^{(1)}, \ldots, U^{(m)})$, the $\boldsymbol{j}$th term of $U^{(i)}$ being $W_j^{(i)}$. Thus,

$$\Pr(\boldsymbol{T}_{\boldsymbol{N}} = \boldsymbol{k}) = \binom{\boldsymbol{N}}{\boldsymbol{k}} \prod_{i=1}^{m} (W_k^{(i)})^{N_i - k_i} \boldsymbol{k}!\, G_{\boldsymbol{k}}(\boldsymbol{1} \mid \boldsymbol{U}). \tag{5.1}$$

Next,

$$\frac{1}{\boldsymbol{N}!} - \frac{1}{\boldsymbol{N}!} \sum_{\boldsymbol{0}\le\boldsymbol{l}<\boldsymbol{k}} \Pr(\boldsymbol{T}_{\boldsymbol{N}} = \boldsymbol{l}) = \frac{1}{\boldsymbol{N}!} - \sum_{\boldsymbol{0}\le\boldsymbol{l}<\boldsymbol{k}} \frac{\prod_{i=1}^{m} (W_l^{(i)})^{N_i - l_i}}{(\boldsymbol{N}-\boldsymbol{l})!} G_{\boldsymbol{l}}(\boldsymbol{1} \mid \boldsymbol{U})$$
$$= G_{\boldsymbol{N}}(\boldsymbol{1} \mid \boldsymbol{U}(\boldsymbol{k})),$$

where $\boldsymbol{U}(\boldsymbol{k}) = (U^{(1)}(\boldsymbol{k}), \ldots, U^{(m)}(\boldsymbol{k}))$, the $\boldsymbol{j}$th element of $U^{(i)}(\boldsymbol{k})$ being $W_j^{(i)}$ if $\boldsymbol{j} < \boldsymbol{k}$, and equal to 0 otherwise. We thus obtain that

$$\Pr(\boldsymbol{T}_{\boldsymbol{N}} < \boldsymbol{k}) = 1 - \boldsymbol{N}!\, G_{\boldsymbol{N}}(\boldsymbol{1} \mid \boldsymbol{U}(\boldsymbol{k})),$$

and hence

$$\Pr(\boldsymbol{T}_{\boldsymbol{N}} \ge \boldsymbol{k}) = \boldsymbol{N}!\, G_{\boldsymbol{N}}(\boldsymbol{1} \mid \boldsymbol{U}(\boldsymbol{k})). \tag{5.2}$$

Note that (5.1) and (5.2) are generalizations of (3.4) and (3.3), respectively. It is instructive to attempt to generalize the argument leading (3.3) to the multi-group epidemic, as it sheds light on the generalization of (2.3) to multi-type Gontcharoff polynomials. For $\boldsymbol{k} \in (\mathbb{Z}^+)^m$ define $\gamma = \boldsymbol{i}_0, \boldsymbol{i}_1, \ldots, \boldsymbol{i}_k$ to be a path from $\boldsymbol{0}$ to $\boldsymbol{k}$, if $k = \sum_{i=1}^{m} k_i$ and $\boldsymbol{0} = \boldsymbol{i}_0 < \boldsymbol{i}_1 < \cdots < \boldsymbol{i}_k = \boldsymbol{k}$. Let $P(\boldsymbol{k})$ denote the set of all such paths. Thus, if $\gamma \in P(\boldsymbol{k})$, then for $l = 1, 2, \ldots, k$, $\boldsymbol{i}_l - \boldsymbol{i}_{l-1}$ is a vector containing $m - 1$ zeros and 1 one; let $\sigma(l)$ denote the coordinate of the one.

For $i \in [1; m]$, let $Q_{(1)}^{(i)} \le Q_{(2)}^{(i)} \le \cdots \le Q_{(N_i)}^{(i)}$ denote the order statistics of $Q_1^{(i)}, Q_2^{(i)}, \ldots, Q_{N_i}^{(i)}$. For $l \in [1; m]$ let $\boldsymbol{i}_j(l)$ denote the lth coordinate of $\boldsymbol{i}_j$. Then, arguing as in Section 3.2, for $\boldsymbol{0} < \boldsymbol{k} \le \boldsymbol{N}$,

$$\{\boldsymbol{T}_{\boldsymbol{N}} \ge \boldsymbol{k}\} = \bigcup_{\gamma \in P(\boldsymbol{k})} A_\gamma,$$

where

$$A_\gamma = \bigcap_{l=1}^{k} \{Q_{\boldsymbol{i}_l(\sigma(l))}^{(\sigma(l))} \le \chi_{\boldsymbol{i}_{l-1}}^{(\sigma(l))}\}.$$

Thus

$$\Pr(\boldsymbol{T}_{\boldsymbol{N}} \geq \boldsymbol{k}) = \Pr\Bigg(\bigcup_{\gamma \in P(\boldsymbol{k})} \bigcap_{l=1}^{k} \{V^{(\sigma(l))}_{N_{\sigma(l)}+1-\boldsymbol{i}_l(\sigma(l))} \geq W^{(\sigma(l))}_{\boldsymbol{i}_{l-1}}\} \Bigg), \tag{5.3}$$

where $(V^{(i)}_{(1)}, V^{(i)}_{(2)}, \ldots, V^{(i)}_{(N_i)})$ $(i \in [1; m])$ are independent and, for $i \in [1; m]$, $(V^{(i)}_{(1)}, V^{(i)}_{(2)}, \ldots, V^{(i)}_{(N_i)})$ has joint probability density function

$$f(v_1, v_2, \ldots, v_{N_i}) = \begin{cases} N_i! & \text{if } 0 < v_1 < v_2 < \cdots < v_{N_i} < 1, \\ 0 & \text{otherwise.} \end{cases}$$

Recalling (5.2), (5.3) can be used to obtain an expression for $G_{\boldsymbol{N}}(\boldsymbol{1} \mid \boldsymbol{U}(\boldsymbol{k}))$, which will be a complicated sum of integrals (note that the events A_γ $(\gamma \in P(\boldsymbol{k}))$ are dependent) and, in this case, is a generalization of (2.3) to m variables. Of course, when $m = 1$, there is only one path from 0 to k, so all the above complications disappear.

We now briefly describe the generalization of Theorem 4.2 to the multi-group setting. For exponential tolerances it is sufficient to set $S^{(i)}(x) = \exp(-x)$ $(x \geq 0)$ for each $i \in [1; m]$, the point here being that we can model differences in tolerance between groups by our choice of $\alpha^{(j,k)}_{(i)}$.

Before proceeding, we define a multi-group version of a general final state random variable. In the single-population case, we defined p random variables for each infected individual to represent p quantities of interest. However, we now define such quantities for each pair (k, l) where $k \in [1; p]$ is a type as before, and $l \in [1; m]$ denotes one of the groups. Thus we can consider quantities of interest that depend not only on an individual, but on each group as well. A simple example is the time spent by each individual in each of the other groups. So for the jth individual to become infected in group i, define for each pair (k, l) a random variable $A^{(k,l)}_{(i,j)}$ distributed according to some underlying random variable $A^{(k,l)}_{(i)}$, with the usual assumptions about independence between individuals. Next, for $\boldsymbol{j} = (j_1, \ldots, j_m)$ define

$$A^{(k,l)}_{(i)}(\boldsymbol{j}) = A^{(k,l)}_{(i)}(j_i) = \sum_{r=-(a_i-1)}^{j_i} A^{(k,l)}_{(i,r)}.$$

Let $\boldsymbol{\Theta} = \{\theta_{ijk} : i \in [1; p],\ j, k \in [1; m]\}$, and define

$$\phi(\boldsymbol{x}, \boldsymbol{\Theta}) = \mathbb{E}\Bigg[\boldsymbol{x}^{\boldsymbol{N}-\boldsymbol{T}} \exp\Bigg(-\sum_{i=1}^{p} \sum_{l=1}^{m} \sum_{r=1}^{m} A^{(i,r)}_{(l)}(\boldsymbol{T}) \theta_{ilr} \Bigg) \Bigg].$$

It follows from (5.1) that

$$\phi(\boldsymbol{x}, \boldsymbol{\Theta}) = \sum_{\boldsymbol{k}=\boldsymbol{0}}^{\boldsymbol{N}} \frac{\boldsymbol{N}!}{(\boldsymbol{N}-\boldsymbol{k})!} \boldsymbol{x}^{\boldsymbol{N}-\boldsymbol{k}} \times \mathbb{E}\Bigg[\Bigg(\prod_{i=1}^{m} S^{(i)}(\chi^{(i)}_{\boldsymbol{k}}) \Bigg) \exp\Bigg(-\sum_{i=1}^{p} \sum_{l=1}^{m} \sum_{r=1}^{m} A^{(i,r)}_{(l)}(\boldsymbol{k}) \theta_{ilr} \Bigg) G_{\boldsymbol{k}}(\boldsymbol{1} \mid \boldsymbol{U}(\boldsymbol{k})) \Bigg]$$

$$= \sum_{\boldsymbol{k}=\boldsymbol{0}}^{\boldsymbol{N}} \frac{\boldsymbol{N}!}{(\boldsymbol{N}-\boldsymbol{k})!}\boldsymbol{x}^{\boldsymbol{N}-\boldsymbol{k}}$$
$$\times \mathbb{E}\left[\left(\prod_{i=1}^{m} S^{(i)}(\chi_{\boldsymbol{k}}^{(i)})\right)\left(\prod_{l=1}^{m}\prod_{q=-(a_l-1)}^{k_l} h(\boldsymbol{\Theta}, \boldsymbol{R}_{(l,q)})\right) G_{\boldsymbol{k}}(\mathbf{1} \mid \boldsymbol{U}(\boldsymbol{k}))\right],$$

where for $l \in [1; m]$,

$$h(\boldsymbol{\Theta}, \boldsymbol{R}_{(l,q)}) = \mathbb{E}\left[\exp\left(-\sum_{i=1}^{p}\sum_{r=1}^{m} A_{(l,q)}^{(i,r)}\theta_{ilr}\right) \mid (R_{(l,q)}^{(1)}, \ldots, R_{(l,q)}^{(m)})\right].$$

The following result is the multi-group version of Theorem 4.2. The proof is identical in structure to the single group case (and hence it is omitted), although now we can also exploit independence between groups as well as between individuals in a group.

Theorem 5.1. *Suppose that for $i \in [1; m]$ and $x \geq 0$, $S^{(i)}(x) = \exp(-x)$. Then*

$$\phi(\boldsymbol{x}, \boldsymbol{\Theta}) = \sum_{\boldsymbol{k}=\boldsymbol{0}}^{\boldsymbol{N}} \frac{\boldsymbol{N}!}{(\boldsymbol{N}-\boldsymbol{k})!}\boldsymbol{\psi}(\boldsymbol{\Theta}, \boldsymbol{k})^{\boldsymbol{N}+\boldsymbol{a}-\boldsymbol{k}} G_{\boldsymbol{k}}(\boldsymbol{x} \mid \boldsymbol{U}^*),$$

where $\boldsymbol{\psi}(\boldsymbol{\Theta}, \boldsymbol{k})$ is an m-vector with lth component

$$\boldsymbol{\psi}_l(\boldsymbol{\Theta}, \boldsymbol{k}) = \mathbb{E}\left[\exp\left(-\sum_{i=1}^{m}\sum_{j=1}^{m} R_{(l)}^{(j)}\alpha_{(l)}^{(j,i)}k_i\right) h(\boldsymbol{\Theta}, \boldsymbol{R}_{(l)})\right],$$

where for $l \in [1; m]$,

$$h(\boldsymbol{\Theta}, \boldsymbol{R}_{(l)}) = \mathbb{E}\left[\exp\left(-\sum_{i=1}^{p}\sum_{r=1}^{m} A_{(l)}^{(i,r)}\theta_{ilr}\right) \mid (R_{(l)}^{(1)}, \ldots, R_{(l)}^{(m)})\right],$$

and $\boldsymbol{U}^* = (U^{*1}, \ldots, U^{*m})$ where for $l \in [1; m]$, U^{*l} has $\boldsymbol{j}$th term $\boldsymbol{\psi}_l(\boldsymbol{\Theta}, \boldsymbol{j})$.

Note that by considering only final severity, so that $p = 1$ and

$$A_{(i)}^{(1,l)}(\boldsymbol{T}) = \sum_{r=(a_i-1)}^{T_i} R_{(i)}^{(l)},$$

then it is straightforward to show that Lemma 5.1 reduces to Theorem 3.1 of Ball and Clancy (1993). Analogous results to Corollaries 4.3, 4.4 and 4.5, and equations (4.7) and (4.8), can be derived for the multi-group model, using obvious generalizations of the previous arguments. We omit the details.

6. Extensions

6.1. Multiple contact models

In this section we suppose that our model is the same as that described in Section 3, except that Q now has a Gamma (s, β) distribution, where $s \geq 2$ is an integer. The model is

then equivalent to one in which, throughout its infectious period, a given infective contacts a given susceptible at the points of a Poisson process of rate β, but now the susceptible has to be contacted s times in total before it becomes infected. Equations (3.5) and (3.6) can, in principle, be used to determine the final size distribution and $\phi(x, \boldsymbol{\theta})$ for this model. However, the simplifications obtained in Section 4.2 cannot be generalized to this case since $S(\chi_k)$ no longer factorizes in a convenient manner. For a small number N of initial susceptibles, the final size distribution can be calculated from (3.5) by first obtaining an explicit expression for $G_k(1 \mid U)$. However, this approach becomes increasingly laborious as N increases.

The case $s = 2$ has previously been considered for a Reed–Frost type model by Scalia-Tomba (1985), who derived an asymptotic approximation to the final size distribution when $N \to \infty$ with $a/N \to \mu > 0$.

6.2. Models with outside infection

Consider now an extension of the model of Section 4.2, in which susceptibles may also be infected from outside the population. Specifcally, we assume that during the course of the epidemic, each of the initial N susceptibles independently avoids infection from outside the population with probability π. Addy *et al.* (1991) considered a multi-group version of such a model and generalized the methods of Ball (1986) to determine properties of its final size and severity. However, the distribution of the final outcome for this model can be obtained by conditioning on the number of initial susceptibles that avoid infection from outside, which has a Binomial (N, π) distribution. Thus, using Theorem 4.2, for this model we have

$$\phi(x, \boldsymbol{\theta}) = \sum_{k=0}^{N} \binom{N}{k} \pi^k (1-\pi)^{N-k} \sum_{i=0}^{k} \frac{k!}{(k-i)!} (\mathbb{E}[\exp(-\beta i R) h(\boldsymbol{\theta}, R)])^{N+a-i} G_i(x \mid \tilde{U}^*).$$

Changing the order of summation yields, after a little algebra,

$$\phi(x, \boldsymbol{\theta}) = \sum_{k=0}^{N} \frac{N!}{(N-k)!} (\mathbb{E}[\exp(-\beta k R) h(\boldsymbol{\theta}, R)])^{N+a-k} \pi^k G_k(x \mid \tilde{U}^*).$$

Further properties of the final outcome now follow as in Section 4.2.

Another approach to the final outcome of this model with outside infection is to introduce a dummy second group, consisting of one initial infective and no susceptibles, whose sole purpose is to imitate the outside infection. Both approaches generalize easily to the multi-group setting.

6.3. Epidemics among households

There has been considerable interest recently in models for the spread of an epidemic among a community of households (see, for example, Becker and Dietz (1995) and Ball *et al.* (1997)). Ball (1996) considers such a model for the spread of an epidemic among a population of m groups (households), each containing n individuals. In this model, infectious individuals have independent and identically distributed *life histories* $\mathcal{H} = (T^{\mathrm{I}}, \eta^{\mathrm{W}}, \eta^{\mathrm{B}})$, where T^{I} is a typical infective's infectious period, and η^{W} and η^{B} are point processes of times, relative to the individual's infection, at which *within-group* and *between-group* contacts are made, respectively. Each within-group (between-group) contact of a specific infective is with an individual chosen independently and uniformly from the n initial susceptibles in the same group (nm individuals in the population). If the individual contacted is still susceptible then it becomes infected, otherwise nothing happens. Suppose that initially there are $mn - 1$

susceptibles and one infective, who has just been infected. As before, the epidemic ceases as soon as there are no infectives left in the population.

Suppose that η^{W} and η^{B} are inhomogeneous Poisson processes with rates, at time t after an individual's infection, of $\lambda_{\mathrm{W}}(t)$ and $\lambda_{\mathrm{B}}(t)$, respectively. If η^{W} and η^{B} are independent and $\lambda_{\mathrm{W}}(t)$ and $\lambda_{\mathrm{B}}(t)$ take the form $\lambda_{\mathrm{W}}(t) = \lambda_{\mathrm{W}}\lambda(t)$ and $\lambda_{\mathrm{B}}(t) = \lambda_{\mathrm{B}}\lambda(t)$ for $t \geq 0$, then setting

$$R = \int_0^{T^{\mathrm{I}}} \lambda(t)\,\mathrm{d}t, \quad \text{and} \quad \lambda(t) \equiv 1$$

yields a model with the same distribution of final outcome as the previous model, and which also is a special case of the model described in Section 5. Thus properties of the final outcome of this household epidemic can, in principle, be obtained from our earlier results. However, in the case of practical interest, namely when m is large and n is small, the calculations quickly become prohibitive.

When m is large, during the early stages of the epidemic each between-group infectious contact is highly likely to be with an individual in a previously uninfected group. Thus the initial stages of the epidemic can be approximated by a branching process, in which the units are single household epidemic processes and the offspring of a given unit are those households that are directly infected by infectives in that given unit. Let C denote the number of offspring of a typical unit in this branching process. Thus a *global epidemic*, i.e. one that infects infinitely many households in the limit as $m \to \infty$, can only occur if $C^* = \mathbb{E}[C] > 1$. Thus C^* provides a threshold parameter for the household epidemic model. The above approximation and threshold parameter can be made exact in the limit as $m \to \infty$, see Ball (1996). We now determine a formula for C^*, for possibly dependent η^{W} and η^{B}, and arbitrary but specified $\lambda_{\mathrm{W}}(t)$ and $\lambda_{\mathrm{B}}(t)$. Let

$$R = \int_0^{T^{\mathrm{I}}} \lambda_{\mathrm{W}}(t)\,\mathrm{d}t \quad \text{and} \quad A = \int_0^{T^{\mathrm{I}}} \lambda_{\mathrm{B}}(t)\,\mathrm{d}t.$$

Then, if global contacts are ignored, the spread of an epidemic within a single household has the same distribution of final outcome as the model described in Section 4.2, with $\beta = 1$, $a = 1$, $N = n - 1$ and infectious periods $R_0, R_1, \ldots, R_{n-1}$ distributed as R above. Let $A_0, A_1, \ldots, A_{n-1}$ be independent copies of A. Then the total number of between-group contacts emanating from infectives in a typical single household epidemic follows a Poisson distribution with random mean $A(T) = \sum_{i=0}^{T} A_i$, where T denotes the final size of the single household epidemic. Thus, by Corollary 4.4,

$$\begin{aligned} C^* &= \mathbb{E}[A(T)] \\ &= (\mathbb{E}[T] + 1)\mathbb{E}[A] \\ &= (1 + \mu_{n-1,1})\mathbb{E}[A], \end{aligned}$$

where $\mu_{n-1,1}$ is given by (4.7). Finally, note that the offspring random variable C has probability generating function

$$\begin{aligned} f(s) &= \mathbb{E}[s^C] \\ &= \mathbb{E}[\mathbb{E}[s^C \mid A(T)]] \\ &= \mathbb{E}[\exp(-A(T)(1-s))] \\ &= \phi(1, 1-s), \end{aligned}$$

where ϕ is analogous to $\phi(x, \boldsymbol{\theta})$ of Section 3. Thus Theorem 4.2 enables $f(s)$, and hence the probability of a global epidemic, to be calculated. Note that the dependence or independence of η^{W} and η^{B} does not affect the threshold parameter C^*, but it does affect the probability of a global epidemic.

Appendix

Proof of Lemma 4.1. We proceed by induction on r. If $r = 0$, then both sides of (4.2) are clearly equal to 1 (under the convention that $\sum_{j=k+1}^{k} R_j = 0$ and $\prod_{j=k+1}^{k} h(\boldsymbol{\theta}, R_j) = 1$). Now

$$\mathbb{E}_{\boldsymbol{R}}\left[\exp\left(-\beta(N-k-r)\sum_{j=k+1}^{k+r} R_j\right)\left(\prod_{i=k+1}^{k+r} h(\boldsymbol{\theta}, R_i)\right) G_r(0 \mid \tilde{U}^{(k)})\right]$$

$$= -\mathbb{E}_{\boldsymbol{R}}\left[\sum_{l=0}^{r-1}\left\{\exp\left(-\beta(N-k-r)\sum_{j=k+1}^{k+r} R_j\right)\left(\prod_{i=k+1}^{k+r} h(\boldsymbol{\theta}, R_i)\right)\right.\right.$$

$$\left.\left.\times \frac{\exp(-\beta(r-l)\sum_{j=k+1}^{k+l} R_j)}{(r-l)!} G_l(0 \mid \tilde{U}^{(k)})\right\}\right],$$

using (2.2). Continuing,

$$= -\sum_{l=0}^{r-1} \mathbb{E}_{\boldsymbol{R}}\left[\left\{\left(\exp\left(-\beta(N-k-r)\sum_{j=k+l+1}^{k+r} R_j\right)\left(\prod_{i=k+l+1}^{k+r} h(\boldsymbol{\theta}, R_i)\right)\right)\Big/(r-l)!\right\}\right.$$

$$\left.\times \exp\left(-\beta(N-k-l)\sum_{j=k+1}^{k+l} R_j\right)\left(\prod_{i=k+1}^{k+l} h(\boldsymbol{\theta}, R_i)\right) G_l(0 \mid \tilde{U}^{(k)})\right],$$

$$= -\sum_{l=0}^{r-1} \frac{(\mathbb{E}_R[\exp(-\beta(N-k-r)R)h(\boldsymbol{\theta}, R)])^{r-l}}{(r-l)!} G_l(0 \mid E^{(N-k-l)}\tilde{U}^*), \tag{A.1}$$

using induction and the fact that the R_j are independent and distributed according to R. Changing the summation variable and using the fact that $G_{r-l}(0 \mid E^l U) = G_r^{(l)}(0 \mid U)$ yields that (A.1) equals

$$-\sum_{l=1}^{r} \frac{(\mathbb{E}_R[\exp(-\beta(N-k-r)R)h(\boldsymbol{\theta}, R)])^{l}}{l!} G_r^{(l)}(0 \mid E^{(N-k-r)}\tilde{U}^*),$$

and the result now follows from Lemma 2.1.

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