



The probability of epidemic fade-out is non-monotonic in transmission rate for the Markovian SIR model with demography



P.G. Ballard^{a,*}, N.G. Bean^{a,b}, J.V. Ross^a

^a School of Mathematical Sciences, The University of Adelaide, Adelaide, SA 5005, Australia

^b ARC Centre of Excellence for Mathematical and Statistical Frontiers, Australia

HIGHLIGHTS

- We calculate the probability of epidemic fade-out for the SIR model with demography.
- We present an efficient algorithm, more accurate than published approximations.
- The probability of epidemic fade-out generally peaks near $R_0 = 2$.
- We explain why epidemic fade-out is more likely near $R_0 = 2$.

ARTICLE INFO

Article history:

Received 21 September 2015

Received in revised form

22 December 2015

Accepted 7 January 2016

Available online 18 January 2016

Keywords:

Diffusion approximation

Efficient algorithms

Epidemic control

Stochastic epidemic model

ABSTRACT

Epidemic fade-out refers to infection elimination in the trough between the first and second waves of an outbreak. The number of infectious individuals drops to a relatively low level between these waves of infection, and if elimination does not occur at this stage, then the disease is likely to become endemic. For this reason, it appears to be an ideal target for control efforts. Despite this obvious public health importance, the probability of epidemic fade-out is not well understood. Here we present new algorithms for approximating the probability of epidemic fade-out for the Markovian SIR model with demography. These algorithms are more accurate than previously published formulae, and one of them scales well to large population sizes. This method allows us to investigate the probability of epidemic fade-out as a function of the effective transmission rate, recovery rate, population turnover rate, and population size. We identify an interesting feature: the probability of epidemic fade-out is very often greatest when the basic reproduction number, R_0 , is approximately 2 (restricting consideration to cases where a major outbreak is possible, i.e., $R_0 > 1$). The public health implication is that there may be instances where a non-lethal infection should be allowed to spread, or antiviral usage should be moderated, to maximise the chance of the infection being eliminated before it becomes endemic.

© 2016 Elsevier Ltd. All rights reserved.

1. Introduction

The ultimate goal of modelling infectious disease dynamics is to gain insight into how to use resources best to eliminate infection. This may be achieved by making invasion difficult through minimising the probability of a major outbreak, for example through the use of prophylactic vaccination, antivirals or contact tracing (Ball, 1983; Ball and Lyne, 2002; Ross and Black, 2015).

For endemic diseases, with wide prevalence, once again the predominant focus is on reducing transmission as much as possible, and there have been a number of studies calculating the

mean time to *endemic fade-out* (van Herwaarden and Grasman, 1995; Näsell, 2001; Kamenev and Meerson, 2008).

Much less attention has been paid to what is the optimal approach to adopt when a major outbreak occurs. Typically, focus has been given to minimising the amount of infection – either the rate of new infections, or the total number of infections over the first wave of an outbreak – for example, through the use of antivirals, and once available, vaccination (e.g., McCaw and McVernon, 2007; Black et al., 2013). Here we instead focus on the probability of *epidemic fade-out* – that is, the probability of infection being eliminated between the first and second waves of infection.

In fact, a more comprehensive understanding of the probability of epidemic fade-out is named as one of the five challenges (for stochastic epidemic models involving global transmission) by Britton et al. (2015), supporting earlier calls (Anderson and May, 1991; Diekmann and Heesterbeek, 2000). The interest in this

* Corresponding author.

E-mail addresses: peter.ballard@adelaide.edu.au (P.G. Ballard), nigel.bean@adelaide.edu.au (N.G. Bean), joshua.ross@adelaide.edu.au (J.V. Ross).

quantity for infection elimination is that following the first wave of an outbreak, the number of infectious individuals drops to a relatively low level. Then, if fade-out does not occur, it is likely that the disease will become endemic. Hence, this “first trough” of infection appears intuitively to be an ideal target for elimination.

We study a Markovian SIR model with demography (van Herwaarden and Grasman, 1995; Näsell, 1999; Andersson and Britton, 2000), and in particular the probability of epidemic fade-out as a function of effective transmission rate, recovery rate, population turnover rate, and population size parameter. We identify the ubiquity of a non-monotonicity property of the probability of epidemic fade-out as a function of effective transmission rate (holding other parameters fixed). In fact, the probability of epidemic fade-out is very often greatest when the basic reproduction number, R_0 , is approximately 2 (restricting consideration to cases where a major outbreak is possible, i.e., $R_0 > 1$). This means that there may be cases when, faced with an infectious outbreak, it would be beneficial to not take action to reduce R_0 .

The identification of this phenomenon was achieved through the development of a numerical method which is highly accurate and efficient for computation of the probability of epidemic fade-out. To our knowledge, as supported by the paper (Britton et al., 2015), there have been only two existing methods proposed, both approximations, for evaluating this probability (van Herwaarden, 1997; Meerson and Sasorov, 2009). These existing methods are asymptotic approximations, with accuracy improving in the limit as the population size parameter tends to infinity. Our method has the benefit of being highly accurate across a wider range of population sizes, including moderate-sized populations, while still using light computer resources and hence scaling well to large population sizes.

In the next section we introduce the Markovian SIR model with demography that we study, before discussing deterministic and diffusion approximations of this model which are relevant to existing methods and our new method for evaluating the probability of epidemic fade-out. We then review the existing approximations. In Section 3 we detail our new method for computing the probability of epidemic fade-out. In Section 4.1 we validate its accuracy and efficiency, and in Section 4.2 we investigate the dependence of the probability of epidemic fade-out on the model parameters, identifying the ubiquity of a non-monotonicity property in the effective transmission rate. Finally, we conclude this work and discuss future research ideas.

2. Background

In this section we present the two existing methods for approximating the probability of epidemic fade-out (van Herwaarden, 1997; Meerson and Sasorov, 2009). To achieve this, we first introduce the underlying model assumed in these earlier studies, and also two asymptotic approximations of this model. These are not only required for both existing methods but also for our new methods to be presented in Section 3.

2.1. The Markovian SIR model with demography

Following previous work (van Herwaarden, 1997; Meerson and Sasorov, 2009), we adopt the Markovian SIR model with demography (van Herwaarden and Grasman, 1995; Näsell, 1999; Andersson and Britton, 2000). However, we note that our methods can be easily modified to suit other SIR models which involve replenishment of susceptibles.

The well-known SIR model puts every individual in the population into one of three classes: “S” for Susceptible, “I” for Infectious, and “R” for Recovered (or Removed). Let S , I and R denote the

number of individuals in the respective states. Then, we assume that susceptible individuals become infectious at rate $\beta SI/N$, and infectious individuals recover at rate γI , where β is the effective transmission rate parameter, $1/\gamma$ is the average infectious period of an individual and N is the total population size. The population is closed, and hence of a constant size.

The SIR model with demography extends the SIR model by also having births (or immigration) of susceptibles, at a fixed rate μN , and deaths (or emigration) from each state at rates μS , μI and μR respectively, where μ is the population turnover rate parameter. We note that this means the actual population size, $S+I+R$, is no longer fixed, but that the birth rate is held constant (i.e., N , the population size parameter, is constant). A consequence of the latter, along with the fact that the number of recovered individuals, R , has no direct bearing on the other states, and that our interest herein is on the number of infectious individuals, is that we may describe the state of the system by (S, I) (Kamenev and Meerson, 2008) with state space $\{(S, I) : 0 \leq S, I\}$. The Markovian SIR model with demography we consider herein is detailed in Table 1 and Fig. 1.

2.2. Asymptotic approximations: the density process

We now state two limiting results of the SIR model with demography, in the limit as N becomes large (Kurtz, 1970, 1971; Pollett, 1990). These approximations assist us in defining the probability of epidemic fade-out, and are furthermore made use of in the two existing methods for approximating the probability of epidemic fade-out, discussed in Section 2.3, and in our own methods to be introduced in Section 3.

Let $Y_N(t)$ be a process following the model defined in Section 2.1, with each value being an (S, I) pair, and with initial value (S_0, I_0) . The associated density process is $X_N(t) = Y_N(t)/N$, with each possible value x being an (s, i) pair, where $s = S/N$ and $i = I/N$; and the initial value is $x_0 = (s_0, i_0) = (S_0/N, I_0/N)$. The density process is important because it allows us to analyse the limiting behaviour as $N \rightarrow \infty$.

Let $f(x, l)$ be the transition rate of the density process from state (x) to state $(x+l/N)$, where l can take on the possible 1-step transition values in Table 1: $(-1, 1)$, $(1, 0)$, $(-1, 0)$ and $(0, -1)$, respectively. Also define for the density process:

$$F(x) = \sum_l f(x, l) = (-\beta si + \mu(1-s), \beta si - (\gamma + \mu)i); \tag{1}$$

$B(x)$, a matrix whose (j, k) th element is given by $b_{j,k} = \frac{\partial f_j}{\partial x_k}$,

$$\Rightarrow B(x) = \begin{pmatrix} -\beta i - \mu & -\beta s \\ \beta i & \beta s - (\gamma + \mu) \end{pmatrix}; \tag{2}$$

Table 1
Events, transitions and their rates for the Markovian SIR model with demography.

Description	Transition	Rate
Infection	$(S, I) \rightarrow (S-1, I+1)$	$\beta SI/N$
Birth of susceptible	$(S, I) \rightarrow (S+1, I)$	μN
Removal of susceptible	$(S, I) \rightarrow (S-1, I)$	μS
Removal of infectious	$(S, I) \rightarrow (S, I-1)$	$(\gamma + \mu)I$

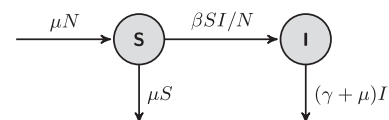


Fig. 1. Diagram of the Markovian SIR model with demography. Note, the “R” state is redundant and has been removed.

Download English Version:

<https://daneshyari.com/en/article/4495873>

Download Persian Version:

<https://daneshyari.com/article/4495873>

[Daneshyari.com](https://daneshyari.com)