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An epidemic model with noisy parameters

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ABSTRACT

We analyse an *SIR* model where the epidemiological parameters are subject to small amplitude random fluctuations. We derive a final size equation and extend the result to an *SEIR* model. We use a small amplitude perturbation to estimate the expected final size of the *SIR* model and its variance, and compare the result with numerical simulations. We show that although individual realisations may exhibit considerable variation around solutions of the deterministic model, the mean of the final size distribution is in good agreement with the deterministic final size, and its standard deviation is small compared to the mean.

1. Introduction

The use of mathematical models for understanding infectious disease dynamics is now well-established [6]. Whereas in the past there may have been a perception that deterministic and stochastic models were applied in mutually exclusive studies [5], there is now a realisation that both types of model have their uses and are appropriate in different circumstances [2,3,13]. For a recent review of progress and the remaining challenges with stochastic epidemic models see [4].

An analysis of a simple deterministic epidemic model frequently involves relating the basic reproduction number $\mathcal{R}_0$ to the final size of the epidemic [6,11]. For a stochastic model the final size may be expressed as a probability distribution, rather than as a number or proportion [2]. Here, we consider a generalisation of the well-known deterministic *SIR* and *SEIR* models, replacing their parameters with a fixed parameter plus a small amplitude randomly fluctuating component. We approximate this fluctuating component with white noise and use results from stochastic calculus [7,10] to analyse the models. The introduced noise may be due to individual hosts responding to infection at different times, with heterogeneous responses, or to environmental fluctuations. This technique has previously been used to establish conditions for the persistence of an endemic state of an *SIS* model [9], and conditions for the stability of the disease-free equilibrium of an endemic *SIR* model [14]. Khaladi and co-workers have analysed an epidemic model in a random environment that changes between a finite number of configurations at times determined according to a Markov process [1,8]. In a previous study we analysed an *SIR* model where $\mathcal{R}_0$ was specified by a distribution rather than a single value [12]. In that model the dynamics were deterministic once the parameters of the distribution had been chosen, although the final size was then specified as a probability distribution.

In Section 2 we discuss an *SIR* model with small amplitude white noise added to the parameters. In Section 3 we derive a quantity whose expected value may be used to determine the final size of an epidemic. In Section 4 we approximate our stochastic model with a linear stochastic process that is a small perturbation of the deterministic model, and derive an expression for the expected final size and its variance, which we compare with numerical simulations of the stochastic model. We extend these results to an *SEIR* model in Section 5.

2. A stochastic *SIR* model

We consider an *SIR* epidemic model [6,11] of the form:

$$\begin{aligned}\dot{x}(t) &= -\beta xy\\ \dot{y}(t) &= \beta xy - \gamma y\end{aligned} \tag{1}$$

with initial conditions $x(0) = x_0$, $0 < x_0 < 1$; and $y(0) = y_0$, $0 < y_0 \ll 1$; where $x(t)$ is the proportion of the population susceptible at time t, and $y(t)$ is the proportion of the population infectious. The basic reproduction number is $\mathcal{R}_0 = \frac{\beta}{\gamma}$. It is well-known [11] that for this model (assuming the population to be large): an epidemic occurs if $\mathcal{R}_0 x_0 > 1$; the proportion of the population that is infected can be approximated initially by $y(t) = y_0 e^{\beta x_0 t - \gamma t}$; during the epidemic $x + y - \mathcal{R}_0^{-1} \log x$ is a conserved quantity; and the proportion of the population that is infected during the entire epi-

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demic, $P = x_0 - x_\infty$, solves the *final size equation*

$$\log\left(1 - \frac{P}{x_0}\right) + \mathcal{R}_0 P = 0 \tag{2}$$

It would be unusual for an epidemic to be allowed to run its course. More generally, if a control measure reduces $\mathcal{R}_0$ to a value $\mathcal{R}_c$ say, when the prevalence of infection is y_1 and a proportion x_1 of the population is susceptible, then the further proportion of the population that will be infected by the time the prevalence reaches y_2 may be found by solving the equation

$$\log\left(1 - \frac{p}{x_1}\right) + \mathcal{R}_c p = \mathcal{R}_c(y_2 - y_1)$$

for p. We will investigate the changes in these results, and in the dynamics of the system, when the contact and recovery rates, and hence the basic reproduction number $\mathcal{R}_0$, are subject to random variation.

Consider the *SIR* model with noise in the contact and recovery rates

$$\begin{aligned} \frac{\mathrm{d}S_t}{\mathrm{d}t} &= -\beta_t S_t I_t \\ \frac{\mathrm{d}I_t}{\mathrm{d}t} &= \beta_t S_t I_t - \gamma_t I_t \end{aligned} \tag{3}$$

We use the subscript t to denote a stochastic process in time. We approximate the noise components of β_t and γ_t on a finite interval $[0, T]$ as follows. Choose integers m and n such that $n\Delta t = 1$ time unit, and $T = m\Delta t$. Define a function $w^{(n)}(t) = w_i$ for $(i-1)\Delta t < t < i\Delta t$ and $i = 1 \ldots m$. Let the w_i be independent and identically distributed random variables, with mean $\bar{w}$ and variance σ^2. We now define

$$W_t^{(n)} = \frac{w^{(n)}(t) - \bar{w}}{\sigma\sqrt{\Delta t}}$$

and observe that

$$\int_0^T W_t^{(n)}\,\mathrm{d}t = \frac{T}{\sigma\sqrt{\Delta t}}\left(\frac{1}{m}\sum_{i=1}^{m} w_i - \bar{w}\right)$$

The summation in the equation above is an estimate of $\bar{w}$ based on m samples, hence it is normally distributed for large m with expected value $\bar{w}$ and variance σ^2/m. The integral $\int_0^T W_t^{(n)}\,\mathrm{d}t$ has expected value zero, and

$$\mathbb{E}\left[\left(\int_0^T W_t^{(n)}\,\mathrm{d}t\right)^2\right] = \left(\frac{T}{\sigma\sqrt{\Delta t}}\right)^2 \frac{\sigma^2}{m} = T$$

Taking the limit as $n \to \infty$, $W_t^{(n)}\Delta t \to W_t \mathrm{d}t = \mathrm{d}B_t$ where W_t is white noise and B_t is Brownian motion. We now write

$$\beta_t(\omega) = \beta\left(1 + \epsilon_\beta \frac{\mathrm{d}B_t^{(\beta)}}{\mathrm{d}t}\right) \qquad \gamma_t(\omega) = \gamma\left(1 + \epsilon_\gamma \frac{\mathrm{d}B_t^{(\gamma)}}{\mathrm{d}t}\right)$$

where ϵ_β and ϵ_γ are positive, and $B_t^{(\beta)}(\omega)$ and $B_t^{(\gamma)}(\omega)$ are two independent Brownian motions for a given realisation ω. We require ϵ_β and ϵ_γ to be small in the sense that $\beta_t(\omega)$ and $\gamma_t(\omega)$ are almost always positive, a requirement satisfied when $\epsilon_\beta^2 + \epsilon_\gamma^2$ is small compared with Δt. Note that ϵ_β and ϵ_γ have units $[\text{time}]^{\frac{1}{2}}$ and W_t has units $[\text{time}]^{-\frac{1}{2}}$. We assume that the dimensionless quantities $\delta_\beta = \epsilon_\beta\sqrt{\beta}$ and $\delta_\gamma = \epsilon_\gamma\sqrt{\gamma}$ are small compared to one.

Eq. (3) can be rewritten

$$\begin{aligned} \mathrm{d}S_t(\omega) &= -\beta S_t I_t \mathrm{d}t - \epsilon_\beta \beta S_t I_t \mathrm{d}B_t^{(\beta)}(\omega) \\ \mathrm{d}I_t(\omega) &= \beta S_t I_t \mathrm{d}t - \gamma I_t \mathrm{d}t + \epsilon_\beta \beta S_t I_t \mathrm{d}B_t^{(\beta)}(\omega) - \epsilon_\gamma \gamma I_t \mathrm{d}B_t^{(\gamma)}(\omega) \end{aligned} \tag{4}$$

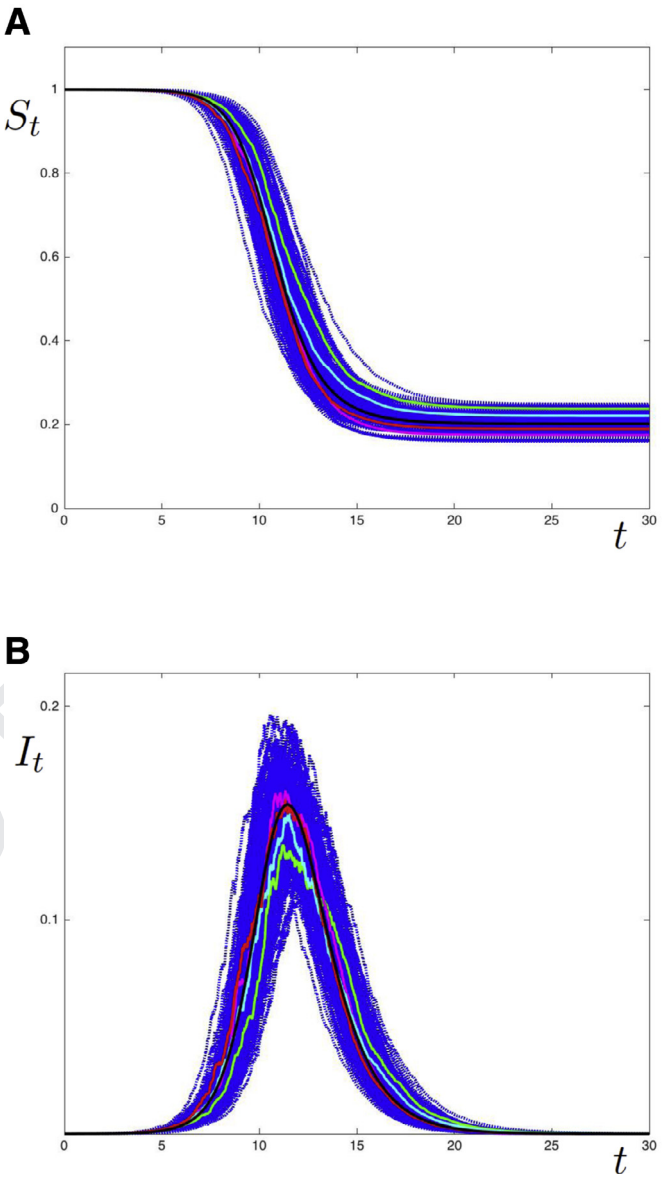

Fig. 1. The dynamics of the stochastic *SIR* model calculated numerically from Eq. (4): (A) S_t the proportion of the population susceptible and (B) I_t the proportion infectious against time. A total of 200 realisations are shown, with four sample plots highlighted in red, green, magenta and cyan, the rest in blue. The deterministic solution is shown in black. Parameter values are $S_0 = 1$, $\beta = 2$, $\gamma = 1$, $\epsilon_\beta = 0.075$, $\epsilon_\gamma = 0.025$. Hence $\delta_\beta = 0.106$ and $\delta_\gamma = 0.025$. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Numerical solutions of multiple realisations of Eq. (4) are presented in Fig. 1.

In the initial part of the epidemic, taking $S_t = S_0$, the second of Eq. (4) becomes a stochastic population growth equation

$$\mathrm{d}I_t(\omega) = (\beta S_0 - \gamma) I_t \mathrm{d}t + \epsilon_0 \gamma I_t \mathrm{d}B_t^{(0)}(\omega) \tag{5}$$

where

$$\epsilon_0 = \sqrt{\left(\frac{\beta S_0}{\gamma}\right)^2 \epsilon_\beta^2 + \epsilon_\gamma^2}$$

and

$$B_t^{(0)}(\omega) = \frac{\beta S_0}{\gamma}\frac{\epsilon_\beta}{\epsilon_0} B_t^{(\beta)}(\omega) - \frac{\epsilon_\gamma}{\epsilon_0} B_t^{(\gamma)}(\omega)$$