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A stochastic vector-borne epidemic model: Quasi-stationarity and extinction

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ABSTRACT

We consider a stochastic model describing the spread of a vector borne disease in a community where individuals (hosts and vectors) die and new individuals (hosts and vectors) are born. The time to extinction of the disease, T_Q, starting in quasi-stationary (conditional on non extinction) is studied. Properties of the limiting distribution are used to obtain an approximate expression for $E(T_Q)$, the mean-parameter in the exponential distribution of the time to extinction, for a finite population. It is then investigated numerically and by means of simulations how $E(T_Q)$ and its approximations depend on the different model parameters.

1. Introduction

Vector borne diseases have a great impact on human health in terms of mortality. Mosquitoes are perhaps the best known disease vectors, with various species playing a role in the transmission of infections such as malaria, yellow fever, dengue fever and West Nile virus. Mathematical modeling of malaria began with Ross's model [1]. The Ross model is deterministic and reflects the basic mechanism that both humans and mosquitoes are necessary for the transmission of infection. Despite its simplicity it has been used to establish an important threshold result and to study the effects of various methods of controlling malaria infection [2–5].

Consider a population in which a vector borne disease is introduced. In the current paper we use stochastic models to answer the question: what might happen? Recurrence of epidemic outbreaks can be explained by the combined influence of epidemic and demographic forces. Stochastic models that account for these two forces in a closed population predict that the infection will eventually become extinct. The time to extinction is an important measure of the persistence of the infection.

Recently, a stochastic model for a vector borne epidemic has been suggested by Llyod et al.[3]. In their model, they have examined the impact of stochastic effects on the invasion and persistence of vector-borne infection. The disease invasion probabilities are derived using branching process methodology. In [6], Bolzoni et al. extended this model to incorporate multiple hosts.

The aim of the present paper is to study the time to extinction for a stochastic model for vector borne diseases. The mathematical problem of determining the time to extinction has proved to be surprisingly difficult (e.g Nåsell [7]) even for human-to-human transmittable disease, and vector borne diseases are more complicated. The basic reproduction number of an infection is the most important concept in mathematical epidemiology, and is important also when studying properties of the extinction time. This quantity, denoted by $\mathcal{R}_0$, can for human-to-human diseases be defined as the expected number of new cases generated by one typical infectious individual in a large susceptible population. For vector borne diseases it is defined similarly, but now this number has to be computed "via" the number of infected vectors. If $\mathcal{R}_0 > 1$, as is assumed in this paper, then we say that the population is above threshold. Introducing an infective to a susceptible community above threshold may, as is well known, lead to a large outbreak. Many of the models that have been employed in vector-borne settings have been deterministic [2,8–11], ignoring the possible importance of random effects. Stochastic effects can be significant during the period immediately after the introduction of the infection into a population [3]: disease invasion is often highly stochastic. Random effects are also the cause leading to extinction from an endemic setting [12]. Deterministic models are hence not of much use when aiming to derive expressions for the time to extinction, because extinction is caused by random fluctuations from the expected (or deterministic) curve.

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The rest of the paper is structured as follows. Section 2 is devoted to a brief review of the deterministic Ross model and the corresponding stochastic formulation. Section 3 is devoted to the law of large numbers of the stochastic epidemic process and Section 4 to its diffusion limit which is the limits of the stochastic models. In Section 5 it is shown that in a finite population the time to extinction is exponentially distributed if the process is started in quasi-stationarity. An approximate expression for τ, the mean parameter of the exponential distribution, is derived in Section 5.3 where we approximate the quasi-stationary distribution by the stationary distribution of the limiting diffusion (e.g Nåsell [7], used the same approach for a different model). In Section 6 we studied the influence of different parameters on the expected time to extinction by using numerical illustrations as well as stochastic simulations.

2. The models

2.1. The deterministic Ross-Macdonald model

The Ross-Macdonald model assumes that each host and vector are, at any point in time, either susceptible to the infection or have the infection and are infectious (incubation periods are hence ignored as well as immunity). The host population size is assumed to be constant and its size is denoted by N_H. The number of hosts that are infectious at time t is written as $I_H(t)$, which means that there are $N_H - I_H(t)$ susceptible hosts. The corresponding fractions of the host population are given by $I_H(t)/N_H$ and $(N_H - I_H(t))/N_H$, respectively.

We write the size of the vector population as N_V and the number of infectious vectors at t as $I_V(t)$. It is assumed that the size of the vector population N_V is constant: the rate at which vectors die balances the rate at which they are born.

Newly born hosts and vectors are taken to be susceptible: it is assumed that no vertical transmission occurs. A susceptible host can acquire infection by being bitten by an infected vector. Assuming that the rate at which a given vector bites hosts is independent of the number of hosts that are present and that the vectors do not have to compete for hosts on which to bite, the overall rate at which bites occur is proportional to the number of vectors but independent of the number of hosts. A single vector is assumed to bite hosts at rate k. The probability of transmission occurring if an infectious vector bites a susceptible host once is denoted by p_{vh}. Once infected, a host remains infectious for an average of $1/\sigma$ time units, after which they recover and become susceptible again. The probability of transmission occurring if a susceptible vector bites an infectious host once is denoted p_{hv}, the per-bite host to vector transmission probability. Once infected, a vector remains infectious until it dies and it is assumed that the infectious vector live for an average of $1/\delta$ time units and that it is replaced by a susceptible vector upon death, thus keeping the vector population constant. The death rate for vectors is the same for infected and susceptible vectors. This leads to the following pair of differential equations:

$$\begin{cases} \dfrac{dI_H}{dt} = kp_{vh}I_V\left(\dfrac{N_H - I_H}{N_H}\right) - \sigma I_H, \\ \dfrac{dI_V}{dt} = kp_{hv}(N_V - I_V)\dfrac{I_H}{N_H} - \delta I_V. \end{cases} \tag{1}$$

The way the model was described the host population satisfies a *SIS* (susceptible-infectious-susceptible) epidemic model while the vector population satisfies a *SI* (susceptible-infectious) epidemic model. Of course this is just a matter of interpretation, hosts have much longer life-length compared to vectors, but since the equations are symmetric, the host and vector could either both be SI, both SIS or one of each, the model only states that the sums of the susceptibles and infectives remain constant.

The basic reproduction number is

$$\mathcal{R}_0 = k^2 p_{hv} p_{vh} N_V / \delta\sigma N_H. \tag{2}$$

We set the derivatives to 0 and then solve them in terms of proportions I_H/N_H and I_V/N_V, thus we obtain two equilibrium states, says, the disease-free state (0, 0) together with the point $(\bar{i}_H, \bar{i}_V)$ given by

$$\bar{i}_H = \frac{\mathcal{R}_0 - 1}{\mathcal{R}_0}\frac{kp_{vh}c_v}{kp_{vh}c_v + \sigma}, \quad \bar{i}_V = \frac{\mathcal{R}_0 - 1}{\mathcal{R}_0}\frac{kp_{hv}}{kp_{hv} + \delta}, \tag{3}$$

where $c_v = N_V/N_H$ denotes the community number of vectors per host. The second state is relevant only if $\mathcal{R}_0 > 1$. The disease-free state is stable for $\mathcal{R}_0 < 1$ and unstable for $\mathcal{R}_0 > 1$, while the point $(\bar{i}_H, \bar{i}_V)$ is stable for $\mathcal{R}_0 > 1$. In other words, if $\mathcal{R}_0 < 1$ the infection is predicted to die out fairly quickly. On the other hand, if $\mathcal{R}_0 > 1$ then it will rise towards a positive infection level, called the endemic level.

2.2. The stochastic Markovian dynamic vector-borne epidemic model

We now define the corresponding Markovian stochastic vector-borne epidemic model. The numbers of hosts and vectors remain constant and are denoted N_H and N_V as before. Each vector bites hosts according to a Poisson process with rate k, each such bite being with a randomly selected host, the times between such bites are hence independent identically distributed according to the exponential distribution with rate k. If the vector is infectious and the host susceptible transmission occurs with probability p_{vh}, and with probability p_{hv} for the opposite scenario (other bites have no effect). A host who gets infected remains so for an exponentially distributed time with rate σ, and then recovers and immediately becomes susceptible again. A vector that gets infected remains infectious for the remainder of its life, and this life length is exponentially distributed with rate parameter δ, just like susceptible vectors. The disease is introduced by having h and v infected hosts and vectors, respectively.

Let

$$I(t) = (I_H(t), I_V(t))$$

denote the process governing the vector borne epidemic. The possible events and their rates are given in Table 1 below. The epidemic model is governed by the bivariate process $I(t) = (I_H(t), I_V(t))$.

3. Law of large numbers for the stochastic vector-borne epidemic

In this section we assume that the populations of hosts and vectors are large. We relabel the numbers of hosts N_H and vectors N_V by $N_H = N$ and $N_V = c_v N$. Further, we relabel $I(t) = (I_H(t), I_V(t))$ by $I^N(t) = (I_H^N(t), I_V^N(t))$. We consider a process $\bar{I}^N(t) = (\bar{I}_H^N(t), \bar{I}_V^N(t)) = (\frac{I_H^N(t)}{N}, \frac{I_V^N(t)}{N})$. We derive a law of large numbers for $\bar{I}^N(t)$ to show that the stochastic process $\bar{I}^N(t)$ converges to a deterministic process $\hat{\bar{i}}(t)$. To obtain a non-trivial limiting deterministic process, we start the proportion process with small positive fractions of infectious hosts and vectors. This leads to $\bar{I}^N(0) = (\bar{I}_H^N(0), \bar{I}_V^N(0)) = (\frac{I_H^N(0)}{N}, \frac{I_V^N(0)}{N}) = (\epsilon_H^N, \epsilon_V^N)$, where $\epsilon_H^N, \epsilon_V^N$ are positive and small. This starting point is arbitrarily chosen and we do not claim that it is exactly here that the stochastic epidemic process will cross when the number of infectives grows in comparison to the population. In what follows, we show that the starting point has negligible effect on the state of the process as long as $(\epsilon_H^N, \epsilon_V^N)$ is close to (0, 0).