



On extinction time of a generalized endemic chain-binomial model



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ABSTRACT

We considered a chain-binomial epidemic model not conferring immunity after infection. Mean field dynamics of the model has been analyzed and conditions for the existence of a stable endemic equilibrium are determined. The behavior of the chain-binomial process is probabilistically linked to the mean field equation. As a result of this link, we were able to show that the mean extinction time of the epidemic increases at least exponentially as the population size grows. We also present simulation results for the process to validate our analytical findings.

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1. Introduction

A chain binomial epidemic model has been developed at the beginning of 20th century by Reed and Frost. The model is widely used in the literature (see for example [1]) and its simplicity stimulated detailed simulation studies [2]. Jacquez [3] criticized the classical formulation of the Reed–Frost model in terms of consistency and reasonability of its assumptions. This critique was initiated by the dimensional analysis of Reed–Frost equation. He followed suggestions of [1] and properly reformulated a more general epidemic model by using probability generating functions of discrete distributions for the number of contacts per person.

Longini [4] modified the classical Reed–Frost process to be able to model diseases such as *gonorrhoea*, *rotavirus*, *meningitis* and *rhinovirus* in which reinfection take place. The model assumes that there is no removed state so that the sum of the number of infected individuals (\mathcal{I}) and of susceptible individuals (\mathcal{R}) in the population remains constant. If the population consists of \mathcal{N} individuals then the transition probabilities are as follows:

$$\begin{aligned} \Pr(\mathcal{I}_{t+1} = x_{t+1} | \mathcal{I}_t = x_t) \\ = \binom{\mathcal{N} - x_t}{x_{t+1}} (1 - q^{x_t})^{x_{t+1}} q^{x_t(\mathcal{N} - x_t - x_{t+1})}. \end{aligned} \quad (1)$$

Here, q is the probability that a susceptible individual escapes from the infection when there is only one infected person in the population. Since this model assumes that there is no immunity against the disease, it may give rise to the existence of an endemic equilibrium. In fact, the mean dynamics of stochastic model (1) has an

endemic equilibrium under the condition that the mean number of contact per person is larger than one (see for example [5]).

While some probabilistic properties of this model has been given in [4], an analytical study on the extinction time of the process remains untouched. The very same problem has been highlighted by Longini [6] as follows:

“An interesting analytical question involves the study of the mean stopping time for the endemic process.”

Mean extinction time of a birth-death type epidemic model has been studied by Kryscio and Lefèvre [7] for large populations and it has been shown that mean extinction time is exponentially increasing in population size. In addition, there are other approaches to study mean absorption times for stochastic population models. For instance, a classical result which applies to all discrete time finite Markov chains regarding mean hitting times is given by Norris [8, Theorem 1.3.5]. In ecology literature, Monte-Carlo simulations are used widely (see e.g. [9,10]) due to easiness of implementation. A different approach to obtain analytical results concerning mean extinction times is to write down the master equations and solve them numerically [11,12]. Lastly, diffusion approximations are used in the literature to derive a formula for mean time to extinction [13,14].

We modify the model proposed by Jacquez [3] for infectious diseases not conferring immunity following infection as done by Longini [6] and study extinction times analytically. To be able to work on this problem, we use an unconventional method, namely deterministic approximations. For chain binomial models, deterministic approximations have been studied by Weiß and Pollett [15] and Buckley and Pollett [16] as limit theorems. Thus these approximations are valid only for large population sizes. Here we find exponential bounds (decreasing in population size) on

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deviation probability of trajectories of chain-binomial Markov chain and its deterministic approximation. Thus we are able to construct a bridge between stochastic model and its mean dynamics which is valid for any population size. Similar results for continuous time and discrete time birth-death type Markov chains has been obtained by Darling and Norris [17] and Benaïm and Weibull [18].

The mean dynamic of the model helps us to determine whether there is an endemic equilibrium. Here we are interested in finding a lower bound on the extinction time of infection in a generalized chain binomial epidemic model when there exists an endemic equilibrium. Using large deviation bounds and properties of deterministic mean dynamics, we will show that one can find an exponentially increasing lower bound on the mean absorption time of the stochastic model.

The paper is organized as follows. We begin by detailing our stochastic model and its mean dynamics in Section 2. In Section 3, we give some useful results concerning the deterministic mean dynamics. In Section 4, we obtain large deviation bounds and use this result to find a lower bound on mean extinction time when the process is endemic. In this section, we also present some simulation results verifying our theoretical findings. Section 5 summarizes our conclusions.

2. Stochastic model and its deterministic counterpart

Given a contact of a susceptible in period t , the probability that it is with an infective is $i_t = I_t / (N - 1)$ where I_t denotes the number of infectives in a population of size N . If an individual makes k contacts in one time step then the probability that none of these contacts is with infectives is $(1 - i_t)^k$. Therefore the probability that at least one of the contacts is with an infective is $1 - (1 - i_t)^k$. More generally, the probability that no effective contact with susceptibles can be taken as a function of $1 - i_t$. To define the function we follow the method suggested by [1] i.e. we assume that this function is a probability generating function of a discrete distribution and has the following form:

$$f(x) = \sum_{k=0}^{\infty} p_k x^k \tag{2}$$

where p_k is the probability that a susceptible makes k contacts during a time interval. Thus in our model the rate of contact depends on the frequency of infectives. In other words, the per capita force of infection increases with the ‘frequency’ of infectives. Thus this model has a frequency dependent transmission term as described by [19]. For density dependent models, in contrast, per capita force of infection increases not only with the number of infectives but also with the population size in an area occupied by the population. Hence, one can easily observe that the classical endemic chain-binomial model proposed by Longini [4] has a density dependent transmission term (see Example E1 below or [3]).

We consider a model not conferring immunity following infection as done by Longini [4]. Hence, we assume that all infected individuals I_t at time t will return to susceptible class at time $t + 1$. In this case, there is no removed state so that $S_t + I_t = N$ for any $N \in \mathbb{N}$. Therefore the number of new infectives at time $t + 1$ is determined by the following conditional probability distribution:

$$\begin{aligned} &Pr(I_{t+1} = x_{t+1} | I_t = x_t) \\ &= \binom{N - x_t}{x_{t+1}} (1 - f(1 - i_t))^{x_{t+1}} (f(1 - i_t))^{N - x_t - x_{t+1}}. \end{aligned} \tag{3}$$

Clearly the mean dynamics for I_t is given by

$$E(I_{t+1} | I_t) = (N - I_t)(1 - f(1 - i_t)).$$

To be able to obtain a scaled difference equation, divide both sides by $N - 1$. Then we get the following logistic equation:

$$i_{t+1} = (a_N - i_t)(1 - f(1 - i_t)) =: g(i) \tag{4}$$

where $a_N = N / (N - 1)$ denotes the carrying capacity as a function of population size N . Note that the sequence $a_N \in (1, \frac{3}{2})$ for $N \geq 3$.

We would like to catalog Eq. (4) for different discrete distributions of the number of contacts. We consider two examples of discrete distributions as follows.

E1 Poisson distribution: Suppose that the number of contacts has a Poisson distribution with mean μ_p . In this case, the probability generating function of this distribution is given by

$$f_p(s) = \exp(-\mu_p(1 - s)).$$

Hence, one can write Eq. (4) as follows:

$$i_{t+1} = (a_N - i_t)(1 - \exp(-\mu_p i_t)).$$

Note that above equation takes the form of the logistic epidemic model studied by Cooke et al. [5] as $N \rightarrow \infty$. In addition there are some similarities to the endemic Reed–Frost model studied by Longini [4]. However, one can easily observe that the Reed–Frost parameter should be taken as $q = \exp(-N\mu_p)$. Hence this parameter is not dimensionless as pointed out by Jacquez [3].

E2 Binomial distribution: Since Poisson distribution is defined on positive integers and zero, it allows unbounded number of contacts. Hence we consider the binomial distribution as an example of distributions defined on bounded intervals. Suppose we divide the infectious period into n equal sub-intervals. Suppose also that in each sub-interval only one contact occurs between people. Let p be the probability of contact in one sub-interval and assume Bernoulli trials. Then the number of contacts follow a binomial distribution with mean $\mu_b = np$ then the probability generating function is given by

$$f_b(s) = (ps + q)^n$$

where $q = 1 - p$. Thus Eq. (4) can be written as

$$i_{t+1} = (a_N - i_t)(1 - (1 - pi)^n).$$

Here we would like to note that other discrete distributions such as geometric distribution can also be considered as done by Jacquez [3] or Ng and Orav [20]. Note also that probability generating functions of these distributions are sufficiently smooth.

Before proceeding to the next section we state our standing assumptions as follows:

Assumption 1.

- There are at least three people in the population i.e. $N \in \mathbb{N}_3 = \mathbb{N} \setminus \{1, 2\}$.
- A random variable with probability generating function f has its first and second moments.

3. Behavior of the deterministic model

We begin this section by defining the basic reproductive number μ as follows:

$$\mu = f'(1).$$

The mean number of contacts for stochastic model (3) is equal to the reproductive number for deterministic model.

The following result determines the effect of the basic reproductive number μ and the population size N on the global stability of the deterministic Eq. (4)

Theorem 2. *The following statements hold for any initial condition $i_0 \in (0, 1)$.*

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