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 gonorrhea, 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 (I) and of susceptible individuals (R) in the population remains constant. If the population consists of N individuals then the transition probabilities are as follows:

\[
Pr(I_{t+1} = x_{t+1} | I_t = x_t) = \binom{N - x_t}{x_{t+1}} (1 - q^h)^{N-x_t-q^h} q^h^{x_{t+1}}.
\]

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
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 Benaim 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 \( t = t_i/(N - 1) \) where \( t_i \) 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 \((1 - t_i)^k\). Therefore the probability that at least one of the contacts is with an infective is \(1 - (1 - t_i)^k\). More generally, the probability that no effective contact with susceptibles can be taken as a function of \( 1 - t_i \). 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:

\[
    f(x) = \sum_{k=0}^{\infty} p_k x^k
\]

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 encyclical 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 \( t_i \) at time \( t \) will return to susceptible class at time \( t + 1 \). In this case, there is no removed state so that \( S_k + I_{t+1} = N \) for any \( N \in \mathbb{N} \). Therefore the number of new infectives at time \( t + 1 \) is determined by the following conditional probability distribution:

\[
    Pr(t_{i+1} = x_{i+1} | h_i = x_i) = \binom{N - x_i}{x_i} \frac{(1 - f(1 - t_i))^{x_i}}{x_{i+1}} (f(1 - t_i))^{N - x_i - x_{i+1}}
\]

Clearly the mean dynamics for \( t_i \) is given by

\[
    E(t_{i+1} | h_i) = (N - t_i)(1 - f(1 - t_i)).
\]

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

\[
    \dot{h}_{i+1} = (a_N - h_i)(1 - f(1 - h_i)) = g(t)
\]

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 \( \mu \). In this case, the probability generating function of this distribution is given by

\[
    f_P(s) = \exp(-\mu(1 - s)).
\]

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

\[
    \dot{h}_{i+1} = (a_N - h_i)(1 - \exp(-\mu p_i)).
\]

Note that above equation takes the form of the logistic epidemic model studied by Cooke et al. [5] as \( N \to \infty \). 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

\[
    \dot{h}_{i+1} = (a_N - h_i)(1 - p^i)^n.
\]

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. \( N \in \mathbb{N} \setminus \{1, 2\} \).
- 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 \( \mu \) 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 \( \mu \) and the population size \( N \) on the global stability of the deterministic Eq. (4).

**Theorem 2.** The following statements hold for any initial condition \( i_0 \) \( \in (0, 1) \).
Since \( f(x) \geq 0 \) for any \( x \in [0, 1] \), it is easy to see that this equilibrium point stays at \( (\frac{a_N}{a_N - 1}, \frac{1}{a_N}) \). By definition of the endemic equilibrium, it is easy to conclude that \( g(i) < i \) at \( (i_e, 1) \) and \( g(i) > i \) at \( (0, i_e) \). This implies the nonexistence of two-periodic solutions and thus the global stability of \( i_e \) by Cull [21]. □

Above given global stability result implies that set \( (0, 1) \) is the basin of attraction for the map \( g \) i.e. \( \lim_{t \to \infty} \hat{g}^t(i_0) = i_e \) for any \( i_0 \in (0, 1) \).

Lemma 3.

(i) \( \rho = \max \{a_N \mu_{-1} + p_0 + (a_N - 1) p_1 \} \) is the Lipschitz constant of the map \( g \).

(ii) If \( a_{0i} \mu > 1 \) then there exists an interval \( I = [a, 1) \subset (0, 1) \) containing the stable fixed point \( i_e \) on which \( g \) is a contraction mapping.

(iii) If \( a_{0i} \mu > 1 \) then there exists an \( \epsilon > 0 \) for which \( g([i_e - \varepsilon, i_e + \varepsilon]) \subset [i_e - x + \varepsilon, i_e + x - \varepsilon] \) for any \( 0 < x < \min(i_e, 1 - i_e) \).

Proof. (i) By (6), it is easy to observe that \( g' \) is a decreasing function of its argument. Hence one can calculate its minimum and maximum values as \( -1 + p_0 + (a_N - 1) p_1 \) and \( a_{0i} \mu \), respectively. This implies that \( |g'(i)| \leq \rho \) for all \( i \in [0, 1] \).

(ii) In the proof of Theorem 2, we showed that \( g(i) > i \) for \( i < i_e \). By the mean value theorem, for any \( \delta \in (0, i_e) \), there exists an \( i_e \in (i_e - \delta, i_e) \) such that

\[
g(i_e - \delta) = i_e - \delta g'(i_e) > i_e - \delta.
\]

This implies that \( g(i_e) < 1 \) for some \( i_e < i_e \). In addition \( g(i) \) decreases in \( i \). Thus we get

\[ -1 < -1 + (a_N - 1) p_1 < g'(i) < 1 \]

for any \( i \in (i_e, 1) \). This implies the existence of an interval \( i_e \in [0, 1] \) on which \( g \) is a contraction.

(iii) Observe that if \( g \) is a contraction mapping on \([i_e, \infty) \) then \( g([i_e - x, i_e - x + \varepsilon]) \subset [i_e - x + \varepsilon, i_e + x - \varepsilon] \). Unless \( g \) is a contraction mapping on the same set then \( g'(y) > 1 \) for some \( y < i_e - x \). By mean value theorem, there exists a \( \gamma \in (0, i_e - x) \) such that \( g'(\gamma) = g'(y)(\gamma - x) > 1 \).

In addition \( g([i_e - x, i_e + x]) \subset (a_N - i_e + x)(1 - f(1 - i_e)) \subset (i_e + x) \). Similarly one can show that \( i_e - x < g(i + x) < i_e + x \). Hence one can find such an \( \varepsilon > 0 \) and thus this completes the proof. □

Above given result gives information about the behavior of our map \( g \) and will be used in the next section to prove our main result.

4. Analysis of the stochastic model

We begin with the following basic result which is a uniform large deviations bound on the parameter \( p \) for the family of binomial random variables \( \text{BIN}(M, p) \).

Proposition 4. For \( M \in \mathbb{N} \) and a real \( p \in [0, 1] \), let \( X \) denote a binomial random variable with the distribution \( \text{BIN}(M, p) \). Then for any constant \( \eta > 0 \),

\[
\Pr(|X - E[X]| > \eta) < 2 \exp\left(-\frac{\eta^2}{2M}\right).
\]

Above given proposition is an easy consequence of a Azuma-Hoeffding inequality given in [22, Theorem 2.17].

4.1. Deterministic approximations and mean time to extinction

In this section, we present our main results concerning deterministic approximation to stochastic model and the mean extinction time. Before proceeding to these results, we define the maximal deviation for bounded time as follows:

\[
D^N(T, i_0) = \max_{0 \leq t \leq T} |i^t - i_0|
\]

and give the following result regarding this stochastic variable.

Theorem 5. Suppose that \( i_0 < N \). For any \( \varepsilon > 0, N \in \mathbb{N} \) and \( T \in \mathbb{N} \)

\[
\Pr(D^N(T, i_0) > \varepsilon | i_0^n = i_0) \leq 2T \exp\left(-\frac{\varepsilon^2 c_T^2}{3(N - 1)}\right)
\]

where \( c_T = (1 - \rho)/(1 - \rho^T) \).

In particular, if \( \rho < 1 \) we have
\[ Pr(D_N^N(T, i_0) > \varepsilon | i_0^N = i_0) \leq 2T \exp \left( -\frac{-\varepsilon^2 (1 - \rho)^2}{3} (N - 1) \right). \] (9)

**Proof.** We have
\[
|n_{k+1} - i_{k+1}| = |n_{k+1} - g(i_k^N) + g(i_k^N) - g(i_k^N)| \\
\leq |n_{k+1} - g(i_k^N)| + |g(i_k^N) - g(i_k^N)| \\
\leq |n_{k+1} - g(i_k^N)| + \rho |i_k^N - i_k^N|.
\]

Define the martingale sequence \( U_k^N := n_{k+1} - g(i_k^N) \). Iterating the last inequality we obtain that
\[
|n_m^N - i_m^N| \leq \sum_{k=0}^{m-1} \rho^{m-k} |U_k^N| \leq \rho m \max_{0 \leq m < m-1} |U_k^N| (10)
\]
where \( \rho m \leq (1 - \rho m - 1)/(1 - \rho) \). Taking the maximum of both sides in (10), one obtains:
\[
Pr(\max_{1 \leq m \leq T} |U_m^N - i_m^N| > \varepsilon) \leq Pr(\max_{0 \leq k \leq T - 1} |U_k^N| > \varepsilon \cdot \varepsilon) \\
\leq \sum_{k=0}^{T-1} Pr(|U_k| > \varepsilon \cdot \varepsilon) \\
= \sum_{k=1}^{T} Pr(|U_k| > \varepsilon \cdot \varepsilon | U_{k-1}) > \varepsilon \cdot \varepsilon) \cdot T - 1).
\]

The last equality is obtained by multiplying both sides of inequality \( |U_m^N| > \varepsilon \cdot \varepsilon \) by \( N - 1 \).

Consider the Markov transition probabilities given by (3). One can easily observe that at time \( t \), the number of infected individuals \( I_t \) given \( i_{t-1} \) is a binomial random variable with the distribution \( Bin(N - i_{t-1}, 1 - f(i_{t-1})) \). Hence, one can use the bound given in Proposition 4 with \( \varepsilon = \varepsilon (N - 1) \) and \( M \leq N \). Note that this bound holds uniformly over \( i_{t-1} = 0, 1, \ldots, N - 1 \). As a result, one can get the following inequality:
\[
Pr\left( \max_{1 \leq m \leq T} |U_m^N - i_m^N| > \varepsilon \right) \leq 2T \exp \left( -\frac{-\varepsilon^2 c_2^2 (N - 1)^2}{2N} \right).
\]
By replacing \( (N - 1)/N \) by 2/3, one can get inequality (8). Now observe that the constant \( c_2 \) used in (10) can be taken as 1 if \( \rho < 1 \). Hence, (9) can be obtained as a consequence of (8). This completes the proof of the theorem. □

Note that this result gives an exponential bound on the probability of deviation for any population size \( N \geq 3 \). Deterministic limits of chain binomial models have been studied by Buckley and Pollett [16] as population size goes to infinity. Since Theorem 5 is valid for small populations, it can be used to find lower bounds on mean extinction time of infectives for any population size \( N \geq 3 \).

To be able to prove our main result, we define the exit times from subsets of \( U \) following [18]. For a Borel subset \( U \subset (0, 1) \) and an integer \( N \in \mathbb{N}_3 \), we denote
\[
T^N_U := \inf\{ t \geq 0 : x^N \notin U \}.
\]
Here \( T^N_U \) is the exit time of the Markov chain \( x^N \) from the set \( U \). Note that only absorbing state of the Markov chain is 0. Here we take \( U = [i_0 - \varepsilon, i_0 + \varepsilon] \subset (0, 1) \) for any \( 0 < \varepsilon < \max_{i_0, 1 - i_0} \).

Denote the mean exit time from set \( U \) and the mean absorption time by \( T^N_U \) and \( \tau^N_0 \), respectively. Then we state our result concerning the mean absorption time. Note that the proof of the following theorem is a modification of a similar result given by Benaim and Weibull [18, Lemma 4.4] for discrete time birth-death chains.

**Theorem 6.** Suppose that \( a_{N, u} > 1, N \in \mathbb{N}_3 \) and \( i_0^N \in U \). Then we have
\[
\tau^N_0 \geq \rho^{\theta^N_N} \]
for some \( \theta > 1 \) and \( p > 0 \).

**Proof.** Recall from item (iii) of Lemma 3 that there exists a constant \( \varepsilon > 0 \) such that \( g(U) \subset U \), where \( U = [i_0 - \varepsilon, i_0 + \varepsilon, i_0 - \varepsilon] \subset (0, 1) \) with \( i_0 \in U \). Consider the following stochastic quantity
\[
D_t = \max_{0 \leq k < t} D^N(1, \nu^N_k).
\]
Suppose that \( D_t < \varepsilon \). Observe that \( i_0^N \in U \) implies that \( g(i_0^N) \in U \), and thus \( i_0^N \in U \). By induction, it is easy to see that \( i_0^N \in U \) for any \( k \in \{0, 1, \ldots, t\} \). Therefore, \( D_t \leq \varepsilon \) implies \( T^N_U > t \).

Hence, one can easily obtain the following relationship:
\[
Pr(T^N_U > t) \leq Pr(D_t < \varepsilon).
\]

Consider right hand side of inequality (12) and observe that
\[
Pr(D_t < \varepsilon) \leq \sum_{k=0}^{t-1} Pr(D^N(1, \nu^N_k) < \varepsilon) \leq \sum_{k=1}^{T} E(Pr(D^N(1, \nu^N_k) < \varepsilon | \nu^N_k)) \leq 2t \theta^{-\gamma (N-1)}.
\]

By integrating the tail method for non-negative random variables and by using inequalities (12) and (13), one can get:
\[
E[T^N_U] = \sum_{k=0}^{\infty} Pr(T^N_U > k) \geq \sum_{k=0}^{\infty} \max\{0, 1 - 2k \theta^{-\gamma (N-1)}\}
\]
\[
\geq \sum_{k=0}^{\infty} (1 - 2k \theta^{-\gamma (N-1)})
\]
\[
= (v + 1)(1 - v \theta^{-\gamma (N-1)})
\]
for any \( v \in \mathbb{N} \). Now choose \( v = \lfloor \rho^{\theta^N_N} \rfloor \). Hence, one can get
\[
T^N_U \geq \rho^{\theta^N_N} \]
by replacing \( v \) and \( v + 1 \) by \( \rho^{\theta^N_N} \) in inequality (14). Choosing \( p = (\theta) \gamma^{-1} \) and recalling the fact that \( U \subset (0, 1) \) complete the proof. □

**Theorem 6** proves that the mean extinction time increases exponentially as the population size increases. We would like to note that the result regarding the mean extinction time of a birth-death type process obtained by Kryscio and Lefèvre [7] is valid for any large initial condition and as population size goes to infinity. Here our results are valid for initial conditions \( i_0 \in U \) as described above. However, for large populations, one can easily see that stochastic process (3) remains close to difference Eq. (4) and enters to the set \( U \) by the limit theorem given in [16] or Theorem 5. Thus one can drop this assumption as population size goes to infinity.

4.2. Numerical validation of the analytical result

In previous subsection, we obtained a lower bound on the mean extinction time. One can numerically examine the behavior of \( \gamma^N_U \) by using Theorem 1.3.5 of [8]. Denote the mean hitting times to 0 with initial condition \( i_0 = i \) by \( \gamma^N_U(i) \) for \( i = 0, 1, \ldots, N-1 \). Then \( \gamma^N_U(0) = 0 \) and
\[
\gamma^N_U(i) = 1 + \sum_{j=1}^{N-1} \gamma^N_U(j)
\]
for \( i = 1, 2, \ldots, N-1 \). We define the transition probabilities by


We also would like to note that our method can also be applied to Longini's chain-binomial model (1) and one can show that the mean time to extinction increases exponentially in population size. His simulation results regarding the mean extinction time of the process (1) are given in [4] and imply at least quadratic increase in population size $N$.

Lastly, the method presented in this paper can be extended to other chain-binomial or chain-multinomial processes. Examples of such processes modeling HIV epidemic are discussed in [23, p. 89–92].

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