

Approximation for Collective Epidemic Model

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Abstract

The collective epidemic model is a quite flexible that describes the spread of an infectious disease of the Susceptible-Infected-Removed type in a closed population. In the present paper a necessary and sufficient condition is derived that generates the weak convergence of the law of this variable to a mixed poisson distribution when the initial susceptible population tends to infinity provided that the out break is severe in a certain sense.

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Introduction

In the mathematical theory of epidemics, an important class of models is concerned with infectious disease of the S(Susceptible)-I(Infected)-R(removed) type. A closed population contains initially n susceptible individuals and m infected individuals. All the infective initial or subsequent are supposed to behave independently. Each of them stays infectious during a certain period of time of random length. After that period it is immune in a permanent way and may thus be regarded as removed from the infectious process. While infected an individual is able to transmit the infection to others. A susceptible if ever contacted by an infective is infected and becomes immediately infectious.

Consider any fixed subject of k susceptible among the n initial ones $1 \leq k \leq n$. It is assumed that any fixed infective does not transmit the infection during its whole infectious period within such a group of k susceptible with a probability $q(k)$ that depends only on the size k of the group (and possibly on n). These $q(k)$'s are fixed and constitute the n parameters of the model.

The collective epidemic terminates at some finite time A as soon as there are no more infective present in the population. Then the ultimate number of susceptible surviving the disease denoted by $S(A)$ say. For simple infection the parameters $q(k)$ can be written as functions of a small number of epidemic components. Any given pair of individuals is now assumed to make contacts at the points of a Poisson process with rate β all these processes being independent. Moreover any infective infectious during a period of random length D_i all the D_i 's being i.i.d and distributed as the variable D say.

We then get

$$q(k) = E[\exp(-k\beta D)], \quad 1 \leq k \leq n$$

In particular the so called general epidemic corresponds to the special case where D is exponentially distributed with parameter μ , here thus $q(k) = \mu / (\mu + k\beta)$. Moreover as long as $S(A)$ is concerned the model covers another standard model known as the Reed-Frost epidemic which is obtained by

Supposing that D is equal to some constant d ; this yields

$$q(k) = q^k \text{ with } q = \exp(-\beta d).$$

For the collective model the exact distribution of $S(A)$ was obtained and studied by Picard and Lefevre(1990). Martin-Lof(1986) established the existence of a threshold phenomenon together with a branching or Gaussian limit approximation. The problem examined in the present paper is the alternative approximation of $S(A)$ by a mixed Poisson law.

Also Daniels(1967) showed for the general epidemic under some conditions $S(A)$ can have a Poisson-like behavior. Later Ball and Barbour(1990) applied the Stein-Chen methodology to derive a Poisson approximation with an order of magnitude for the model of Martin-Lof(1986). Recently Lefevre and Utev(1995) obtained a necessary and sufficient condition that guarantees the validity of such a Poisson limit for the generalized epidemic. Our purpose here is to go further in this subject by deriving now a mixed Poisson approximation for the final state of the collective epidemic.

Branching process

Definition1

Let the random variables $x_0, x_1, x_2, \dots, x_n \dots$ denote the size of (or the number of objects in) the $0^{th}, 1^{st}, 2^{nd} \dots$ generation respectively. Let the probability that an object (irrespective of the generation to which it belongs) generates k similar objects be denoted by p_k where $p_k \geq 0, k = 0, 1, 2, 3, \dots$ $\sum p_k = 1$.

The sequence $\{x_n, n = 0, 1, 2, 3, \dots\}$ constitutes a Galton-Watson branching process with offspring distribution $\{p_k\}$.

Properties of generating functions of Branching process.

We have

$$x_{n+1} = \sum_{r=1}^{x_n} \zeta_r \text{ where } \zeta_r \text{ are i.i.d variables with distribution } \{p_k\}.$$

Let $P(s) = \sum_k \Pr\{\zeta_r = k\}S^k = \sum_k P_k S^k$ be the p.g.f of $\{\zeta_r\}$ and let

$$P_n(s) = \sum_k \Pr\{X_n = k\}s^k, n = 0, 1, 2, \dots \text{ be the p.g.f of } \{x_n\}.$$

We assume that $x_0 = 1$, clearly $P_0(s) = S$ and $P_1(s) = P(s)$.

We start by associating with the collective epidemic an equivalent model of branching type. By equivalent we mean that the final susceptible state $S_n(\infty)$ can be obtained as the first-crossing level of some decreasing branching model in a linearly decreasing barrier.

Let $\{z_{n,1}, z_{n,2}, \dots, z_{n,n}\}$ be a family of n exchangeable Bernoulli random variables with parameters $q_n(k), 1 \leq k \leq n$. For $t=1, 2, 3, \dots$ Let $\{z_{n,1}(t), \dots, z_{n,n}(t)\}$ be i.i.d copies of that family.

The Markov Chain $\{x_n(t), t \geq 0\}$ defined by $x_n(0) = n$ and $x_n(t) = \sum_{i=1}^{x_n(t-1)} z_{n,i}(t), t \geq 1$.

This chain is decreasing overtime. Its transient distribution is given below.

Lemma1

For each $t \geq 1$

$$E \binom{x_n(t)}{K} = \binom{n}{k} [q_n(t)]^t, 1 \leq k \leq n$$

ie $x_n(t)$ is distributed as the sum of n exchangeable Bernoulli random variables with parameters $[q_n(k)]^t, 1 \leq k \leq n$.

Proof

Let $z_{n,i}^{(j)}$ denote the indicator of the event (susceptible i escapes infection from infective j during the epidemic spread). From the definition of the model we see that each vector $\{z_{n,1}^{(j)}, \dots, z_{n,n}^{(j)}\}$ is a family of n exchangeable Bernoulli random variables and all the vectors are i.i.d copies of the family $\{z_{n,1}, \dots, z_{n,n}\}$ say with $q_n(k) = P(z_{n,1} = z_{n,2} = \dots = z_{n,k} = 1), 1 \leq k \leq n \rightarrow (1)$

At this point we emphasize that the probabilities (1) corresponds to the parameters usually introduced when constructing the joint law of n exchangeable Bernoulli random variables $\{z_{n,1}, \dots, z_{n,n}\}$. In particular consider the partial sums $x_{n,u} = z_{n,1} + \dots + z_{n,u} 1 \leq u \leq n$. We have the distribution $x_{n,u}$ when specified by its

binomial moments is given by $E \binom{x_{n,u}}{k} = \binom{u}{k} q_n(k) 1 \leq k \leq u$. Hence for $t=1$ the

statement of lemma is true. For $t \geq 2$ we obtain that

$$E \binom{X_n(t)}{k} = E \left\{ E \binom{X_n(t)}{k} / X_n(t-1) \right\} = E \binom{X_n(t-1)}{k} q_n(k)$$

Which leads to the proof of the lemma by induction.

To make the link with the epidemic model consider the decreasing line $n + m_n - 1$ and let T_n be the first time when the branching model crosses the line

$$T_n = \inf \{ t \geq 0 : x_n(t) \geq n + m_n - t \}$$

Clearly $1 \leq T_n \leq n + m_n$.

Proposition 1

The process $\{x_n(t), t \geq 0\}$ is a decreasing Markov chain with

$$X_n(t) =_d MB(n, \prod_{s=1}^t Q_n, s), t \geq 1 \quad \rightarrow (2)$$

At time T_n , the state $X_n(T_n)$ has the same law as the variable $s_n(\infty)$ which is provided by the following n relation

$$E \left\{ \binom{X_n(T_n)}{k} / [E(Q_n^k)]^{n+m_n-X_n(T_n)} \right\} = \binom{n}{k} \quad 1 \leq k \leq n \quad \rightarrow (3)$$

Proof

The first assertion is obvious from

$$X_n(t) = \sum_{i=1}^{X_n(t-1)} Z_{n,i^{(t)}}, t \geq 1$$

The law (2) for $X_n(t)$ is obtained from

$$X_n(t) =_d MB(X_n(t-1), Q_{n,t}), t \geq 1 \text{ by induction and well known fact that}$$

$MB(B(l, u), v) =_d B(l, uv)$ from (2) we get $1 \leq k \leq n$ that

$$E \left[\binom{X_n(t)}{k} \right] = \binom{n}{k} [E(Q_n^k)]^t, t \geq 0$$

Which shows that the process

$$\left\{ \binom{X_n(t)}{k} [E(Q_n^k)]^{-t}, t \geq 0 \right\}$$

Forms a martingale.

Now from

$$T_n = \inf \{ t : t + X_n(t) = n + m_n \}$$

T_n is a Markov time and applying the optional stopping theorem that yields the n relation (3).

These constitutes a triangular set of n linear equations in the n ultimate state probabilities $P[S_n(T_n) = k]$, $1 \leq k \leq n$. The probability for $k=0$ follows. Finally we

note that the system (3) is identical with n relation providing the law of $S_n(\infty)$.

This leads to the following proposition.

Proposition 2

The branching model intersects the barrier at T_n . That is $X_n(T_n) = n + m_n - T_n \rightarrow (4)$

Furthermore $X_n(T_n)$ has the same distribution as $S_n(\infty)$ which is provided by n relation

$$E \left\{ \binom{S_n(\infty)}{k} / [q_n(k)]^{n+m_n-S_n(\infty)} \right\} = \binom{n}{k}, 1 \leq k \leq n$$

This representation has a simple interpretation.

Returning to the epidemic model we make a change of time scale and we define a new artificial time $t=1, 2, \dots$ as the cumulative number of removals in the course of real time.

Put $X_n(0) = n$ and let $X_n(t), t \geq 1$ denote the number of individuals that escape infection contacts with the first t infective removed. Moreover put $I_n(0) = m_n$ and let $I_n(t), t \geq 1$ be the number of infected individuals still present after the t^{th} removal. By construction $t + X_n(t) + I_n(t) = n + m_n$. Thus the first time when there are no more infective present in the population is quite identical with T_n and (4) does not hold true. We then feel intuitively that $X_n(T_n)$ and $S_n(\infty)$ are equidistributed.

Conclusion

Hence we conclude that $X_n(T_n)$ does satisfy a Poisson Limit Theorem.

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