

Stochastic Epidemic and its Asymptotic Distribution

Dr. Muthuramakrishnan

*Associate Professor of Mathematics, National College,
Trichirappalli, Tamil Nadu, India.*

Mr. A. Martin

*Assistant Professor of Mathematics, Avvaiyar Government College for Women,
Karaikal, Puducherry U.T, India.*

Abstract

This paper examines in detail about SIR epidemic Model and its properties. Suppose one or (more) infected person is introduced in to a community of individuals more or less susceptible to the disease. The disease spreads from the affected to the unaffected by contact infection. Each infected person runs through the course of his sickness and finally is removed from the number of those who are sick by recovery or by death. As the epidemic spreads the number of unaffected members of the community becomes reduced. Suppose the number of persons who escape infection tends to large (infinity) the total number of persons who escapes infection converges in distribution to a poisson random variable with mean b where $0 < b < \infty$. The stochastic process of the above type shows that when the threshold is large but the population is much larger the distribution of the remaining uninfected in a large epidemic has approximately the poisson form.

Keywords: Threshold, poisson form, SIR.

Introduction:

The early work on the mathematical theory of epidemics was invariably of a deterministic nature and assured that for given number of susceptible and infections individuals and given attack and removal rates, a certain definite number of fresh cases would occur in any specified time. However it is widely realized than an appreciable element of chance enters into the conditions under which new infections or removals take place.

Deterministic Treatment

Let us first glance at the results obtained in the deterministic case. The following treatment, with constant infection and removal rates is substantially that given by Kermack and Mckendrick though with some slight alterations to their notation.

Let us consider a homogeneously mixing community of n individuals of whom at time t there are x susceptible, y infectious cases in circulation and z individuals who are isolated, dead or recovered and immune.

Thus we have $x + y + z = n$.

Now suppose that there is a constant infection rate β and constant removal rate so that the number of new infections in time dt is $\beta xydt$ and the number of removals from circulation is γydt . Let us choose our time scale so that t is replaced by βt . Then it is easy to see that the course of the epidemic is represented by the differential equations.

$$\left. \begin{aligned} dx/dt &= -xy \\ dy/dt &= xy - \rho y \\ dz/dt &= \rho y \end{aligned} \right\} \quad (1)$$

Where $\rho = \gamma / \beta$ the ratio of the removal to infection rate initially when $t = 0$. we can assume that x is approximately equal to n . It is then clear from (1) that epidemic can start to build up as this requires $(dy/dt)_{t=0} > 0$. Kermack and Mckendrick obtained an approximate solution to (1) for epidemics of small magnitude and showed that if $\rho = n - v$ where v is small compared with n , an epidemic of total size $2v$ will occur. This constitutes the Kermack and Mckendrick's Threshold Theorem.

Stochastic Treatment :

Let us use the same definitions of x, y and z and shall replace t by βt as before. Then on the assumption of homogeneous mixing of the susceptible and infectious individuals in circulation the Probability of one new infection taking place in time dt is $xydt$, while the probability of one infected person being removed from circulation in time dt is ρydt . Let $P_{rs(t)}$ be the probability that at time t there are r susceptible still uninfected and s infectious individuals in circulation.

Let us assume that the epidemic is started by the introduction of a infectious cases into a population of n susceptible. It is now easy to show by the usual methods that the whole process can be characterized by the partial differential equation for the probability generating function π :

$$\frac{\partial \Pi}{\partial t} = (v^2 - uv) \frac{\partial^2 \Pi}{\partial u \partial v} + \rho(1-v) \frac{\partial \Pi}{\partial v} \quad (2)$$

$$\text{where } \Pi = \sum_{r,s} u^r v^s p_{rs} \quad (3)$$

$$\text{with limits } 0 \leq r+s \leq n+a, 0 \leq r \leq n, 0 \leq s \leq n+a \quad (4)$$

Equation (2) is substantially that given by Bartlett putting his immigration rate equal to zero.

Let us now use the Laplace transform and its inverse with respect to time given by

$$\phi^*(\lambda) = \int_0^{\infty} e^{-\lambda t} \phi(t) dt$$

$$\phi(t) = \frac{1}{2\pi i} \int_{c-i\infty}^{c+i\infty} e^{\lambda t} \phi^*(\lambda) d\lambda \quad R(\lambda) > 0 \quad (5)$$

where

$$\int_{c-i\infty}^{c+i\infty} \equiv \lim_{w \rightarrow \infty} \int_{w-i\infty}^{w+i\infty} \quad \text{and } c \text{ is positive and greater than the abscissa}$$

of all the residues.

Taking transforms of (2) and (3), and using the boundary condition

$$P_{na}(0) = 1 \quad (6)$$

We obtain

$$(v^2 - uv) \frac{\partial^2 \Pi^*}{\partial u \partial v} + \rho(1-v) \frac{\partial \Pi^*}{\partial v} - \lambda \Pi^* + u^n v^a = 0 \quad (7)$$

$$\text{and } \Pi^* = \sum_{r,s} u^r v^s p_{rs}^* = \sum_{r,s} u^r v^s q_{rs} \quad (8)$$

$$\text{where } q_{r,s}^* = p_{r,s}^* = \int_0^{\infty} e^{-\lambda t} p_{r,s}(t) dt \quad (9)$$

Substituting (8) in (7) and equating coefficients of $u^r v^s$, yields fields the recurrence relations

$$(r+1)(s-1)q_{r+1,s-1} - \{s(r+\rho) + \lambda\} q_{rs} + \rho(s+1)q_{r,s+1} = 0$$

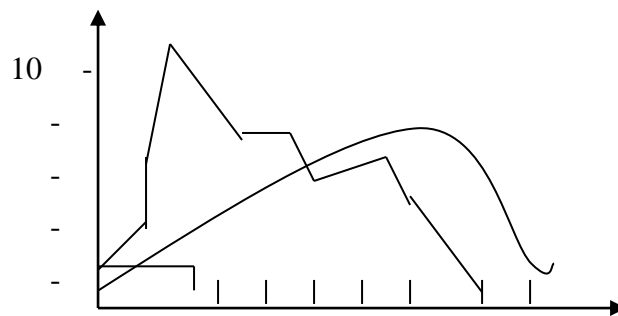
and $-\{a(n+\rho) + \lambda\} q_{na} + 1 = 0 \quad (10)$

with $0 \leq r+s \leq n+a, 0 \leq r \leq n, 0 \leq s \leq n+s$

Any q_{rs} whose suffix falls outside the prescribed ranges is taken to be identically zero.

David G. Kendall in his paper deterministic and stochastic epidemics in closed populations finds that when $m > \rho$ that the sample epidemic curves will fall broadly into classes; those (Corresponding to mode A) which peter out fairly, quickly and those (Corresponding to mode B) which approximate to the deterministic epidemic curve associated with the k and k equations.

Epidemic curve (Stochastic epidemic).



0.5

t

The continuous curves show that conditional means for model A (J-Shaped) and mode B (Peaked).

H.E. Davets arrive at an appropriate formulae for the distribution of total epidemic size which are appropriate for large populations.

Let $p(x|\xi, \eta)$ be the probability that there are ultimately x uninfected individuals when initially that were ξ susceptible and η infective.

When the threshold is large but the population size is much large, the

distribution of the number remaining uninfected in a large epidemic has

approximately the Poisson forms with the deterministic mean $\frac{\xi}{\rho}$ $\xi e^{-\xi/\rho}$.

Construction of the Epidemic Process:

Let n be originally healthy individuals indexed by $i, 1 \leq i \leq n$

and let m be originally infectious individuals indexed by $j, 1 \leq j \leq m$.

Let $\{s_j\}_{j=1}^m$ and $\{s_i\}_{i=1}^n$ be independent and identically distributed random

Variables(i.i.d) with density $\rho e^{-\rho t}$ on $[0, \infty)$, individual j in the original infectious group will remain infectious for s_j time units before removal from the population. Individual i in the original healthy group will remain infections for s_i time units if he becomes infected.

Let $\{p_i\}_{i=1}^n$ be i.i.d random variables with density e^{-t} on $[0, \infty)$,

independent of the s_j 's and s_i 's. The variable p_i will be thought of as the "resistance to infection" of individual i in the original healthy group. Let

$\{p_{(k)}\}_{k=1}^n$ be the associated order statistics so that $p_{(1)} < p_{(2)} < \dots < p_{(n)}$

Let $s_i^{(k)} = s_i$ if $p_{(k)} = p_i$.

Now let the epidemic process proceed as follows. The originally infected individuals j remains in the population for s_j time units after which he is removed. The healthy individuals i accumulates exposure to infection at a rate equal to the number of infected individuals present. When the total exposure to infection of healthy individuals i reaches p_i individuals i becomes infected and then remains in the population for an additional s_i time units before removal.

It remains to show that the resulting process is Markov with the correct transition probabilities. Suppose $(X(t), Y(t)) = (x, y)$. The probability that a particular infected individual is removed in the time interval $[t, t + \delta]$ is $\rho\delta + o(\delta)$ because the

distribution of the s_j 's and s_i 's has constant hazardrate ρ . The probability that exactly one of the y infected individuals is removed in $[t, t + \delta]$ is therefore $\rho y \delta + o(\delta)$. The probability that a particular one of the x healthy individuals will become infected in $[t, t + \delta]$ is $y \delta + o(\delta)$, so that the probability that exactly one of the healthy individuals becomes infected is $xy \delta + o(\delta)$. It follows that the transition probabilities are as desired.

Let γ be the number of new infections occurring during the course of the epidemic.

If $p_{(1)} > \sum_{j=1}^m s_j$, then all originally infectious individuals are

removed before the resistance to infection of any healthy individual has exceeded, so that $\gamma = 0$. Otherwise, the originally healthy individuals associated with $p_{(1)}$ becomes the first new infection and $\gamma \geq 1$. An easy induction argument shows that $\gamma + 1$ is the smallest k , $1 \leq k \leq n$, for which

$$p_{(k)} > \sum_{j=1}^m s_j + \sum_{i=1}^{k-1} s^{(i)}$$

It this equality does not hold for any k , $1 \leq k \leq n$, then $\gamma = n$.

Define

$$R = \sum_{j=1}^m s_j + \sum_{i=1}^{\gamma} s^{(i)} \quad (11)$$

Then R is the amount of exposure to infection withstood by those individuals who remain healthy at the end of the epidemic and $X(\infty) = n - \gamma$ is the number of p_i 's greater than R .

Consider a sequence of epidemics with parameter n_k, m_k and ρ_k $1 \leq k < \infty$. Let γ_k be the number of new infections in a realization of the k^{th} epidemic, so that $X_k(\infty) = n_k - \gamma_k$ is the number of individuals who escape infection.

Theorem 1.1

If $n_k \rightarrow \infty, \rho_k \rightarrow \infty$ and

$n_k \exp\left\{-\left(\frac{n+m}{\rho_k}\right)\right\} \rightarrow b \quad 0 < b < \infty$, then $x_k(\infty)$ converges in distribution to a Poisson random variable with mean b .

The proof is given in the following by suppressing the subscript k .

The fact that ρ is $o(n+m)$ implies that with high probability all but a tiny fraction of the population becomes infected. Thus R will be close to

$$\sum_{j=1}^m s_j + \sum_{i=1}^n s_i,$$

which is in turn close to $(m+n)/\rho$ with high probability. If R is close enough to $(m+n)/\rho$, then $X(\infty)$ will equal the number of p_i 's which are greater than $(m+n)/\rho$. The number of p_i 's greater than $(m+n)/\rho$ has the distribution Binomial $\left(n, e^{-(m+n)/\rho}\right)$, which converges in distribution to Poisson (b) .

The subscript k will again be suppressed. Taking logarithms in

$$n e^{-(m+n)/\rho} \rightarrow b \text{ yields}$$

$$\log n - \frac{n+m}{\rho} \rightarrow \log b$$

so that $\rho \sim \frac{m+n}{\log n}$. Thus ρ is $o(m+n)$, but

$$(m+n)^\gamma \text{ is } o(\rho) \text{ for } 0 < \gamma < 1$$

Lemma 1.1

Let $0 < \varepsilon < 1$ be given. If $\rho < \varepsilon^2(m+n)$, then

$$P\{X(\infty) > \varepsilon(m+n)\} < \left[\frac{\rho}{\varepsilon(m+n)}\right]^m < \varepsilon^m \leq \varepsilon$$

Proof

We can view the population of infected individuals as a continuous - time birth and death process with a variable birth – rate.

The ratio of death – rate to birth rate is $\rho / x(t)$, which is less than $\rho / (\varepsilon(m+n))$, until $X(t) \leq \varepsilon(m+n)$. The probability that a birth – and – death process starting at m and with a death – rate to birth – rate ratio $q < 1$ is ever absorbed at zero is q^m .

Lemma 1.2

Let $0 < \varepsilon < 1$. For n sufficiently large,

$$P\left\{ R < \frac{(1-2\varepsilon)(m+n)}{\rho} \right\} < 2\varepsilon$$

Proof

We have by lemma 1.1, R is greater than the sum of the first $(1-\varepsilon)(m+n)$ terms of $\{s_1, s_2, \dots, s_m, s^{(1)}, s^{(2)}, \dots, s^{(n)}\}$ with probability greater than $(1-\varepsilon)$ for sufficiently large n . The sum of first $(1-\varepsilon)(m+n)$ terms has mean

$(1-\varepsilon)(m+n) / \rho$ and variance $(1-\varepsilon)(m+n) / \rho^2$. The chebyshev inequality implies the lemma 1.2.

Lemma 1.3

Let $0 < \varepsilon < 1$. For n sufficiently large

$$P\left\{ X(\infty) > n^{3\varepsilon} \right\} < 3\varepsilon$$

Proof:

The number of p_i 's which are greater than $(1-2\varepsilon)(m+n) / \rho$ is Binomial $\left(n, e^{-(1-2\varepsilon)(m+n) / \rho}\right)$.

This distribution has mean

$$ne^{-(1-2\varepsilon)(m+n)/\rho} \sim n(b/n)^{(1-2\varepsilon)} = b^{(1-2\varepsilon)} n^{2\varepsilon}$$

Markov inequality and application of lemma 1.2 completes the proof of lemma 1.3.

From lemma 1.3, it is easy to see that $x(\infty)$ is $O(\sqrt{n})$ in probability. Thus except on a set of small probability, R is greater than the sum of the first $m+n - \sqrt{n}$ terms of

$$\left\{ s_1, s_2, \dots, s_m, s^{(1)}, s^{(2)}, \dots, s^{(n)} \right\}.$$

R is of course less than or equal to the sum of all the terms. By the proof of lemma 1.2 shows that with probability approaching one

$$\frac{(m+n)}{\rho} - \frac{(m+n)^{\frac{2}{3}}}{\rho} < R < \frac{(m+n)}{\rho} + \frac{(m+n)^{\frac{2}{3}}}{\rho} \tag{12}$$

The number of p_i 's greater than

$$\frac{(m+n)}{\rho} \pm \frac{(m+n)^{\frac{2}{3}}}{\rho}$$

is distributed as a

Binomial $\left(n, \exp \left\{ -\frac{(m+n)}{\rho} \mp \frac{(m+n)^{\frac{2}{3}}}{\rho} \right\} \right)$ which has mean $n \exp \left\{ -\frac{(m+n)}{\rho} \mp \frac{(m+n)^{\frac{2}{3}}}{\rho} \right\}$

$$n \exp \left\{ -\frac{(m+n)}{\rho} \mp \frac{(m+n)^{\frac{2}{3}}}{\rho} \right\} \sim b \exp \left\{ \mp \frac{(m+n)^{\frac{2}{3}}}{\rho} \right\} \rightarrow b \tag{13}$$

Thus with probability approaching one, $x(\infty)$ is less than a Binomial

$$\left(n, \exp \left\{ -\frac{(m+n)}{\rho} + \frac{(m+n)^{\frac{2}{3}}}{\rho} \right\} \right)$$

random variable and greater than

$$\text{Binomial} \left(n, \exp \left\{ -\frac{(m+n)}{\rho} - \frac{(m+n)^2}{\rho} \right\} \right) \quad \text{random variable.}$$

CONCLUSION:

Since both of these distributions converge in law to a Poisson with mean b , the theorem is proved. That is when the threshold is large but the population is much larger the distribution of the number remaining uninfected in a large epidemic has approximately the Poisson form with mean b .

REFERENCES

- [1] Bailey, N.T.J., The Mathematical theory of Infectious Diseases and its Application, London Griffin, 1975.
- [2] Daniels, H.E., The Distribution of the total size of an Epidemic, Proceeding of the 5th Berkeley Symposium on Mathematical Statistics and Probability vol.4, pp. 281-293.
- [3] Kendal, D.G., Deterministic and Stochastic Epidemics in closed Population. Proceedings of the third Berkeley Symposium on Mathematical Statistics and Probability. Vol. 4, pp 149-165.
- [4] Kermack W.O. and Mckendrick.A.G., Contribution to the Mathematical Theory of Epidemics. Proc. Roy.Soc. Ser. A, vol.115(1927) pp. 700-721.
- [5] Mckendrick,A.G., Application of Mathematics to Medical problems. Proc. Edinburg Math.Soc., vol 44(1926), pp. 700-721.
- [6] Whittle.P, The Outcome of a Stochastic Epidemic a Note on Bailey's Paper ,Biometrika , vil.42(1955), pp 116-122.