Stochastic Epidemic Model with Poisson Infection and Poisson Removal Rates

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ABSTRACT: In this paper, we have developed a stochastic epidemic model with Poisson infection and Poisson removal rates. Poisson infection rate is depending on the number of persons infected in the system, and Poisson removal rate is depending on the number of persons removed in the system.

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I. INTRODUCTION

Mathematical and theoretical biology is an interdisciplinary scientific research field with wide range of applications in biology, medicine and biotechnology. The field may be referred to as mathematical biology or biomathematics to stress the mathematical side, or as theoretical biology to stress the biological side. It includes at least four major subfields: biological mathematical modeling, relational biology/complex systems biology (CSB), bioinformatics and computational bio modeling / bio computing. Mathematical biology aims at the mathematical representation, treatment and modeling of biological processes, using a variety of applied mathematical techniques and tools. It has both theoretical and practical applications in biological, biomedical and biotechnology research. For example, in cell biology, protein interactions are often represented as cartoon models, which, although easy to visualize, do not accurately describe the systems studied. In order to do this, precise mathematical models are required. By describing the systems in a quantitative manner, their behaviour can be better simulated, and hence properties can be predicted that might not be evident to the experimenter. Mathematical biology is a very active and fast growing interdisciplinary area in which mathematical concepts, techniques, and models are applied to a variety of problems in developmental biology and biomedical sciences.

The occurrence of more cases of a disease than would be expected in a community or region during a given time period is called an epidemic. An epidemic is the rapid spread of infectious disease to a large number of people in a given population within a short period of time, usually two weeks or less. An epidemic may be restricted to one location; however, if it spreads to other countries or continents and affects a substantial number of people, it may be termed a pandemic [16].

Epidemiology is one of the most important fields of research. The modeling and analysis of infectious diseases have been done by many authors. The classical theoretical papers on epidemic models by Kermack and Mekendrick [8, 9, 10] have had a major influence in the development of mathematical models. The modeling literature is now extensive and growing very quickly. Bailey [2] gave a good introduction to the variety of problems and models for the spread and control of infectious disease. The article by Hethcote [6] reviewed three basic epidemiological models. Diekmann and Heesterbeek [5] presented a concentrated review to this field and they discussed how to use biological assumptions in constructing models and present applications.

In mathematics and physics, a deterministic system is a system in which no randomness is involved in the development of future states of the system [17]. A deterministic model will thus always produce the same output from a given starting condition or initial state [18]. For example, physical laws that are described by differential equations represent deterministic systems, even though the state of the system at a given point in time may be difficult to describe.
explicitly. Markov chains and other random walks are not deterministic systems, because their development depends on random choices.

Stochastic means being or having a random variable. A stochastic model is a tool for estimating probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. The random variation is usually based on fluctuations observed in historical data for a selected period using standard time series techniques. Distributions of potential outcomes are derived from a large number of simulations which reflect the random variation in the input.

Basic Concepts
The term epidemiology is the study of health-event, health-characteristic, or health-determinant patterns in a society. Now before we go further in this study, here the basic concepts are introduced which will be useful in the following sections.

Definition 1.1 [3]
An epidemic is an unusually large short – term outbreak of a disease, such as Cholera and Plague etc.

The spread of disease depends on:
- The mode of transmission.
- Susceptibility.
- Infections period.
- Resistance.
and many other factors.

Definition 1.2 [11]
Any group of individuals, usually of a single species, occupying a given area at the same time is known as population.

The population in an epidemiological model can be classified into three types: Susceptible, Infected and Removal which are denoted by \( S(t) \), \( I(t) \) and \( R(t) \) respectively, where \( S(t) \) represent the number of individuals in the population who can be infected, while \( I(t) \) represent the number of infected individuals in the population, that is, those with the disease who are actively transmitting it, \( R(t) \) denotes the number of individuals removed from the population by recovery, death, immunization or other means [7].

In probability theory, a Poisson process is a stochastic process that counts the number of events and the time points at which these events occur in a given time interval. The time between each pair of consecutive events has an exponential distribution with parameter \( \lambda \) and each of these inter-arrival times is assumed to be independent of other inter-arrival times. The process is named after the Poisson distribution introduced by French mathematician Simeon Denis Poisson [13]. It describes the time of events in radioactive decay [4], telephone calls [15] or request for documents on a web server under certain conditions [1], and many other phenomena, where events occur independently from each other. The number of arrivals \( N(t) \) in a finite interval of length \( t \) obeys the Poisson \((\lambda t)\) distribution,

\[
P\{N(t) = n\} = \frac{(\lambda t)^n}{n!} e^{-\lambda t}.
\]

Moreover, the numbers of arrivals \( N(t_1, t_2) \) and \( N(t_3, t_4) \) in non-overlapping intervals \( (t_1 \leq t_2 \leq t_3 \leq t_4) \) are independent.

An infection rate is an estimate of the rate of progress of a disease, based on proportional measures of the extent of infection at different times.

In probability theory, the probability generating function of a discrete random variable is a power series representation of the probability mass function of the random variable. Probability generating functions are often
employed for their succinct description of the sequence of probabilities Pr(X = i) in the probability mass function for a random variable X, and to make available the well developed theory of power series with non-negative coefficients.

**Definition 1.3 [12]**

Consider a random variable X, i.e, a discrete random variable taking non-negative values.

Write

\[ P_k = P(X = k), \quad k = 0, 1, 2, \ldots \]

The probability generating function of X is defined as

\[ G_X(S) = \sum_{k=0}^{\infty} P_k S^k = E(S^k). \]

Note that \( G_X(1) = 1 \), so the series converges absolutely for \( |S| \leq 1 \). Also \( G_X(0) = P_0 \).

**Theorem 1.4 [12] (Total and Compound Probability)**

Let \( A_1, A_2, \ldots, A_n \) be a partition of \( \Omega \). For any event B,

\[ \Pr(B) = \sum_{j=1}^{n} \Pr(A_j) \Pr(B/A_j). \]

In this paper, we have developed a stochastic epidemic model with removal with Poisson infection and Poisson removal rates. Poisson infection rate is depending on the number of persons infected in the system, and Poisson removal rate is depending on the number of persons removed in the system.

**II. EPIDEMIC MODEL**

In this section we study the characterizations of the stochastic epidemic model with removal with Poisson infection and Poisson removal rates.

2.1. Stochastic Epidemic Model with Poisson Infection and Poisson Removal Rates

Let \( P_{m,n}(t) \) be the probability that there are m susceptible and n infectives in the population at time t. If \( N \) is the total size of the population, then the number of persons in the removed category is \( N - m - n \).

Let the probability of susceptible being infected in the time interval \( (t, t+\Delta t) \) be \( \beta mn \Delta t + O(\Delta t) \), and let the corresponding probability of one infected being removed in the same time interval be \( \gamma n \Delta t + O(\Delta t) \).

In this case, let us assume that \( \beta mn \) is the Poisson rate of susceptible becomes infected with parameter \( \lambda I \), and \( \gamma n \) is the Poisson rate of an infective becomes removed with parameter \( \lambda R \).

\[ \beta mn = \frac{e^{-\lambda I} (\lambda I)^m}{m!}, \quad m \geq 0 \]  
\[ \gamma n = \frac{e^{-\lambda R} (\lambda R)^n}{n!}, \quad n \geq 0. \]

Here, \( \lambda I \) be the rate of infection from susceptible to infected, and \( \lambda R \) be the rate of removal from infective to removed.

The probability that there is no change in the time interval \( (t, t+\Delta t) \) is then given by

\[ 1 - \beta mn \Delta t - \gamma n \Delta t + O(\Delta t) \]

Now there can be m susceptibles and n infected persons at time \( t + \Delta t \) if there are
(i) \( m+1 \) susceptibles and \( n-1 \) infectives at time \( t \) and if one person has become infected in time \( \Delta t \),
(or)

(ii) \( m \) susceptibles and \( n+1 \) infectives at time \( t \) and if one infected person has been removed in time \( \Delta t \),
(or)

(iii) \( m \) susceptibles and \( n \) infectives at time \( t \) and if there is no change in time \( \Delta t \).

We assume that the probability of more than one change in time \( \Delta t \) is \( O(\Delta t) \).

Then, using the theorems of total and compound probability, we get

\[
P_{m,n}(t+\Delta t) = P_{m+1,n-1}(t)\beta(m+1)(n-1)\Delta t + P_{m,n+1}(t)\gamma(n+1)\Delta t + P_{m,n}(t)(1-\beta mn)\Delta t - \gamma n \Delta t + O(\Delta t)
\]

So that,

\[
P_{m,n}(t+\Delta t) - P_{m,n}(t) = P_{m+1,n-1}(t)\beta(m+1)(n-1)\Delta t + P_{m,n+1}(t)\gamma(n+1)\Delta t - P_{m,n}(t)\beta mn\Delta t - \gamma n \Delta t + O(\Delta t)
\]

\[
\frac{P_{m,n}(t+\Delta t) - P_{m,n}(t)}{\Delta t} = P_{m+1,n-1}(t)\beta(m+1)(n-1) + P_{m,n+1}(t)\gamma(n+1) - P_{m,n}(t)\beta mn - \gamma n
\]

Proceeding to the limit as \( \Delta t \rightarrow 0 \) in (5), we get

\[
\lim_{\Delta t \rightarrow 0} \frac{P_{m,n}(t+\Delta t) - P_{m,n}(t)}{\Delta t} = P_{m+1,n-1}(t)\beta(m+1)(n-1) - P_{m,n}(t)\beta mn + P_{m,n+1}(t)\gamma(n+1) - \gamma n + O(\Delta t)
\]

Therefore,

\[
\frac{d}{dt}(P_{m,n}(t)) = \beta(m+1)(n-1)P_{m+1,n-1}(t) - \beta mn P_{m,n}(t) + \gamma(n+1)P_{m,n+1}(t) - \gamma n P_{m,n}(t)
\]

Initially, let there be \( s \) susceptibles and \( a \) infectives. Then we define the probability generating function by

\[
\phi(x,y,t) = \sum_{m=0}^{s} \sum_{n=0}^{a-m} P_{m,n}(t) x^m y^n
\]

Multiplying (6) by \( x^m y^n \) and summing over \( n \) from 0 to \( s+a-m \) and \( m \) from 0 to \( s \), we get

\[
\frac{\partial}{\partial t} \left( \sum_{m=0}^{s} \sum_{n=0}^{s+a-m} P_{m,n}(t) x^m y^n \right) = \sum_{m=0}^{s} \sum_{n=0}^{s+a-m} \frac{d}{dt}(P_{m,n}(t)) x^m y^n
\]

So that,

\[
\frac{\partial \phi}{\partial t} = \sum_{m=0}^{s} \sum_{n=0}^{s+a-m} \left[ \beta(m+1)(n-1)P_{m+1,n-1}(t) - \beta mn P_{m,n}(t) + \gamma(n+1)P_{m,n+1}(t) - \gamma n P_{m,n}(t) \right] x^m y^n
\]

(Using (6) and (7))
\[
\sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( \beta (m+1)(n-1)P_{m+1,n-1}(t) \right)x^m y^n - \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \beta mn P_{m,n}(t)x^m y^n \\
+ \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( \gamma (n+1)P_{m,n+1}(t) \right)x^m y^n - \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \gamma n P_{m,n}(t)x^m y^n \\
\frac{\partial \varphi}{\partial t} = \beta \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( (m+1)(n-1)P_{m+1,n-1}(t) \right)x^m y^n - \beta \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} mn P_{m,n}(t)x^m y^n \\
+ \gamma \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( (n+1)P_{m,n+1}(t) \right)x^m y^n - \gamma \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} n P_{m,n}(t)x^m y^n
\]

(8)

Now, the definition of probability generating function, we have

\[
x \frac{\partial \varphi}{\partial x} = \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} m P_{m,n}(t)x^m y^n; \quad (9)
\]

\[
y \frac{\partial \varphi}{\partial y} = \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} n P_{m,n}(t)x^m y^n; \quad \text{and} \quad (10)
\]

\[
x y \frac{\partial^2 \varphi}{\partial x \partial y} = \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} mn P_{m,n}(t)x^m y^n \quad (11)
\]

Equation (8) can be written as,

\[
\frac{\partial \varphi}{\partial t} = \beta y^2 \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( (m+1)(n-1)P_{m+1,n-1}(t) \right)x^m y^{n-2} - \beta xy \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} mn P_{m,n}(t)x^{m-1} y^{n-1} \\
+ \gamma \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} \left( (n+1)P_{m,n+1}(t) \right)x^m y^n - \gamma xy \sum_{m=0}^{\infty} \sum_{n=0}^{\infty} n P_{m,n}(t)x^m y^{n-1}
\]

(12)

Using the relations (9), (10) and (11) in (12), we get

\[
\frac{\partial \varphi}{\partial t} = \beta y^2 \frac{\partial^2 \varphi}{\partial x \partial y} - \beta xy \frac{\partial^2 \varphi}{\partial x^2} + \gamma \frac{\partial \varphi}{\partial x} - \gamma y \frac{\partial \varphi}{\partial y}
\]

(13)

We have to solve (13) subject to the initial condition,

\[
\varphi(x, y, 0) = x^3 y^3
\]

(14)

2.2. Classification of the solution

In this section, to find the classification of the solution of the partial differential equation (13) derived in section 2.1.

Now, the given equation (13) is a linear partial differential equation of the second order in three independent variables \( x, y, t \).

By using the result of section A.4.7 in [14], equation (13) can be re-written as

\[
0 \cdot \varphi_{xx} + \beta \left( y^2 - xy \right) \varphi_{xy} + 0 \cdot \varphi_{xt} + \beta \left( y^2 - xy \right) \varphi_{yx} + 0 \cdot \varphi_{yy} + 0 \cdot \varphi_y + 0 \cdot \varphi_t = 0
\]

(15)

Let us define the matrix \( A \), is given by
\[
A = \begin{bmatrix}
\text{coeff. of } u_{xx} & \text{coeff. of } u_{xy} & \text{coeff. of } u_{xz} \\
\text{coeff. of } u_{yx} & \text{coeff. of } u_{yy} & \text{coeff. of } u_{yz} \\
\text{coeff. of } u_{zx} & \text{coeff. of } u_{zy} & \text{coeff. of } u_{zz}
\end{bmatrix}
\]

Therefore,
\[
A = \begin{bmatrix}
0 & \beta \left(y^2 - xy\right) & 0 \\
\beta \left(y^2 - xy\right) & 0 & 0 \\
0 & 0 & 0
\end{bmatrix}
\]

(Using (15) and (16))

Since, \(a_{ij} = a_{ji}\), \(A = \begin{bmatrix} a_{i,j} \end{bmatrix}_{3 \times 3}\) is a symmetric matrix of order 3x3.

So that,
\[
|A| = \begin{vmatrix}
0 & \beta \left(y^2 - xy\right) & 0 \\
\beta \left(y^2 - xy\right) & 0 & 0 \\
0 & 0 & 0
\end{vmatrix} = 0
\]

Also, the Eigen values of \(A\) is given by the form \(|A - \lambda I| = 0\)

That is,
\[
\begin{vmatrix}
-\lambda & \beta \left(y^2 - xy\right) & 0 \\
\beta \left(y^2 - xy\right) & -\lambda & 0 \\
0 & 0 & -\lambda
\end{vmatrix} = 0
\]

\[-\lambda^2 + \beta^2 \left(y^2 - xy\right)^2 = 0\]
\[
\lambda \left(\beta^2 \left(y^2 - xy\right)^2 - \lambda^2\right) = 0
\]
\[
\lambda = 0; \quad \lambda^2 - \beta^2 \left(y^2 - xy\right)^2 = 0
\]

Therefore,
\[
\lambda = 0; \quad \lambda = \pm \beta \left(y^2 - xy\right).
\]

In equations (17) and (18), the determinant value of \(A\) is zero and one of the Eigen values of \(A\) is also zero.

By using case (ii) of section A.4.7 in [14], the solution of the given partial differential equation (13) is of parabolic type.

III. CONCLUSION

Here, we have developed a stochastic epidemic model with Poisson infection and Poisson removal rates. Poisson infection rate is depending on the number of persons infected in the system, and Poisson removal rate is depending on the number of persons removed in the system. This result can be extended to epidemic models with carriers in consideration with vaccination.

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