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Application of Markov Chains in Epidemiology

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ABSTRACT

Recently, mathematical models are used to describe epidemic disease spread. Epidemic disease transmission outbreaks are modeled among Markov chain in order to monitor and control epidemic spreads. In this paper SIS (Susceptible- Infections- Susceptible) and SIR (Susceptive- Infectious- Recovered) models with discrete Markov chain are represented. These models are developed to see how the number of infected individuals changes over time. In this paper a review of a discrete model of Markov chain for describing epidemic spread is represented. The aim of this review is to explain the formulation of SIR and SIS epidemic models for the spread of infectious disease and to estimate transmission rate and recovery rates.

KEYWORDS

Epidemiology, mathematical method, Markov chain

1 Introduction

Epidemiology studies the cause, distribution and control of disease in a given population or region (city, state or globally). Mathematical models are used to understand disease outbreaks and spread, predict future occurrence of events and the effecton the population. By analyzing these mathematical models certain measures can be taken in order the disease to be controlled. In this paper, depending on the dependence between susceptible, infected and recovered individuals, two types of mathematical models are considered.

The Susceptible- Infected- Susceptible (SIS) model divides the population into two subgroups: susceptible and infected individuals. This model, presumes that recovered individuals from the population do not have permanent immunity and immediately may and can become infectious again. The results for stochastic SIS model in [1] show normal distribution nature of the quasi- stationary distribution when the population size is large and the reproduction number is greater than 1. In [2] transmission parameter is considered to be function of the population size.

The Susceptible- Infected- Recovered (SIR) model divides the population into three subgroups: susceptible, infected and removed/ recovered (dead, immunity) individuals. In this model a susceptible individual that has been infected, recovers the infection and obtains permanent immunity. The main aim of this model is to predict the trajectory of

epidemic transmission as transitions are made from one to another subgroups. This model was developed by [3]. More complex SIR models are obtained from [3] by making more assumption and more parameters areconsidered [5, 6].

2 SIS Epidemic Model

In discrete- time stochastic SIS epidemic model, shown on figure 1, susceptible individual (S) becomes infected (I) but after recovery does not develop immunity and can immediately become infected again, $S \to I \to S$. The first assumption in this model is that newborns aren't born infected and are placed in susceptible subgroups which means that there is not vertical transmissions. Secondly, infected individuals are infectious and can pass the infection to other individuals from susceptible subgroup. Thirdly, the total population size remains constant over time. This means that the number of births is equal to number of deaths at any time stamp,$N = S(t) + I(t)$.

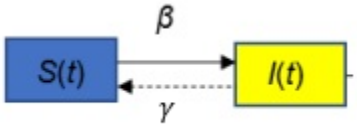

Figure 1: Markov chain of transition in SIS epidemic model

The SIS epidemic model is formulated using discrete time Markov chain. Let with$S(t)$ and$I(t)$are denoted random discrete variables at time $t \in T = \{0, \Delta t, 2\Delta t, ..\}$ with $S(t), I(t) \in \{0,1,2, \dots, N\}$. Because the total population at any time is assumed to be constant follows:

$$\frac{dN}{dt} = \frac{dS(t)}{dt} + \frac{dI(t)}{dt} = 0$$

By choosing enough small time steps can be assumed that at most one transmission occurs during each time step. For small enough time step Δt and for $I(t) = i$ only one of the following states can occur:

$$i \overset{\Delta t}{\to} i + 1, \quad i \overset{\Delta t}{\to} i - 1, \quad i \overset{\Delta t}{\to} i$$

These means that at every time change, one new individual may get infected, recover and become susceptible again or there may not be change in the number of infectious individuals in the population. The number of susceptible individuals decreases if a new individuals get infected. A recovery of infected individuals'part of the population means that the infection subgroup decreases and susceptible subgroup increases, but the total population remains constant. Several factors affected the transmission of infection disease such as contact transmission, pathogen factors, environmental factor, clime etc. The transmission and recovery rates of the population are denoted as $\beta > 0$ and $\gamma > 0$, respectively. The transmission rate β does not change with population size and transmission rate remains constant even as the number of infected individuals increases. The numbernewly infectedsusceptible individuals at time step t is given as:

$$\frac{\beta S(t) I(t)}{N}$$

The number of infectious individuals that become susceptible depends on the number of infected individuals in a population and is determined by the recovery rate. The rate of infected individuals that become susceptible at any time t is given by $\gamma I(t)$. Time changes of susceptible subgroup is defined as:

$$\frac{dS(t)}{dt} = -\frac{\beta S(t) I(t)}{N} + \gamma I(t)$$

The probability of transiting from i to $i + 1$ is:

$$p_{i+1\leftarrow i}(\Delta t) = \frac{\beta i(N-i)}{N}\Delta t$$

where $S = N - I$. The number of individuals recovering at time t is given by $\gamma I(t)$ and for every recovery the changes of the infectious subgroup is:

$$\frac{dI(t)}{dt} = \frac{\beta S(t)I(t)}{N} - \gamma I(t)$$

The probability of transiting from i to $i-1$ is:

$$p_{i-1\leftarrow i}(\Delta t) = \gamma i \Delta t$$

The sum of probabilities of all possible transitions states must be equal to one. Thus, the probability that the number of infection subgroup remains unchanged after a time step is:

$$p_{i\leftarrow i}(\Delta t) = 1 - \left[\frac{\beta i(N-i)}{N} + \gamma i\right]\Delta t$$

For simplification $b(i) = \frac{\beta i(N-1)}{N}$ and $d(i) = \gamma i$. In order transition probability to be between 0 and 1, the time stepΔt should be sufficiently small enough so that following condition is satisfied:

$$max_i = \{[b(i) + d(i)]\Delta t\} \leq 1$$

The transition matrix $P(\Delta t)$that gives the probabilities of transitioning from one state to another in one time step is defined as follows:

$$\begin{pmatrix} 1 & d(1)\Delta t & 0 & \dots & 0 & 0 \\ 0 & 1-[b(1)+d(1)]\Delta t & d(2)\Delta t & \dots & 0 & 0 \\ 0 & b(1)\Delta t & 1-[b(2)+d(2)]\Delta t & \cdots & 0 & 0 \\ 0 & 0 & b(2)\Delta t & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & d(N-1)\Delta t & 0 \\ 0 & 0 & 0 & \dots & 1-[b(N-1)+d(N-1)]\Delta t & d(N)\Delta t \\ 0 & 0 & 0 & \dots & b(N-1)\Delta t & 1-d(N)\Delta t \end{pmatrix}$$

The state $p_{00} = 1$ is an absorbing state of the transition matrixthat denotes the probability that the epidemic will die-off. If transitions from i to j and from j to i are possible than$i$ and j are part of same communicating class. The state $i = 0$ forms a communicating class and another communicating class is formedforstates $i > 0$. In the class when$i > 0$ the probability of transitioning between any two states in the population is positive, and also the probability of transitioning from any one of the states out of the class to $i = 0$ is positive.

3 SIR Epidemic Model

In the discrete- time stochastic SIR model, shown on figure 2, the total population is assumed to be constant and divided into three subgroups: susceptible, infected and recovered. Let $S = (t), I(t)$ and $R(t)$are random numbers that denotes the number of susceptible, infected and recovered (immune) individuals at time $t \in T = \{0, \Delta t, 2\Delta t, ..\}$, respectively. The total population at any time is $N = S(t) + I(t) + R(t)$. The assumption in this model is that there is no latent period, which means that infected individuals are also infectious.

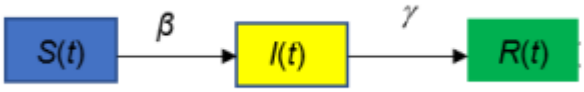

Figure 2: Markov chain of transition in SIR epidemic model

The population size is constant at any time, so that follows:

$$\frac{dN}{dt} = \frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0$$

In order dimension of the system to be reduced, the number of recovered individuals is computed by means of susceptible and infected subgroups as:

$$R(t) = N - S(t) - I(t)$$

The other assumption is that at most one transition can occur during each time step if the time steps are sufficient small enough. The process is bivariate because the recovered subgroup depends on susceptible and infectious subgroups so that for time step Δtonly one of the following transitions can occur:

$$(s,i) \overset{\Delta t}{\rightarrow} (s-1, i+1), \quad (s,i) \overset{\Delta t}{\rightarrow} (s, i-1), \quad (s,i) \overset{\Delta t}{\rightarrow} (s,i)$$

Only one individual from the population may get infected, recover from the infection and not becoming susceptible again or there may not be any changes of the number of infectious individuals for every time step. When new infection occurs in the population, the number of susceptible individuals decreases while the number of infection individuals increases.

For discrete time Markov chain SIR model, the change of susceptible subgroup at time t is defined as:

$$\frac{dS(t)}{dt} = -\frac{\beta S(t) I(t)}{N}$$

Because it is presumed the recovered individuals develop immunity, the susceptible individuals are transiting to infection subgroup with no individual returning to the susceptible subgroup. This means that over time the number the susceptible individuals in the population decreases andthe probability of new infection is defined as:

$$p_{(s-1,i+1)\leftarrow(s,i)}(\Delta t) = \frac{\beta si}{N}\Delta t$$

Infected individuals are recovering and transiting to the recovery subgroup, so thusthe time change of infection subgroup at time t is defined as:

$$\frac{dI(t)}{dt} = \frac{\beta S(t) I(t)}{N} - \gamma I(t)$$

Recovery is transition from state (s,i) to state$(s, i-1)$with probability:

$$p_{(s,i-1)\leftarrow(s,i)}(\Delta t) = \gamma i \Delta t$$

The total population size is constant so that each death is accompanied by a birth. Thus, the probability that the number of infectious individuals remains unchanged after one time step is:

$$p_{(s,i)\leftarrow(s,i)}(\Delta t) = 1 - \left[\frac{\beta si}{N} + \gamma\right]\Delta t$$

The transition matrix for SIR epidemic model cannot be expressed in a simple form, but there is a single absorbing state at the origin for $s = 0$ and $i = 0$.

4 Conclusion

SIS and SIR epidemic models are most simple mathematical models that are used analyzing the spread of infectious diseases. Markov chains are important tool for mathematical modeling of epidemiology results. The mathematical

models which are based on Markov chains can be used for prediction of spreading diseases and for prediction on outcomes of taking measures for stopping the spread of infections. On the other hand, binominal epidemics models as Greenwood model and Reed- Frost model can be used for estimate duration size of the epidemic. In the future, the authors will consider more complex mathematical models like SEIR, SEIR+D for prediction of epidemiological process in their research.

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