Claremont Graduate University

Discrete Mathematical Modeling

Fall 2016

A Markov Chain Model of SIR Epidemics

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December 15, 2016

1 Abstract

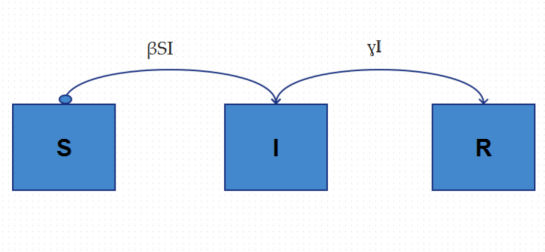
We propose a Markov chain model for epidemics of SIR (Susceptible-Infected-Recovered) type over closed population. This Markov chain model is analogous to the famous Kermack-McKendrick continuous SIR model. We further find its stationary distribution and show that under our assumption the epidemic converges to the state in which each individual in the population is recovered.

2 Introduction

Mathematical modeling is used in many ways academically and professionally. One of the most important modeling techniques is to model and study behaviors of epidemics. Epidemics modeling began in the eighteenth century and has never been absent. Epidemics modeling utilizes both continuous and discrete techniques. This SIR model is good for predicting the behavior of a disease but not suitable for preventing a disease since it does not consider the probability of each individual getting infected. (Yaesoubi et al.)Depending on the purposes, one uses different techniques. In this paper, we will focus on SIR model, which stands for Susceptible, Infected and Recovered, in both continuous and discrete fashion. And discuss what the advantage of discrete epidemics model has over its continuous counterpart.

2.1 The Continuous SIR Model

We categorize the total population into three groups:



- Susceptible: Individuals who are healthy and can be infected. Denote their number at time t by $S(t)$.
- Infective: individuals who are infected and able to transmit the disease. Their number at time t is denoted by $I(t)$.
- Recovered: individuals who are immune to the disease because they have been infected but then recovered.

The Kermack and McKendrick's SIR Model, proposed in 1927, consists of three differential equations as follows:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta SI}{n} \\ \frac{dI}{dt} &= \frac{\beta SI}{n} - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$

where β is the infection rate, $\frac{1}{\gamma}$ is the recovery period for the infected and n is the total population. n is set to be fixed without spatial distribution.
We shall simplify Kermack McKendrick SIR Model as follows to coop-

erate well with our model:

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$

3 The Markov Chain Model

3.1 Model Construction

We consider the spread of an epidemic in a closed population using the SIR model in which the population is divided into three categories as described in the continuous model. For the Markov chain, let n denote the total population. The state of an indivisual i at time t is denoted by $X_i(t)$ and can take one of the values in $\{0, 1, 2\}$: 0 for susceptible, 1 for infected and 2 for recovered. β is the probability that a susceptible person is infected in the next time step, and δ is the probability that an infected person becomes recovered in the next time step. As with the continuous model, individuals in the recovered group are immune to the disease, meaning that they stay at this state with probability 1. The state of the whole population at time t is represented as:

$$X(t) = (X_1(t), X_2(t), \ldots, X_n(t))$$

Since for each i, $X_i(t) \in \{0, 1, 2\}$, the Markov chain has a total of $N := 3^n$ states.

Let P be the transition matrix of the Markov chain with transition probability from state A to state B denoted by P_{AB}. Then the element P_{AB} is given by:

$$
\begin{aligned}
P_{A,B} &= \Pr\{X(t+1) = B | X(t) = A\} \\
&= \prod_{i=1}^{n} \Pr\{X_i(t+1) = B_i | X(t) = A\}
\end{aligned} \tag{1}
$$

We can further calculate these probabilities from the model assumptions as follows:

$$
\Pr\{X_i(t+1) = B_i | X(t) = A\} = \begin{cases}
1-\beta, & (A_i, B_i) = (0,0) \\
\beta & (A_i, B_i) = (0,1) \\
0 & (A_i, B_i) = (0,2) \\
0 & (A_i, B_i) = (1,0) \\
1-\delta & (A_i, B_i) = (1,1) \\
\delta & (A_i, B_i) = (1,2) \\
0 & (A_i, B_i) = (2,0) \\
0 & (A_i, B_i) = (2,1) \\
1 & (A_i, B_i) = (2,2)
\end{cases} \tag{2}
$$

Note here that equations (1) and (2) above describes the Markov chain fully. However, there are two crucial observations to the analysis that will follow:

1. Elements in the main diagonal of P have the form $(1-\beta)^{m_1}(1-\delta)^{m_2}$, where $m_1, m_2 \geq 0$. In particular, the element $P_{NN} = 1$.

2. All elements below the main diagonal are 0 because each contains at least one transition from infected to susceptible, recovered to infected or recovered to susceptible; none of which is allowed in the SIR model.

For illustration purposes, we write down the 9×9 transition matrix when $n = 2$ (2 people in the population):

$$P = \begin{array}{c} \text{states} \\ (0,0) \\ (0,1) \\ (0,2) \\ (1,0) \\ (1,1) \\ (1,2) \\ (2,0) \\ (2,1) \\ (2,2) \end{array} \begin{array}{c} \begin{array}{ccccccccc} (0,0) & (0,1) & (0,2) & (1,0) & (1,1) & (1,2) & (2,0) & (2,1) & (2,2) \end{array} \\ \begin{pmatrix} (1-\beta)^2 & (1-\beta)\beta & 0 & \beta(1-\beta) & \beta^2 & 0 & 0 & 0 & 0 \\ 0 & (1-\beta)(1-\delta) & (1-\beta)\delta & 0 & \beta(1-\delta) & \beta\delta & 0 & 0 & 0 \\ \vdots & 0 & 1-\beta & 0 & 0 & \beta & 0 & 0 & 0 \\ & \vdots & 0 & (1-\delta)(1-\beta) & (1-\delta)\beta & 0 & \delta(1-\beta) & \delta\beta & 0 \\ & & \vdots & 0 & (1-\delta)^2 & \delta(1-\delta) & 0 & \delta(1-\delta) & \delta^2 \\ & & & \vdots & 0 & 1-\delta & 0 & 0 & \delta \\ & & & & \vdots & 0 & 1-\beta & \beta & 0 \\ & & & & & \vdots & 0 & 1-\delta & \delta \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{pmatrix} \end{array}$$

3.2 Model Analysis

In this section, we study the Markov chain constructed in the previous section. In particular, we find a stationary distribution, its uniqueness and whether the Markov chain converges to it or not. For the purpose of the following results, let $\vec{e}_X$ denote the unit row vector with 0's everywhere and 1 at the Xth element.

Proposition 3.1. *Let $\vec{\pi}$ be a row vector in $\mathbb{R}^N$. Then $\vec{\pi} = \vec{e}_N$ is a stationary distribution of the Markov chain defined by* (1) *and* (2).

Proof. Denote the ith element of $\vec{\pi}$ by π_i, and let $\vec{v}_i$ be the ith column vector in the transition P. It's sufficient to prove that $\pi_i = 0$ for all $1 \leq i \leq N-1$ since $\sum_{i=1}^{n} \pi_i = 1$ by normalization of the probabilities. We prove this by induction. First note that $\pi_1 = \vec{\pi} \cdot \vec{v_1} = \pi_1 v_1(1)$, where $v_i(j)$ denote the jth element of $\vec{v_i}$. Since $v_1(1) = (1-\beta)^N > 0$, it follows that $\pi_1 = 0$. Assume now that $\pi_i = 0$ for all $i \leq k-1$ for some $k < N$. Then for $i = k$, we have

$$\pi_k = \sum_{i=1}^{N} \pi_i v_k(i) = \sum_{i=k}^{N} \pi_i v_k(i) = \pi_k v_k(k) \tag{3}$$

The second equality above follows from the induction hypothesis and the last equality is due to the fact that all elements below the main diagonal of P are 0; i.e. $v_i(j) = 0 \ \forall j > i$. Because $0 < v_k(k) < 1$, we have $\pi_k = 0$. □

Now consider the graph G with nodes representing the state of the Markov chain and edges connecting nodes i and j whenever $P_{ij} > 0$. It's easy to see that this graph is connected and therefore the Markov chain is irreducible. Moreover, since the Markov chain contains self-loops, it's also aperiodic. We can now state the following main result.

Proposition 3.2. *The stationary distribution $\vec{\pi}$ is unique. Furthermore, the Markov chain defined by* (1) *and* (2) *converges to $\vec{\pi}$.*

4 Future study

A major advantage of this model is that it takes into account the state of each individual in the population. This advantage can be further utilized by considering the individuals interaction in the disease transmission. Define a new parameter k_i to be a uniformly distributed random variable representing the number of infected people with access to individual i. Then instead of assuming a constant infection probability, we can assume that disease transmission follows a binomial distribution with parameters k_i and β, where β represents the probability of infection with each interaction; that is

$$\Pr\{X_i(t+1) = 1 | X_i(t) = 0\} = \binom{n}{k_i} \beta^{k_i} (1-\beta)^{n-k_i} \tag{4}$$

This assumption captures the dynamic of infectious diseases more accurately. However, we will not study this construction further, and we leave it to possible future work.
One significant concern that remains to be studied is the mixing time of the Markov chain which examines how long it takes for the epidemic to die out.

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