IOP Conf. Series: Journal of Physics: Conf. Series **855** (2017) 012024 doi:10.1088/1742-6596/855/1/012024

Discrete time Markov chains (DTMC) susceptible infected susceptible (SIS) epidemic model with two pathogens in two patches

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Abstract. The SIS epidemic model describes the pattern of disease spread with characteristics that recovered individuals can be infected more than once. The number of susceptible and infected individuals every time follows the discrete time Markov process. It can be represented by the discrete time Markov chains (DTMC) SIS. The DTMC SIS epidemic model can be developed for two pathogens in two patches. The aims of this paper are to reconstruct and to apply the DTMC SIS epidemic model with two pathogens in two patches. The model was presented as transition probabilities. The application of the model obtain that the number of susceptible individuals decreases while the number of infected individuals increases for each pathogen in each patch.

1. Introduction

Health is the important thing in human life. Health can be impaired due to an infectious disease. The spread of infectious diseases that occurs in a long period of time can lead to the occurrence of an epidemic. The epidemic can be represented in a mathematical model (Hethcote [5]).

In 1927, the epidemic model was first introduced by Kermack and McKendrick [6]. In 1994, Allen [2] has been written the susceptible infected susceptible (SIS) epidemic models. The characteristic of the model is a susceptible individual, after a successful contact with an infectious individual, becomes infected and infectious, but it does not develop immunity to the disease. In the SIS epidemic models, the individuals conditions are classified into two categories, there are susceptible (S) and infectious (I). The number of susceptible and infected individuals is random events that depend on time so it follows the stochastic process (Allen [2]). The number of susceptible and infected individuals at time $t+1$ depends only on the individuals at time t, so these follow the discrete time Markov process. It can be described as an epidemic model of discrete time Markov chains (DTMC) SIS (Allen [1]).

According to Allen and Kiruparahan [3] in 2005, a susceptible individual can be infected more than one pathogen. In 2007, McCormack and Allen [7] represented that the spread of the disease also can occur in one or more patch, due to their individual displacement occurred from one patch to another. Then Allen et al.[4] developed a model of an epidemic DTMC SIS for

two pathogens in the two patches. By referring to Allen et al., the aims of this research are to reconstruct and to apply the DTMC SIS epidemic model with two pathogens in two patches.

2. DTMC SIS Epidemic Models with One Pathogen

In 2003, Allen [1] introduced the DTMC SIS epidemic model. There are four assumptions on the model i.e. total population size N is constant, the birth rate that equals to the death rate, homogeneously population, and the individuals born are susceptible individuals. Let $S(t)$ and $I(t)$ denote discrete random variables for the number of susceptible and infected individuals at time t. The total population size N is constant so $S(t) + I(t) = N$. Let $S(t) = s$ and $I(t) = i$, s and i are state, the joint probability function for $S(t)$ and $I(t)$ is given by

$$p_{(s,i)}(t) = P\{S(t) = s, I(t)) = i\},$$

where $s, i = 0, 1, 2, \ldots, N$ and $t = 0, \Delta t, 2\Delta t, \ldots$.

A transition is a change in the number of susceptible and infected individuals during the time period Δt. The time period Δt is chosen sufficiently small such that the number of susceptible and infected individuals changes by at most one during the time period Δt, that is -1 if it decreases, 0 if it fixed, or 1 if it increases. During the time period Δt, if the change in the number of susceptible and infected individuals is h and j, where h and $j \in \{-1, 0, 1\}$, so the transitions are from state s to $s+h$ and from state i to $i+j$. According to Allen [1], the DTMC SIS epidemic model satisfy

$$p_{(s+h,i+j),(s,i)}(\Delta t) = \begin{cases} \frac{\beta is}{N}\Delta t, & (h,j) = (-1,1); \\ \gamma i \Delta t, & (h,j) = (1,-1); \\ \delta i \Delta t, & (h,j) = (0,-1); \\ 1 - \left(\frac{\beta is}{N} + \gamma i + \delta i\right)\Delta t, & (h,j) = (0,0); \\ 0, & (h,j) \text{ others}, \end{cases}$$

where δ denotes the birth rate that equals to the death rate, β denotes the contact rate, and γ denotes the recovery rate.

3. DTMC SIS Epidemic Models with Two Pathogens

According to Allen et al.[4], the individuals can be infected with more than one pathogen through direct contact between an infected individual and a susceptible one. Let $S(t)$ and $I_k(t)$ denote discrete random variables for susceptible and infected individuals with pathogen k at time t, where $k = 1$ and 2. The assumptions of the DTMC SIS epidemic model with two pathogens equal to the assumptions of the DTMC SIS epidemic model one pathogen. Let $S(t) = s$, $I_k(t) = i_k$, and the change in the number of susceptible and infected individuals with pathogen k during the time period Δt is j_k, with $j_k \in \{-1, 0, 1\}$, then the DTMC SIS epidemic model is given by

$$p_{(s+h,i_k+j_k),(s,i_k)}(\Delta t) = \begin{cases} \beta_k \frac{i_k}{N} s \Delta t, & (h,j_k) = (-1,1); \\ \gamma_k i_k \Delta t, & (h,j_k) = (1,-1); \\ \delta_k i_k \Delta t, & (h,j_k) = (0,-1); \\ 1 - a & (h,j_k) = (0,0); \\ 0, & (h,j_k) \text{ others}, \end{cases}$$

where $a = \left(\frac{\beta_1 s}{N} i_1 + \gamma_1 i_1 + \delta_1 i_1 + \frac{\beta_2 s}{N} i_2 + \gamma_2 i_2 + \delta_2 i_2\right)\Delta t$, with $\delta_k, \beta_k, \gamma_k$ denote the birth rate that equals to the death rate, the contact rate, and the recovery rate of pathogen k.

4. Main Results

4.1. The Reconstruction Model

The reconstruction of the DTMC SIS epidemic model with two pathogens in two patches refers to Allen et al.[4]. The assumptions of the DTMC SIS epidemic model with two pathogens in two patches equal to the assumptions of the DTMC SIS epidemic model with two pathogens. There are two processes in the model i.e. an infection process and an dispersal process. The infection process discusses about the contact of susceptible and infected individuals in the same patch. The dispersal process discusses about an individual movement from one patch to another.

Let $S_d(t)$ and $I_{dk}(t)$ indicate discrete random variables for the number of susceptible individuals at time t in patch d and the number of infected individuals by pathogen k at time t in patch d, respectively, where $S_d(t), I_{dk}(t) \in \{0, 1, 2, \ldots, N\}$. Let N_1 and N_2 indicate the population size in patch d, $d = 1, 2$ and the total population size is $N_1 + N_2 = N$, where N_1 and N_2 are constant. Let $S_d(t) = s_d$ and $I_{dk}(t) = i_{dk}$, the joint probability function for $S_d(t)$ and $I_{dk}(t)$ is given by

$$p_{(s_d,i_{dk})}(t) = P\{S_d(t) = s_d, I_{dk}(t) = i_{dk}\},$$

where $s_d, i_{dk} = 0, 1, 2, \ldots, N$ and $t = 0, \Delta t, 2\Delta t, \ldots$.

If the change in the number of susceptible and infected individuals during the time period Δt are h_d and j_{dk}, then the transitions are from *state* s_d to state $s_d + h_d$ and from *state* i_{dk} to *state* $i_{dk} + j_{dk}$. The transition probability for s_d to $s_d + h_d$ and i_{dk} to $i_{dk} + j_{dk}$ is

$$\begin{aligned} p_{(s_d+h_d,i_{dk}+j_{dk}),(s_d,i_{dk})}(\Delta t) &= P\{(S_d(t+\Delta t), I_{dk}(t+\Delta t)) = (s_d + h_d, i_{dk} + j_{dk}) | \\ &\quad (S_d(t), I_{dk}(t)) = (s_d, i_{dk})\}. \end{aligned}$$

If there is a new infection, so state (s_d, i_{dk}) transition to state $(s_d - 1, i_{dk} + 1)$. The transition occurs due to a susceptible individual becomes infected by pathogen k. If there are i_{dk} infected individuals in N_d population, then the probability of contact between infected individuals and susceptible individuals is $\frac{i_{dk}}{N_d}$. If β_{dk} is the contact rate of infected individuals by pathogen k in patch d, then the transition probability from state (s_d, i_{dk}) to state $(s_d - 1, i_{dk} + 1)$ satisfy

$$p_{(s_d-1,i_{dk}+1),(s_d,i_{dk})}(\Delta t) = \beta_{dk} \frac{i_{dk}}{N_d} s_d \Delta t.$$

If an infected individual by pathogen k recovers from the infection, then state (s_d, i_{dk}) transition to *state* $(s_d + 1, i_{dk} - 1)$. If γ_{dk} is the recovery rate of pathogen k in patch d, then the transition probability from state (s_d, i_{dk}) to state $(s_d + 1, i_{dk} - 1)$ is given by

$$p_{(s_d+1,i_{dk}-1),(s_d,i_{dk})}(\Delta t) = \gamma_{dk} i_{dk} \Delta t.$$

If an infected individual with pathogen k dies from the infection, then state (s_d, i_{dk}) transition to state $(s_d, i_{dk} - 1)$. If δ_{dk} is the death rate of pathogen k in patch d, then the transition probability from state (s_d, i_{dk}) to state $(s_d, i_{dk} - 1)$ is

$$p_{(s_d,i_{dk}-1),(s_d,i_{dk})}(\Delta t) = \delta_{dk} i_{dk} \Delta t.$$

There is a possibility that during the time period Δt, no event occurs. The probability no event occurs during the time period Δt is given by

$$p_{(s_d,i_{dk}),(s_d,i_{dk})}(\Delta t) = 1 - \left(\frac{\beta_{d1} s_d}{N_d} i_{d1} + \gamma_{d1} i_{d1} + \delta_{d1} i_{d1} + \frac{\beta_{d2} s_d}{N_d} i_{d2} + \gamma_{d2} i_{d2} + \delta_{d2} i_{d2} \right) \Delta t,$$

where $s_d + i_{d1} + i_{d2} \in \{0, 1, 2, \ldots, N_d\}$.

Let $b = (\frac{\beta_{d1} s_d}{N_d} i_{d1} + \gamma_{d1} i_{d1} + \delta_{d1} i_{d1} + \frac{\beta_{d2} s_d}{N_d} i_{d2} + \gamma_{d2} i_{d2} + \delta_{d2} i_{d2})\Delta t$, then the DTMC SIS epidemic model for the infection process in patch d for pathogen k satisfy

$$p_{(s_d+h_d, i_{dk}+j_{dk}),(s_d,i_{dk})}(\Delta t) = \begin{cases} \beta_{dk} \frac{i_{dk}}{N_d} s_d \Delta t, & (h_d, j_{dk}) = (-1, 1); \\ \gamma_{dk} i_{dk} \Delta t, & (h_d, j_{dk}) = (1, -1); \\ \delta_{dk} i_{dk} \Delta t, & (h_d, j_{dk}) = (0, -1); \\ 1 - b, & (h_d, j_{dk}) = (0, 0); \\ 0, & (h_d, j_{dk}) \text{ yang lain}, \end{cases} \tag{1}$$

where β_{dk}, γ_{dk}, and δ_{dk} are positive.

There is a dispersal process after the infection process. The dispersal process refers to the movement of individuals from one patch to another. In this process, the populations size N_1 and N_2 are constant. Thus, if there is the movement of individuals from patch 1 to patch 2 then also there is the movement of individuals from patch 2 to patch 1. If the susceptible individuals move from one patch to another with probability p_d, then the remains of the susceptible individuals which don't move from one patch to another have a probability $1 - p_d$. If the infected individuals by pathogen k move from one patch to another with probability p_{dk}, then the remains of the infected individuals by pathogen k which don't move from one patch to another have a probability $1 - p_{dk}$. Thus, the DTMC SIS epidemic model for the dispersal process in patch d for pathogen k satisfy

$$p = \begin{cases} p_d, \\ 1 - p_d, \end{cases} \quad \text{and} \quad q = \begin{cases} q_{dk}, \\ 1 - q_{dk}. \end{cases}$$

4.2. The Model Application

In this section, the parameters value were selected by referring to Allen et al.[4]. The parameters value are contact rate $\beta_{11} = 0.1$, $\beta_{12} = 0.05$, $\beta_{21} = 0.05$, $\beta_{22} = 0.075$, recovery rate $\gamma_{11} = 0.05$, $\gamma_{12} = 0.025$, $\gamma_{21} = 0.033$, $\gamma_{22} = 0.05$, the birth rate that equals to the death rate $\delta_{dk} = 0$, the population size $N = 200$, $N_1 = 100$ and $N_2 = 100$. By using the parameters into the model (1), it is obtained the transition probabilities. By knowing the transition probabilities, it is also known the transition from state (s_d, i_{dk}) to state $(s_d + h_d, i_{dk} + j_{dk})$, then the number of susceptible and infected individuals at time t can be known. By using initial conditions $I_{11}(0) = I_{12}(0) = I_{21}(0) = I_{22}(0) = 1$ and $S_1(0) = S_2(0) = 98$ into the model (1) with the parameters value which refers to Allen et al., the number of susceptible and infected individuals at an interval 600 first period of times is presented in the Figure 1 and 2.

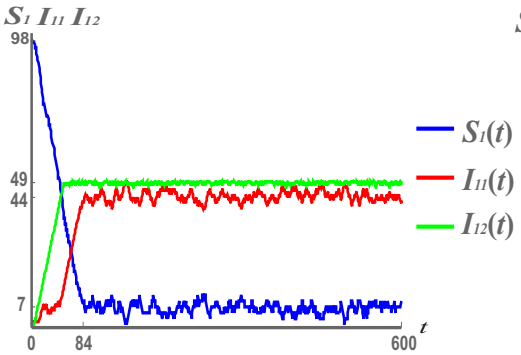

Figure 1. The number of $S_1 I_{11} I_{12}$ at an interval 600 first period times.

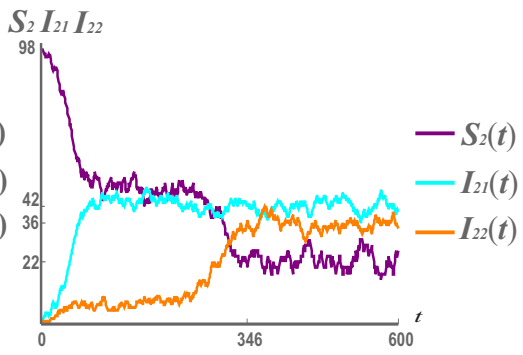

Figure 2. The number of $S_2 I_{21} I_{22}$ at an interval 600 first period times.

Figure 1 shows that the number of susceptible individuals at time 84th decreases from 1 to 7. At time 84th to time 600th, the number of susceptible individuals fluctuates in number 5 to 9. The number of infected individuals by the first pathogen increases from 1 to 44 at time 84th, then it fluctuates in number 41 to 47. The number of infected individuals by the second pathogen increases from 1 to 49, then it fluctuates in number 48 to 50. Figure 2 shows that the number of susceptible individuals decreases from 98 to 22 at time 346th, then it fluctuate until time 600th in number 18 to 26. At time 346th, the number of infected individuals by the first pathogen increases from 1 to 42, then it fluctuates until time 600th in number 39 to 45. The number of infected individuals by the second pathogen increases from 1 to 36, then it fluctuates until time 600th in number 31 to 40.

To observe the change in the number of infected individuals at time t and to calculate the transition probabilities, we present the disease spread at an interval 10 first period of times in Figure 3 and 4.

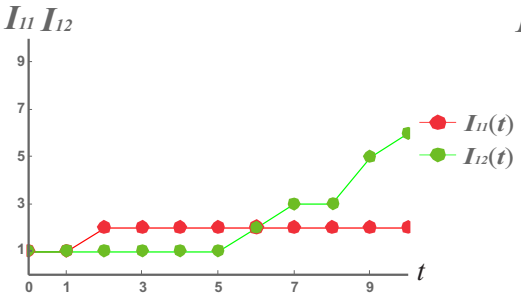

Figure 3. The number of $I_{11}I_{12}$ at an interval 10 first period of times.

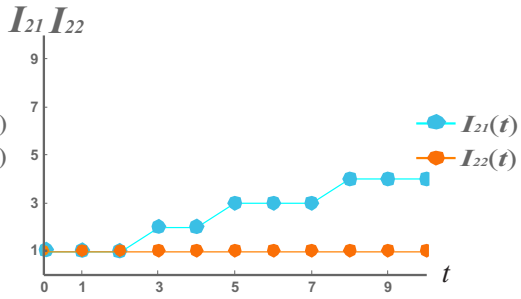

Figure 4. The number of $I_{21}I_{22}$ at an interval 10 first period of times.

The transition probabilities of diseases spread in Figure 3 and 4 can be calculated by using model (1). Figure 3 shows the change in the number of infected individuals, $I_{11}(1) = 1$ to $I_{11}(2) = 2$. There is a transition of a susceptible individual that it can be infected by the first pathogen at a time period Δt. The transition probability of $I_{11}(1) = 1$ to $I_{11}(2) = 2$ by using model (1) is 0.098. Figure 4 shows the change in the number of infected individuals $I_{21}(2) = 1$ to $I_{21}(3) = 2$. The transition probability of $I_{21}(2) = 1$ to $I_{21}(3) = 2$ is 0.049. In the same way, the transition probability at every time can be easily calculated.

The transition probabilities of the movement individuals in the dispersal process were selected by referring to Allen et al.[4]. The transition probability of the movement susceptible individuals is $p_d = 0.01$. Allen et al. assumes that the infected individuals are isolated, then the transition probability of the movement infected individuals is $q_{dk} = 0$. Thus, the transition probability of no occur the movement susceptible individuals is $1 - p_d = 0.99$.

5. Conclusions

From this paper, we have two conclusions.

(i) The DTMC SIS epidemic model with two pathogens in two patches is given by

(a) the transition probabilities of the infection process are

$$p_{(s_d+h_d,i_{dk}+j_{dk}),(s_d,i_{dk})}(\Delta t) = \begin{cases} \beta_{dk}\frac{i_{dk}}{N_d}s_d\Delta t, & (h_d, j_{dk}) = (-1, 1); \\ \gamma_{dk}i_{dk}\Delta t, & (h_d, j_{dk}) = (1, -1); \\ \delta_{dk}i_{dk}\Delta t, & (h_d, j_{dk}) = (0, -1); \\ 1 - b, & (h_d, j_{dk}) = (0, 0); \\ 0, & (h_d, j_{dk}) \text{ others}, \end{cases}$$

with β_{dk}, γ_{dk}, and δ_{dk} are positive, where $b = (\frac{\beta_{d1}s_d}{N_d}i_{d1} + \gamma_{d1}i_{d1} + \delta_{d1}i_{d1} + \frac{\beta_{d2}s_d}{N_d}i_{d2} + \gamma_{d2}i_{d2} + \delta_{d2}i_{d2})\Delta t$.

(b) the transition probabilities of the dispersal process are

$$p = \begin{cases} p_d, \\ 1 - p_d, \end{cases} \quad \text{and} \quad q = \begin{cases} q_{dk}, \\ 1 - q_{dk}. \end{cases}$$

(ii) The application of the model which refers to Allen shows the pattern of disease spread DTMC SIS epidemic model with two pathogens in two patches. In patch one, at time 84th, the number of susceptible individuals decreases from 98 to 7, the number of infected individuals by the first pathogen increases from 1 to 44, and the number of infected individuals by the second pathogen increases from 1 to 49. In patch two, at time 346th, the number of susceptible individuals decreases from 98 to 22, the number of infected individuals by the first pathogen increases from 1 to 42, and the number of infected individuals by the second pathogen increases from 1 to 36.

References

[1] Allen L J S 2008 *An Introduction to Stochastic Epidemic Models* (Texas: Texas Tech University)
[2] Allen L J S 2003 *An Introduction to Stochastic Processes with Applications to Biology* (New Jersey, Upper Saddla River: Prentice Hall)
[3] Allen L J S and Kirupaharan N 2005 Asymptotic Dynamics of Deterministic and Stochastic Epidemic Models with Multiple Pathogens *International Journal of Numerical Analysis and Modeling* **2** 3 pp 329-344
[4] Allen L J S, Kirupaharan N, and Wilson S M 2004 SIS Epidemic Mode ls with Multiple Pathogen Strains *Journal of Difference Equations and Applications* **10** 1 pp 53-75
[5] Hethcote H W 2000 The Mathematics of Infectious Diseases *SIAM Review* **42** 4 pp 599-653
[6] Kermack W O and McKendrick A G 1927 A Contribution to the Mathematical Theory of Epidemics *Proceeding of the Royal Society of London, Series A, Containing Papers of a Mathematical and Physical Character* **115** pp 700-721
[7] McCormack R K and Allen L J S 2007 Multi-patch Deterministic and Stochastic Models for Wildlife Diseases *Journal of Biological Dynamics* **1** 1 pp 63-85