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Using Stochastic SIS Epidemic Model with Markovian Environment for Infectious Diseases

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Highlights

- **The number of infected individuals depends on the values of β and γ. It cannot be seen dying out unless β< γ.**
- **The equilibrium level of infected individuals decreases as β value decreases.**
- **The disease prevalence is decreasing at a fixed time.**

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ABSTRACT

There are various types of stochastic epidemic models that can be formulated to deal with different types of diseases. In this project (SIS) epidemic model Susceptible - Infected- Susceptible will be considered relating to the Continuous Time Markov chains process. Each type of the epidemic models studies the disease according to its status. In particular, the SIS epidemic model regards infectious diseases. The Maple code is provided in this project, which is created to produce and predict the number of infected individuals and the disease prevalence at a fixed time.

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1. Introduction

Mathematical models have been used in epidemiology since the eighteenth century, and in the early nineties, the dynamical systems approaches were commonly enforced in this field, which played a very important role in the development of theoretical epidemiology. The process of modeling infectious diseases purposes to recognize the prevalence of a species with respect to the factors that allocate incidence, distribute, and continuance.

Therefore, epidemiological models can be used to be aware of how an infectious disease spreads between individuals and how can be affected by different complexities. There are several epidemic models that can be applied for different infection statuses, such as SI, SIS and SIR. The SI and SIR models take the dynamics of severe infections that either kill or confer immunity when the infection is recovered, whereas the SIS model, which will be considered in this project, studies the infectious diseases that do not confer long-lasting immunity. For example, sexually transmitted infections, HIV and bacterial infections, by which individuals can be infected many times during their lives, and in which susceptible individuals recover from infection and then become liable to be infected again Keeling, M and Rohani, P (2008). Moreover, because of the interactions between populations, it is very difficult to deal with the spread of all infectious diseases without a mathematical model. Therefore, epidemiological models are used to understand and predict the macroscopic behaviour of the disease prevalence through a population. Thus, the purpose of this project is to outline the (SIS) epidemic model regarding the continuous time Markov chains. Furthermore, the Maple code will be also described.

2. Continuous-Time Markov Chains

Assume {X(t)} is a continuous-time stochastic process and (t≥0). Therefore, {X(t); t ≥0}can be called a Continuous-Time Markov Chain if the stochastic process {X(t)} has the Markovian property, *if, in addition*, P{X(t + s) = j / X(s) = i}is independent of s, then the continuous-time Markov chain is said to have stationary or homogeneous transition probabilities in which the future behavior of the process depends only on the present and it does not depend on the past (Ross, S., 2007). This means the conditional distribution of X(t+s) (the future) given X(s), s ≥0 (the present) and X(u), 0 ≤ u < s (the past) is defined as the following:

P(X(t + s)=j/X(s)=i, X(u)=x(u); 0≤u< s)=P(X(t+s)=j/X(s)=i)

3. SIS Epidemic Model

There are diverse types of stochastic epidemic models that can be formulated by different stochastic processes, such as SIS Susceptible -Infected-Susceptible as shown in Fig. 1 and SIR Susceptible - Infected- Recovered. In this work, the SIS epidemic model for infectious diseases will be applied with its direct relation to the Continuous Time Markov Chain (CTMC) model. In the CTMC model, the time scale is defined on the continuous period, t ∈[0;∞). However, the states random variables S(t); I(t) are discrete, (Allen, 2008).

According to Clancy (2005), the SIS model can be defined as the model, which regards a fixed population size N = S+I at time t ≥0 with S(t); I(t) susceptible and infective host individuals respectively. In addition, the time for the next infective host individual belongs to the exponential distribution with mean

$$(\beta/N\, I(t)(N - I(t)) + \gamma\, I(t))^{-1}$$

$$\frac{dS(t)}{dt} = N - \beta_{r(t)}S(t)I(t) + \gamma_{r(t)}I(t) - S(t)$$

$$\frac{dI(t)}{dt} = \beta_{r(t)}S(t)I(t) + \gamma_{r(t)}I(t)$$

Where N is the population, $\beta > 0$ is the infection rate, $\gamma > 0$ is the recovery rate, S(t) is the number of susceptible indivduals at time t, I(t) is the number of infectious individuals at time tsubject to N=S(t)+I(t) and r(t) is a Markov chain with a finite state space defined on continuous period, $t \in [0, \infty)$.

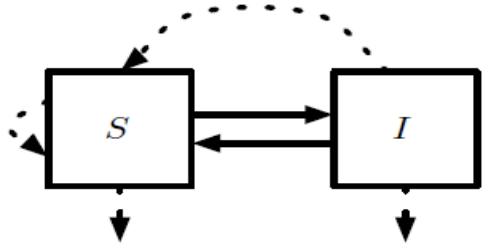

Fig. 1. SIS diagram (Allen, 2008).

4. The Description of Maple Code

It has been generated a sample from the exponential distribution with a Parameter

$$(\beta/N\, Y(t)(N - Y(t)) + \gamma\, Y(t))^{-1}$$

and probability $\frac{\gamma}{\gamma+\beta/N(N-Y)}$

If (Y=Y−1). Otherwise, (Y=Y+1). With different values of the population size N, β, γ, Y_0 and t_{max}. In this case we used {Y (t)} instead of {I(t)}.

The Maple code produces the number of infective host individuals during a period of time (t) and it can be seen how long each individual stays infected and then return susceptible. We can run the program for several times with different parameters' values to see how we can get different numbers of individuals for a long time. In addition, the program can be run to see the number of infective individuals $Y(t_0)$ at a fixed time. For example, the value of Y with the time t_{max}, $Y(t_{max})$, which is the highest value oft, in this case we produced a histogram to show the prevalence of diseases at a fixed time with various values of the other parameters regarding the change in the number of the infective individuals with the change of the other parameters' values, such as β, γ and Y_0.

5. The effect of β and γ values on the graph

If β value is greater than γ value, the graph's trend is going upwards, in this case the number of infected individuals(Y) cannot be seen dying out, we can just see how this number is increasing and decreasing during a period of time (t) as it is shown in the graph in Fig. 2, in which β= 2 and γ= 1

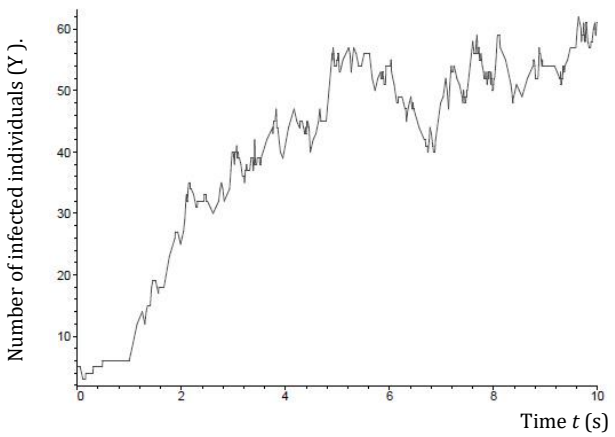

Fig. 2. Graph showing the number of infected individuals wnen β>γ.

Whereas If β value is smaller than γ value the graph's trend is going downwards. Similarly, it can be identified from the graph that how the number of infected individuals (Y) is changing up and down until it is nearly or completely died out in a period of time (t) as it is provided in the graph shown in Fig. 3, in which β= 1 and γ=2.

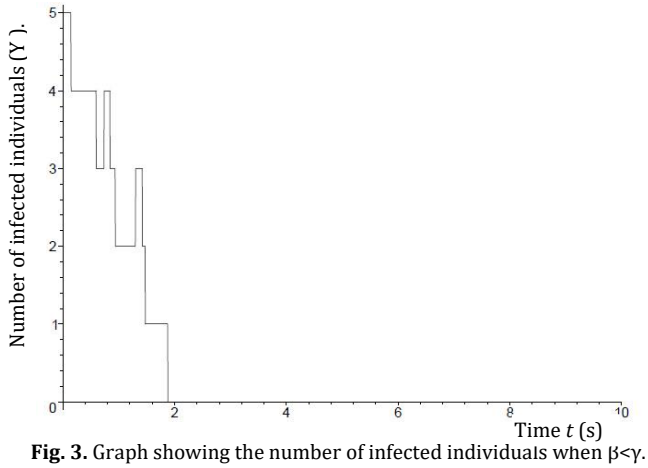

Fig. 3. Graph showing the number of infected individuals when β<γ.

6. The equilibrium level of the infected individuals

The equilibrium level is shown in Fig. 4 when β>γ and in Fig. 5 when β<γ respectively. According to the graphs the equilibrium level of the host individuals when β>γ is approximately 20 infected individuals. However, in the case β<γ the equilibrium level is about five infected individuals. This means that the equilibrium level increases as the β value increases, in which the number of infected individuals enhances at one level that can be clearly seen in the graph.

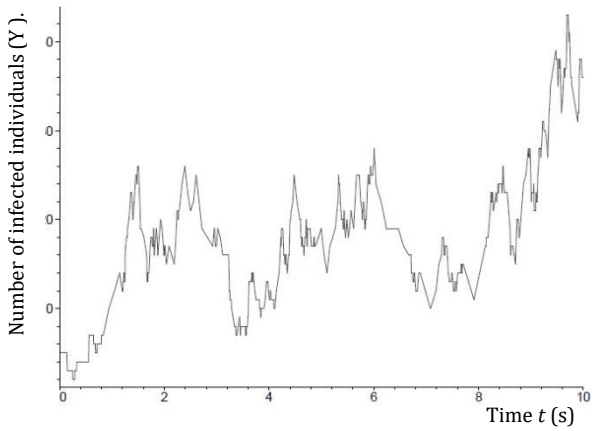

Fig. 4. Graph showing the equilibrium level when β>γ.

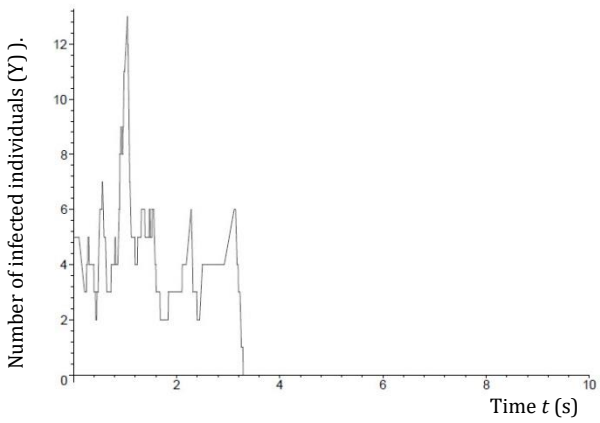

Fig. 5. Graph showing the equilibrium level when β<γ.

7. The number of infective individuals at specific Time

As it has been mentioned previously the Maple code produces the number of infective individuals at a fixed time $Y(t_{max})$, which is demonstrated in three histograms, each one illustrates different data from the others. Fig. 6 shows the number of infective individ-

uals at specific time t_{max}=10 with a higher value of Y to see the difference when we start the experiment with a quite high number of infective individuals.

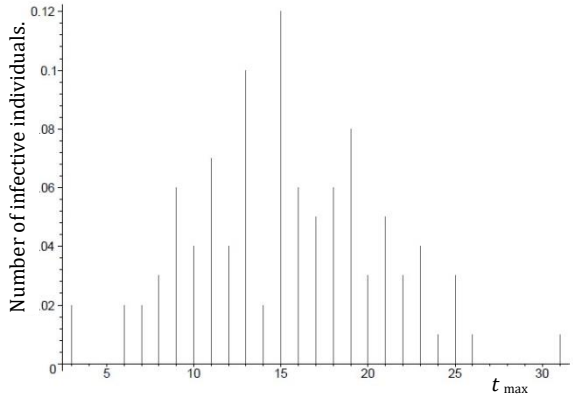

Fig. 6. Number of infective individuals at specific time(Y = 50; β= 2; γ= 3).

Fig. 7 shows that the prevalence of the disease at the fixed time (t_{max}) is decreasing starting with about 0.4 at level zero ending with a very small amount at level ten.

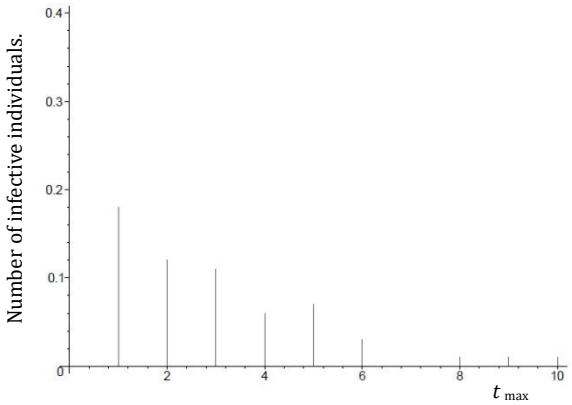

Fig. 7. Number of infective individuals at specific time(Y = 5; β= 3; γ= 2).

According to the information in Fig. 8, the number of infective individuals has almost the same behavior as in Fig. 7, although in both graphs we changed β and γ values to see if there is any difference, it does not seem to.

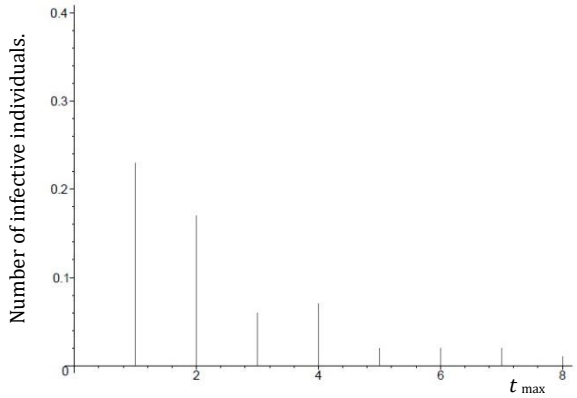

Fig. 8. Number of infective individuals at specific time(Y=5; β=2; γ=3).

8. The equilibrium level for the disease's prevalence at the fixed time

The histogram in Fig. 9 demonstrates the equilibrium level for the number of infected individuals at a specific time t_{max}. In this case and as it is shown in the graph the equilibrium level is about 15.

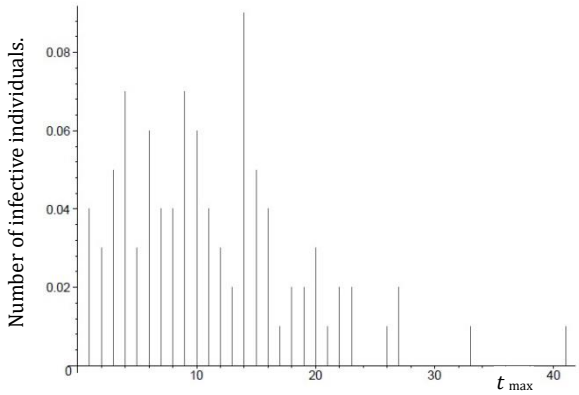

Fig. 9. Graph showing the equilibrium level for the diseases prevalence at specific time (Y = 50, β= 3, γ= 2, t_{max} = 10).

9. The Maple Code

The Maple code includes three procedures, which are First Step, Raga Function and Second Step. These procedures have different inputs as well as the outputs. For instance, the first step of the procedure has an exponential random variable T from which the sample x is generated as a list, Z is a Bernoulli random variable and two lists (Y list and t list), Y list consists of the initial value Y0 and Y-1 if the probability of Z is 1 otherwise Y+1 and t list consists of t values that include the initial value t=0 adding x each time reaching to t_{max}. The output of this procedure produces Y list and t list and plot them. Raga Function procedure has the same lists and the real number t_{max} as the First Step procedure with a real number s that should be between 0 and t_{max}, this procedure produces the ith element of Y list, where i is a positive integer with s between i^{th} and $i+1^{st}$ element of t list. In addition, Second Step procedure has the almost same inputs as the previous procedures with Y t_{max}, which is a list of Y values as a function of t_{max} values by this procedure, and Raga Function we can obtain a histogram shows Y values at a fixed time t_{max}. Finally, because some variables have not defined from the First Step the Maple code needs to be run three times.

10. Conclusion

This project has provided a simple account of improvements in modeling infectious diseases by stochastic models. In particular, using SIS epidemic model with a fixed population size N, susceptible and infective host individuals and time (t) to predict the disease's prevalence. We used Maple program to understand and see how the infectious disease spreads between a population. In addition, the prevalence of the disease has also been examined at a specific time, which done by producing some graphs regarding different values of parameters that may affect the results and the time.

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