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Deterministic and Stochastic SIS Model of Common Cold in Universiti Malaysia Perlis

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ABSTRACT

The epidemiological of common cold with Susceptible- Infected- Susceptible (SIS) model is the description of the dynamics of a disease that is contact transmitted with no long lasting immunity. This is the first attempt to develop SIS model on common cold. The purpose of this study is to compare between the deterministic and stochastic SIS model with demography and without demography (presence of births and deaths), to derive the reproductive number, R_0 between the models and to compare the SIS models demography without pharmacological treatment and with pharmacological treatment. There are two groups tested in SIS model which is UniMAP's students and UniMAP's staffs and these data were taken from UniMAP's university health centre on September 2015. In this study, SIS models were implemented as set of deterministic ordinary differential equations (ODE) that can be solved by using different numerical methods and a discrete time Markov chain (DTMC) process in stochastic simulations. Gillespie algorithm had been used to generate stochastic simulations efficiently in R program. Then, differential equations will be constructed which described the mean statistics of each process. Hence, the derivation of reproductive number, R_0 had been obtained by using the next generation operator method. In these cases, the number of infected persons in SIS demography will continuously decrease as there are presence of births and deaths in the population. Pharmacological treatment had been used to improve and control the infection of common cold from spread to population. This control measures help to minimize the numbers of infected individuals in the population. Therefore, the pharmacological treatment increases the recovery rate and helps them to recover more quickly. Basic reproductive number, R_0 for every models without demography and with demography were derived for determining whether a disease persist in the population or not. The disease will continuously spread out into population if $R_0 > 1$ as all the models are greater than 1.

Keywords: SIS model, reproduction number, deterministic, stochasticity

1. INTRODUCTION

Susceptible- Infected- Susceptible (SIS) model is a model of the behaviour of an infectious disease in a large population. The SIS model consist of susceptible state and infected state. These states are generally called compartments, and the corresponding models are called compartment models. Individuals in population are appoints into different compartments and letters are used to show the different stages in compartmental models. Compartmental model briefly explains what happens at the population scale (Vynncycky & White, 2010). Deterministic modelling is described by ordinary differential equations (ODEs) that can be deal with by using different numerical methods. It is applicable for large population and deterministic simulation that contain no random variables and no degree of randomness. The output of the model is fully determined by the parameter values and the initial conditions.

Stochastic model is developed as a stochastic process with a collection of random variables evolving time (Allen, 2008). The behaviour of dynamics stochastic modelling can be interpreted by discrete time Markov Chain (DTMC) (Vynnycky & White, 2010). The discrete time stochastic SIS model is a Markov chain with finite state space and assumed that at most one event occurs in the time period Δt (Allen & Burgin, 2000). The same set of parameter values and initial conditions will lead to an ensemble of different outputs. Event- driven approach is a method that requires explicit consideration of events. Population forms that emerge from the irregular way of occasions at level of the individual or otherwise called as transition rates is portrayed as demography stochastic (Keeling & Rohani, 2008). The transition probabilities can be performed with individuals experience different rates due to each event (Bloomfield, 2014).

Infectious diseases are defined as a disease caused by an infectious agent and have been characterized by their biological properties. It can be difficult to distinguish between the common cold and influenza. The differences between these diseases are the type of pathogen involved in the disease. For common cold, pathogen involved were rhinoviruses while influenza were influenza viruses A or B. This pathogen can be transmitted by an infected individual and this epidemiology is deal with populations (Krämer & Krickberg, 2010). Common cold can be categorized as SIS model. Common cold is a sickness brought about by virus infection situated in the nose and Figure 1 shows an anatomy of the nose. It is because of infection by an extensive variety of respiratory infections, of which the rhinoviruses are the most widely recognized (Kumar et al., 2007). Rhinoviruses are spread effortlessly through individual-to-individual contact because there are no less than 100 different antigenic strains of rhinovirus, making it troublesome for the immune system to confer protection (Kumar & Clark, 2009).

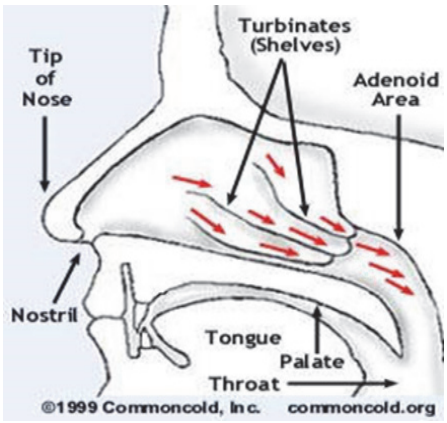


Figure 1. An illustration anatomy of the nose.

2. METHODS

2.1 Method 1: Without demography

The simplest model without demography, no birth, no death and no migration which is also known as closed population was used. Le β e the size of the population. Schematic of the model in Figure 2 showed that the transition rates, indicated by arrow, between each compartment shown. Parameters β and γ represent the transition rates between compartmental model of susceptible and infected. Let S be the number of susceptible individuals and I be the number of infected individuals. The transmission rate is denoted by β while recovery rate is γ. The infected individuals return to be susceptible class on recovery because the disease confers no immunity against infection.

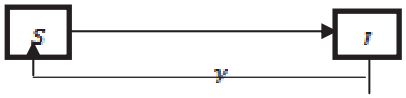


Figure 2. A schematic SIS general model diagram (Chitnis, 2011)

Deterministic of SIS model

The SIS model is given in the following set of equations:

$$\frac{dS}{dt} = \gamma I - \beta SI \quad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (2)$$

where,

βSI = susceptible individuals makes contact with infected individuals to transmit disease, β in unit time, *t*.

γI = infected individuals who recover then enter again in susceptible class in unit time, *t*. The discrete time deterministic SIS model with the total population held constant has the form (Allen & Burgin, 2000).

$$S(t + \Delta t) = S(t) + (-\beta SI + \gamma I)\,\Delta t \quad (3)$$

$$I(t + \Delta t) = I(t) + (\beta SI - \gamma I)\,\Delta t \quad (4)$$

where $\Delta t = n\Delta t, n = 0,1,2, \ldots, \Delta t$ is a fixed timed interval (days), $S(0) > 0, I(0) > 0$ and $S(0) + I(0) = N$. Let *S(t)* be the number of susceptible individuals in the population at time *t* and *I(t)* be the number of infected individuals in the population at time *t*. $S(t + \Delta t)$ is defined by the increase in the number of susceptible individuals from time *t* to time $t + \Delta t$ while $I(t + \Delta t)$ is defined by the number of infected individuals from time *t* to time $t + \Delta t$. The total population *S(t) + I(t) = N* is constant. The model is set to disease free state to obtain reproductive number. For disease free state, consider infected compartment, $I = 0$.

Stochastic SIS model

Gillespie algorithm will be used in R program to generate stochastic simulation. The idea of the Gillespie algorithm is to determine when the next event will occur. The discrete time stochastic version of the Markovian model SIS (without demography) model with finite state space is defined by the following events and rates in Table 1 (Keeling & Rohani, 2008).

Table 1 Transition rates and change in state space of the process $S(t), I(t)$ to the next event in small time, Δt.

Event	Transition	Transition rate
Infection of susceptible	$s \to s-1$ & $i \to i+1$	βsi
Recovery of infection	$i \to i-1$ & $s \to s+1$	γi

2.2 Method 2: With demography (Without pharmacological treatment)

The natural birth and death rates are included in this model and assumed that all births are susceptible and death rate is equal for all compartments. Let the birth and death rates are equal so that the total population remains constant with respect to time. Birth rate is defined as the birth rate per capita and death rate indicates the measure of deaths per capita.

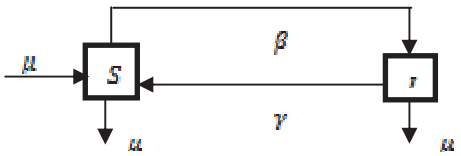


Figure 3. A schematic SIS model with demography diagram (Hethcote, 1989).

Deterministic SIS model with demography

This system is described by the following equations:

$$\frac{dS}{dt} = \mu - \beta SI + \gamma I - \mu S \quad (5)$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I \quad (6)$$

New parameter, birth and death rate, μ was added into Eq. (5) and (6). By adding the equations, it is shown that the total population is constant at any instant t is $S(t) + I(t) = N$. Then,

$$\frac{dS}{dt} + \frac{dI}{dt} = 0 \quad (7)$$

Hence, the discrete time deterministic SIS model has the form:

$$S(t + \Delta t) = S(t) + (\mu - \beta SI + \gamma I - \mu S)\,\Delta t \quad (8)$$

$$I(t + \Delta t) = I(t) + (\beta SI - \gamma I - \mu I)\,\Delta t \quad (9)$$

where $\Delta t = n\Delta t, n = 0,1,2,\ldots,\Delta t$ is a fixed timed interval (in days), $S(0) > 0, I(0) > 0$ and $S(0) + I(0) = N$. Where the total population $S(t) + I(t) = N$ is constant. Let all the parameters are positive, $\beta > 0, \gamma > 0$ and $\mu > 0$. Let $S(t)$ be the number of susceptible individuals in the population at time t and $I(t)$ be the number of infected individuals in the population at time t. $\mu\Delta t$ is the number of births or deaths per individuals during the time interval. $\gamma\Delta t$ is the number of individuals that recover in the time interval, Δt. Infected individuals immediately become susceptible once they have recovered because they do not develop immunity towards common cold.

Stochastic SIS model with demography

In the stochastic DTMC model, Gillespie algorithm will be used in this study to generate stochastic simulation and the idea of the Gillespie algorithm is to determine when the next event will occur. The discrete time stochastic version of the Markovian model SIS (with demography) model with finite state space is defined by the following events and rates in Table 2 (Keeling & Rohani, 2008).

Table 2 Transition rates and change in state space of the process $S(t)$, $I(t)$ to the next event in small time, Δt.

Event	Transition	Transition rate
Birth of susceptible	$s \to s+1$	μ
Death of susceptible	$s \to s-1$	μs
Infection of susceptible	$s \to s-1$ & $i \to i+1$	βsi
Recovery of infection	$i \to i-1$ & $s \to s+1$	γi
Death of infection	$i \to i-1$	μi

2.3 Method 3: With demography (Pharmacological treatment)

There are many ways to improve and control the infection from spreading to the population. These control measure help to minimize the risk of transmission between infectious and susceptible humans. Hence, the intervention method for managing common cold is pharmacological treatment.

Deterministic SIS model with demography (pharmacological treatment)

Birth and death rate parameters, μ was added into the equations below. The population as a whole is assumed to be constant, *S(t) + I(t) = N.* This system is described by the following equations:

$$\frac{dS}{dt} = \mu - \beta SI + pI - \mu S \tag{10}$$

$$\frac{dI}{dt} = \beta SI - \mu I - pI \tag{11}$$

Hence, the discrete time deterministic SIS model has the form:

$$S(t+\Delta t) = S(t) + (\mu - \beta SI + pI - \mu S)\,\Delta t \tag{12}$$

$$I(t+\Delta t) = I(t) + (\beta SI - \mu I - pI)\Delta t \tag{13}$$

where $\Delta t = n\Delta t, n = 0,1,2,\ldots,\Delta t$ is a fixed timed interval (in days), $S(0) > 0, I(0) > 0$ and $S(0) + I(0) - N$. Where the total population *S(t) + I(t) = N* is constant. Let all the parameters are positive, $\beta > 0, p > 0$ and $\mu > 0$. Let *S(t)* be the number of susceptible individuals in the population at time t and *I(t)* be the number of infected individuals in the population at time *t.* $\mu\Delta t$ is the number of births or deaths per individuals during the time interval. $p\Delta t$ is the recovery rate from pharmacological treatment taken by infected individuals to recover in the time interval, Δt before enter again in the susceptible class because there are no long- lasting immunity.

Stochastic SIS model with demography (pharmacological treatment)

The stochastic version of the Markovian SIS (with pharmacological treatment) model is defined by the following events and rates as in Table 3 (Chowell et al., 2009).

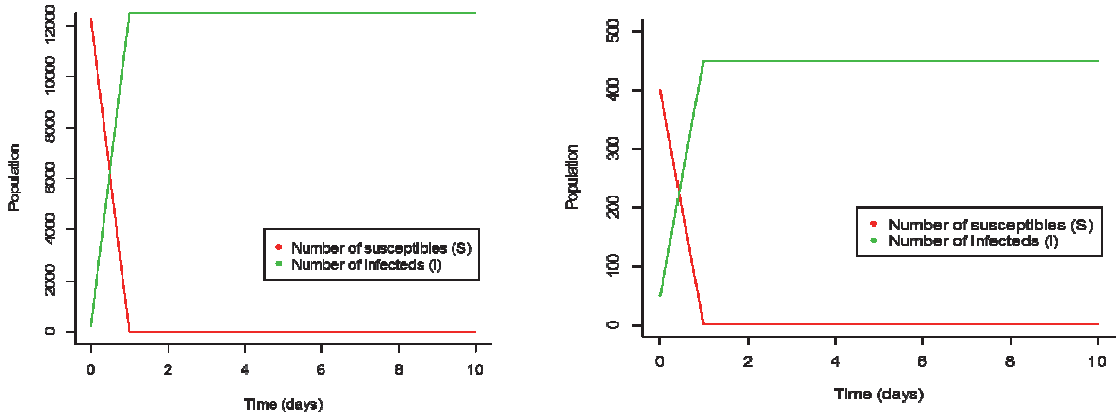
Table 3 Transition rates and change in state space of the process $S(t), I(t)$ to the next event in small time, Δt.

Event	Transition	Transition rate
Birth of susceptible	$s \to s+1$	μ
Death of susceptible	$s \to s-1$	μs
Infection of susceptible	$s \to s-1$ & $i \to i+1$	βsi
Recovery of infection from pharmacological treatment	$i \to i-1$ & $s \to s+1$	γi
Death of infection	$i \to i-1$	μi

3. RESULTS

Discrete time deterministic model and stochastic models are formulated and analysed for SIS models with different population sizes for two groups which are UniMAP's students and UniMAP's staffs. The discrete time model is directly applicable to particular disease such as common cold. The population of UniMAP's students comprise of approximately 12500 individuals while UniMAP's staffs consist of approximately 450 individuals. There will be three methods (without demography, without demography pharmacological treatment and with demography pharmacological treatment) tested in SIS models.

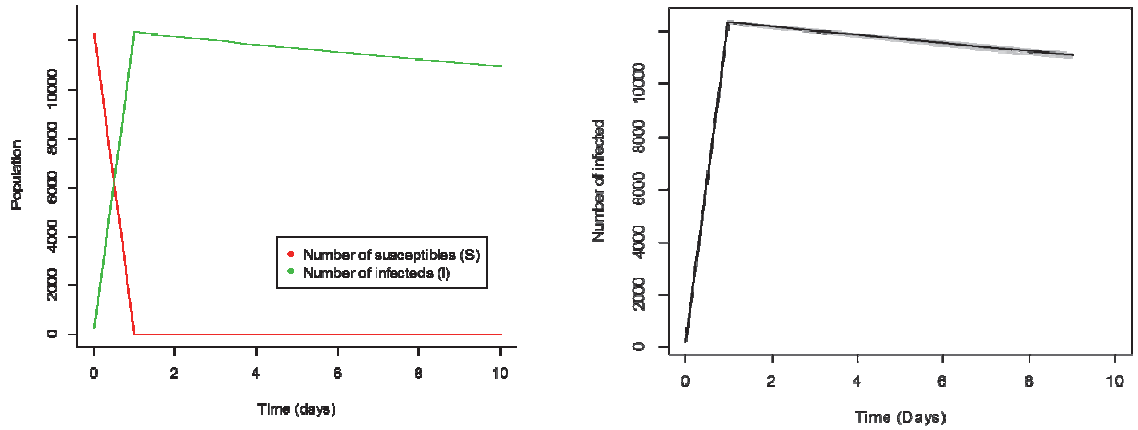
3.1 Method 1: Without demography



(a) (b)

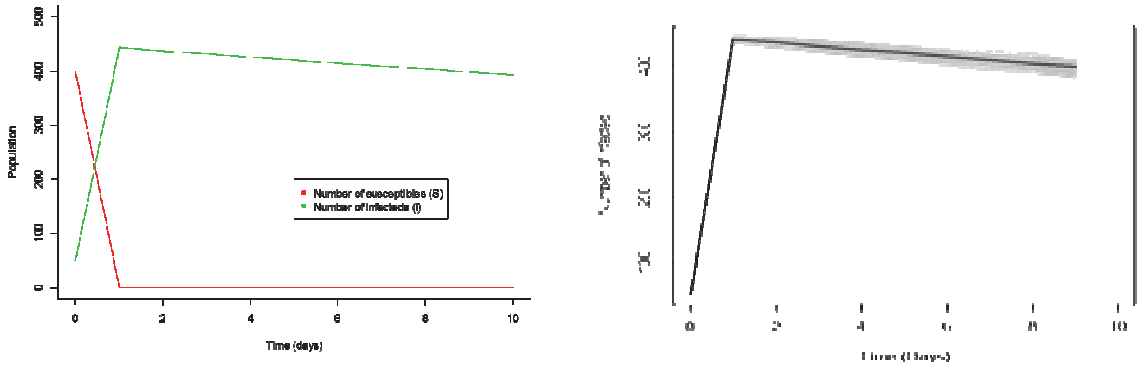
Figure 4. The deterministic SIS model without demography for (a) UniMAP's students and (b) UniMAP's staffs.

3.2 Method 2: Without demography (Without pharmacological treatment)



(a) (b)

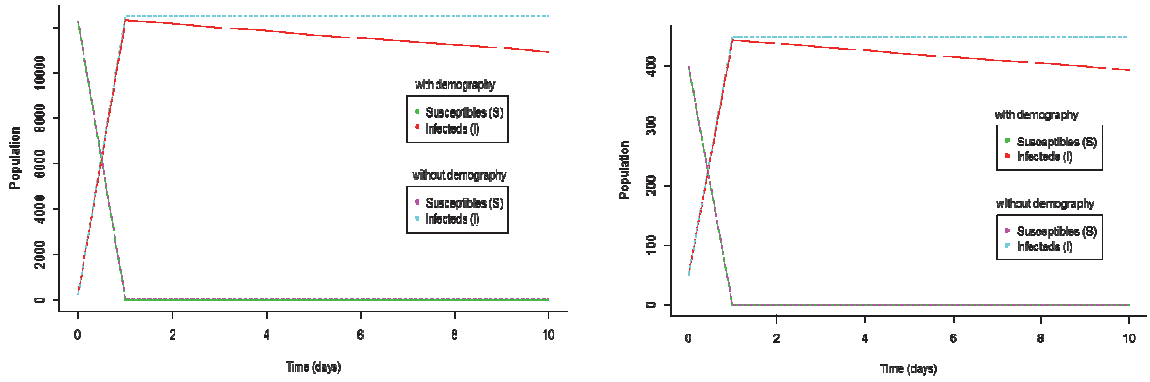
Figure 5. (a) The deterministic SIS model with demography for UniMAP's students and (b) 100 simulations of the stochastic SIS model using Gillespie's Method.



(a) (b)

Figure 6. (a) The deterministic SIS model with demography for UniMAP's staffs and (b) 100 simulations of the stochastic SIS model using Gillespie's Method.

3.3 Method 3: With demography (With pharmacological treatment)



(a) (b)

Figure 7. Comparison between without demography and with demography deterministic SIS model of (a) UniMAP's students and (b) UniMAP's staffs.

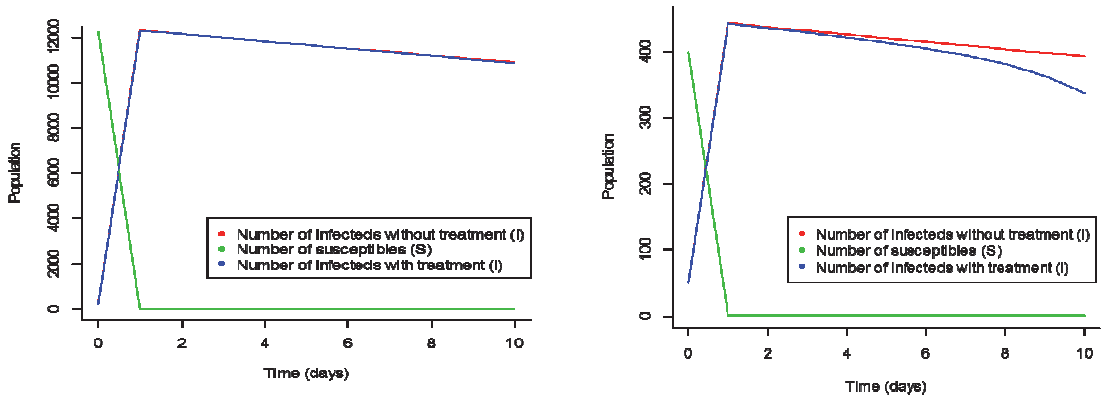


Figure 8. Comparison deterministic SIS model with and without pharmacological treatment for (a) UniMAP's students and (b) UniMAP's staffs.

3.4 Comparison for three methods between UniMAP's students and UniMAP's staffs

Table 4 Comparison for three methods on UniMAP's students

	Without demography	**With demography**	
		Pharmacological treatment	
		With	**With**
μ	-	0.0133	
β	0.3333		
γ	0.1429		-
ρ	-		0.3
R_0	2.3324	2.1338	1.0638

Table 5 Comparison for three methods on UniMAP's students

	Without demography	**With demography**	
		Pharmacological treatment	
		With	**With**
μ	-	0.0133	
β	0.3333		
γ	0.10		-
ρ	-		0.3
R_0	3.333	2.9417	1.0638

4. CONCLUSIONS

It can be concluded that the behaviour of SIS models with and without demography are nearly the same. Stochastic models such as Markov chain model provides alternative to deterministic models and ease some of the problems with the deterministic formulations (Allen & Allen, 2003). Knowledge of the similarities and differences between models is useful in selecting the correct formulation. In this case, the difference is just the number of infected in demography which slightly decreases compared to without demography before it reaches the equilibrium

state. This is due to the presence of birth and death rate in the population. Gillespie algorithm was used to simulate stochastic models in R by drawing a process randomly from all events in process according to their respective probabilities.

The basic reproductive number R_0 plays an important role whether the disease is eliminated or persists in population. Reproduction number of all SIS models were derived from DFE and it can be concluded that if $R_0 > 1$, the disease will remain and continuously spread out in the population which agrees with the findings of Heatcote (1989), Allen and Burgin (2000) and Chitnis (2011). In this case, numerical test shown that when all reproductive number in all models are greater than 1, virtually everyone in population will sooner or later remains infected as the disease will continuously spread out into population (Haran, 2009).

By implementing pharmacological treatment that increases the recovery rate, p it helps to reduce the basic reproductive rate of a disease. This shows that if the recovery rate is high, the number of infected will continuously decrease and less compared to without pharmacological treatment. So, if recovery rate is larger, then the infected individuals that are recovering in larger numbers than the same sized pool would recover otherwise which is in agreement with Tassier (2013). This is because of the case that they speed up the rate of recovery. Reproductive number, R_0 can be reduced through an increase in the recovery rate through medication (Chitnis, 2011).

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APPENDIX

If any, the appendix should appear directly after the references without numbering, and on a new page.