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The Dynamics of SIS Epidemic Model with Emphasis on Deterministic Approach

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Abstract

The rate of spread of sexually transmitted diseases like gonorrhea, syphilis and Chlamydia in the third world countries is so alarming. Hence, in this paper, we present SIS epidemic model using deterministic approach in a closed population. It was shown that the dynamics of the model are determined by the basic reproduction ratio R_O (with brief biological interpretation). It was also shown that the asymptotic dynamics of the model are well determined for a disease free equilibrium and for an endemic equilibrium.

Keywords: susceptible, infective, basic reproduction ratio, asymptotic dynamics, disease free equilibrium, endemic equilibrium.

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1.0 Introduction

The issue of sexually transmitted disease (STD) such as gonorrhea, syphilis and Chlamydia is a global problem that has plagues the human race for a very long time now. In this work, we present the SIS epidemic model from a deterministic perspective. In an SIS epidemic model, a susceptible individual, becomes infected and infections, but does not develop immunity to the disease. Hence, after recovery, infected individuals return to the susceptible class.

Many models and methods have been devised for the study of SIS epidemic model. Allen [1] considered differential equations describing the dynamics of an SIS epidemic model

$$\frac{ds}{dt} = -\frac{\beta}{N}SI + (b+\gamma)I \quad and \qquad \frac{dI}{dt} = \frac{\beta}{N}SI - (b+\gamma)I \quad \text{.....(1)}$$

With $R_o = \dfrac{\beta}{b+\gamma,}$

Neal [2] analysed both deterministic and stochastic models.

Enatsu et. al [3] proposed a discrete-time SIS epidemic model with immigration of infective by the back-ward Euler's method. Reluga [4] analysed the rational expectation equilibrium in an epidemiology game with two interacting subpopulations of equal size where decisions change the prevalence and transmission patterns of an infectious disease.

Marva et. al [5] consider a spatially distributed periodic multi-strain SIS epidemic model. They allow susceptible and infected individuals migrate between patches with periodic migration rate.

Gray et. al [6] discussed the effect of telegraph noise in the well known SIS epidemic model and also established the explicit solution of the stochastic SIS epidemic model which is useful in performing computer simulations.

Artalejo et. al [7] Developed computational schemes for the corresponding distributions in a transient regime and still absorption.

Jianquan al [8] analysed the SIS epidemic model with a single vaccination was investigated and the efficiency of vaccine. The disease related death rate and vague population dynamics were also considered.

Lijun and Xiao-Diang [9] investigated the global dynamics of a periodic SIS epidemic model with maturation delay. They also analysed and obtained sufficient conditions for the single population growth equation to admit a globally attractive positive periodic solution.

Iggidr. et. al [10] consider an SIS epidemiological model with demographic effects, births, mortality and mortality caused by infection.

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2.0 The Model Formulation

We shall adopt the epidemic model [11] for the purpose of formulating this model. The SIS model is a model where there is movement from classes (1). Hence, the figure below.

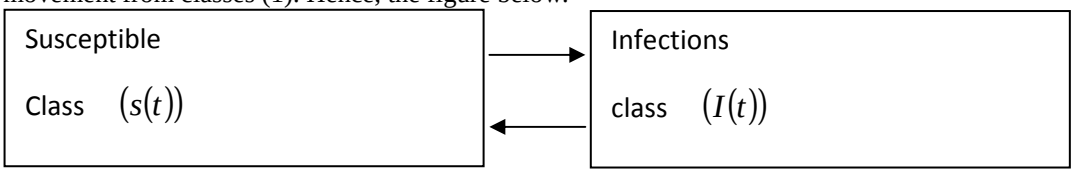

Figure 1: SIS compartmental diagram (1)

We assume that the probability that an infective recovers during time Δt is given by $\tau\Delta t$. Then, the total number of infective people that recover during time Δt is given by $\tau\Delta t\ I(t)$. The expected number of newly infected people in the total population during time Δt is $\beta\Delta t s(t)I(t)$.

Thus

$$I(t+\Delta t) = I(t) + \beta\Delta t s(t)I(t) \quad \text{.....(2)}$$

$$I(t+t) - I(t) = \beta\Delta t s(t)I(t) - I\Delta t I(t) \quad \text{.....(3)}$$

$$I(t+\Delta t) - I(t) = \Delta t(\beta sIt)I(t) - \tau I(t) \quad \text{.....(4)}$$

Dividing equation (4) by Δt, then take limit as $\Delta t \to 0$

$$\text{Lin}\,\Delta t \to 0 \lim_{\Delta t\to 0}\left\{\frac{I(t+\Delta) - I(t)}{\Delta t}\right\} = \lim_{\Delta t\to 0}\left\{\frac{\beta s(t)I(t) - \tau I(t)}{1}\right\} \quad \text{.....(5)}$$

$$\text{Lin}\ \Delta t \to 0 \quad \lim_{\Delta t\to 0}\left\{\frac{I(t+\Delta t) - I(t)}{\Delta t}\right\} = \frac{dI}{dt} = \beta s(t)I(t) - \tau I(t) \quad \text{.....(6)}$$

Similarly,

$$\frac{ds}{dt} = -\beta s(t)I(t) + \tau I(t) \quad \text{.....(7)}$$

Therefore, our model is

$$\frac{dS}{dt} = -\beta S(t)I(t) + \tau I(t) \ \ and \ \ \frac{dI}{dt} = \beta S(t)I(t) - \tau I(t) \quad \text{..... ....(8)}$$

2.1 Parameters and Symbols

S (t) = susceptible class (individuals) at time t
I (t) = infected class (individuals) at time t
Z (t) = probability that an individual is infected at time t = 0 is still infected at time t
β = contact rate (or transmission rate)
τ = recovering rate
N = total population size

2.2 Assumptions

i. We assume that the disease does not confer – long lasting immunity. Hence, after recovering infected individuals returns to the susceptible class.
ii. There are no birth and death, and so the population size N is constant.
iii. The population is well mixed

2.3 The model

Recall from (8) $\frac{dS}{dt} = -\beta S(t)I(t) + \tau I$ and $\frac{dI}{dt} = \beta S(t)I(t) - \tau I$

Therefore $s(t)+I(t)=N$ …… .(9)

If $\frac{ds}{dt}+\frac{dI}{dt}=0$ therefore, $\frac{dN}{dt}=0$ …… …(10)

the initial conditions satisfy

$S(0)>0, I(0)>0$ and $s(0)+I(0)=N$ …… ……(11)

The dynamics of the model (8) are determined by the basic reproduction ratio (R_o). The basic reproduction ratio is the number of secondary infection caused by one infected individuals in an entirely susceptible population [1]. The basic reproduction ratio for model (8) is defined as

$$R_o=\frac{\beta N}{\tau} \text{.....(12)}$$

this can be obtained from (8)

The asymptotic dynamics of the model (8) are summarized in the theorem below.

Theorem: Let S(t) and I (t) be a solution to model (8)

Case 1: if $R_0 \le 1$, then $\lim_{t\to\infty}\{S(t), I(t)\}=(N,0)$ is a disease free equilibrium.

If Case 2: then $R_o>1$, $\lim_{t\to\infty}\{S(t), I(t)\}=\left(\frac{N}{R_o}, N\left(1-\frac{1}{R_o}\right)\right)$ is an endemic equilibrium.

3.0 Solution of the model

We consider the infections case (from equation (8)) $\frac{dI}{dt}=\beta SI-\tau I$

this can also be written as

$$\frac{dI}{dt}=\tau(R_o-1)I\left(1-\frac{I}{N\left(1-\frac{1}{R_o}\right)}\right) \text{.....(13)}$$

Set $k=N\left(1-\frac{1}{R_o}\right)$ in (13) therefore,

$$\frac{dt}{dt}=\tau(R_o-1)I\left(1-\frac{I}{k}\right) \text{.....(14)}$$

If

$$\frac{dI}{I\left(1-\frac{I}{k}\right)}==\tau(R_o-1)dt \text{.....(15)}$$

Integrate both sides of (15) we have

$$\int_0^I I\frac{dt}{I\left(1-\frac{I}{k}\right)}=\tau(R_o-1)t \text{.....(16)}$$

Decomposing the left hand side of (16) using partial fraction, then we shall have

$$\int_0^I \frac{dI}{I}+\frac{1}{k}\int_o^I \frac{-\frac{dI}{k}}{-\frac{1}{k}\left(1-\frac{I}{k}\right)}=\tau(R_o-1)t \text{.....(17)}$$

$$InI-In\left(1-\frac{I}{k}\right)=\tau(R_o-1)t \text{.....(18)}$$

$$In\left(\frac{I}{\frac{k-I}{k}}\right) = \tau(R_o - 1)t \quad \text{..... (19)}$$

$$I = \frac{k}{(I + ke^{-\tau(R_o-1)t})} \quad \text{.....(20)}$$

Recall from (13)

$k = N\left(1 - \frac{1}{R_o}\right)$ therefore,

$$I(t) = \frac{N\left(1 - \frac{1}{R_o}\right)}{(I + N\left(1 - \frac{1}{R_o}\right)e^{-\tau(R_o-1)t})} \quad \text{..... ....(21)}$$

But,

$N = s(t) + I(t) \Rightarrow s(t) = N - I(t)$

$$s(t) = N - \left\{\frac{N\left(1 - \frac{1}{R_o}\right)}{\left(1 + N\left(1 - \frac{1}{R_o}\right)e^{-\tau(R_o-1)t}\right)}\right\} \quad \text{.....(22)}$$

Therefore, the solution for $I(t)$ and $S(t)$ are equation (21) and (22) respectively.

4.0 Analysis of the model

From (11), when t=0 at initial time

$$S(0) = N\left(1 - \frac{\left(1 - \frac{1}{R_o}\right)}{1 + N\left(1 - \frac{1}{R_o}\right)}\right) > 0 \quad \text{..... (23)}$$

$$I(0) = \frac{N\left(1 - \frac{1}{R_o}\right)}{1 + N\left(1 - \frac{1}{R_o}\right)} > 0 \quad \text{..... (24)}$$

S(0) + I(0) = N.

We can give a biological interpretation to the basic reproduction ratio R_o. Let $Z(t)$ be the probability that an individual initially infected at t = 0 is still infected at time, t. Since, the probability of being infective at time $t + \Delta t$ is equal to the probability of being infective at time t times the probability of not being recovering during time Δt, we have

$$Z(t + \Delta t) = Z(t)(1 - \tau\Delta t) \quad \text{.....(25)}$$

$$\lim_{\Delta t \to 0}\left\{\frac{Z(t + \Delta t) - Z(t)}{\Delta t}\right\} = \frac{dZ}{dt} = -\tau Z(t) \quad \text{..... (26)}$$

With initial condition $Z(0)$. Then,

$$\frac{dZ}{dt} = -\tau Z \Rightarrow Z(t) = e^{-\tau t} \quad \text{..... ...(27)}$$

Now, the expected number of secondary infections produced by a single primary infection over the time period, $(t, t + dt)$ is given by probability that the primary infective is still infectious at time t multiplied by the expected number of secondary infections produced by a single infective during time dt, is $Z(t) \times S(t)\beta dt$. We assume that the total number of secondary

infections from a single infective individual is small relative to the population size N. Therefore, the expected number of secondary infective produced by a single primary infective introduced into a completely susceptible population

$\int_0^\infty \beta Z(t)S(t)dt \approx \beta N \int_0^\infty Z(t)dt, \quad S(t) \approx N$

$= \beta N \int_0^\infty e^{-\pi} dt$

$= \frac{\beta N}{\tau}$

$= R_o$..... ....(28)

If a single infected individual introduced into a completely susceptible population produces more than one secondary infection before recovering, then $R_o \succ 1$ and the disease becomes endemic (Chasnov [11]. But, when $R_o \leq 1$ is a disease free population.

Case 1.

If $R_o \leq 1$ as $t \to \infty$ from equation (21) and (22), we have $\lim_{t\to\infty}\{S(t), I(t)\} = (N, o)$ as a disease free equilibrium which inform with our therein above. The implication of this as that the entire population (N) is susceptible to the disease as t becomes very large. Numerical analysis of case 1: We assume values for the parameters at different time.

R_0 = 0.5, N = 500, $\beta = 0.005$ and $\tau = 5$

Table 1: Disease free equilibrium ($R_o \leq 1$)

$s(t)$	R_o	t	β	τ	N	$s(t)$	$I(t)$
S(0)	0.5	0	0.005	5	500	499	1.002
S(1)	0.5	1	0.005	5	500	499.9	0.082
S(2)	0.5	2	0.005	5	500	500	0.007
.		.					.
.		.					.
.		.					.
S(50)	0.5	50	0.005	5	500	500	0

Case 2.

If $R_o > 1$ as $t \to \infty$ from equation (21) and (22), we have $\lim_{t\to\infty}\{S(t), I(t)\} = \left(\frac{N}{R_o}, N\left(1 - \frac{1}{R_o}\right)\right)$ is an endemic equilibrium.

The implication of this is that the entire population (N) becomes infective to the disease as t becomes very large.

Numerical analysis of case 2: We assume values for the parameters at different time.

R_0 = 5, N = 500, $\beta = 0.003$ and $\tau = 0.25$

Table2:An endemic equilibrium. (R_o >1)

$S(t)$	R_o	t	β	τ	N	$S(t)$	$I(t)$
S(0)	0.5	0	0.003	0.25	500	499.0024938 ≈ 499	1
S(1)	0.5	1	0.003	0.25	500	497.3000661 ≈ 497	3
S(2)	0.5	2	0.003	0.25	500	492.7449636 ≈493	7
.		.					.
.		.					.
.		.					.
.		.					.
S(50)	0.5	50	0.003	0.25	500	100	400

4.1 Discussion

In this paper we have been able to formulate the SIS epidemic model by considering both the infectious class $I(t)$ and the susceptible class. The solution of the model at t=0 shows that $S(0)+I(0)=N$, signifying a constant population size (satisfying the initial conditions of the model). The model is analysed. It was shown that the dynamic of model (8) are determined by basic reproduction ratio R_o.
The model was further analysed by considering the asymptotic dynamics of the model.

Case 1:

It was shown that when $R_o \leq 1$ at the initial stage an individual is infected with the disease but as t increases the population *N* becomes entirely free from the disease (susceptible)

Case 2:

It was also shown that when $R_o > 1$ at the initial stage an individual is infected with the disease and as t increases the number of individual infected with disease become very large and approaches the population size (N). Signifying that infected individuals produces more than one secondary infection before recovering.

5.0 Summary and Conclusion

We have been able to established that from the above model

Case 1.If $R_o \leq 1$ we have $\lim_{t\to\infty}\{S(t), I(t)\} = (N, o)$ as a disease free equilibrium signifying that the entire population N becomes susceptible.

Case 2.If $R_o > 1$ we have $\lim_{t\to\infty}\{S(t), I(t)\} = \left(\frac{N}{R_o}, N\left(1-\frac{1}{R_o}\right)\right)$ is an endemic equilibrium, also signifying that as t becomes very large, the entire population becomes infective.

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