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Stability Analysis of A Non Vaccinated Sir Epidemic Model

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Abstract:
A proper mathematical model structure is required to understand the dynamics of the spread of infectious diseases. In this paper I have discussed about a general SIR epidemic model which represents the direct transmission of infectious disease. Local and global stabilities of both the disease free and the endemic equilibrium are derived by using the evaluated reproduction number R_0.

Key words: Mathematical model, Local Stability, Epidemic Model, Reproduction Number

1.0 Introduction

Any infectious diseases mainly caused by pathogenic microorganisms, such as viruses, bacteria, fungi and parasites. The diseases can spread directly or indirectly from one person to another or from animals to humans. These diseases are one of the main causes of worldwide death. In spite of all the advancement in medicines, infectious disease outbreaks still pose a significant threat to the public health and economy [1-6]. The spread rates of different infectious diseases are rising due to changes in human behavior, inappropriate use of antibiotic drugs, increased trade and travel, larger and denser cities and the emergence of new and resurgent pathogens.

Mathematical modeling is a valuable tool to understand the dynamics of infectious diseases and to support the development of control strategies. A lot of Mathematical models for different infectious diseases were proposed by several researchers and scientists. Shulgin et al.[5] considered a simple Susceptible-Infected-Recovered (SIR) epidemic model with pulse vaccina-tion. In their work they presented that if certain conditions regarding the magnitude of vaccination proportion together with period of pulses are satisfied then the pulse vaccination leads to epidemic eradication. Kribs-Zaleta and Velasco-Henandez [3] considered a simple two dimensional SIS model with vaccination showing backward bifurcation. In this paper I have discussed the stability analysis of a general Susceptible-Infected-Recovered (SIR)
epidemic model of infectious disease. I have presented both disease-free equilibrium and the endemic equilibrium of the proposed model. The local dynamics of a general SIR is determined by the basic reproduction number R_0 which depends on the parameter values. For $R_0 \le 1$ the disease-free equilibrium is locally asymptotically stable while for $R_0 > 1$ the endemic equilibrium exists. By using the theory of Lyapunov function, I have presented the global asymptotic stability.

2.0 Mathematical Formulation

In this section, I formulate an epidemic model for the spread of a general infectious disease. I
split the total population N(t), into three distinct subclasses which are susceptible S(t), infectious
I(t) and recovered R(t). Now the model can be represented by the following system of differentials
equations.

$$\left.\begin{aligned} \frac{dS(t)}{dt} &= \mu - \lambda S(t)I(t) - \mu S(t) \\ \frac{dI(t)}{dt} &= \lambda S(t)I(t) - \gamma I(t) - \mu I(t) \\ \frac{dR(t)}{dt} &= \gamma I(t) - \mu R(t) \end{aligned}\right\} \text{-----(1)}$$

with the initial conditions $S(0) \ge 0, I(0) \ge 0, R(0) \ge 0 \big] - - - - - - (2)$

Here μ is the recruitment and natural death rate, λ is the effective contact rate between susceptible
and infected individuals and γ is the recovery rate of infected individuals.By considering the total population density, we have

$S(t) + I(t) + R(t) = 1 \Rightarrow R(t) = 1 - S(t) - I(t) \big]$ Therefore it is enough to consider

$$\left.\begin{aligned} \frac{dS(t)}{dt} &= \mu - \lambda S(t)I(t) - \mu S(t) \\ \frac{dI(t)}{dt} &= \lambda S(t)I(t) - \gamma I(t) - \mu I(t) \end{aligned}\right\} - -(3)$$

The feasible region for the above system is $\Omega = \left\{ \big(S(t), I(t)\big) \in \Re^2_+, S(t) + I(t) \le 1 \right\}$

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Since $\left.\begin{aligned} S(t)=0 \Rightarrow \frac{dS(t)}{dt}=\mu>0 \\ I(t)=0 \Rightarrow \frac{dI(t)}{dt}=0 \end{aligned}\right]$

Thus Ω is positively invariant.

3.0 Threshold Analysis

Here we will discuss about the stability analysis.

Here the disease free equilibrium point is $E_0=(1,0)$. To find the endemic equilibrium point $E_1=(S^*,I^*)$ we making the right hand side of the system (3) equal to zero and thus we have

$S^*=\frac{\gamma+\mu}{\lambda},\ I^*=\frac{\mu}{\lambda}(R_0-1),$

where $R_0=\frac{\lambda}{\mu+\lambda}$

In mathematical epidemiology an important concept is related to the basic reproduction number R_0. As it serves as a threshold parameter that governs the spread of infectious diseases in a population.This is defined as the second expected number produced from just one individual in a susceptible population. For any infectious disease, one of the most important concerns is its ability to invade a population [2]. This can be expressed by a threshold parameter R_0. If $R_0<1$, then each infected individual in its entire period of infectivity, will produce less than one infected individual on average. In DFE case the system is locally asymptotically stable, which shows that the disease will be wiped out of the population.

If $R_0>1$, then the each infected individual in its entire infective period having contact with susceptible individuals will produce more than one infected individual, which will then lead to the disease invading the susceptible population, and the DFE is unstable [6].

The linearization by Routh Hurwitz criteria around the endemic equilibrium point E_1 in [3] is locally asymptotically stable for $R_0>1$.

To show that the proposed system is globally asymptotically stable, we use the Lyapunov function theory for both the disease free and the endemic equilibrium. First we present the global stability of the disease-free equilibrium.

Theorem 3.1. If $R_0\le 1$, then the disease-free equilibrium E_0 of the system is globally asymptotically stable on Ω.

Proof. To establish the global stability of the disease free equilibrium E_0, we construct the following Lyapunov function $V:\Omega\to R$:

$V(S,I)=I(t)$

Calculating the time derivative of V along the solution of the proposed system, we obtain

$V'(t)=\lambda S(t)I(t)-(\gamma+\mu)I(t)=(\gamma+\mu)(R_0S(t)-1)I(t)$

Here we can observe that $V'(t)\le 0$ for $R_0<1$

Now if $R_0<1$, then $V'(t)=0\Leftrightarrow I(t)=0$ and if $R_0=1$, then $V'(t)=0\Leftrightarrow S(t)=1$

Hence by LaSalle's invariance principle [4] the diseases-free equilibrium point E_0 is globally asymptotically stable on Ω.

Theorem 3.2. The endemic equilibrium $E_1=(S^*,I^*)$ of the system is globally asymptotically stable on Ω.

Proof. For the global stability of the endemic equilibrium E_1, we construct the Lyapunov function $L:\Omega_+\to R$, where $\Omega_+=\{(S(t),I(t))\in\Omega\,|\,S(t)>0,I(t)>0\}$ is given by

$L(S,I)=W_1\left[S-S^*\ln\left(\frac{S}{S^*}\right)\right]+W_2\left[I-I^*\ln\left(\frac{I}{I^*}\right)\right]$

Where W_1 and W_2 are positive constant to be chosen latter. By taking the derivative of the above function, we have

$\frac{dL}{dt}=W_1(S-S^*)\left(-\lambda I-\mu+\frac{\mu}{S}\right)+W_2(I-I^*)(\lambda S-(\gamma+\mu))$

Considering the equilibrium point, we have

$-\mu=\lambda I^*-\frac{\mu}{S}$ and $-(\gamma+\mu)=-\lambda S^*$

Thus the above equation reduces to

$\frac{dL}{dt}=\lambda(W_2-W_1)(S-S^*)(I-I^*)-W_1\mu(S-S^*)^2$

For $W_1=W_2=1$, we have $\frac{dL}{dt}=-\mu\frac{(S-S^*)^2}{SS^*}\le 0$,

Also we have $\frac{dL}{dt}=0\Leftrightarrow S=S^*$

Hence by LaSalle's invariance principle [4] the endemic equilibrium point E_1 is globally asymptotically stable on Ω.

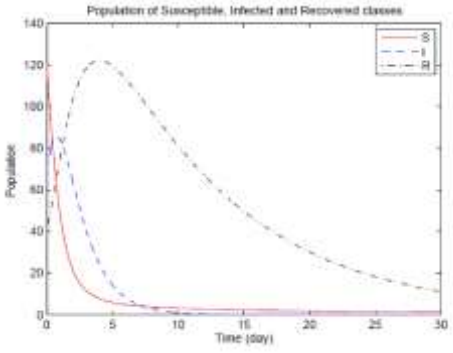

Figure 1. The plot shows the population of susceptible, infected and recovered individuals.

4.0 Numerical Simulation and Conclusion

In this section I have used an iterative method to find the numerical simulation. For numerical simulation I have consider the parameter value $\mu = 0.1$, $\lambda = 0.0098$ and $\gamma = 0.5$. By using Runge-Kutta order 4 scheme, I have solved the proposed model (1).The plot in Figure1, shows the population of susceptible, infected and recovered individuals.

The main objective of this paper is to give the idea that the transmission of infection can be easily studied by epidemic models. Analysis of the model showed that there are two equilibria one is disease-free equilibria
and the other one is endemic equilibria. The local dynamics of the model are determined by the basic reproduction number R_0 which depends on the parameter values. It can be also observe from the analysis that for $R_0 \leq 1$ the disease-free equilibrium is locally asymptotically stable while for $R_0 > 1$ the endemic equilibrium exists.

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