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A SIR EPIDEMIOLOGICAL MODEL WITH STABILITY ANALYSIS

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Abstract: A SIR epidemiological model is introduced and analyzed both analytically and numerically. The model possesses a number of stable and unstable equilibrium states which reflects the true nature of a realistic model. Stability of the equilibrium states is discussed by a suitable Lyapunov function. The numerical results are given through graphical representation.

Key words: Epidemiological model, stability, lyapunov function

Introduction

The study of epidemiology has a long history with a vast variety of models and explanations. Population dynamics concerns the effects of infectious diseases in regulating natural populations, decreasing population sizes, reducing natural fluctuations, or causing destabilizations of equilibria into oscillations of the population states. There are two types of mathematical models: deterministic and stochastic. The deterministic model is to determine the value of underlying properties while the stochastic model aims to predict possible outcome of the system. A SIR model is a deterministic model to determine the number of susceptible, infected and removal classes standing for *S*, *I* and *R* respectively in an environment (Korobeinikov *et al*., 2002). In an environment mostly people are susceptible to a particular disease. After infection a susceptible comes to an infected class. After immunity an infected individual becomes a removal class. When the infection does not lead to immunity, so that infected become susceptible again after recovery, the disease is called an SIS disease. When infected have permanent immunity after recovery, the disease is called an SIR disease. Bacterial infections tend to be SIS, while viral infections correspond to SIR diseases (Mena-Lorca *et al*., 1992).

Materials and Methods

Formulation: We divide the whole population into three classes, the susceptible, the infected and the removal class, symbolically identified by *S*, *I* and *R* respectively. We also assume that the whole population is constant that is birth rate and death rate are equal. We consider immunity here as permanent immunity so that no member of removal class reenter into susceptible class. A model on these assumptions is well known as SIR model. The transfer diagram of this model is in Fig.1. An individual becomes susceptible with a constant rate γ. The natural death rate of susceptible and infected individuals is σ. The transmission of disease can be made through contacts between susceptible, a horizontal transmission, and through parents to a newly born child, a vertical transmission. The horizontal transmission, we assume according to bilinear incidence rate of $\beta SI/N$. The

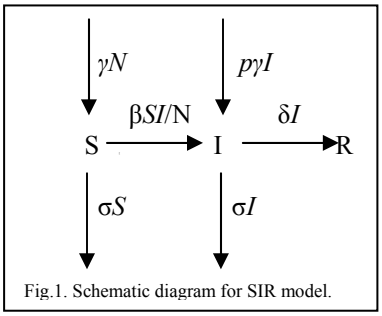

Fig.1. Schematic diagram for SIR model.

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vertical transmission is proportional to the birth rate γ and this flux must be related to the infected individuals as $p\gamma I$, where p is the fraction of newborn infected at birth. Thus the model for SIR epidemiology becomes as

$$\dot{S} = \gamma N - \beta SI / N - p\gamma I - \sigma S$$
$$\dot{I} = \beta SI / N - (\delta + \sigma - p\gamma) I \qquad (1)$$

where $1/\delta$ is the average period of infected individual. The relation for removal class R is not considered as $S + I + R = \text{constant}$.

The equilibrium states of the model (1) is given by considering $\dot{S} = 0$
$\dot{I} = 0$

This gives an infection free equilibrium state $E_o = (S_0, I_0)$, with $S_0 = \frac{\gamma}{\sigma} N, \qquad I_0 = 0$

and also an endemic equilibrium state $E_e = (S_e, I_e)$, with $S_e = \frac{\gamma}{\sigma}\frac{N}{R_0}, \qquad I_e = \frac{\gamma N}{\sigma + \delta}\left(1 - \frac{1}{R_0}\right)$

where the parameter $R_0 = \frac{\beta\gamma}{\sigma(\delta + \sigma - p\gamma)}$ which is also known as reproduction number. For the existence of the endemic equilibrium state R_0 must be greater than unity.

Results

In the model (1), if initial infection $I_0 = 0$, then it remains zero for all the time regardless the value of S. Thus for an endemic infection, there must be at least a single infected species. This is natural phenomenon because no infection can be made without infected individual for epidemiology. On the other hand if initially the number of susceptible is zero, then $\frac{dS}{dt}$ will be negative as long as $I > \frac{N}{p}$, so the number of susceptible might be negative. This makes the model unrealistic because we are concerned only for non negative individual. However, the case $I > \frac{N}{p}$ is very unlikely to happen. These along with various cases are shown in the Fig. 2.

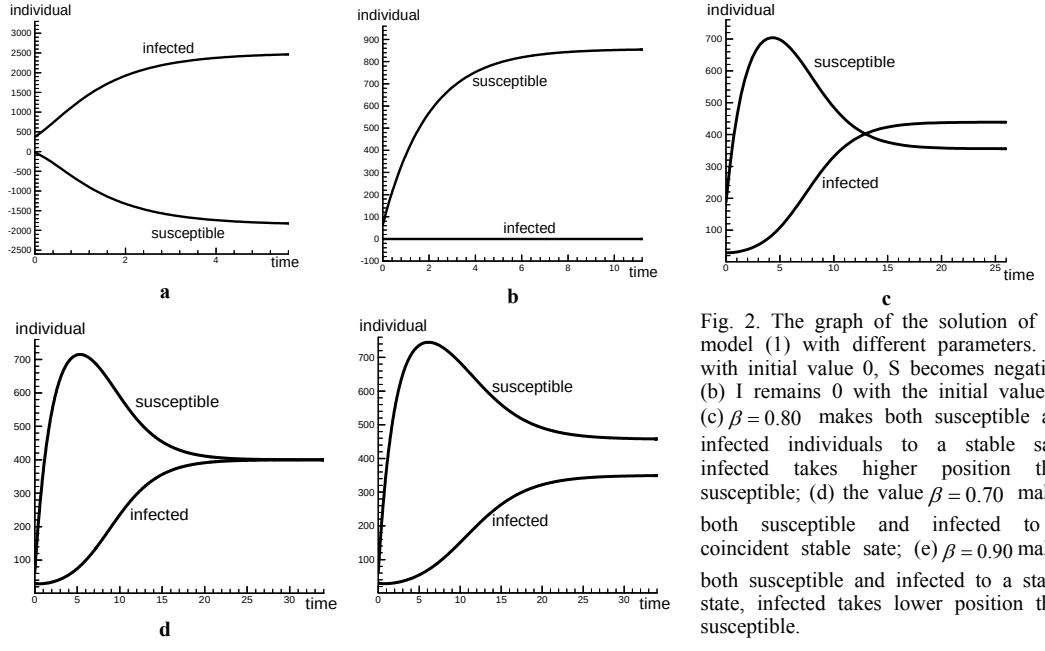

Fig. 2. The graph of the solution of the model (1) with different parameters. (a) with initial value 0, S becomes negative; (b) I remains 0 with the initial value 0; (c) $\beta = 0.80$ makes both susceptible and infected individuals to a stable sate, infected takes higher position than susceptible; (d) the value $\beta = 0.70$ makes both susceptible and infected to a coincident stable sate; (e) $\beta = 0.90$ makes both susceptible and infected to a stable state, infected takes lower position than susceptible.

e

In Fig. 2 we obtained the graphs through changing only the value of the parameter β, however the similar result can be obtained by changing the value of γ. Now to remove the weakness of the model let us take the substitution as $S = Y - \frac{p\gamma N}{\beta}$. Under this substitution the model (1) becomes

$$\frac{dY}{dt} = \gamma N - \beta\left(Y - \frac{p\gamma N}{\beta}\right)\frac{I}{N} - p\gamma I - \sigma\left(Y - \frac{p\gamma N}{\beta}\right)$$
$$= \left(1 + \frac{\sigma p}{\beta}\right)\gamma N - \frac{\beta}{N} YI - \sigma Y$$
$$= \hat{\gamma} N - \frac{\beta}{N} YI - \sigma Y$$

where $\hat{\gamma} = \left(1 + \frac{\sigma p}{\beta}\right)\gamma$

$$\frac{dI}{dt} = \frac{\beta I}{N}\left(Y - \frac{p\gamma N}{\beta}\right) - (\delta + \sigma - p\gamma)I$$
$$= \frac{\beta IY}{N} - (\delta + \sigma)I$$
$$= \frac{\beta IY}{N} - \hat{\delta} I$$

where $\hat{\delta} = \delta + \sigma$. That is, $\frac{dY}{dt} = \hat{\gamma} N - \frac{\beta}{N} YI - \sigma Y$ and $\frac{dI}{dt} = \frac{\beta IY}{N} - \hat{\delta} I$ (2)

In the new model (2), with zero initial value, Y will not lead to a negative value. The new endemic equilibrium is given by $\hat{\gamma} N - \frac{\beta}{N} YI - \sigma Y = 0,\ \frac{\beta IY}{N} - \hat{\delta} I = 0$ (3)

Solving this we get, $Y_e = \frac{N\hat{\gamma}}{R_0},\ I_e = \frac{\hat{\gamma}}{\hat{\delta}}\left(1 - \frac{1}{R_0}\right)N$

The equation (3) also gives the following relation $\frac{\beta IY}{N} = \hat{\gamma} N - \sigma Y = \hat{\delta} I$ (4)

Stability analysis: To examine the local stability of the infection free equilibrium of (1), we linearize the system about $E_o = (S_0, I_0)$. The corresponding Jacobian matrix is

$$J_0 = \begin{bmatrix} -\sigma & -\frac{\beta\gamma}{\sigma} - p \\ 0 & \frac{\beta\gamma}{\sigma} - \delta + p\gamma \end{bmatrix}$$

The eigenvalues of J_0 are $-\sigma$ and $\frac{\beta\gamma}{\sigma} + p\gamma - \delta$. Therefore the infection free equilibrium $E_o = (S_0, I_0)$ is asymptotically stable if $\delta > \frac{\beta\gamma}{\sigma} + p\gamma$.

To test the stability of endemic equilibrium E_e consider the following Lyapunov function

$$L(Y, I) = Y_e\left(\frac{Y}{Y_e} - \ln\frac{Y}{Y_e}\right) + I_e\left(\frac{I}{I_e} - \ln\frac{I}{I_e}\right) \quad \text{for all } Y,\ I > 0 \quad \ldots \ \ldots \ \ldots \quad (5)$$

Therefore,

$$\frac{dL}{dt} = \frac{\partial L}{\partial Y}\frac{\partial Y}{dt} + \frac{\partial L}{\partial I}\frac{\partial I}{dt}$$
$$= \left(1 - \frac{Y_e}{Y}\right)\left(\hat{\gamma} N - \frac{\beta}{N} YI - \sigma Y\right) + \left(1 - \frac{I_e}{I}\right)\left(\frac{\beta}{N} YI - \hat{\delta} I\right)$$
$$= \hat{\gamma} N\left(1 - \frac{Y_e}{Y}\right) + \sigma\left(Y_e - Y\right) + \hat{\delta}\left(I_e - I\right) + \frac{\beta}{N}\left(Y_e I - YI_e\right)$$

Using relation (4)

$$\frac{dL}{dt} = \hat{\gamma}N\left(1-\frac{Y_e}{Y}\right)+\sigma Y_e-\sigma Y+\hat{\gamma}N-\sigma Y_e-\hat{\delta}I+\hat{\delta}I-Y\left(\frac{\hat{\gamma}N}{Y_e}-\sigma\right)$$

$$= \hat{\gamma}N\left(2-\frac{Y_e}{Y}\right)-\frac{\hat{\gamma}NY}{Y_e}$$

$$= \hat{\gamma}N\left(2-\frac{Y_e}{Y}-\frac{Y}{Y_e}\right)$$

$$= -\hat{\gamma}N\frac{Y_e}{Y}\left(1-2\frac{Y}{Y_e}+\left(\frac{Y}{Y_e}\right)^2\right)$$

$$= -\hat{\gamma}N\frac{Y_e}{Y}\left(1-\frac{Y}{Y_e}\right)^2 \le 0 \quad \forall\ Y, I \ge 0$$

As $\frac{dL}{dt}$ is non-positive, therefore, by the asymptotic stability theorem E_e is globally asymptotic stable.

Discussion

In this paper a SIR epidemiological model is introduced. The solution of the model exhibits some realistic behaviour. The only unrealistic characteristics of the model is that when the susceptible individual is zero the subsequent individual might be negative for sufficient large number of infected individuals. This model has two equilibrium states; one is infection free equilibrium and the other is endemic equilibrium state. To remove the unrealistic solution we modified the model through a suitable substitution of the variable. The new model has also two equilibrium states but does not lead the negative susceptible individual if it is disappeared earlier. The linearization of the modified model at the infection free equilibrium reveals that the state is asymptotically stable after certain parameter values unless it is unstable. To perform a stability analysis of the endemic equilibrium state we considered an auxiliary function (5) most commonly known as Lyapunov function (Lyapunov, 1992). This endemic equilibrium is also asymptotically stable. Fig.2 gives the static view of stable nature of the equilibrium state.

Conclusion

The analysis of the SIR epidemiological model ensures the existence of stable endemic equilibrium state. The model can be used to analyse the epidemiological behaviour of infectious diseases of different species with necessary modification.

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