

Local Stability of Equilibrium Points of a SIR Mathematical Model of Infectious Diseases

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Abstract— In this paper, we studied a SIR mathematical model of infectious diseases. We formulate a theorem on existence and uniqueness of solutions and establish the proof of the theorem. We showed that the model has two equilibrium points: disease-free and endemic equilibrium. Local stability of the equilibrium points was obtained using reliable Jacobian matrices and basic reproduction number (R_0). The analysis reveals that the disease-free equilibrium is locally asymptotically stable if $R_0 < 1$, the infection is temporal and will disappear with time. On the other hand, if $R_0 > 1$, the number of infections rises, an epidemic results and the endemic equilibrium is locally stable.

Index Terms— Mathematical model, equilibrium points, existence and uniqueness of solutions, mathematical model, SIR, stability analysis.

I. INTRODUCTION

Transmission dynamics of infectious diseases has been modeled by many mathematicians and scientists. Starting in 1927, Kermack and Mckendrick [1-3] developed theoretical papers on some infectious diseases using differential equations. After that, many deterministic models have been formulated and applied to a variety of infectious diseases [4-11].

In the modeling of disease transmission dynamics, it is common to divide the total population into various groups depending on the infection status of an individual [12]. A sequence of letters such as SIR, describes the movement of individuals from susceptible (S) to infectious (I) and finally recover (R). These models are suitable for diseases which confer permanent immunity after recovery. Models of SEIR type has a susceptible group(s) exposed or latent group (E), infectious (I) and recovered (R) are used to study diseases with temporary immunity.

In this paper, we propose a SIR model to study the dynamics of infectious diseases in a population. The propose model is appropriate for tuberculosis, hepatitis B, malaria, typhoid, cholera, measles and small pox.

The paper is organised as follows: In section 2, we state the equations of the model. The equilibrium points of the model and basic reproduction number are derived in section 3. Local stability of equilibrium points is performed in section 4 while section 5 concludes the presentation.

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II. MODEL FORMULATION

We consider a SIR type disease (e.g cholera). The model has a susceptible group denoted by S, an infected group I and a recovered group R. we assume recruitment rate π into the population while denotes movement of susceptible in individual into the infected group (transmission rate). γ is the death rate due to disease and μ is the natural death rate.

The differential equations for the SIR model are as follows:

$$\frac{ds}{dt} = \pi - \beta SI - \mu S \quad (1)$$

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

$$\frac{dR}{dt} = -\mu R \quad (3)$$

By using the next generation matrix method proposed by Van den Driessche and Watmough [13] for calculating R_0 . The basic reproduction number (R_0) of the model is the largest (dominant) eigenvalue of matrix FV^{-1} where F is the rate of new infections while V is the rate of transfer of infections from one compartment to another. Thus, the basic reproduction number of model system (1) - (3) is

$$R_0 = \frac{\beta}{\gamma + \mu} \quad (4)$$

III. EQUILIBRIUM POINTS

The model has two equilibrium points namely disease-free equilibrium (DFE) and endemic equilibrium.

At the equilibrium points,

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0 \quad (5)$$

Hence, the following equations are solved for equilibrium points

$$\pi - \beta SI - \mu S = 0 \quad (6)$$

$$\beta SI - (\gamma + \mu)I = 0 \quad (7)$$

$$-\mu R = 0 \quad (8)$$

In a DFE, the population is from disease and consequently $I = 0$, so that we now have from equations (6) - (8),

$$\pi - \mu S = 0 \tag{9}$$

$$-\mu R = 0 \tag{10}$$

Solving (9) and (10), we obtain the DFE point

$$T_0 = (S_0, I_0, R_0) = \left(\frac{\pi}{\mu}, 0, 0 \right) \tag{11}$$

In the endemic state, the infection persists and $I \neq 0$. We solve the following equations for endemic equilibrium $T^* = (S^*, I^*, R^*)$:

$$\pi - \beta S^* I^* - \mu S^* = 0 \tag{12}$$

$$\beta S^* I^* - (\gamma + \mu) I^* = 0 \tag{13}$$

$$\mu R^* = 0 \tag{14}$$

Solving (13), we get

$$S^* = \frac{\gamma + \mu}{\beta} \tag{15}$$

Substituting (15) into (12) gives

$$I^* = \frac{\pi\beta - \mu(\gamma + \mu)}{\beta(\gamma + \mu)} \tag{16}$$

From (14) $R^* = 0$ (17)

Thus, the endemic equilibrium T^* of the model (1) - (3) is given by equations (15) - (17).

IV. LOCAL STABILITY OF EQUILIBRIUM POINTS

We investigate the local stability of equilibrium points of the model by the theorem below:

Theorem 1 [14]

Let

$$\frac{dx}{dt} = P(x, y), \frac{dy}{dt} = Q(x, y), X = \begin{pmatrix} x \\ y \end{pmatrix}$$

Suppose $X_1 = \begin{pmatrix} x_1 \\ y_1 \end{pmatrix}$ is an equilibrium point of the plane

$$X_1 = g(X) = \begin{pmatrix} P(x, y) \\ Q(x, y) \end{pmatrix}$$

autonomous system where $P(x, y)$ and $Q(x, y)$ have continuous first partial derivatives in a neighbourhood X_1 . Then we have following:

If the eigenvalues of $A = g^1(X_1)$ have negative real parts, then X_1 is a locally asymptotically stable equilibrium point.

If $A = g^1(X_1)$ has an eigenvalue with positive real part, then X_1 is an unstable equilibrium point.

Stability of disease-free equilibrium

The Jacobian matrix at the DFE T_0 is given by

$$J(T_0) = \begin{pmatrix} -\mu & 0 & 0 \\ 0 & -(\gamma + \mu) & 0 \\ 0 & 0 & -\mu \end{pmatrix} \tag{18}$$

We solve $|J - \lambda I| = 0$ where λ is the eigenvalue.

Hence,

$$\lambda_1 = \lambda_2 = -\mu, \lambda_3 = -(\gamma + \mu) \tag{19}$$

Equation (19) shows that all the eigenvalues have negative real parts. It follows then by Theorem 1, that the disease-free equilibrium T_0 is locally asymptotically stable.

Remark 1: By using the basic reproduction number, the local stability of T_0 can also be conducted by using the theorem below.

Theorem 2: If $R_0 < 1$, the equilibrium point T_0 is locally stable

Proof

Using parameter values of the model:

$\beta = 0.012, \gamma = 0.34, \mu = 0.1$. then, according to equation (4) $R_0 = 0.353 < 1$. This shows that the disease-free equilibrium is locally stable.

Stability of endemic equilibrium

It should be noted that by using the Jacobian matrix at the endemic equilibrium T^* , all the eigenvalues can be shown to have negative real part. It follows then that the endemic equilibrium is stable.

Theorem 3: if $R_0 > 1$, the endemic equilibrium point T^* is stable.

Proof

Let $\beta = 0.31, \gamma = 0.6, \mu = 0.1$. Using equation (4), $R_0 = 5.167 > 1$. Hence, T^* is stable

V. DISCUSSION OF RESULTS AND CONCLUSION

A model for the transmission of infectious diseases have been analysed. The analysis showed that the model has a disease-free equilibrium which is locally stable for $R_0 < 1$ and endemic equilibrium which is stable for $R_0 > 1$. The stability of endemic equilibrium suggests a wiping out of the population. Hence, treatment measures aimed at reducing R_0 below 1 should be intensified to control the disease.

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