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Research Article

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The Dynamics of a Nonlinear Incidence Rate in an Sir Model

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Abstract In this paper, we study the dynamical behavior of an SIR epidemic model with a nonlinear incidence rate. By carrying out qualitative and numerical analysis, the relationship of the basic reproduction number (R_0) with the stability of the model is proposed. It is established that the system has a stable disease free equilibrium point for (R_0<1). For (R_0> 1), conditions for the stability of the endemic equilibrium point are established.

Keywords Epidemic model, Nonlinear incidence rate, Basic Reproduction number, Stability, Disease free equilibrium, Endemic equilibrium.

1. Introduction

In this paper, we consider an SIR model and assume a nonlinear incidence rate of the form $\phi SI(1+\alpha I)$, where α, $(0 \leq \alpha \leq 1)$, is an inhibitory parameter. Introduction of the inhibitory parameter makes the model more realistic because the number of effective contacts between infective individuals and susceptible individuals is controlled by the inhibitory parameter. At $\alpha = 0$, i.e. no inhibitory effect, the system assumes a bilinear force of infection, but at $\alpha = 1$, we have full inhibition. Systems with this type of nonlinear incidence rates are widely studied [1–10].

Analytically, we derive a threshold value (R_0) and prove that when R_0< 1, the disease free equilibrium point is locally asymptotically stable and at R_0>1, the endemic equilibrium comes into existence and is locally asymptotically stable. Numerical simulations support our analytical calculations and also show that we have global asymptotic stability of the disease free and endemic equilibria for R_0 < 1 and R_0>1respectively. The paper is organized as follows: The model is described in Section 2. The basic reproduction number and relevant results for the stabilities of the disease free and endemic equilibria could be found in Section 3. We have numerical simulations in 4 and conclusion in Section 5.

2. Derivation of the Model

We consider an SIR deterministic model with a three dimensional differential equation system. Individuals are assumed to be in one of the following epidemiological states: S-Susceptibles (at risk of contracting the disease), I-Infectives (infected and capable of transmitting the disease), and R-Recovered (population recovered from the infection). All recruitment is into the susceptible class, and occurs at a constant rate β. We assume a nonlinear incidence rate of the form $\phi SI(1+\alpha I)$, where ϕ is the infection rate and α, $(0 \leq \alpha \leq 1)$, is an inhibitory parameter. We present the model as follows:

$$\begin{aligned} \frac{dS}{dt} &= \beta - \mu S - \phi SI(1+\alpha I) \\ \frac{dI}{dt} &= \phi SI(1+\alpha I) - (\mu + \Upsilon)I \\ \frac{dR}{dt} &= \Upsilon I - \mu R \end{aligned} \qquad (1)$$

This model has the death rate μ, which represent death rate as a result of natural causes. An infected individual has a recovery rate of (Υ) into the recovery compartment. Since this model is for human population, we assume that all its state variables and parameters are nonnegative for all t≥ 0. The region biologically relevant is given by

$$\Omega = \left\{(S, I, R) \in \mathcal{R}_+^3 : 0 \leq S + I + R \leq \frac{\beta}{\mu}\right\} \quad (2)$$

The total human population is given by N = $S + I + R$, so that $dN/dt \leq \beta - \mu N$, thus $N \to \beta/\mu$ as$t \to$ □.

3. Stability Analysis

The basic reproduction number for the model obtained by the first generation matrix approach introduced by Diekmann et al [11] is given as

$$R_0 = \frac{\phi\beta}{\mu(\mu + \Upsilon)} \quad (3)$$

The disease-free equilibrium given by $E^0 = (S^0, I^0, R^0)$ is the only equilibrium for $R_0 \leq 1$, where

$$S^0 = \frac{\beta}{\mu}, \quad I^0 = 0, \quad R^0 = 0$$

If $R_0 > 1$, then there is also an endemic equilibrium given by $E^* = (S^*, I^*, R^*)$, where S^* is the root of the following

$$\mu\phi\alpha S^{*2} + (-\phi\alpha\beta - \mu\phi - \phi\Upsilon)S^* + \mu^2 + 2\mu\Upsilon + \Upsilon^2 = 0$$

And I^* and R^* are given below in terms of S^*

$$I^* = -\frac{(\phi S^* - \mu - \Upsilon)}{\phi\alpha S^*}$$

$$R^* = \frac{\Upsilon(\phi S^* - \mu - \Upsilon)}{(\mu\phi\alpha S^*)} \quad (4)$$

Local Stability of the Disease Free Equilibrium.

The characteristics equation after linearizing (1) about the disease free equilibrium E^0 gives

$$(\lambda + \mu)^2(\mu^2 + \mu\Upsilon + \mu\lambda - \phi\beta) = 0 \quad (5)$$

This gives $\lambda_{1,2} = -\mu$ and the solution to the following equation

$$\mu^2 + \mu\Upsilon + \mu\lambda - \phi\beta = 0 \quad (6)$$

(6) gives

$$\lambda = \{\mu + \Upsilon\}(R_0 - 1)$$

The first two eigenvalues λ_1 and λ_2 are negative and if $R_0 < 1$, λ in (6) is also negative giving us the following theorem.

Theorem 1.

The disease-free equilibrium point of the System (1) is locally asymptotically stable when $R_0 < 1$, marginally stable when $R_0 = 1$ and unstable when $R_0 > 1$.

Local Stability of the Endemic Equilibrium

We analyse the local stability of the endemic equilibrium point in this section. The characteristics equation at the endemic equilibrium point E^*gives

$$\lambda^3 + \mu^2\phi\alpha I^{*2} + \phi\alpha\mu\Upsilon I^{*2} + 2\mu\phi\alpha I^{*2}\lambda + \phi\alpha\Upsilon I^{*2}\lambda + \phi\alpha I^{*2}\lambda^2 - 2\mu^2\phi\alpha I^* S^* - 4\mu\phi\alpha I^* S^*\lambda - 2\phi\alpha I^* S^*\lambda^2 + \mu^2\phi I^* + \mu\phi\Upsilon I^* + 2\mu\phi I^*\lambda + \phi I^*\lambda^2 + \mu^2\Upsilon - \mu^2\phi S^* - 2\phi\mu S^*\lambda - \phi S^*\lambda^2 + \mu^3 + 3\mu^2\lambda + 2\mu\Upsilon\lambda + 3\mu\lambda^2 + \Upsilon\lambda^2 + \phi\Upsilon I^*\lambda = 0 \quad (7)$$

Equation (7) simplifies to

$$(\lambda + \mu)(\mu\phi\alpha I^{*2} + \phi\alpha\Upsilon I^{*2} + \phi\alpha I^{*2}\lambda - 2\mu\phi\alpha I^* S^* - 2\phi\alpha I^* S^*\lambda + \mu\phi I^* + \phi\Upsilon I^* + \phi I^*\lambda - \phi\mu S^* - \phi S^*\lambda + \mu^2 + \mu\Upsilon + 2\mu\lambda + \Upsilon\lambda + \lambda^2) = 0 \quad (8)$$

Giving $\lambda = -\mu$ and the solution to the following equation

$A_1\lambda^2 + A_2\lambda + A_3 = 0$

Where,

$A_1 = \phi\alpha S^{*2}$

$A_2 = \phi^2\alpha S^{*3} - \phi\alpha\Upsilon S^{*2} - \phi\mu S^* - \phi\Upsilon S^* + \mu^2 + 2\mu\Upsilon + \Upsilon^2$

$A_3 = \phi^2\alpha\mu S^{*3} - \phi\alpha\mu^2 S^{*2} - \phi\alpha\mu\Upsilon S^{*2} - \phi\mu^2 S^* - 2\phi\mu\Upsilon S^* - \phi\Upsilon^2 S^* + \mu^3 + 3\mu^2\Upsilon + 3\mu\Upsilon^2 + \Upsilon^3$

Conditions: Let the following hold for $R_0 > 1$

(i) $A_1 > 0, \quad A_2 > 0, \quad A_3 > 0$

(ii) $A_1A_2 - A_3 > 0$

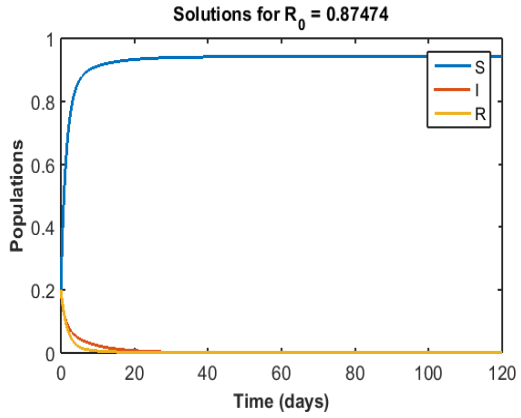
If conditions (i) and (ii) hold, we are guaranteed stability from the Routh Hurwitz criteria giving us the following theorem.

Theorem 2.

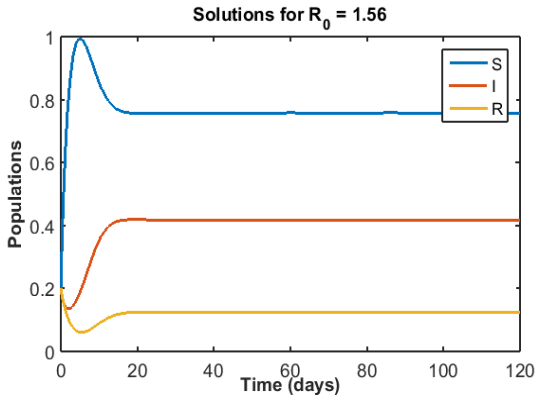
The endemic equilibrium point (E^*) of System (1) is locally asymptotically stable whenever $R_0 > 1$ if conditions (i) and (ii) above is satisfied.

4. Numerical Simulation

In this section, we show numerically the established results in earlier sections about the stability of the disease free and the endemic equilibria of the System (1) as it relates to the basic reproduction number (R_0). We use the ode23 suite in Matlab to simulate the System (1) with the parameters as shown below the figures. The parameters are chosen solely for simulation convenience and do not reflect actual collected data.



(a) $R_0 = 0.8747 < 1$, $\mu = 0.69$



(b) $R_0 = 1.56 > 1$, $\mu = 0.5$

Figure 1: Other parameters are: β = 0.65, ϕ = 0.78, α = 024 and Υ= 0.15

In Fig. 1(a), $R_0 = 0.8747 < 1$, hence the disease free equilibrium becomes stable which shows that the infection dies out of the population. Fig. 1(b) shows the stable endemic equilibrium for $R_0 = 1.56 > 1$, this means that the disease will persist in the population. This simulation agrees with Theorems (1) and (2) in Section 3.

In the next figures, we show the effect of the inhibition parameter αon System (1) by plotting the number of infectives for different values of α.

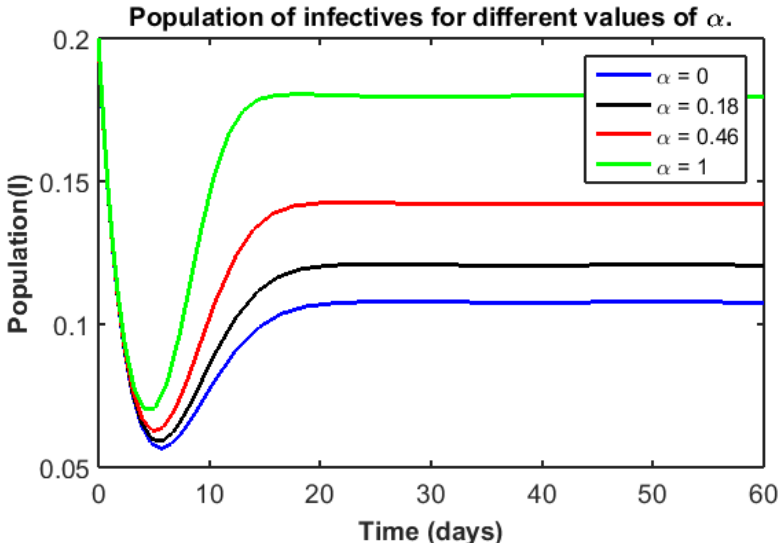


Figure 2: Simulation of the evolution of the number of infected individuals for different values of α. Other parameters are: β = 0.65, μ = 0.5, φ=0.78 and ϒ= 0.15.

We easily notice a remarkable increase in the number of infectives as the inhibition parameter is increased in Fig. 2. Notice that at $\alpha = 0$, we have the bilinear force of infection, but at $\alpha = 1$, we have full inhibition.

5. Conclusion

In this paper, we formulated an SIR epidemic model with a nonlinear incidence rate. The threshold value R_0 was found and analytical calculations and numerical simulations show that the local and global dynamics of the System (1) are completely determined by the values of the threshold number R_0.

We found that if $R_0 < 1$, the disease free equilibrium point is always stable for $(0 \leq \alpha \leq 1)$ and the endemic equilibrium point is always stable for $(0 \leq \alpha \leq 1)$ if $R_0 > 1$. The inhibitory parameter α is such that at $\alpha = 0$, i.e. no inhibitory effect, the system assumes a bilinear force of infection giving lower infectives in the population, but at full inhibition ($\alpha = 1$), we have higher levels of infectives, Fig (2).

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