Journal of Mathematical Sciences and Modelling, 4 (3) (2021) 133-138
Research Article

Journal of Mathematical Sciences and Modelling

Journal Homepage: www.dergipark.gov.tr/jmsm
ISSN 2636-8692
DOI: http://dx.doi.org/10.33187/jmsm.1009561

Stability of an SIRS Epidemic Model with Saturated Incidence Rate and Saturated Treatment Function

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Article Info

Keywords: *Global stability, Lyapunov function, SIRS epidemic model.*
2010 AMS: *34D20, 34D23*
Received: *14 Octobrt 2021*
Accepted: *22 December 2021*
Available online: *29 December 2021*

Abstract

In this paper the global dynamics of susceptible-infected-recovered-susceptible (SIRS) epidemic model with saturated incidence rate and saturated treatment function is studied. Firstly, the basic reproduction number R_0 is calculated and the existence of the disease-free and positive equilibria is showed. In addition, local stability of the equilibria is investigated. Then, sufficient conditions are achieved for global stability of disease-free and endemic equilibria. Finally, the numerical examples are presented to validate the theoretical results.

1. Introduction

In epidemiology, mathematical modeling is an important tool for observing the dynamic evolution and effects of infectious disease [1]. Using mathematical models, researchers can identify trends in disease, analyze epidemiological studies, and make general predictions about disease. For this purpose, stability and bifurcation analysis of many SIRS epidemic models have been investigated in [2]-[6]. The total population consists of three subpopulations based on disease status in classical infectious disease models: S(t)-susceptible population, I(t)-infective population and R(t)-recovered population, at any given time t. The classic SIRS epidemic model, assuming that the recovering population has transient immunity, can be given as

$$\begin{aligned} \frac{dS}{dt} &= A-\rho S-f(I)S+\delta R, \\ \frac{dI}{dt} &= f(I)S-(\rho+\gamma)I-T(I), \\ \frac{dR}{dt} &= \gamma I-(\rho+\delta)R+T(I). \end{aligned}$$

where the parameter A denotes the natality of susceptible population, ρ is the mortality rate and δ shows the rate of loss of immunity and return to the susceptible class of recovered individuals. γ is the recovery rate of the infected population. $f(I)S$ denotes the incidence rate, and the $f(I)$ function measures the infectious strength of the disease.
In this study, we take a saturated incidence rate

$$f(I)=\frac{\beta I}{1+\alpha I},$$

which firstly presented by Capasso and Serio in [2]. Here, βI calculates the infectious strength of the disease and $\frac{1}{1+\alpha I}$ calculates the inhibitory effect from behavioral change or crowding of infective individuals when the number of susceptible individuals increases.
In addition, we take saturated treatment function as

$$T(I)=\frac{rI}{1+\varepsilon I},$$

which is continuous and differentiable [3]. Here, $rI>0$ and $\varepsilon\geq 0$. r means the cure rate and ε quantifies the extent of the effect of delaying the infected to cure.

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In this paper, we present the SIRS epidemic model with saturated incidence rate and saturated treatment function as follows:

$$\frac{dS}{dt} = A - \frac{\beta SI}{1+\alpha I} - \rho S + \delta R, \tag{1.1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{1+\alpha I} - (\rho+\gamma)I - \frac{rI}{1+\varepsilon I}, \tag{1.2}$$

$$\frac{dR}{dt} = \gamma I - (\rho+\delta)R + \frac{rI}{1+\varepsilon I}. \tag{1.3}$$

The remainder of this article is organized as follows. In Section 2, the local stability of the equilibria is examined. In Section 3, adequate conditions for global stability of equilibria are provided by using Lyapunov functions. In Section 4, to validate our theoretical results, some numerical examples are given.

2. Equilibria and Local Dynamics

We start with investigating the positivity and boundedness properties of solutions for system (1.1)-(1.3), for the purpose of ensuring that the model is biologically well-behaved.

Theorem 2.1. *If the initial conditions are $S(0) \geq 0, I(0) \geq 0, R(0) \geq 0$, the solutions of system (1.1)-(1.3) are nonnegative and bounded for all $t \geq 0$.*

Proof. From the model system (1.1)-(1.3), we have

$$\frac{dS}{dt}|_{S=0} = A + \delta R, \quad \frac{dI}{dt}|_{I=0} = 0, \quad \frac{dR}{dt}|_{R=0} = \gamma I + \frac{rI(t)}{1+\varepsilon I(t)}.$$

It is clear that these ratios are not negative in the bounding planes of the non-negative cone of $\mathbb{R}^3$. Therefore, if we start inside this cone, we will always stay inside this cone in the inward direction of the vector field in all bounding planes. Consequently, all solutions of (1.1)-(1.3) are not negative.
For the proof of boundedness, we denote the total population size as $M = S + I + R$. Adding Eqns. (1.1)-(1.3), we obtain

$$\frac{dM}{dt} = A - \rho M. \tag{2.1}$$

If we solve the Eq. (2.1), we find

$$M(t) = \frac{A}{\rho} - \left(\frac{A}{\rho} - M(t_0)\right) e^{-\rho(t-t_0)}$$

where $M(t_0) > 0$ is an initial condition. Thus,

$$\lim_{t\to\infty} M(t) = \frac{A}{\rho}$$

which shows the conclusion. □

From the above theorem, we obtain the following region:

$$\Gamma = \{(S,I,R) \in \mathbb{R}^3_+ | S + I + R \leq \frac{A}{\rho}, S \geq 0, I \geq 0, R \geq 0\}$$

which is a positively invariant set for Eqns. (1.1)-(1.3).
Since the limit set of Eqns. (1.1)-(1.3) is on the plane $S + I + R = \frac{A}{\rho}$, we can concentrate on the following reduced system:

$$\frac{dI}{dt} = \frac{\beta I}{1+\alpha I}\left(\frac{A}{\rho} - I - R\right) - (\rho+\gamma)I - \frac{rI}{1+\varepsilon I}, \tag{2.2}$$

$$\frac{dR}{dt} = \gamma I - (\rho+\delta)R + \frac{rI}{1+\varepsilon I} \tag{2.3}$$

Clearly,

$$\Lambda = \left\{(I,R) | I \geq 0, R \geq 0, I + R \leq \frac{A}{\rho}\right\}.$$

is the positively invariant set of system (2.2)-(2.3)
To put the model in dimensionless form, we build the following variable change:

$$I' = \frac{\beta}{\rho+\gamma} I, \quad R' = \frac{\beta}{\rho+\gamma} R, \quad t' = (\rho+\gamma)t.$$

To avoid making the mathematical notation look bad, we still indicate (I', R', t') by (I, R, t). Then we get

$$\frac{dI}{dt} = \frac{I}{1+mI}(B-I-R)-I-\frac{pI}{1+qI}, \tag{2.4}$$

$$\frac{dR}{dt} = rI-nR+\frac{pI}{1+qI} \tag{2.5}$$

where $m=\frac{\alpha(\rho+\gamma)}{\beta}$, $B=\frac{\beta A}{\rho(\rho+\gamma)}$, $p=\frac{r}{\rho+\gamma}$, $q=\frac{\varepsilon(\rho+\gamma)}{\beta}$, $r=\frac{\rho}{\rho+\gamma}$, $n=\frac{\rho+\delta}{\rho+\gamma}$. It can be seen that $m,n,p,q,r,B>0$ and the positively invariant set of system (2.4)-(2.5) is

$$\tilde{\Lambda}=\{(I,R)|I\geq 0, R\geq 0, I+R\leq B\}.$$

Clearly, system (2.4)-(2.5) always has a unique disease-free equilibrium $E^0=(I^0,R^0)=(0,0)$. The positive equilibria of system (2.4)-(2.5) can be obtained by solving the following equation

$$f(I)=A_1I^2+B_1I+C_1=0 \tag{2.6}$$

where

$$\begin{aligned} A_1 &= \left(1+m+\frac{r}{n}\right)q, \\ B_1 &= q(1-B)+1+m+\frac{r+p}{n}+pm, \\ C_1 &= (p+1)\left(1-\frac{B}{p+1}\right), \end{aligned}$$

Denote $R_0=\frac{B}{p+1}$.

$$R^*=\frac{1}{n}\left(rI^*+\frac{pI^*}{1+qI^*}\right)$$

where I^* is the positive root of the Eq. (2.6). Therefore, system (2.4)-(2.5) has a unique endemic equilibrium $E^*=(I^*,R^*)$.
The Jacobian matrix corresponding to the model Eqns. (2.4)-(2.5) is as follows:

$$J=\begin{pmatrix} \frac{1}{(1+mI)^2}(B-I-R)-\frac{I}{1+mI}-\frac{p}{(1+qI)^2}-1 & -\frac{I}{1+mI} \\ r+\frac{p}{(1+qI)^2} & -n \end{pmatrix}.$$

Now using the variable matrix J obtained above, we get the local stability of the equilibria.

Theorem 2.2. *(i) If $R_0<1$ the disease free equilibrium E^0 of the system (2.4)-(2.5) is locally asymptotically stable otherwise it is unstable. (ii) If $R_0>1$, $A_2<0$ and $B_2>0$, then the unique endemic equilibrium E^* locally asymptotically stable.*

Proof. (i) The Jacobian matrix corresponding to $E^0=(0,0)$ of Eqns. (2.4)-(2.5) is as follows

$$J^0=\begin{pmatrix} B-p-1 & 0 \\ r+p & -n \end{pmatrix}.$$

The eigenvalues of J^0 are

$$\lambda_1=-n,\ \ \lambda_2=B-p-1.$$

Obviously, $\lambda_1<0$. Note that if $R_0<1$, $\lambda_2<0$ and so the disease-free equilibrium E^0 is locally asymptotically stable. Conversely, if $R_0>1$, $\lambda_2>0$ and so E^0 is unstable.
(ii) The Jacobian matrix corresponding to $E^*=(I^*,R^*)$ of Eqns. (2.4)-(2.5) is as follows

$$J^*=\begin{pmatrix} \frac{1}{(1+mI^*)^2}(B-I^*-R^*)-\frac{I^*}{1+mI^*}-\frac{p}{(1+qI^*)^2}-1 & -\frac{I^*}{1+mI^*} \\ r+\frac{p}{(1+qI^*)^2} & -n \end{pmatrix}.$$

The roots of the equation

$$\lambda^2+A_2\lambda+B_2=0$$

are the eigenvalues of J^*. Here

$$\begin{aligned} A_2 &= n+1+\frac{p}{(1+qI^*)^2}+\frac{I^*}{1+mI^*}+\frac{1}{(1+mI^*)^2}(I^*+R^*-B), \\ B_2 &= n\left(1+\frac{p}{(1+qI^*)^2}+\frac{I^*}{1+mI^*}+\frac{1}{(1+mI^*)^2}(I^*+R^*-B)\right) \\ &+ \left(r+\frac{p}{(1+qI^*)^2}\right)\left(\frac{I^*}{1+mI^*}\right). \end{aligned}$$

If $A_2<0$ and $B_2>0$, the eigenvalues of J^* are negative. Thus, proof is completed. □

3. Global Stability

In this chapter, we have obtained the sufficient conditions for global stability for E^0 and E^*.

Theorem 3.1. *If $R_0 < 1$, the disease-free equilibrium $E^0 = (0,0)$ of Eqns. (2.4)-(2.5) is globally asymptotically stable provided that the following condition holds:*

$$Bq < (p+1)m.$$

Proof. Now we will construct a Lyapunov function and use the direct method of Lyapunov to prove the global stability of E^0. Take into the following Lyapunov function

$$V_0(I,R) = I.$$

Clearly V_0 is a positive definite function. If we differentiate V_0 with respect to t, we get

$$\begin{aligned}
\frac{dV_0}{dt} &= \frac{dI}{dt} \\
&= \frac{I}{1+mI}(B-I-R) - I - \frac{pI}{1+qI} \\
&\leq \frac{BI}{1+mI} - \frac{(p+1)I}{1+qI} - \frac{qI^2}{1+qI} \\
&\leq \frac{B-(p+1)}{(1+qI)(1+mI)}I + \frac{Bq-(p+1)m}{(1+qI)(1+mI)}I^2
\end{aligned}$$

Obviously, if $R_0 < 1$ and $Bq < (p+1)m$, then $\frac{dV_0}{dt} \leq 0$. Furthermore, $\frac{dV_0}{dt} = 0$ if and only if $I = 0$. According to LaSalle's principle of invariance [5], this means that all solutions in $\tilde{\Lambda}$ approach the plane $I = 0$ and $R = 0$ as $t \to \infty$. Therefore, we conclude that E^0 is globally asymptotically stable in $\tilde{\Lambda}$. □

Theorem 3.2. *If $R_0 > 1$, then the infected equilibrium $E^* = (I^*, R^*)$ is globally asymptotically stable supplied that the following condition holds:*

$$z_{11} < 0.$$

Proof. To verify the global asymptotic stability of E^*, we apply the method of Lyapunov functions integrated with the Volterra-Lyapunov stable matrices theory [5, 7]. For this, we determine the Lyapunov function as follows:

$$V^* = w_1(I-I^*)^2 + w_2(R-R^*)^2,$$

where w_1, w_2 are positive constants. If we differentiate V^* with respect to time, we get

$$\begin{aligned}
\frac{dV^*}{dt} &= 2w_1(I-I^*)\frac{dI}{dt} + 2w_2(R-R^*)\frac{dR}{dt} \\
&= 2w_1\left(\frac{I}{1+mI}(B-I-R) - \frac{I^*}{1+mI^*}(B-I^*-R^*) - (I-I^*) - \frac{pI}{1+qI} + \frac{pI}{1+qI}\right)(I-I^*) \\
&+ 2w_2\left(r(I-I^*) - n(R-R^*) + \frac{pI}{1+qI} - \frac{pI}{1+qI}\right)(R-R^*) \\
&= 2w_1\left(\frac{B-I-R-(1+mI)I^*}{(1+mI)(1+mI^*)} - \frac{p}{(1+qI)(1+qI^*)}\right)(I-I^*)^2 \\
&- 2w_1\frac{I^*}{(1+mI^*)}(I-I^*)(R-R^*) + 2w_2\left(r + \frac{p}{(1+qI)(1+qI^*)}\right)(I-I^*)(R-R^*) \\
&- 2w_2 n(R-R^*)^2 \\
&= Y(WZ + Z^TW^T)Y^T.
\end{aligned}$$

Here, $Y = (I-I^*, R-R^*)$, $W = diag(w_1, w_2)$ and

$$Z = \begin{pmatrix} z_{11} & z_{12} \\ z_{21} & z_{22} \end{pmatrix},$$

where

$$\begin{aligned}
z_{11} &= \frac{B-I-R-(1+mI)I^*}{(1+mI)(1+mI^*)} - \frac{p}{(1+qI)(1+qI^*)} \\
z_{12} &= -\frac{I^*}{1+mI^*} \\
z_{21} &= r + \frac{p}{(1+qI)(1+qI^*)} \\
z_{22} &= -n
\end{aligned}$$

It is clear that $z_{12} < 0$, $z_{21} > 0$ and $z_{22} < 0$. If $z_{11} < 0$, then Z is Volterra-Lyapunov stable matrix. Therefore, $\frac{dV^*}{dt} < 0$, and by LaSalle's invariance principle [5], E^* is globally asymptotically stable in the interior of $\tilde{\Lambda}$. □

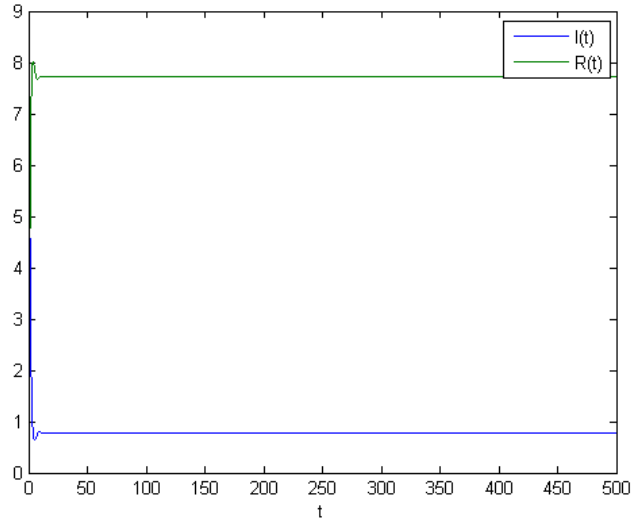

Figure 4.1: The infected equilibrium is $E^* = (I^*, R^*) = (0.7737, 7.7221)$ and it is globally asymptotically stable

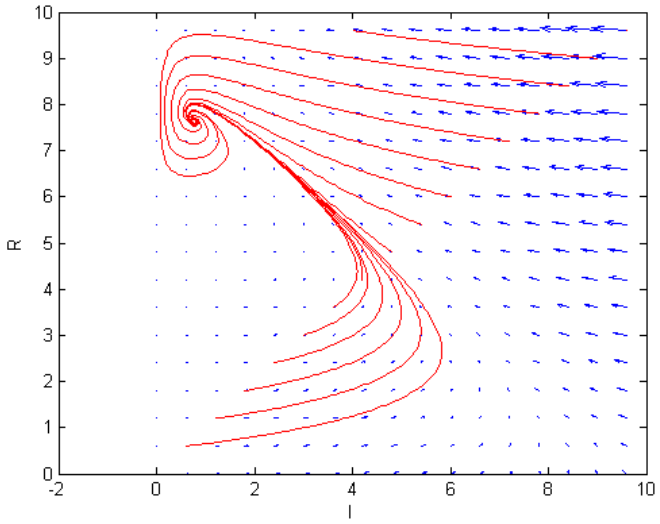

Figure 4.2: When $R_0 > 1$, the phase portrait of Eqns. (2.4)-(2.5) with $E^* = (0.7737, 7.7221)$.

4. Numerical Simulations

We now present some examples to confirm the global stability of the model investigated in Section 3.
Example 4.1: In this example, we set the hypothetical initial values as $(I(0), R(0)) = (5, 1)$. We also take the parameter values as $m = 0.005$, $n = 0.1$, $B = 1$, $p = 0.5$, $q = 0.005$, $r = 0.5$. Thus, $R_0 > 1$ and the infected equilibrium is $E^* = (I^*, R^*) = (0.7737, 7.7221)$. Therefore $E^* = (I^*, R^*) = (0.7737, 7.7221)$ is globally asymptotically stable (See Fig. 4.1 and Fig. 4.2).
Example 4.2: In this example, we set the hypothetical initial values as $(I(0), R(0)) = (5, 1)$. We also take the parameter values as $m = 0.005$, $n = 0.1$, $B = 10$, $p = 0.5$, $q = 0.004$, $r = 0.5$. Thus, $R_0 < 1$ and the disease-free equilibrium $E^0 = (0, 0)$ is globally asymptotically stable (See Fig. 4.3).

5. Conclusion

In this paper, the local and global stability of a SIRS epidemic model with a saturated incidence ratio and a saturated treatment function has been investigated. The basic reproduction number R_0 has been obtained for this model. Next, when $R_0 < 1$ it has been shown that the disease-free equilibrium is globally asymptotically stable , and the infected equilibrium is globally asymptotically stable when $R_0 > 1$. This means that if $R_0 < 1$, the disease has disappeared, otherwise the disease becomes endemic. In this context, we can say that our theoretical results are confirmed by numerical results.

Acknowledgements

The author would like to express their sincere thanks to the editor and the anonymous reviewers for their helpful comments and suggestions.

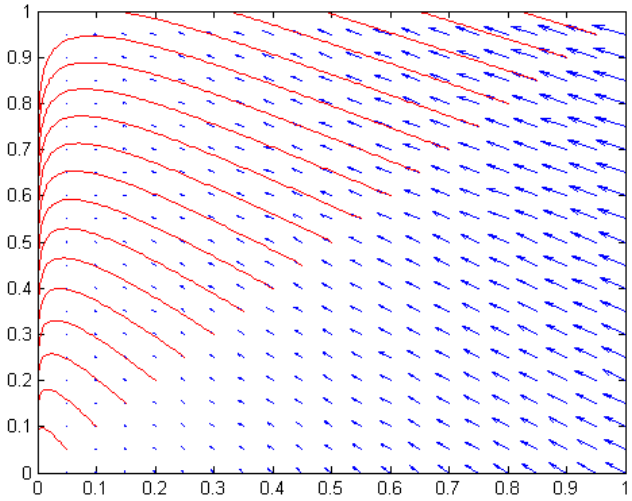

Figure 4.3: When $R_0 < 1$, the phase portrait of Eqns. (2.4)-(2.5) with $E^0 = (0,0)$.

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