MODELING AND ANALYSIS OF AN EPIDEMIC MODEL WITH CLASSICAL KERMACK-MCKENDRICK INCIDENCE RATE UNDER TREATMENT

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ABSTRACT. An epidemic model with Classical Kermack-Mckendrick incidence rate under a limited resource for treatment is proposed to understand the effect of the capacity for treatment. We have assumed that treatment function is strictly increasing function of infective individuals and becomes constant when the number of infective is very large. Existence and stability of the disease free and endemic equilibrium are investigated, boundedness of the solutions are shown. Even in this simple version of the model, backward bifurcation and multiple epidemic steady states can be observed with some sets of parameter values. Hopf-bifurcation analyses are given and numerical examples are provided to help understanding.

1. INTRODUCTION

Mathematical models have become important tools in analyzing the spread and control of infectious diseases. By setting up a good epidemic model and understanding well we can have many advantages of preventing invasion of infection to population. In recent times, epidemiological models have received much attention from researchers. Several epidemics models and reviews on theoretical developments are described in Anderson and May [1], Brauer and Castillo-Chavez [2], Britton [3], Diekmann and Heesterbeeck [4], Hethcote [5], Lizana and Rivero [6], Ruan and Wang [7], Takeuchti et al. [8], Wang and Ma [9], Wang [10], Stanek [11], Stepak and Hlubinka [12], Brauer [13], Huang and Villasana [14] and Brauer [15]. Also we want to mention here a survey paper (Hethcote [16]) and some books (see Bailey [17], Heesterbeeck [18]). The incidence rate in an epidemic model is the rate at which susceptible become infectious. The form of incidence rate that is used in our model is the classical

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Received by the editors November 16 2009; Accepted December 7 2009.

2000 Mathematics Subject Classification. 92D30, 34K20.

Key words and phrases. Epidemic, endemic equilibrium, treatment, basic reproductive number, limit cycle.

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Kermack-McKendrick model [19], i.e. the simple mass action $\alpha SI$, $\alpha$ is called the transmission coefficient. Here susceptible become infectious by contact with infectious individuals. Later they may recover and join the group of immune (or dead) individuals. Treatment plays an important role to control or decrease the spread of diseases such as flu, tuberculosis, and measles (see Feng and Thieme [20], Wu and Feng [21], Hyman and Li [22]). In classical epidemic models, the treatment rate is assumed to be proportional to the number of the infectious, which is almost impossible in real perspective because in that case the resources for treatment should be quite large. In fact, every country or society should have a suitable capacity for treatment. If it is too large, the country or society pays for unnecessary cost. If it is too small, the country or society has the risk of the outbreak of a disease. As the member of infective individuals increases Government or Society of a country extend the existing capacity of treatment accordingly. But each country or society has certain maximum capacity of treatment for infective. Traditionally, the treatment function as taken as $T(I) = \alpha I$. It embodies the unrealistic feature that there is unbounded linear increase in $T$ with respect to $I$. This unrealistic feature can largely be removed and the above feature can be included by adapting the alternative treatment function $T(I) = bI/(1 + aI)$. Here we see that when $I \to \infty$ i.e. when the numbers of infectious individuals become very large treatment become constant $(b/a)$.

The paper is organized as follows. The model and its basic properties are given in section 2. Detailed qualitative analysis is given in section 3 (local stability), section 4 (global stability) and section 5 (bifurcation investigation). Some numerical evidence and discussions are given in section 6.

2. Model, Basic Properties and Backward Bifurcation:

To construct our model we make the following assumptions:

$H_1$: In the absence of disease the susceptible population grows according to a logistic growth, with carrying capacity $K(>0)$, and with an intrinsic birth rate $r(>0)$.

$H_2$: We assume that only susceptible population $S$ is capable of reproducing with logistic growth rate, the infectious population $I$ is removed by death with a constant death rate $d(>0)$ a portion of susceptible populations are recovered from disease by natural processes and some are recovered by treatment with a treatment rate $T(I) = bI/(1 + aI)$.

Obviously the treatment function that we consider is a strictly increasing function and become constant when number of infectious individuals becomes very large.

$H_3$: We assume that the disease spreads with a simple mass action $\alpha SI$ among the susceptible population only and is not genetically inherited. The infected populations never become susceptible.

Based on these assumptions the model is described by the following system of nonlinear differential equation

$$\frac{dS}{dt} = rS \left(1 - \frac{S + I}{K}\right) - \alpha SI,$$

$$\frac{dI}{dt} = \alpha SI - (d + \gamma)I - \frac{bI}{1 + aI}.$$
\[
\frac{dR}{dt} = \gamma I + \frac{bI}{1 + aI} - dR, \quad (2.3)
\]
where \(S(t), I(t)\) and \(R(t)\) denotes the numbers of susceptible, infective, and recovered individuals at time \(t\), respectively. \(r(>0)\) is the intrinsic growth rate of susceptible, \(K\) is the carrying capacity of the susceptible in the absence of infective, \(\alpha\) is the proportionality constant, \(d\) is the natural death rate of the population, \(\gamma\) is the natural recovery rate of infective individuals. Here we consider the treatment function as \(T(I) = \frac{bI}{1 + aI}\). In our model recovered individuals never become susceptible. Since the first two equations of (2.1)-(2.3) are independent of the variable \(R\), it suffices to consider the following reduced model
\[
\frac{dS}{dt} = rS \left(1 - \frac{S + I}{K}\right) - \alpha SI, \quad \frac{dI}{dt} = \alpha SI - (d + \gamma)I - \frac{bI}{1 + aI}.
\]
The system of equation always has the trivial equilibrium \(E_0(0, 0)\) and the boundary equilibrium \(E_1(K, 0)\). To find the positive equilibria, set
\[
r \left(1 - \frac{S}{K}\right) - \left(\alpha + \frac{r}{K}\right)I = 0, \quad (2.4)
\]
\[
\alpha S - (d + \gamma) - \frac{b}{1 + aI} = 0. \quad (2.5)
\]
From (2.4), we get
\[
S = K - \left(\frac{\alpha K + r}{r}\right)I, \quad (2.6)
\]
and from (2.5), we get
\[
S = \frac{d + \gamma}{\alpha} + \frac{b}{\alpha(aI + 1)}. \quad (2.7)
\]
Hence from (2.6) and (2.7) we get
\[
a\alpha(K\alpha + r)I^2 + I \left\{\alpha(K\alpha + r) + ar(d + \gamma - K\alpha)\right\} + r(d + \gamma + b - K\alpha) = 0. \quad (2.8)
\]
Thus if \(E^*(S^*, I^*)\) denotes the interior equilibrium,
\[
S^* = K - \left(\frac{K\alpha + r}{r}\right)I^* = \frac{d + \gamma}{\alpha} + \frac{b}{\alpha(1 + aI^*)},
\]
where \(I^*\) is positive root of equation (2.8).

There is a threshold quantity which determines whether an epidemic occurs or the disease simply dies out. This quantity is called basic reproductive number, denoted by \(R_0\), which can be defined as the number of secondary infections caused by a single infected introduced into a population made up entirely of susceptible individuals over the course of infection of this single infective.

We define the basic reproduction number \(R_0\) as follows:
\[
R_0 = \frac{K\alpha}{d + \gamma + b}. \quad (2.9)
\]
If $R_0 > 1$, then (2.8) admits a unique positive solution $I^*$, and $I^*$ is given by

$$I^* = \frac{-B + \sqrt{B^2 - 4AC}}{2A},$$

(2.10)

where

$$A = \frac{a\alpha(K\alpha + r)}{K\alpha}, \quad B = \frac{\alpha(K\alpha + r) + ar(d + \gamma - K\alpha)}{K\alpha}, \quad C = \frac{r(d + \gamma + b - K\alpha)}{K\alpha}.$

So, for $R_0 > 1$, there exists a unique endemic equilibrium $(S^*, I^*)$ of the system (2.1)-(2.2), where

$$I^* = \frac{-B + \sqrt{B^2 - 4AC}}{2A}, \quad S^* = \frac{d + \gamma}{\alpha} + \frac{b}{a(1 + aI^*)}.$$

Now if $R_0 < 1$, then (2.8) has no positive root if $B > 0$, but if $R_0 < 1$ and $B < 0$, then (2.8) has either two positive roots or no positive root. So for $R_0 < 1$ and $B > 0$, (2.8) has a pair of positive roots if $B^2 - 4AC > 0$.

Equation (2.8) can be written as

$$AI^2 + BI + r\left(\frac{1}{R_0} - 1\right) = 0.$$

Therefore, when $R_0^* < R_0 < 1$ and $B < 0$, (2.8) has a pair of positive roots, where $R_0^* = 4Ar/(B^2 + 4Ar)$. Again $B < 0$, if $K\alpha > r\{(a + a(d + \gamma))/ar - \alpha\}$.

The above analysis can be stated through a proposition as follows

**Proposition 2.1.**

1. The trivial equilibrium $E_0(0, 0)$ and the disease free equilibrium $E_1(K, 0)$ always exist.
2. For $R_0 > 1$, a unique positive endemic equilibrium exists in addition to the disease free equilibrium.
3. For $R_0^* < R_0 < 1$ and $\alpha K > r\{(\alpha + a(d + \gamma))/\alpha - \alpha\}$, two positive equilibriums exist in addition to the disease free equilibrium.
4. For $0 < R_0 < R_0^*$ or ($R_0^* < R_0 < 1$ and $\alpha K < r\{(\alpha + a(d + \gamma))/\alpha - \alpha\}$) there is only the disease free equilibrium.
5. For $R_0 = 1$ and $\alpha K > r\{(\alpha + a(d + \gamma))/\alpha - \alpha\}$, a unique positive endemic equilibrium exists in addition to the disease free equilibrium.

For $\alpha K > r\{(\alpha + a(d + \gamma))/\alpha - \alpha\}$ the model (2.1)-(2.2) exhibit a backward bifurcation. Apart from the disease-free equilibrium $E_1(K, 0)$ there can exist a single unique endemic steady state or two positive steady states depending on the solutions to a quadratic equation. The endemic steady state value of $S^*$ is obtained from $S^* = \frac{d + \alpha}{a\alpha + \frac{b}{(1 + aI^*)}}$, where $I^*$ is the solution of the quadratic equation (2.8). Equation (2.8) has one or two feasible (i.e. positive, real) solutions, depending on the values of the parameters. As seen in the previous discussion, there is a unique positive endemic equilibrium for the case when $R_0 > 1$. For $R_0 < 1$, the situation is more complicated. For $\alpha K > r\{(\alpha + a(d + \gamma))/\alpha - \alpha\}$, there is a region of values for $R_0 < 1$, where there are two feasible solutions.
To test whether the system (2.1)-(2.3) is positively invariant or not let us suppose that 
\((S(t), I(t), R(t))\) is a solution of (2.1)-(2.3). If \(S(t) > 0, I(t) > 0, R(t) > 0\) for \(0 \leq t < t_0\) and \(I(t_0) = 0\), it is natural to assume that \((S(t), I(t), R(t))\) satisfies
\[
\frac{dS}{dt} = rS \left(1 - \frac{S}{K}\right), \quad I(t) = 0, \quad \frac{dR}{dt} = -dR, \quad \text{for } t \geq t_0
\]

Consequently, \(R_3^+\) is positively invariant for the system (2.1)-(2.3). Now we consider the boundedness of solutions of the system (2.1)-(2.3).

**Theorem 2.2.** All the solutions of the system (2.1)-(2.3) which initiate in \(R_3^+\) are uniformly bounded.

**Proof.** Let us consider a function
\[
U = S + I + R. \tag{2.11}
\]

Now, the time derivative of (2.11) along the solutions of (2.1)-(2.3) is
\[
\frac{dU}{dt} = rS \left(1 - \frac{S}{K}\right) - \frac{r}{K}SI - \alpha SI + \alpha SI - (d + \gamma)I \\
- \frac{bI}{1+aI} + \gamma I + \frac{bI}{1+aI} - dR \\
= rS \left(1 - \frac{S}{K}\right) - \frac{r}{K}SI - dI - dR \\
\leq rS \left(1 - \frac{S}{K}\right) - dI - dR.
\]

Or,
\[
\frac{dU}{dt} + cU \leq \left\{ r \left(1 - \frac{S}{K}\right) + c \right\} S + (c - d) I + (c - d) R,
\]

where \(c\) is some positive constant. Now choosing \(c = d\),
\[
\frac{dU}{dt} + dU < \left\{ r \left(1 - \frac{S}{K}\right) + d \right\} S,
\]

\[
\Rightarrow \quad \frac{dU}{dt} + dU < \mu,
\]

where \(\mu = K(r + d)^2/4r\). Applying the theory of differential inequality (Birkoff and Rota [23]) we obtain \(0 < U(S, I, R) < \left(1 - e^{-at}\right) \mu/d + U(S(0), I(0), R(0))e^{-at}\), which, upon letting \(t \to \infty\), yield \(0 < U < \mu/d\). So, we have that all the solutions of the system (2.1)-(2.3) that start in \(R_3^+\) are confined to the region \(G\), where \(G=\{(S, I, R) \in R_3^+: U = (\mu/d) + \varepsilon, \text{ for any } \varepsilon > 0\}\). Hence the theorem. □
3. DYNAMIC BEHAVIOR

In this section we study the stability properties of different equilibriums. Stability analysis is critical in this study since we would be able to know whether endemic equilibrium would be stable so that the disease would persist or not. The Jacobian matrix of the system (2.1)-(2.2) at the trivial equilibrium \( E_0(0, 0) \) is given by

\[
M_0 = \begin{pmatrix}
r & 0 \\
0 & -(d + \gamma + b)
\end{pmatrix}.
\]

Hence, the eigen values of this system are the roots of the equation

\[
(r - \lambda)(-d - \gamma - b - \lambda) = 0.
\]

Therefore, \( E_0(0, 0) \) is always a unstable saddle point.

Jacobian matrix for \( E_1(K, 0) \) is given by

\[
M_1 = \begin{pmatrix}
r & -(K\alpha + r) \\
0 & K\alpha - (d + \gamma + b)
\end{pmatrix}.
\]

The eigen values of the matrix are \(-r\) and \(K\alpha - (d + \gamma + b)\). Hence \( E_1(K, 0) \) is locally asymptotically stable when \( K\alpha < (d + \gamma + b) \) i.e. when \( R_0 < 1 \), and unstable when \( K\alpha > (d + \gamma + b) \) i.e. when \( R_0 > 1 \). It is observed that when unique endemic equilibrium \( E^*(S^*, I^*) \) exists, \( E_1(K, 0) \) is unstable. Also we can observe that, the disease-free equilibrium \( E_1(K, 0) \) can exist simultaneously with two positive equilibriums of the system. The Jacobian matrix of the system at \( E^*(S^*, I^*) \), the interior equilibrium is given by

\[
M = \begin{pmatrix}
W & X \\
Y & Z
\end{pmatrix},
\]

where \( W = -(r/K)S^* \), \( X = -(K\alpha + r)/K \), \( Y = \alpha I^* \), \( Z = abI^*/(aI^* + 1)^2 \).

The characteristic equation is

\[
\lambda^2 + \lambda \text{Trace}(M) + \text{Det}(M) = 0.
\]

Here

\[
\text{Trace}(M) = -\left(\frac{r}{K}\right)S^* + \frac{abI^*}{(aI^* + 1)^2}, \quad \text{Det}(M) = \left[\frac{\alpha(K\alpha + r)}{K} - \frac{r}{K} \frac{ab}{(aI^* + 1)^2}\right] S^* I^*.
\]

The stability and classification of the equilibrium \( E^*(S^*, I^*) \) dependents on the sign of the \( \text{Trace}(M) \) and \( \text{Det}(M) \).

1. If \( \text{Trace}(M) < 0 \), and \( \text{Det}(M) > 0 \), then \( E^*(S^*, I^*) \) is a stable node or a stable spiral.
2. If \( \text{Trace}(M) > 0 \), and \( \text{Det}(M) > 0 \), then \( E^*(S^*, I^*) \) is an unstable node or unstable spiral.
3. If \( \text{Det}(M) < 0 \), then \( E^*(S^*, I^*) \) is a saddle point.
4. If \( \text{Trace}(M) = 0 \), then there are some limit cycles.
Trace \( (M) = \frac{-r}{K} S^* + \frac{abI^*}{(aI^* + 1)^2} = \frac{-r(d + \gamma)(aI^* + 1)^2 - rb(aI^* + 1) + abK\alpha I^*}{K\alpha (aI^* + 1)^2} \). 

So, the sufficient condition for negative Trace is \( \alpha < \frac{r}{K} \) i.e. if the proportionality constant less than the biotic potential of the species.

Again, 

\[
\text{Det}(M) = \left[ \frac{\alpha(K\alpha + r)}{K} - \frac{rab}{K(aI^* + 1)^2} \right] S^* I^* 
= \frac{S^* I^*}{K(aI^* + 1)^2} \left[ \alpha(K\alpha + r)a^2 I^* + 2\alpha(K\alpha + r)I^* + \alpha(K\alpha + r) - rab \right].
\]

Obviously, \( \text{Det}(M) > 0 \) for \( K\alpha > \frac{r}{\alpha} (ab - \alpha) \).

Therefore the unique positive equilibrium of the system is asymptotically stable if

\[
\min \left\{ d + \gamma + b, \frac{r}{\alpha} (ab - \alpha) \right\} < K\alpha < r.
\]

But when there exist two positive equilibriums, the positive equilibrium which satisfies (3.1) must be asymptotically stable.

Now there exists a limit cycle near the unique endemic equilibrium point if Trace \( (M) = 0 \) at that point. Trace \( (M) = 0 \) implies \( J_1 I^* + J_2 I^* + J_3 = 0 \), where 

\[
J_1 = ra^2(d + \gamma), \quad J_2 = 2ar(d + \gamma) + ab(r - K\alpha), \quad J_3 = r(b + \gamma + d).
\]

Again from the equation of equilibrium we have \( J'_1 I^* + J'_2 I^* + J'_3 = 0 \), where 

\[
J'_1 = a\alpha(K\alpha + r), \quad J'_2 = \alpha(K\alpha + r) + ar(d + \gamma - K\alpha), \quad J'_3 = d + \gamma + b - K\alpha.
\]

Therefore, if \( R_0 > 1 \), and \( I^* = \frac{J_1J'_2 - J_1J'_3}{J_2J'_1 - J_1J'_2} \), there exists a limit cycle near the unique endemic equilibrium point.

### 4. Global Stability

In this section we investigate the global stability of both the disease free equilibrium and endemic equilibrium.

#### 4.1. The global stability of the disease free equilibrium.

**Theorem 4.1.** The disease-free equilibrium \( E_1(K, 0) \) always exists and is globally stable if \( K\alpha < (d + \gamma - r) \).
Proof. To investigate the global stability of the disease-free equilibrium $E_1(K, 0)$, we consider the Lyapunov function as follows

$$V_1 = S - K - K \ln \left( \frac{S}{K} \right) + I.$$ 

Calculating the derivative of $V_1$ along the solutions of the system (2.4)-(2.5)

$$\frac{dV_1}{dt} = (S - K) \frac{1}{S} \frac{dS}{dt} + \frac{dI}{dt} \leq - \frac{r}{K} (S - K)^2 - (d + \gamma - K\alpha - r)I < 0$$

in the interior of $R_+^2$ for $K\alpha \leq (d + \gamma - r)$.

Therefore, by Lyapunov-La Salle (Hale [24]), it follows that $E_1(K, 0)$ is locally asymptotically stable and all trajectories starting in Int $R_+^2$ approach $E_1(K, 0)$ as $t$ goes to infinity if the inequality $K\alpha \leq (d + \gamma - r)$ holds. This establishes the global stability of disease-free equilibrium $E_1(K, 0)$. So, $E_1(K, 0)$ always exists and is globally stable for $K\alpha \leq (d + \gamma - r)$. □

4.2. The global stability of the endemic equilibrium. To investigate the global dynamic behavior of the endemic equilibrium, the following discussion consists of two cases: $R_0 > 1$ and $R_0^* < R_0 < 1$.

Case 1. $R_0 > 1$.

Theorem 4.2. For $R_0 > 1$, the unique endemic equilibrium exists and is globally stable in the region $G_1 = \{(S, I) \in R_+^2 : S > \frac{Kb}{a} \}$ if $r \frac{ab - \alpha}{\alpha} < K\alpha < r$.

Proof. We know that the existence and stability of limit cycle is related to the existence and stability of a positive equilibrium. Also we know that, if there is no limit cycle and the endemic equilibrium is unique, the unique endemic equilibrium is globally stable. So, the limit cycles of (2.1)-(2.2) plays crucial roles on structure of dynamical behavior of the model. For this reason, we take Dulac function as $D(S, I) = 1/SI$.

Let $f_1(S, I) = rS \left( 1 - \frac{S}{K} \right) - (\alpha + \frac{r}{K}) SI$, and $f_2(S, I) = \alpha SI - (d + \gamma)I - \frac{bI}{1 + aI}$. Then we have,

$$\frac{\partial}{\partial S} (Df_1) + \frac{\partial}{\partial I} (Df_2) = - \frac{r}{KI} + \frac{ab}{S(1 + aI)^2} = - \frac{r}{KSI} \left[ S - \frac{KabI}{r(1 + aI)^2} \right] \leq 0,$$

if $S > \max \left\{ \frac{KabI}{r(1 + aI)^2} \right\}$ i.e. $S > \frac{Kb}{4r}$.

For $R_0 > 1$, the unique positive equilibrium exists and is globally stable in the region $G_1 = \{(S, I) \in R_+^2 : S > \frac{Kb}{4r} \}$ for $r \frac{ab - \alpha}{\alpha} < K\alpha < r$. Hence proved. □

Case 2. $R_0^* < R_0 < 1$. 


Theorem 4.3. For $R^*_0 < R_0 < 1$, the positive equilibrium will be globally stable if

$$\frac{r}{\alpha} (ab - \alpha) < K\alpha < \min \{r, d + \gamma\}.$$ 

Proof. To test the global stability of endemic equilibrium, we construct the Lyapunov function as $V = S - K \ln (S) + I$.

Now taking time derivative of $V$ along the solutions of equations (2.1)-(2.2), we get

$$\frac{dV}{dt} = \frac{dS}{dt} - \frac{K}{S} \frac{dS}{dt} + \frac{dI}{dt}$$

$$= \left(1 - \frac{K}{S}\right) \left\{rS \left(1 - \frac{S + I}{K}\right) - \alpha SI\right\} + \alpha SI - (d + \gamma)I - \frac{bI}{1 + aI}$$

$$= -(K - S) \left\{r \left(1 - \frac{S + I}{K}\right)\right\} + \alpha KI - \alpha SI + \alpha SI - (d + \gamma)I - \frac{bI}{1 + aI}$$

$$= -(K - S) \left\{r \left(1 - \frac{S + I}{K}\right)\right\} - (d + \gamma - K\alpha)I - \frac{bI}{1 + aI}.$$ 

Therefore, $\frac{dV}{dt} \leq 0$, if $K\alpha < d + \gamma$. Hence by La Salle’s theorem (Khalil [25]) the trajectories starting in $\text{Int} R^2_+$ approach $E^*(S^*, I^*)$ as $t$ goes to infinity if $K\alpha < d + \gamma$. This establishes the global stability of $E^*(S^*, I^*)$. Hence for $R^*_0 < R_0 < 1$, the positive equilibrium will be globally stable if $\frac{r}{\alpha} (ab - \alpha) < K\alpha < \min \{r, d + \gamma\}$.

5. Hopf bifurcation and periodic solutions

Epidemiological models with constant parameters are often found to approach a steady state in which the species coexist in equilibrium. But if parameters used in the model are changed, other types of dynamical behavior may occur and the critical parameter values at which such transitions happen are called bifurcation points. When a stable steady state goes through a bifurcation will in general either lose its stability or disappear entirely. Even if the system ends up in another steady state the transition to that state will often involve the extinction of one or more species of the system. On the other hand the entire system may survive in a non-stationary state, but further bifurcation may lead to local extinction of species. In order to preserve the system under consideration in its natural state, crossing bifurcation should be avoided and in doing so it is of great importance to determine the critical parameter values at which bifurcation occur. However in order to understand the general mechanisms leading to bifurcations in ecosystems much simpler models are needed.

From the equation of equilibrium we have

$$P_1 I^{*2} + P_2 I^* + r(P_3 + b) = 0, \quad (5.1)$$

where $P_1 = a\alpha(K\alpha + r), P_2 = \alpha(K\alpha + r) + a(r(d + \gamma - K\alpha)), P_3 = d + \gamma - K\alpha$.

$$I^* = \frac{-P_2 + \sqrt{P_2^2 - 4rP_2P_3 - 4rP_1b}}{2P_1} = \frac{\sqrt{P_1^2 - P_5b}}{2P_1} - \frac{P_2}{2P_1} = P_6\sqrt{P_4 - P_3b} - P_7,$$
where \( P_4 = P_2^2 - 4rP_1P_3, \ P_5 = 4rP_1, \ P_6 = 1/2P_1, \ P_7 = P_2/2P_1. \) Now
\[
\text{Trace}(M) = 0 \Rightarrow P_5I^* + (P_0 + P_{10}b)I^* + r(P_{11} + b) = 0, \tag{5.2}
\]
where \( P_8 = ra^2(d + \gamma), \ P_9 = 2ar(d + \gamma), \ P_{10} = a(r - K\alpha), \ P_{11} = (d + \gamma). \)

Now putting the value of \( I^* \) in (5.2), we get
\[
P_8 \left\{ P_6\sqrt{P_4 - bP_5} - P_7 \right\}^2 + \left( P_6\sqrt{P_4 - bP_5} - P_7 \right) \left( P_9 + bP_{10} \right) + r(P_{11} + b) = 0.
\]
Or,
\[
P_{12} + bP_{13} = \left( \sqrt{P_4 - bP_5} \right) \left( P_{14} - bP_{15} \right),
\]
where
\[
P_{12} = P_8P_3P_6^2 + P_8P_2^2 - P_7P_5 + rP_{11},
\]
\[
P_{13} = -P_8P_3P_6^2 - P_7P_{10} + r, \ P_{14} = 2P_6P_7P_8 - P_6P_9,
\]
\[
P_{15} = P_6P_{10}.
\]
Or,
\[
(P_{12} + bP_{13})^2 = (P_4 - bP_5) (P_{14} - bP_{15})^2.
\]
Or,
\[
P_{12}^2 + 2P_{12}P_{13}b + P_{13}b^2 = (P_4 - bP_5) \left( P_{14} - 2P_{14}P_{15}b + P_{15}b^2 \right).
\]
Or
\[
a_0b^3 + 3a_1b^2 + 3a_2b + a_3 = 0,
\]
where
\[
a_0 = P_{13}^2 P_5,
a_1 = \left( P_{13}^2 - P_4 P_{15}^2 - 2P_5 P_{14} P_{15} \right) / 3,
a_2 = \left( 2P_{12} P_{13} + 2P_4 P_{14} P_{15} + P_5 P_{14}^2 \right) / 3,
a_3 = \left( P_{12}^2 - P_4 P_{13}^2 \right).
\]
Now applying Cardan’s method we get \( b = \{(p - a_1) - (H/p)\}/a_0, \) where \( H = a_0a_2 - a_1^2, \)
\( G = a_0^3a_3 - 3a_0a_1a_2 + 2a_1^3, \ G^2 + 4H^3 > 0 \) and \( p = \left\{ \left( -G + \sqrt{G^2 + 4H^3} \right) / 2 \right\}^{1/3}. \)

But if \( G^2 + 4H^3 < 0, \) three real roots of \( b \) are \( 2\sqrt{-H} \cos \frac{\theta}{3}, 2\sqrt{-H} \cos \left( \frac{2\pi + \theta}{3} \right), 2\sqrt{-H} \cos \left( \frac{4\pi + \theta}{3} \right), \) where \( r_1(\cos \theta) = -G/2, r_1(\sin \theta) = \sqrt{-G^2 + 4H^3}/2, \) and \( r_2^2 = -H^3. \)

We now present a Hopf-bifurcation analysis of the system (2.1)-(2.2). Suppose that the parameter \( b^* \) is such that \( \text{Trace}(M) = 0 \) at the endemic equilibrium. Now if for any \( b = b^*, \) \( \frac{d}{db} \left( \text{Trace}(M) \right) \neq 0, \) then by using the Hopf-bifurcation theorem (Hassard et al [26]), the system (2.1)-(2.2) enters into Hopf type small amplitude periodic solution at parametric value \( b = b^* \) near the positive interior equilibrium.

For our model it is very difficult to test \( \frac{d}{db} \left( \text{Trace}(M) \right) \neq 0 \) analytically, but examples are provided to help understanding.
6. Numerical analysis and discussion

Our proposed model consists of three nonlinear ordinary differential equations, namely, a susceptible population, an infective population and recovered population. We have shown that all the solutions are bounded in the region $G = \{(S, I, R) \in R^3_+ : U = (\mu/d) + \varepsilon, \text{for any positive } \varepsilon\}$. For the reduced model, both the trivial equilibrium $E_0(0, 0)$ and a disease free equilibrium $E_1(K, 0)$ exist, among which $E_0(0, 0)$ is always unstable. Conditions for the unique endemic equilibrium or two endemic equilibriums are obtained. We have considered the treatment function as $T(I) = bI/(1 + aI)$, and it is realized that it plays an important role for the existence of different equilibriums. We take the values of different parameters as follows, $r = 3, K = 100, \alpha = 0.1, d = 0.5, \gamma = 0.3, a = 0.1, 0 < b < 18$.

![Figure 1](image-url)

**Figure 1.** Existence diagram of different equilibrium points in $(b, R_0)$ plane.

In Figure 1, we see that when $b < 9.2$ the basic reproductive number, $R_0 > 1$ and there exists a unique positive equilibrium. For $b = 8$, we get the corresponding unique positive equilibrium $(42.31783, 13.31127)$, where $R_0 = 1.136364 > 1$. Now for $b \in [9.2, 10.566)$ the corresponding values of $R_0 \in [R_0^*, 1)$, where $R_0^* = 0.879752$. We see that, when $b = 9.2$ there exists unique positive equilibrium $(51.33, 11.23)$ and when $b = 9.3$, there exist two positive endemic equilibriums $(52.24, 11.02)$ and $(99.09, 0.209)$, corresponding value of $R_0$ is $0.990099$. But if we take $b = 10.567$, value of $R_0$ becomes $0.8797396$ which is less than $R_0^*$. So in that case there exists no real interior equilibrium point.

To understand the role of treatment to the stability of unique endemic equilibrium, we have drawn Figure 2. Here we take the values of the parameters same as before.

In Figure 2, we see that, $\text{Det}(M)$ is always positive and $\text{Trace}(M) < 0$ for $b < 1.956$. So, for $0 < b < 1.956$, $R_0 > 1$ and the unique endemic equilibrium is stable. For $b = 1$ and
values of all other parameters same as before, we get the unique endemic equilibrium point (11.28, 20.47). Here $R_0 = 5.555556$, $\text{Trace}(M) = -0.1179772$, $\text{Det}(M) = 2.928028$ respectively, and hence the equilibrium is a stable spiral, see Figure 3.

For $b = 2.1$, the unique endemic equilibrium is (15.096, 19.593) and the corresponding values of $\text{Trace}(M)$, $\text{Det}(M)$ and $R_0$ are 0.01694339, 3.632401 and 3.448276 respectively. So, here both of $\text{Trace}(M)$ and $\text{Det}(M)$ are positive and hence the unique endemic equilibrium is unstable (see Figures 4).
System (2.1)-(2.2) has a unique endemic equilibrium (15.096, 19.593), which is an unstable focus. There exists a unique stable periodic solution. Again for $b=1.965$, Trace($M$) = 0 and Det($M$) > 0 and in that case limit cycle occur, see Figure 5.

Now, if we take the values of parameters as follows: $r = 1.5$, $K = 120$, $\alpha = 0.05$, $d = 1$, $\gamma = 0.1$, $a = 2.7$, $b = 5$, we get the corresponding value of $R_0 = 0.9836066$ and $R_0^* = 0.08771911$. So, here $R_0^* < R_0 < 1$, and we get two interior equilibriums (23.89, 19.22) and
For the equilibrium (23.89, 19.22) the corresponding values of Trace($M$) and Det($M$) are -0.2058972 and 1.407367 respectively, and for the equilibrium (119.96, 0.77), the corresponding values of Trace($M$) and Det($M$) are -1.399669 and -0.1468361 respectively. Therefore the equilibrium point (23.89, 19.22) is stable and (119.96, 0.77) is unstable, see Figures 6.

![Figure 6](image)

**Figure 6.** Figures correspond the case $R_0^* < R_0 < 1$, where one of the positive endemic equilibrium is globally stable.

Again, if we take $r = 3$, $K = 100$, $\alpha = 0.1$, $d = 0.8$, $\gamma = 1.4$, $a = 0.3$, $b = 8$, we get $R_0 = 0.9803922$, $R_0^* = 0.588543$ and the corresponding two endemic equilibriums are (36.9, 14.56) and (99.54, 0.105656). For (36.9, 14.56), the values of Trace($M$) and Det($M$) are 0.1055624 and 5.642884 respectively. Also for (99.54, 0.105656), those values are -2.748032 and -0.5747029 respectively. Therefore in this case both of two equilibriums are unstable and only the disease-free equilibrium $E_1(K, 0)$ is stable here (see Figures 7).

In this paper, by combining qualitative and bifurcation and analyses we have studied the global behavior of an SIR epidemic model with treatment. This model can be more significant when it is transformed to adjust to a specific transmittable disease; by using specific parameter values and adding some extra terms into a model would do this.

**References**


Figure 7. Figures correspond the case $R_0^* < R_0 < 1$, where both of the positive endemic equilibriums are unstable and only the disease free equilibrium is globally stable.


