Global Stability and Sensitivity Analysis of SEIQR Worm Virus Propagation Model with Quarantined State in Mobile Internet

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Abstract

The mobile Internet plays a significant role in everyday life. In recent years, it has developed very quickly and continues to offers us more and more functionalities and facilities. At present, Wi-Fi is widely used for mobile devices to connect to the Internet, but there has been a rapid increase in computer worms and viruses in the Wi-Fi base station. These worms and viruses expose the devices to the dangerous environment. In this paper, a worm propagation model with a quarantined state is proposed for studying how to control worm propagation in Wi-Fi stations. The quarantined state \((Q)\) is introduced and used to protect the infected nodes from transmitting the worm sources to the Internet or Wi-Fi base station. We determine the basic reproduction number \(R_0\) and sensitivity index that can show which parameter has the most effect in reducing \(R_0 < 1\) rapidly. We then prove the local and global asymptotic stabilities at worm-free equilibrium \(P_0\) when \(R_0 < 1\). Moreover, at the worm endemic equilibrium \(P^*\), we also prove the locally stable and the global asymptotic stability by applying Bennison criteria, when \(R_0 > 1\). Graphs of numerical results show that increasing the quarantined rate can reduce the worms propagated on Wi-Fi network. These results indicate that our model can predict the mechanism for combating worm propagating in Wi-Fi stations.

AMS subject classification:

Keywords: SEIQR model, Wi-Fi station, Global stability analysis, Sensitivity analysis.

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1. Introduction

Malware epidemic models describing the dynamic behaviors and characteristics of computer worms and viruses in the Internet are of great issue in computer networks or Wi-Fi base stations because mathematics can help to devise effective mechanisms for controlling the spread of computer worms and viruses, [1, 2, 3, 4], [5, 7, 8, 9]. A computer worm is a kind of computer program that can replicate itself. They can spread throughout the Internet network or Wi-Fi base station and send sources to other nodes without any user’s intervention. Moreover, computer worms can cause large scale network congestions [10]-[11], [12], [13], [14] and can rapidly infect millions of computers and bring about huge economic and financial losses. [15],[16]

According to a report by China Internet Network Information Center in 2015 [17], mobile devices have become increasingly pervasive as there are about 5.57 billion smartphone users in China, which is far greater than the number of computer users. This large number attracts attackers to spread worm programs among mobile devices. However, most smartphones do not have any effective methods to prevent worm attacks, leaving them vulnerable to such attacks. Smartphones affected by worms can cause great losses to users, including the leakage of data, system damage, and even financial loss.

In the past decades, computer networks have been the main focus of researchers who have proposed many different mathematical models to explore the dynamic behaviors and characteristics of computer worms present in the Internet, which the Wi-Fi base station can help control by either continuing or disrupting the connection. Specifically, Wi-Fi base stations can quarantine infected nodes by cutting off the connection between the infected nodes and other nodes.

In this paper, we first define the Quarantined state $(Q)$, to represent the infected nodes quarantined by the Wi-Fi base station, and then build a new propagation model, the SEIQR (Susceptible-Exposed-Infectious-Quarantined-Recovered) model, for mobile device worms. This model can describe the dynamic behaviors of the worms spreading in the Wi-Fi environment as the following state transition.

![Figure 1: State transition graph of the SEIQR model.](image-url)
2. SEIQR worm propagation model

In this model, a new state, the Quarantined state \( Q \) is introduced. If the mobile devices are quarantined from the infectious state, then they cannot spread the worm. Therefore, the quarantine rate \( \xi \), has a significant impact on the propagation of the worm. We can take measures to remove the worm sources from quarantined mobile nodes so that these nodes will be in the recovered state forever. All the nodes \( N \) are divided into five classes: the Susceptible nodes \( S \), the Exposed nodes \( E \), the Infected nodes \( I \), the Quarantined nodes \( Q \) and the Recovered nodes \( R \). Hence,

\[
S(t) + E(t) + I(t) + Q(t) + R(t) = N \tag{2.1}
\]

Based on these transition relationships, the SEIQR worm propagation model can be formulated by the following differential equations:

\[
\begin{align*}
\frac{dS}{dt} &= \mu N - \beta SI - \mu S, \\
\frac{dE}{dt} &= \beta SI - \eta E - \epsilon E - \mu E, \\
\frac{dI}{dt} &= \eta E - \mu I - \xi I - \gamma I, \tag{2.2} \\
\frac{dQ}{dt} &= \xi I - \phi Q - \mu Q, \\
\frac{dR}{dt} &= \epsilon E + \gamma I + \phi Q - \mu R,
\end{align*}
\]

with an initial condition \((S(0), E(0), I(0), Q(0), R(0)) \in \mathbb{R}^5_+\).

The parameter \( \mu \) is the Wi-Fi connection rate or disconnection rate, \( \beta \) is the rate at which susceptible state is attacked by the infected state, \( \eta \) is the state transition rate from \( E \) to \( I \), \( \epsilon \) is the state transition rate of \( E \) to \( R \), \( \gamma \) is the state transition rate from \( I \) to \( R \), \( \xi \) is the quarantine rate that affects the worm propagation, and \( \phi \) is the state transition rate from \( Q \) to \( R \). The feasible region of the system (2.2) can be described as \( \Omega \):

\[
\Omega = \{(S, E, I, Q, R)|S, E, I, Q, R \geq 0, S + E + I + Q + R = N\}, \tag{2.3}
\]

which is a positively invariant for the system (2.2).

3. Model analysis

This section is devoted to study the system (2.2) theoretically. The analysis of this model comprises the existence of the worm-free equilibrium, the worm endemic equilibrium, and the basic reproduction number. Secondly, we prove the local and global stabilities of the worm-free equilibrium. Finally, the global stability of the worm endemic equilibrium is proved.
3.1. Equilibriums

**Theorem 3.1.** The worm propagation system (2.2) has the unique worm-free equilibrium,

\[ P_0 = (N, 0, 0, 0, 0), \]

and the worm endemic equilibrium: \( P_1 = (S^*, E^*, I^*, Q^*, R^*) \), where

\[
S^* = \frac{(\eta + \varepsilon + \mu)(\xi + \gamma + \mu)}{\eta \beta}, \quad E^* = \frac{\mu(\mu + \xi + \gamma)}{\beta \eta}(R_0 - 1),
\]

\[
I^* = \frac{\mu}{\beta}(R_0 - 1), \quad Q^* = \frac{\mu + \xi}{\beta(\varphi + \mu)}(R_0 - 1),
\]

\[
R^* = \left( \frac{\varepsilon + \xi + \gamma}{\beta}(R_0 - 1) + \gamma + \varphi \frac{\xi}{\varphi + \mu} \right) \frac{R_0 - 1}{\beta},
\]

where \( R_0 = \frac{\eta \beta N}{(\eta + \varepsilon + \mu)(\mu + \xi + \gamma)} \).

**Proof.** Solving the following algebraic equations

\[
-\beta S^* I^* + \mu N - \mu S^* = 0, \\
\beta S^* I^* - \eta E^* - \varepsilon E^* - \mu E^* = 0, \\
\eta E^* - \mu I^* - \xi I^* - \gamma I^* = 0, \\
\xi I^* - \varphi Q^* - \mu Q^* = 0, \\
\varepsilon E^* + \gamma I^* + \varphi Q^* - \mu R^* = 0.
\]

If \( I^* = 0 \), we obtain the unique worm-free equilibrium \( P_0 = (N, 0, 0, 0, 0) \), otherwise, the unique worm endemic equilibrium, \( P_1 = (S^*, E^*, I^*, Q^*, R^*) \),

\[
S^* = \frac{(\eta + \varepsilon + \mu)(\xi + \gamma + \mu)}{\eta \beta}, \quad E^* = \frac{\mu(\mu + \xi + \gamma)}{\beta \eta}(R_0 - 1), \quad I^* = \frac{\mu}{\beta}(R_0 - 1),
\]

\[
Q^* = \frac{\mu + \xi}{\beta(\varphi + \mu)}(R_0 - 1), \quad R^* = \left( \frac{\varepsilon + \xi + \gamma}{\varphi + \mu} + \gamma + \varphi \frac{\xi}{\varphi + \mu} \right) \frac{R_0 - 1}{\beta},
\]

where \( R_0 > 1 \). The proof is completed. \( \blacksquare \)

**Remark 3.2.** The system (2.2) always has a unique worm endemic equilibrium, if \( R_0 > 1 \). grows, while if \( R_0 < 1 \), then the number of worm virus would decrease to zero.

3.2. The basic reproduction number \((R_0)\)

Now, we derive the basic reproduction number of system (2.2) which is the most fundamental parameter used by epidemiologists. We apply the next generation method [21] to
derive the basic reproduction number. First, the model (2.2) can be written in the matrix form as

\[
\begin{pmatrix}
\frac{dE}{dt} \\
\frac{dS}{dt} \\
\frac{dI}{dt} \\
\frac{dQ}{dt} \\
\frac{dR}{dt}
\end{pmatrix} =
\begin{pmatrix}
\beta SI \\
0 \\
0 \\
0 \\
0
\end{pmatrix} -
\begin{pmatrix}
(\eta + \epsilon + \mu)E \\
\beta SI - \mu N - \mu S \\
(\mu + \xi + \gamma)I - \eta E \\
\phi Q + \mu Q - \xi I \\
\mu R - \epsilon E - \gamma I - \varphi Q
\end{pmatrix} = F - V. \tag{3.5}
\]

The $5 \times 5$ Jacobian matrices that are obtained

\[
F = \begin{bmatrix}
0 & \beta I & \beta S & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{bmatrix}, \quad \text{and}
\]

\[
V = \begin{bmatrix}
(\eta + \epsilon + \mu) & 0 & 0 & 0 & 0 \\
0 & \beta I - \mu & \beta S & 0 & 0 \\
-\eta & 0 & (\mu + \xi + \gamma) & 0 & 0 \\
-\epsilon & 0 & -\xi & \varphi + \mu & 0 \\
0 & 0 & -\gamma & -\varphi & \mu
\end{bmatrix}. \tag{3.6}
\]

Substituting $P_0 = (N, 0, 0, 0, 0)$ into both Jacobian matrices and then, finding the next generation matrix is defined as $FV^{-1}$,

\[
FV^{-1} = \begin{bmatrix}
\frac{\eta \beta N}{(\eta + \epsilon + \mu) (\mu + \xi + \gamma)} & 0 & \frac{\beta N}{(\mu + \xi + \gamma)} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0
\end{bmatrix}.
\]

We determine its eigenvalues, $(\lambda)$ from the characteristic equation

\[
\begin{vmatrix}
\frac{\eta \beta N}{(\eta + \epsilon + \mu) (\mu + \xi + \gamma)} - \lambda & 0 & \frac{\beta N}{(\mu + \xi + \gamma)} & 0 & 0 \\
0 & -\lambda & 0 & 0 & 0 \\
0 & 0 & -\lambda & 0 & 0 \\
0 & 0 & 0 & -\lambda & 0 \\
0 & 0 & 0 & 0 & -\lambda
\end{vmatrix} = 0. \tag{3.7}
\]
that gives $\lambda_1 = \frac{\eta\beta N}{(\eta + \varepsilon + \mu)(\mu + \xi + \gamma)}$ and $\lambda_2 = \lambda_3 = \lambda_4 = 0 = \lambda_5 = 0$. Hence, denote the basic reproduction number of system (2.2) which is determined by the spectral radius as follows:

$$R_0 = \rho_0(FV^{-1}) = \frac{\eta\beta N}{(\eta + \varepsilon + \mu)(\mu + \xi + \gamma)}. \quad (3.8)$$

**Remark 3.3.** If $R_0 > 1$, then the number of worm viruses grow, while if $R_0 < 1$, then the number of worm viruses would decrease to zero.

### 3.3. Local stability of the worm-free equilibrium

**Theorem 3.4.** If $R_0 < 1$, the worm-free equilibrium $P_0$ of the system (2.2) is locally asymptotically stable.

**Proof.** According to the system (2.2), the Jacobian matrix is given by

$$J = \begin{bmatrix}
-\beta I_0 - \mu & 0 & -\beta S_0 & 0 & 0 \\
\beta I_0 & -(\eta + \varepsilon + \mu) & \beta S_0 & 0 & 0 \\
0 & \eta & -(\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & \xi & -(\varphi + \mu) & 0 \\
0 & \varepsilon & \gamma & \varphi & -\mu
\end{bmatrix}. \quad (3.9)$$

At the worm-free equilibrium $P_0 = (N, 0, 0, 0, 0)$, we have the Jacobian matrix as:

$$J_0^* = \begin{bmatrix}
-\mu & 0 & -\beta N & 0 & 0 \\
0 & -(\eta + \varepsilon + \mu) & \beta N & 0 & 0 \\
0 & \eta & -(\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & \xi & -(\varphi + \mu) & 0 \\
0 & \varepsilon & \gamma & \varphi & -\mu
\end{bmatrix}. \quad (3.10)$$

and the characteristic equation

$$\begin{vmatrix}
\lambda + \mu & 0 & \beta N & 0 & 0 \\
0 & \lambda + (\eta + \varepsilon + \mu) & -\beta N & 0 & 0 \\
0 & -\eta & \lambda + (\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & -\xi & \lambda + (\varphi + \mu) & 0 \\
0 & -\varepsilon & -\gamma & -\varphi & \lambda + \mu
\end{vmatrix} = 0, \quad (3.11)$$

$$(\lambda + \mu)^2(\lambda + \varphi + \mu) \begin{vmatrix}
\lambda + (\eta + \varepsilon + \mu) & -\beta N & 0 & 0 \\
-\eta & \lambda + (\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & -\varphi & \lambda + \mu \\
0 & -\varepsilon & -\gamma & \lambda + (\mu + \xi + \gamma)
\end{vmatrix} = 0.$$

Therefore, three of the eigenvalues of $J_0^*$ are $\lambda_1 = -\mu, \lambda_2 = -\mu$ and $\lambda_3 = -(\varphi + \mu)$ which have negative real parts. The two remaining eigenvalues are solutions of the quadratic equation

$$\lambda^2 + a_1\lambda + a_2 = 0, \quad (3.12)$$
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where

\[ a_1 = (\xi + \gamma + \mu) + (\eta + \epsilon + \mu) > 0, \]
\[ a_2 = (\eta + \epsilon + \mu) + (\xi + \gamma + \mu) - \eta \beta N, \]

Using the Routh-Hurwitz conditions, we consider:

\[ a_1 = (\xi + \gamma + \mu) + (\eta + \epsilon + \mu) > 0, \]
\[ a_1 a_2 = ([\xi + \gamma + \mu] + (\eta + \epsilon + \mu) \big( (\eta + \epsilon + \mu) + (\xi + \gamma + \mu) - \eta \beta N \big) \big( \eta + \epsilon + \mu \big) + \eta \beta N \big( 1 - R_0 \big) > 0, \quad R_0 < 1. \]

So, \( a_1 > 0 \) and \( a_1 a_2 > 0 \), according to the Routh-Hurwitz Criterion, two roots of Eq. (3.12) have negative real parts, \( \Re(\lambda_4) < 0, \Re(\lambda_5) < 0 \), where \( R_0 < 1 \), thus all eigenvalues of the characteristic equation (3.11) have negative real parts. Hence the worm-free equilibrium \( P_0 \) of system (2.2) is locally asymptotically stable.

3.4. Global stability of the worm-free equilibrium

In this section, we apply the Lyapunov theory to prove the globally asymptotically stability of the system (2.2) at worm-free equilibrium \( P_0 \).

**Theorem 3.5.** If \( R_0 < 1 \), the worm-free equilibrium \( P_0 \) of the system (2.2) is globally asymptotically stable on the feasible region \( \Omega_1 \), otherwise, unstable.

**Proof.** We construct the Lyapunov function

\[ L(t) = \eta E(t) + m I(t), \quad m > 0. \]

Then, calculating the derivative of \( L \) along the solutions of the model (2.2), we obtain

\[
\frac{dL}{dt} = \eta \frac{dE}{dt} + m \frac{dI}{dt} \\
= \eta[\beta SI - (\eta + \epsilon + \mu)E] + m[\eta E - (\mu + \xi + \gamma)I] \\
= \eta \beta SI + \eta(m - \eta - \epsilon - \mu)E - m(\mu + \xi + \gamma)I.
\]

(3.13)

The second term would be positive, we let \( m = \eta + \epsilon + \mu \) and \( S < N \) from the feasible region \( \Omega \).

\[
\frac{dL}{dt} < [\eta \beta N - (\eta + \epsilon + \mu)(\mu + \xi + \gamma)]I \\
= (\eta + \epsilon + \mu)(\mu + \xi + \gamma)\left[ \frac{\eta \beta N}{(\eta + \epsilon + \mu)(\mu + \xi + \gamma)} - 1 \right]I \\
= (\eta + \epsilon + \mu)(\mu + \xi + \gamma)(R_0 - 1)I.
\]

Hence, \( R_0 < 0 \), it implies that \( L'(t) < 0 \) on \( \Omega \). According to LaSalle Invariance Principle [20], we obtain that the worm-free equilibrium \( P_0 \) is globally asymptotically stable on \( \Omega \).
Remark 3.6. Theorem 3.5 implies that computer worm viruses on Wi-Fi base stations would tend to become extinct when the basic reproduction number is less than or equal to unity.

3.5. Local stability of the worm endemic equilibrium

Now we are ready to investigate the stability of the worm endemic equilibrium.

Theorem 3.7. If \( R_0 > 1 \), the worm endemic equilibrium \( P_1 \) in Eq. (3.4) of the system (2.2) is locally asymptotically stable.

Proof. The Jacobi matrix (3.9) of the system (2.2) at \( P_1 \) is given by

\[
J P^* = \begin{bmatrix}
-\beta I^* - \mu & 0 & -\beta S^* & 0 & 0 \\
\beta I^* & -(\eta + \varepsilon + \mu) & -\beta S^* & 0 & 0 \\
0 & \eta & -(\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & \xi & -(\varphi + \mu) & 0 \\
0 & \varepsilon & \gamma & \varphi & -\mu \\
\end{bmatrix}.
\] (3.14)

The characteristic equation is

\[
\left| \begin{array}{ccccc}
\lambda + \beta I^* + \mu & 0 & -\beta S^* & 0 & 0 \\
-\beta I^* & \lambda + (\eta + \varepsilon + \mu) & -\beta S^* & 0 & 0 \\
0 & -\eta & \lambda + (\mu + \xi + \gamma) & 0 & 0 \\
0 & 0 & -\xi & \lambda + (\varphi + \mu) & 0 \\
0 & -\varepsilon & -\gamma & -\varphi & \lambda + \mu \\
\end{array} \right| = 0.
\]

Simplifying, we have

\[
(\lambda + \mu)[\lambda + (\varphi + \mu)] \left| \begin{array}{ccc}
\lambda + \beta I^* + \mu & 0 & -\beta S^* \\
-\beta I^* & \lambda + (\eta + \varepsilon + \mu) & -\beta S^* \\
0 & -\eta & \lambda + (\mu + \xi + \gamma) \\
\end{array} \right| = 0.\tag{3.15}
\]

Two of the eigenvalues of \( J_0^* \) are \( \lambda_1 = -\mu \) and \( \lambda_2 = -(\varphi + \mu) \) which have negative real parts and other three remaining eigenvalues satisfy the following equation

\[
\lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0,
\]

where

\[
a_1 = (\eta + \varepsilon + \mu) + (\beta I^* + \mu) + (\mu + \xi + \gamma) > 0,
\]

\[
a_2 = (\beta I^* + \mu)(\eta + \varepsilon + \mu) + (\eta + \varepsilon + \mu)(\mu + \xi + \gamma)
\]

\[+ (\beta I^* + \mu)(\mu + \xi + \gamma) - \eta \beta S^*, \]

\[
a_3 = (\beta I^* + \mu)(\eta + \varepsilon + \mu)(\mu + \xi + \gamma) - \eta \beta S^* \mu.
\]
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We consider

\[ a_1 = (\eta + \varepsilon + \mu) + (\beta I^* + \mu) + (\mu + \xi + \gamma) \]
\[ = \eta + \varepsilon + \gamma + \mu(2 + R_0) > 0, \]

\[ a_1a_2 - a_3 = [(\eta + \varepsilon + \mu) + (\beta I^* + \mu) + (\mu + \xi + \gamma)] \]
\[ \cdot [(\eta + \varepsilon + \mu)(\mu + \xi + \gamma) + (\mu + \xi + \gamma)(\beta I^* + \mu) \]
\[ + (\beta I^* + \mu)(\eta + \varepsilon + \mu) - \eta \beta S^*] \]
\[ - [(\eta + \varepsilon + \mu)(\mu + \xi + \gamma)(\beta I^* + \mu) - \mu \eta \beta S^*] \]
\[ = [\eta + \varepsilon + \xi + \gamma] + \mu(2 + R_0) + [\varepsilon + \gamma + \mu(1 + R_0)](\varepsilon + \gamma + \mu) \mu R_0 \]
\[ + \mu(\eta + \varepsilon + \mu)(\mu + \xi + \gamma) > 0, \]

\[ a_3(a_1a_2 - a_3) = (a_1a_2 - a_3)[(\eta + \varepsilon + \mu)(\beta I^* + \mu)(\mu + \xi + \gamma) - \mu \eta \beta S^*] \]
\[ = (a_1a_2 - a_3)(\eta + \varepsilon + \mu)(\mu + \xi + \gamma)(R_0 - 1) > 0, \quad R_0 > 1. \]

So \( a_1 > 0, a_1a_2 - a_3 > 0, \) and \( a_3(a_1a_2 - a_3) > 0 \) satisfy the Routh-Hurwitz Criterion, which gives \( \Re(\lambda_3) < 0, \Re(\lambda_4) < 0, \) and \( \Re(\lambda_5) < 0, \) where \( R_0 > 1, \) thus all eigenvalues of Eq. (3.15) have negative real parts. Hence the disease-free equilibrium \( P_1 \) of system (2.2) is locally asymptotically stable.

3.6. Globally asymptotically stability

We investigate the globally asymptotically stability of the worm endemic equilibrium \( P_1 \) of the model (2.2) by using the Bendixon criterion [18]. The existence of a robust Bendixon criterion for the system which is associated to the existence and unicity of an equilibrium determines the global dynamics of the system which requires the use of Lozinski Logarithmic norm. Since three populations \( S, E \) and \( I \) do not depend on the populations \( Q \) and \( R, \) so the system (2.2) can be reduced to the model that has three equations,

\[
\begin{align*}
\frac{dS}{dt} &= -\beta SI + \mu N - \mu S, \\
\frac{dE}{dt} &= \beta SI - (\eta + \varepsilon + \mu)E, \\
\frac{dI}{dt} &= \eta E - (\mu + \xi + \gamma)I.
\end{align*}
\]

Applying the method of Li and Muldowney[18], the Bendixson criterion can help to prove the global stability of an endemic equilibrium.

Theorem 3.8. If \( R_0 > 1, \) the worm endemic equilibrium \( P_1 \) of the system (3.16) is globally asymptotically stable on \( \Omega, \) otherwise, unstable.
Proof. The Jacobian matrix of the system (3.16) is given by
\[
J = \begin{bmatrix}
-\beta I - \mu & 0 & -\beta S \\
\beta I & -(\eta + \varepsilon + \mu) & \beta S \\
0 & \eta & -(\mu + \xi + \gamma)
\end{bmatrix},
\] (3.17)
and its second additive compound Jacobian matrix \(J^{[2]}\) is defined by
\[
J^{[2]} = \begin{bmatrix}
-\beta I - 2\mu - \eta - \varepsilon & \beta S \\
\eta & -\beta I - 2\mu - \xi - \gamma & \beta S \\
0 & \beta I & -\eta - \varepsilon - 2\mu - \xi - \gamma
\end{bmatrix}.
\] (3.18)

We also define the matrix function \(P\) of \(E, I\) as:
\[
P := \begin{bmatrix}
1 & 0 & 0 \\
0 & E & 0 \\
0 & 0 & E
\end{bmatrix},
P^{-1} = \begin{bmatrix}
1 & 0 & 0 \\
0 & I & 0 \\
0 & 0 & I
\end{bmatrix}.
\]
Calculation the derivative of matrix \(P\) with respect to \(t\), we obtain
\[
P_f = \frac{dP}{dt} = \begin{bmatrix}
\frac{d(1)}{dt} & 0 & 0 \\
0 & \frac{d}{dt} \left(\frac{E}{I} \right) & 0 \\
0 & 0 & \frac{d}{dt} \left(\frac{E}{I} \right)
\end{bmatrix} = \begin{bmatrix}
0 & 0 & 0 \\
0 & E \left(\frac{\dot{E}}{E} - \frac{\dot{i}}{I} \right) & 0 \\
0 & 0 & E \left(\frac{\dot{E}}{E} - \frac{\dot{i}}{I} \right)
\end{bmatrix}.
\]

We have two products of the matrices as:
\[
P_f P^{-1} = \begin{bmatrix}
0 & 0 & 0 \\
0 & \frac{\dot{E}}{E} - \frac{\dot{i}}{I} & 0 \\
0 & 0 & \frac{\dot{E}}{E} - \frac{\dot{i}}{I}
\end{bmatrix},
\]
and
\[
P J^{[2]} P^{-1} = \begin{bmatrix}
-\beta I - 2\mu - \eta - \varepsilon & \frac{\beta SI}{E} & \frac{\beta SI}{E} \\
E \eta & -(\beta I - 2\mu - \xi - \gamma) & 0 \\
0 & \beta I & (\eta - \varepsilon - 2\mu - \xi - \gamma)
\end{bmatrix}.
\]
Then, the Bendixson matrix is defined by \(B = P_f P^{-1} + P J^{[2]} P^{-1}\) as:
\[
B = \begin{bmatrix}
-\beta I - 2\mu - \eta - \varepsilon & \frac{\beta SI}{E} & \frac{\beta SI}{E} \\
E \eta & \frac{\dot{E}}{E} - \frac{\dot{i}}{I} - \beta I - 2\mu - \xi - \gamma & 0 \\
0 & \beta I & \frac{\dot{E}}{E} - \frac{\dot{i}}{I} - \eta - \varepsilon - 2\mu - \xi - \gamma
\end{bmatrix}.
\]
which can be written in the partition matrix form as:
\[ B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix}. \]  
(3.19)

where
\[ B_{11} = [-\beta I - 2\mu - \eta - \varepsilon], \quad B_{12} = \begin{bmatrix} \frac{\beta S I}{E} & \frac{\beta S I}{E} \end{bmatrix}, \quad B_{21} = \begin{bmatrix} E I & 0 \end{bmatrix}^T, \]
\[ B_{22} = \begin{bmatrix} \dot{E} - \frac{\dot{i}}{I} - \beta I - 2\mu - \xi - \gamma & 0 \\ \frac{\dot{E}}{I} - \frac{i}{I} - \eta + \varepsilon - 2\mu - \xi - \gamma & \frac{\dot{E}}{E} \end{bmatrix}. \]

Let \((a_1, a_2, a_3)\) be a vector in \(R^3\). We choose a vector norm in \(R^3\) as
\[ |(a_1, a_2, a_3)| = \max \{|a_1|, |a_2| + |a_3|\} \]  
(3.20)

and a matrix norm \(\mu_1\) is defined by \(\mu_1(B_{nn}) = \max(a_{kk} + \sum_{i,j \neq k} |a_{ik}|)\) as described in [22].

We consider the function \(g_1(S, E, I)\) defined by
\[ g_1(S, E, I) = \mu_1(B_{11}) + |B_{12}| \]
\[ = \max\{-\beta I - 2\mu - \eta - \varepsilon\} + \max\left\{\left|\frac{\beta S I}{E}\right|, \left|\frac{\beta S I}{E}\right|\right\} \]
\[ = -\beta I - 2\mu - \eta - \varepsilon + \frac{\beta S I}{E}. \]

From (3.3), we have \(\frac{\beta S I}{E} = \frac{\dot{E} - \frac{\dot{i}}{I} - 2\mu - \xi - \gamma}{E} + (\eta + \varepsilon + \mu)\), so it obtains
\[ g_1(S, E, I) = -\beta I - 2\mu - \eta - \varepsilon + \left(\frac{\dot{E}}{E} + (\eta + \varepsilon + \mu)\right) \]
\[ = \frac{\dot{E}}{E} - \mu - \beta I \leq \frac{\dot{E}}{E} - \mu, \]

and the function \(g_2(S, E, I)\)
\[ g_2(S, E, I) = \mu_1(B_{22}) + |B_{21}| \]
\[ = \max\left\{\frac{\dot{E}}{E} - \frac{i}{I} - 2\mu - \xi - \gamma, \frac{\dot{E}}{E} - \frac{i}{I} - \eta - \varepsilon - 2\mu - \xi - \gamma\right\} \]
\[ + \max\left\{\frac{E I}{\eta}, 0\right\} \]
\[ = \frac{\dot{E}}{E} - \frac{i}{I} - \mu - (\mu - \xi + \gamma) + \frac{E}{I} \eta. \]
The relation \(-(\mu + \xi + \gamma) = \frac{i}{I} - \frac{\eta E}{I}\) in Eq.(3.3), we have

\[ g_2(S, E, I) = \frac{\dot{E}}{E} - \frac{i}{I} - \mu + \frac{\dot{i}}{I} - \frac{\eta E}{I} + \frac{E}{I} \eta = \frac{\dot{E}}{E} - \mu. \]

Let \(\mu\) be the Lozinski measure with respect to this norm and the bound of Lozinski measure of Benison matrix is given by

\[ \mu(B) \leq \sup(g_1, g_2) = \frac{\dot{E}}{E} - \mu. \]

This holds along each solution \((S(t), E(t), I(t))\) of the system (3.16) with initial condition \((S(0), E(0), I(0)) \in \Omega\), where \(\Omega\) is the compact absorbing set. By Benison criterion, define the quantity \(q_2\) as:

\[ q_2 = \lim_{t \to \infty} \sup \sup_{x \in K} \frac{1}{t} \int_0^t \mu(B(s, x_0)) ds \leq \lim_{t \to \infty} \sup \sup_{x \in K} \frac{1}{t} \int_0^t \left( \frac{\dot{E}}{E} - \mu \right) ds. \]

\[ = \lim_{t \to \infty} \sup \sup_{x \in K} \frac{1}{t} \left( \ln E \bigg|_0^t - \mu s \bigg|_0^t \right) = \lim_{t \to \infty} \sup \sup_{x \in K} \frac{1}{t} (\ln E(t) - \ln E(0) - \mu(t - 0)) \]

\[ = \lim_{t \to \infty} \sup \sup_{x \in K} \frac{1}{t} \left( \ln \frac{E(t)}{E(0)} - \mu t \right) = -\mu \leq -\frac{\mu}{2} < 0, \]

which implies \(q_2 \leq -\frac{\mu}{2} < 0\), it implies that \(P_1\) is globally asymptotically stable. ■

3.7. Sensitivity analysis of basic reproduction number \(R_0\)

The basic reproduction number \(R_0\) is a function that depends on five parameters \(\varepsilon, \eta, \beta, \xi, \mu,\) and \(\gamma\). In order to reduce the computer worm viruses, it is necessary to control the parameter values to make \(R_0 < 1\). We are therefore interested in finding the rate of change of \(R_0\) as the parameter values are changed.

The rate of change of \(R_0\) for a change in value of parameter \(h\) can be estimated from a normalized sensitivity index, \(SI(h)\) defined as follows:

\[ SI[h] = \frac{k}{R_0} \cdot \frac{\partial R_0}{\partial k}. \]  

(3.21)

The normalized sensitivity indices of the reproduction number with respect to \(\varepsilon, \eta, \beta, \xi, \mu,\)
and γ are given by

\[SI[\varepsilon] = -\frac{\varepsilon}{\eta + \varepsilon + \mu}, \quad SI[\eta] = \frac{\varepsilon + \mu}{\eta + \varepsilon + \mu},\]

\[SI[\beta] = 1, \quad SI[\xi] = -\frac{\xi}{\xi + \gamma + \mu},\]

\[SI[\mu] = -\frac{\mu(\mu^2 + \eta + \varepsilon + \xi + \gamma)}{(\eta + \varepsilon + \mu)(\xi + \gamma + \mu)}, \quad SI[\gamma] = -\frac{\gamma}{\xi + \gamma + \mu}.\] (3.22)

The sensitivity indices \(SI[\eta]\) and \(SI[\beta]\) are positive, i.e., the value of \(R_0\) decreases as \(\eta\) and \(\beta\) values decrease. The remaining indices are negative, i.e., the value of \(R_0\) decreases as \(\varepsilon, \xi, \mu\) and \(\gamma\) values increase.

Table 1: Parameter values corresponding to the disease-free equilibrium point

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>infection rate of susceptible nodes by infected nodes ((\beta))</td>
<td>0.000004</td>
<td>day(^{-1})</td>
</tr>
<tr>
<td>rate of losing immunity ((\xi))</td>
<td>0.05</td>
<td>day(^{-1})</td>
</tr>
<tr>
<td>rate for recovery ((\gamma))</td>
<td>0.01</td>
<td>day(^{-1})</td>
</tr>
<tr>
<td>transition rate ((\mu))</td>
<td>0.000003</td>
<td>day(^{-1})</td>
</tr>
<tr>
<td>transition rate ((\eta))</td>
<td>0.05</td>
<td>day(^{-1})</td>
</tr>
<tr>
<td>rate at which the exposed ((\varepsilon))</td>
<td>0.000003</td>
<td>day(^{-1})</td>
</tr>
</tbody>
</table>

As an example, we have computed the normalized sensitivity indices for the special case of parameter values given in Table 1. The sensitivity indices and corresponding % values in Table 2 represent the changes in parameter values required to give a 1% decrease in \(R_0\).

Table 2: Normalized sensitivity indices of \(R_0\) and change in parameter for 1% change in \(R_0\)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Sensitivity indices of (R_0)</th>
<th>corresponding % changes</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\beta)</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>(\xi)</td>
<td>-0.833</td>
<td>-1.200</td>
</tr>
<tr>
<td>(\gamma)</td>
<td>-0.167</td>
<td>-6</td>
</tr>
<tr>
<td>(\mu)</td>
<td>-0.110 \times 10^{-4}</td>
<td>-90909.893</td>
</tr>
<tr>
<td>(\eta)</td>
<td>1.200 \times 10^{-5}</td>
<td>83334.333</td>
</tr>
<tr>
<td>(\varepsilon)</td>
<td>-0.6 \times 10^{-5}</td>
<td>-1.667 \times 10^{-5}</td>
</tr>
</tbody>
</table>

In Table 2, the parameters that have the most effect on reducing the basic reproduction number (\(R_0 < 1\)) are listed in descending order, from the rate (\(\beta\)) of susceptible state
that receives worm, the quarantine rate ($\xi$), the recover rate ($\gamma$) of state $Q$ to state $R$, respectively. For example, in order to get a 1% decrease in the value of $R_0$, it is necessary to decrease the value of $\beta$ by 1%. Also, in order to get a 1% decrease in the value of $R_0$, it is necessary to increase the values of $\xi$ and $\gamma$ by 1.2% and 6.0%. Therefore, from the sensitivity indices, the most effective methods of reducing the value of $R_0$ are to decrease the rate of infected of susceptible node ($\beta$), decrease the growth rate of the population ($\xi$), and increase the rate of treatment rate ($\gamma$), respectively.

4. Numerical simulation

In this section, some numerical simulations are given to show the geometric impression of our results. With the set of the parameter values in Table 1, Fig 2 demonstrates the global stability of worm-free solution $P_0(100000, 0, 0, 0, 0)$ and $R_0 = 0.83 < 1$ of the system (2.2) and various initial conditions.

Figure 2: Graphs of numerical solutions for system (2.2) tends to $P_0(100000, 0, 0, 0, 0)$
Table 3: Parameter values corresponding to the endemic equilibrium point

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>infection rate of susceptible nodes by infected nodes ($\beta$)</td>
<td>0.000004</td>
<td>day$^{-1}$</td>
</tr>
<tr>
<td>rate of losing immunity ($\xi$)</td>
<td>0.05</td>
<td>day$^{-1}$</td>
</tr>
<tr>
<td>rate for recovery ($\gamma$)</td>
<td>0.01</td>
<td>day$^{-1}$</td>
</tr>
<tr>
<td>transition rate ($\mu$)</td>
<td>0.000003</td>
<td>day$^{-1}$</td>
</tr>
<tr>
<td>transition rate ($\eta$)</td>
<td>0.05</td>
<td>day$^{-1}$</td>
</tr>
<tr>
<td>rate at which the exposed ($\epsilon$)</td>
<td>0.000003</td>
<td>day$^{-1}$</td>
</tr>
</tbody>
</table>

Figure 3: Graphs of numerical solutions for system (2.2) tends to $P_1$.

To demonstrate the permanence of system (2.2), we take the set of the parameter values in Table 3, which runs for some choices of the initial conditions, in this case, we have
\( R_0 = 6.67 > 1 \) and the endemic equilibrium \( P_1(77501.005, 0.135, 0.022, 0.131, 22498.708) \) that shows globally asymptotically stable in Fig 4.

Consider system (2.2) with the parameter values in Table 3. For the transition rate \( \beta = 3 \times 10^{-6}, 5 \times 10^{-6}, 10^{-5}, 9 \times 10^{-4}, 10^{-3} \). Fig 4a shows how the infectious individuals \( I(t) \) evolves with time. It can be seen that a larger \( \beta \) favours computer worm virus spreading.

For the quarantined rate \( \xi = 0, 0.01, 0.02, 0.05, 0.08, 1 \). Fig 4b shows how the infectious group \( I(t) \) evolves with time. It can be seen that a smaller \( \xi \) favours computer worm virus spreading.

\[ \begin{align*}
\text{(a)} & \quad \text{The transition rate } \beta \text{ effects to } I(t) \\
\text{(b)} & \quad \text{The quarantined rate } \xi \text{ effects to } I(t) \\
\text{(c)} & \quad \text{The rate from } E(t) \text{ to } R(t) \\
\text{(d)} & \quad \text{The rate from } I(t) \text{ to } R(t)
\end{align*} \]

Figure 4: Graphs of numerical results show the impacts of \( \beta, \xi, \epsilon, \gamma \) to the infectious individual \( I(t) \) of system (2.2)

Consider system (2.2) with the parameter values in Table 2. For the quarantined rate \( \xi = 0, 0.01, 0.02, 0.05, 0.08, 1 \). Fig 4 shows how the infectious group \( I(t) \) evolves with time. It can be seen that a smaller \( \xi \) favours computer worm virus spreading.
5. Discussion

In this paper, a worm propagation model with a quarantined state is proposed. The quarantined state \((Q)\) can protect the infected nodes from transmitting the worm sources to the Internet or Wi-Fi base station. We determine the basic reproduction number \(R_0\) and also show sensitivity indices that show which parameter has the most effect in reducing \(R_0 < 1\) rapidly. We then prove the local and globally asymptotically stabilities at worm-free equilibrium \(P_0\) when \(R_0 < 1\). Moreover, at the worm endemic equilibrium \(P^*\), we also prove the locally stable and the globally asymptotically stability by applying Bennison criteria, when \(R_0 > 1\). Graphs of numerical results show that increasing the quarantined rate can reduce the worm propagated on Wi-Fi network.

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References


