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Global Dynamics of an SIQR Model with Vaccination and Elimination Hybrid Strategies

Yanli Ma [1], Jia-Bao Liu [2,*] and Haixia Li [1]

[1] Department of General Education, Anhui Xinhua University, Hefei 230088, China; Linda-mayanli@163.com (Y.M.); learain1@126.com (H.L.)
[2] School of Mathematics and Physics, Anhui Jianzhu University, Hefei 230601, China
* Correspondence: liujiabaoad@163.com or liujiabao@ahjzu.edu.cn

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Abstract: In this paper, an SIQR (Susceptible, Infected, Quarantined, Recovered) epidemic model with vaccination, elimination, and quarantine hybrid strategies is proposed, and the dynamics of this model are analyzed by both theoretical and numerical means. Firstly, the basic reproduction number R_0, which determines whether the disease is extinct or not, is derived. Secondly, by LaSalles invariance principle, it is proved that the disease-free equilibrium is globally asymptotically stable when $R_0 < 1$, and the disease dies out. By Routh-Hurwitz criterion theory, we also prove that the disease-free equilibrium is unstable and the unique endemic equilibrium is locally asymptotically stable when $R_0 > 1$. Thirdly, by constructing a suitable Lyapunov function, we obtain that the unique endemic equilibrium is globally asymptotically stable and the disease persists at this endemic equilibrium if it initially exists when $R_0 > 1$. Finally, some numerical simulations are presented to illustrate the analysis results.

Keywords: basic reproductive number; equilibrium; stability; SIQR epidemic model; vaccination; elimination

1. Introduction

As we know, infectious diseases cause the loss of billions of lives and bring great pain to millions of families. The whole world has devoted efforts to avoid the outbreak of the disease. Mathematical models have become important tools in analyzing the spread and control of infectious diseases. Almost 250 years ago, Bernoulli presented some works on human epidemiology with the help of mathematical models. Toward the beginning of the 2nd quarter of the 20th century, Kermack and McKendric [1] established the classical SIR model on epidemiology. Later on, many mathematical models had been proposed for the transmission dynamics of infectious diseases [2–9]. In recent years, some works have been studied for mathematical analysis of human diseases and epidemic models also utilising dynamical system approaches as stability analysis, LaSalle's invariance principle, Routh-Hurwitz criterion, or Lyapunov function in combination with numerical studies [10–14]. These models provided theoretical and quantitative bases for the prevention and control of infectious diseases.

Quarantine is the most direct control strategy for the spread of infectious disease. It has been used to reduce the transmission of human diseases such as leprosy, plague, cholera, typhus, yellow fever, smallpox, diphtheria, tuberculosis 25, and measles etc, and also been used to tackle animal diseases such as rinderpest, foot and mouth disease, psittacosis, asian fowl plague, and rabies etc. Hence, it is very important to study the infectious disease models with quarantine [15–18]. Vaccination is considered to be the most effective intervention strategy. It has been used to tackle diseases such as measles, mumps, rubella, diphtheria, tetanus, influenza, polio, etc. Recently, the epidemiological models with vaccination strategy have been analyzed by many authors in [19–27]. For example,

Li et al. [19] discussed the global analysis of SIS epidemic model with a simple vaccination and multiple endemic equilibria; Liu et al. [20] established two SVIR models by considering the time for them to obtain immunity and the possibility for them to be infected before this; Trawicki [21] proposes a new SEIRS model with vital dynamics (birth and death rates), vaccination, and temporary immunity provides a mathematical description of infectious diseases and corresponding spread in biology; T.K. Kar et al. [23] focused on the study of a nonlinear mathematical SIR epidemic model with a vaccination program, and the results showed that an accurate estimation of the efficiency of vaccination is necessary to prevent and control the spread of disease. We also refer the readers to [26,27] for relative studies on this respect. Elimination is also an effective measure to eliminate the source of infection, it is that the infected individuals were killed when they are found. It has been used to tackle diseases caused by animals or spreading in animals such as avian in uenza, tuberculosis, tetanus, rotavirus infection, etc. However, these models only consider a single prevention and control strategy, there is scarce research on the hybrid case of these strategies.

Our objective of this paper is to consider an SIQR model with vaccination, elimination, and quarantine hybrid strategies. The rest of the paper is organized as follows. In Section 3, we formulate an SIQR model with vaccination, elimination and quarantine hybrid strategies. In Section 4, we determine the basic reproduction number R_0 and obtain the existence of equilibriums. In Section 5, we discuss and analyze the local stability and the global stability of the equilibriums by Routh-Hurwitz criterion theory and constructing suitable Lyapunov functions. In Section 6, we carry out numerical simulations to illustrate the theoretical results. In Section 7, we present some discussions and illustrations about the characteristics of different prevention and control strategies according to the expression of the basic reproductive number R_0. In the last section, we give a conclusion and prospect for the research work.

2. Model Formulation

In this section, we formulate an SIQR model with vaccination, elimination, and quarantine hybrid strategies.

We assume that the total population is divided into four distinct epidemiological subclasses of individuals which are susceptible, infectious, quarantine, and recovered (removed) with sizes denoted by $S(t)$, $I(t)$, $Q(t)$, and $R(t)$, respectively. The total population size at time t is denoted by $N(t)$, with $N(t) = S(t) + I(t) + Q(t) + R(t)$. We establish the following SIQR epidemic model of ordinary differential equations

$$\begin{cases} \frac{dS}{dt} = \Lambda - \beta SI - \mu S - pS, \\ \frac{dI}{dt} = \beta SI - (\mu + \alpha_1 + \gamma + q + \delta)I, \\ \frac{dQ}{dt} = \delta I - (\varepsilon + \mu + \alpha_2)Q, \\ \frac{dR}{dt} = pS + \gamma I + \varepsilon Q - \mu R. \end{cases} \tag{1}$$

where Λ is the recruitment rate of the population, μ is the natural death rate of the population, α_1 is the disease-related death rate of the infective class, α_2 is the disease-related death rate of the quarantine class, β is the effective contact rate between the susceptible class and the infective class, γ is the natural recovery rate of the infective class, p is the vaccination rate of the susceptible class, δ is the quarantine rate of the infective class, ε is the removed rate from the quarantine class to the recovered class, q is the elimination rate of the infective class.

3. Equilibrium and Basic Reproductive Number

In this section, we determine the basic reproduction number R_0 and obtain the existence of the disease-free equilibrium E_0 and the endemic equilibrium E^* of system (1).

Summing up the four equations of system (1) and denoting

$$N(t) = S(t) + I(t) + Q(t) + R(t),$$

having

$$N'(t) = \Lambda - \mu N - (\alpha_1 + q)I - \alpha_2 Q \leq \Lambda - \mu N.$$

By solving the formula of $N'(t)$, we obtain

$$N(t) \leq N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t}),$$

thus

$$\lim_{t \to +\infty} \sup(N(t)) = \frac{\Lambda}{\mu}.$$

From biological considerations, we study system (1) in the the following feasible region

$$D = \left\{ (S, I, Q, R) | S \geq 0, I \geq 0, Q \geq 0, R \geq 0, S + I + Q + R \leq \frac{\Lambda}{\mu} \right\}.$$

Set the right sides of system (1) equal zero, that is,

$$\begin{cases} \Lambda - \beta SI - \mu S - pS = 0, \\ \beta SI - (\mu + \alpha_1 + \gamma + q + \delta)I = 0, \\ \delta I - (\varepsilon + \mu + \alpha_2)Q = 0, \\ pS + \gamma I + \varepsilon Q - \mu R = 0. \end{cases} \tag{2}$$

We determine a disease-free equilibrium $E_0 \left(\frac{\Lambda}{\mu + p}, 0, 0, \frac{\Lambda p}{(\mu + p)\mu} \right)$ of system (1) using (2). Further, if $\Lambda\beta > (\mu + p)(\mu + \alpha_1 + \gamma + q + \delta)$, we obtain an unique endemic equilibrium $E^*(S^*, I^*, Q^*, R^*)$ of system (1) using (2), where

$$S^* = \frac{\mu + \alpha_1 + \gamma + q + \delta}{\beta}, \quad I^* = \frac{\mu + p}{\beta} \left(\frac{\Lambda}{\mu + p} \frac{\beta}{\mu + \alpha_1 + \gamma + q + \delta} - 1 \right),$$

$$Q^* = \frac{\delta}{\mu + \alpha_2 + \varepsilon} \frac{\mu + p}{\beta} \left(\frac{\Lambda}{\mu + p} \frac{\beta}{\mu + \alpha_1 + \gamma + q + \delta} - 1 \right), \quad R^* = \frac{\gamma I^* + pS^* + \varepsilon Q^*}{\mu}.$$

Define

$$R_0 = \frac{\Lambda}{\mu + p} \frac{\beta}{\mu + \alpha_1 + \gamma + q + \delta}.$$

The R_0 is called the basic reproduction number of system (1). It is easy to obtain the following theorem.

Theorem 1. *For system (1), there is always a disease-free equilibrium E_0, and there is also an unique endemic equilibrium E^* when $R_0 > 1$.*

4. Global Stability of Equilibriums

In this section, we study the global stability of the disease-free equilibrium $E_0 \left(\frac{\Lambda}{\mu + p}, 0, 0, \frac{\Lambda p}{(\mu + p)\mu} \right)$ and the endemic equilibrium $E^*(S^*, I^*, Q^*, R^*)$ of system (1) by Routh-Hurwitz criterion theory and LaSalle's invariance principle.

Theorem 2. *If $R_0 < 1$, the disease-free equilibrium E_0 of system (1) is locally asymptotically stable. If $R_0 > 1$, the disease-free equilibrium E_0 is unstable.*

Proof. The Jacobian matrix of system (1) at the disease-free equilibrium E_0 is

$$J(E_0) = \begin{pmatrix} -\mu - p & 0 & 0 & 0 \\ 0 & \beta\frac{\Lambda}{\mu+p} - (\mu + \alpha_1 + \gamma + q + \delta) & 0 & 0 \\ 0 & \delta & -\mu - \alpha_2 - \varepsilon & 0 \\ p & \gamma & \varepsilon & -\mu \end{pmatrix}.$$

The four eigenvalues of matrix $J(E_0)$ are

$$\lambda_1 = -\mu - p, \quad \lambda_2 = \frac{\beta}{\mu + \alpha_1 + \gamma + q + \delta}(R_0 - 1), \quad \lambda_3 = -(\mu + \alpha_2 + \varepsilon), \quad \lambda_4 = -\mu.$$

Obviously, if $R_0 < 1$, we have the relation $\lambda_2 < 0$. Therefore, all eigenvalues of matrix $J(E_0)$ have negative real parts. Hence, the disease-free equilibrium E_0 is locally asymptotically stable. If $R_0 > 1$, we get the relation $\lambda_2 > 0$. Therefore, the matrix $J(E_0)$ has at least an eigenvalue with positive real part. Thus, the disease-free equilibrium E_0 is unstable. This completes the proof. □

Theorem 3. *If $R_0 < 1$, the disease-free equilibrium E_0 of system (1) is globally asymptotically stable.*

Proof. Consider the following Lyapunov function

$$V(t) = I(t).$$

Calculating the derivative of $V(t)$ along the positive solution of system (1), it follows that

$$\begin{aligned} \left.\frac{dV}{dt}\right|_{(1)} = \left.\frac{dI}{dt}\right|_{(1)} &= \beta SI - (\mu + \alpha_1 + \gamma + q + \delta)I \\ &= (\beta S - (\mu + \alpha_1 + \gamma + q + \delta))\, I \\ &\leq \left(\beta\frac{\Lambda}{\mu + p} - (\mu + \alpha_1 + \gamma + q + \delta)\right) \\ &= (\mu + \alpha_1 + \gamma + q + \delta)(R_0 - 1)I \\ &\leq 0. \end{aligned}$$

Furthermore, $V' = 0$ only if $I = 0$. The maximum invariant set in $\{(S, I, Q, R)|V' = 0\}$ is the singleton $\{E_0\}$. When $R_0 < 1$, according to LaSalle's invariance principle [28,29], it follows that

$$\lim_{t \to +\infty} I(t) = 0.$$

Then, we obtain the limit equations of system (1)

$$\begin{cases} \frac{dS}{dt} = \Lambda - \mu S - pS, \\ \frac{dQ}{dt} = -(\varepsilon + \mu + \alpha_2)Q, \\ \frac{dR}{dt} = pS + \varepsilon Q - \mu R. \end{cases}$$

So, the disease-free equilibrium E_0 is globally attractive in the region D. Therefore, the disease-free equilibrium E_0 of system (1) is globally asymptotically stable when $R_0 < 1$ combined with the local asymptotical stability of the disease-free equilibrium E_0. Thus we complete the proof. □

Theorem 4. *If $R_0 > 1$, the endemic equilibrium E^* of system (1) is locally asymptotically stable.*

Proof. The Jacobian matrix of system (1) at the endemic equilibrium E^* is

$$J(E^*) = \begin{pmatrix} -\mu - p - \beta I^* & -\beta S^* & 0 & 0 \\ \beta S^* & \beta\frac{\Lambda}{\mu+p} - (\mu + \alpha_1 + \gamma + q + \delta) & 0 & 0 \\ 0 & \delta & -\mu - \alpha_2 - \varepsilon & 0 \\ p & \gamma & \varepsilon & -\mu \end{pmatrix}.$$

The two eigenvalues of matrix $J(E^*)$ are

$$\lambda_3 = -(\mu + \alpha_2 + \varepsilon), \quad \lambda_4 = -\mu.$$

The other two eigenvalues are also the eigenvalues of following matrix

$$J^*(E^*) = \begin{pmatrix} -\mu - p - \beta I^* & -\beta S^* \\ \beta S^* & \beta\frac{\Lambda}{\mu+p} - (\mu + \alpha_1 + \gamma + q + \delta) \end{pmatrix}$$

$$= \begin{pmatrix} R_0 & -\beta S^* \\ \beta S^* & (\mu + \alpha_1 + \gamma + q + \delta)(R_0 - 1) \end{pmatrix}$$

Obviously, if $R_0 > 1$, it follows that

$$tr(J^*(E^*)) = R_0 + (\mu + \alpha_1 + \gamma + q + \delta)(R_0 - 1) > 0,$$

$$det(J^*(E^*)) = R_0(R_0 - 1)(\mu + \alpha_1 + \gamma + q + \delta) + \beta^2(S^*)^2 > 0.$$

Therefore, all eigenvalues of matrix $J(E^*)$ have negative real parts. According to Routh-Hurwitz criterion, we obtain the endemic equilibrium E^* of system (1) is locally asymptotically stable. Thus the proof is completed. □

The global asymptotic stability of the endemic equilibrium is proved below.

Theorem 5. *If $R_0 > 1$, the endemic equilibrium E^* of system (1) is globally asymptotically stable.*

Proof. Since the front two equations of system (1) can be independent, we consider the following subsystem

$$\begin{cases} \frac{dS}{dt} = \Lambda - \beta SI - \mu S - pS, \\ \frac{dI}{dt} = \beta SI - (\mu + \alpha_1 + \gamma + q + \delta)I. \end{cases} \tag{3}$$

Consider the following Liapunov function

$$V(t) = \frac{1}{2}(S - S^*)^2 + S^*\left(I - I^* - I^* ln\frac{I^*}{I}\right).$$

Calculating the derivative of $V(t)$ along the positive solution of system (3), it follows that

$$\begin{aligned} \left.\frac{dV}{dt}\right|_{(3)} &= (S - S^*)S' + S^*(I - I^*)\frac{I'}{I} + (Q - Q^*)Q' + (R - R^*)R' \\ &= -(\mu + p)(S - S^*)^2 - \beta I(S - S^*)^2 \\ &\leq 0. \end{aligned}$$

Obviously, we can obtain that $V(t)$ is positive definite and $V'(t)$ is negative definite. Hence, the solution (S^*, I^*) of system (3) is globally asymptotically stable. When $R_0 > 1$, any solutions of system (3) converge to (S^*, I^*), equivalently, $\lim_{t\to+\infty} S(t) = S^*$, $\lim_{t\to+\infty} I(t) = I^*$.

Then prove: $\lim_{t\to+\infty} Q(t) = Q^*$, $\lim_{t\to+\infty} R(t) = R^*$.

Consider the third equation of system (1), we derive limit equation

$$\frac{dQ}{dt} = \delta I^* - (\varepsilon + \mu + \alpha_2)Q. \tag{4}$$

It is easy to show that Q^* is the solution of Equation (4) and Q^* is globally asymptotically stable. According to the relation between limit system and original system, we therefore obtain that $\lim_{t\to+\infty} Q(t) = Q^*$. In the same way, we also obtain that $\lim_{t\to+\infty} R(t) = R^*$.

Noting that if $R_0 > 1$, the endemic equilibrium E^* of system (1) is locally asymptotically stable, we conclude that if $R_0 > 1$, the endemic equilibrium E^* of system (1) is globally asymptotically stable. This completes the proof. □

5. The Numerical Simulation

In this section, we give numerical simulations to illustrate the main theoretical results above.

In system (1), let $\Lambda = 0.26$, $\mu = 0.02$, $q = 0.12$, $\alpha_1 = 0.1$, $\alpha_2 = 0.01$, $\gamma = 0.1$, $p = 0.05$, $\delta = 0.12$, $\varepsilon = 0.3$. When $\beta = 0.1$, by computing, we derive $R_0 = 0.8075 < 1$ and system (1) has a disease-free equilibrium $E_0 = (3.735, 0, 0, 9.265)$. And we set twelve initial conditions $(1.5, 2.5, 1, 4.6)$, $(4, 0.4, 6, 2.5)$, $(5.5, 3.8, 0.5, 2)$, $(0.8, 1.6, 2.1, 8.9)$, $(3, 5.1, 1.8, 2)$, $(4.2, 1.5, 2, 3.2)$, $(6.5, 2.5, 1, 1.5)$, $(1.3, 0.4, 2, 9.5)$, $(8.5, 0.8, 0.5, 0.5)$, $(4.8, 1.6, 2.1, 4.3)$, $(3.6, 3.1, 4.8, 0.9)$, and $(0.5, 0.1, 1.4, 10.1)$, the numerical simulation is shown in Figure 1. From Theorem 3, it follows that E_0 is globally asymptotically stable. Figure 1 shows the dynamic behaviors of system (1).

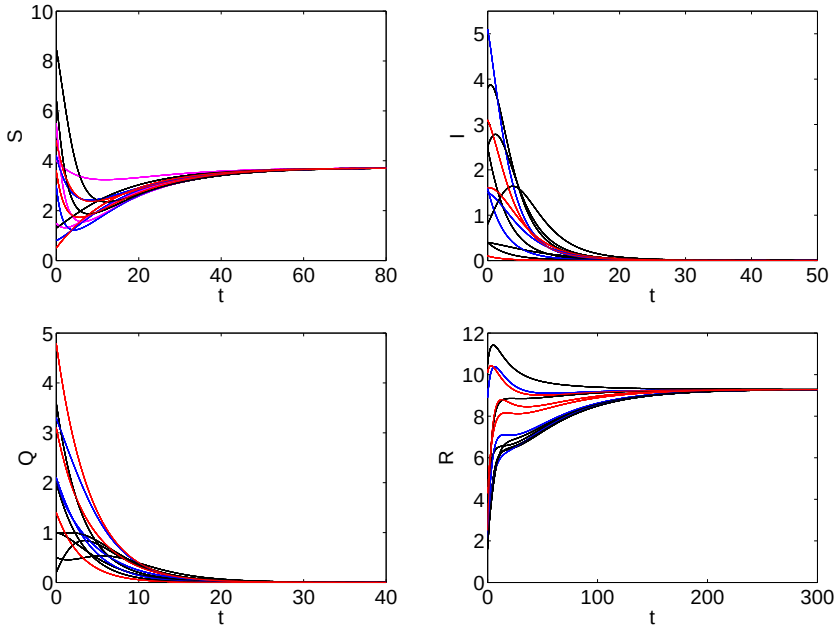

Figure 1. Variational curves of S, I, Q, and R with time t when $R_0 = 0.8075 < 1$.

In system (1), let $\Lambda = 0.26$, $\mu = 0.02$, $q = 0.12$, $\alpha_1 = 0.1$, $\alpha_2 = 0.01$, $\gamma = 0.1$, $p = 0.05$, $\delta = 0.12$, $\varepsilon = 0.3$. When $\beta = 0.3$, by computing, we derive $R_0 = 2.4224 > 1$ and system (1) has an endemic equilibrium $E^* = (1.535, 0.3321, 0.1221, 7.313)$. We set the same initial conditions as in Figure 1, the numerical simulation is shown in Figure 2. From Theorem 5, we notice that E^* is globally asymptotically stable. Numerical simulation illustrates this fact in Figure 2.

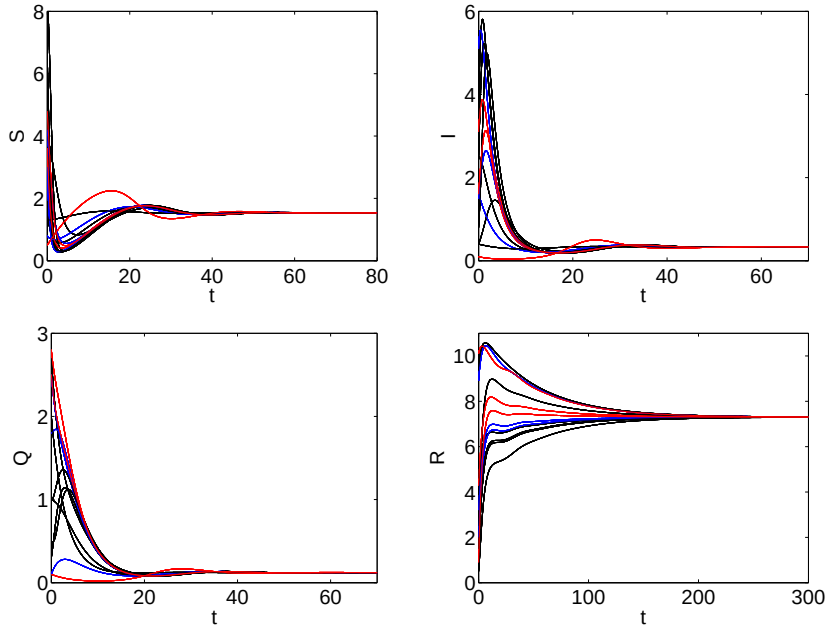

Figure 2. Variational curves of S, I, Q, and R with time t when $R_0 = 2.4224 > 1$.

In addition, we set the same initial conditions and parameters as in Figure 2 and obtain the following illustrations (see Figures 3–5). The reproduction number R_1 for quarantine-free ($\delta = 0$) and vaccination-free ($p = 0$) model is $R_1 = 11.4706 > 1$, the numerical simulation is shown in Figure 3. The reproduction number R_2 for elimination-free ($q = 0$) and vaccination-free ($p = 0$) model is $R_2 = 11.47 > 1$, the numerical simulation is shown in Figure 4. The reproduction number R_3 for elimination-free ($q = 0$) and quarantine-free ($\delta = 0$) model is $R_3 = 5.0649 > 1$, the numerical simulation is shown in Figure 5.

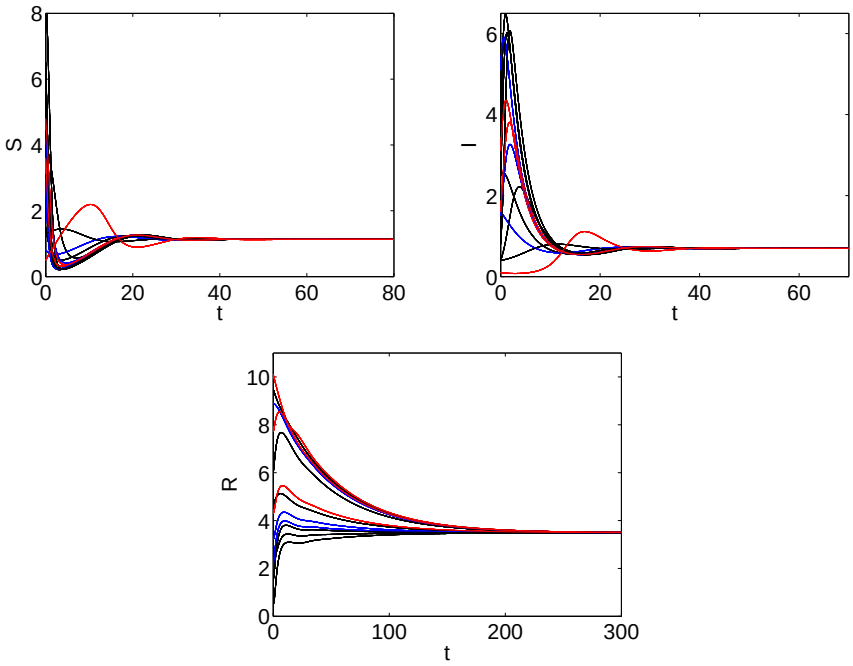

Figure 3. Variational curves of S, I, and R with time t when $R_1 = 11.4706 > 1$ for the same initial values and parameters of Figure 2 except $\delta = p = 0$.

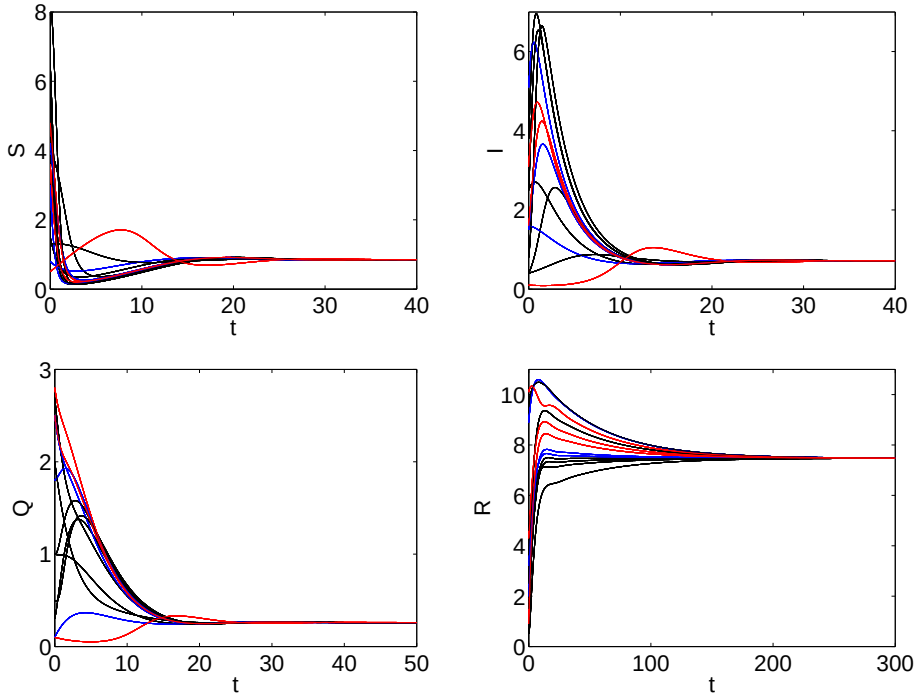

Figure 4. Variational curves of S, I, Q, and R with time t when $R_2 = 11.47 > 1$ for the same initial values and parameters of Figure 2 except $p = q = 0$.

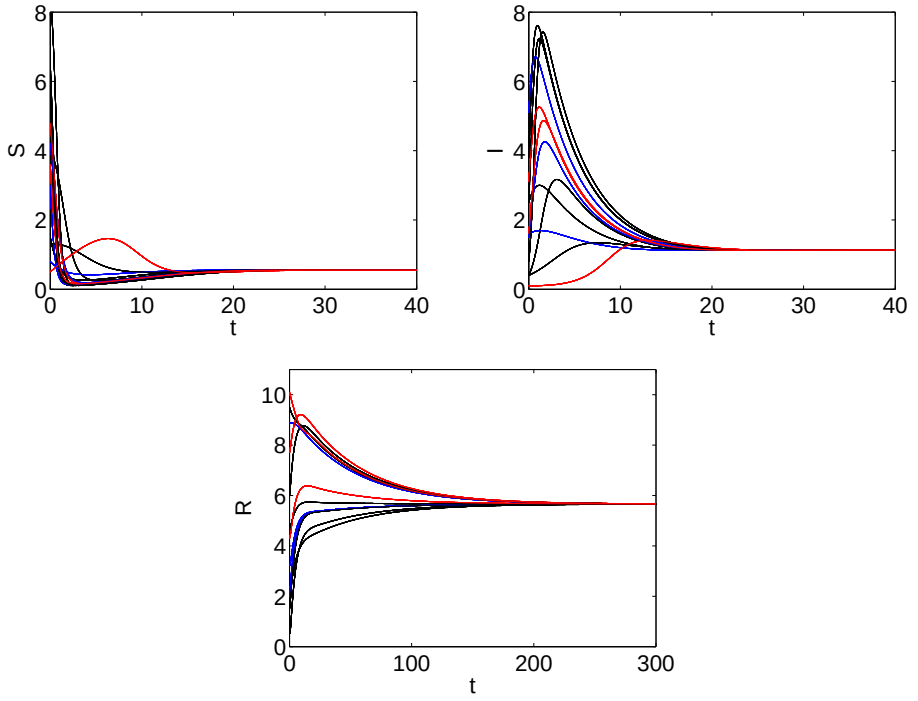

Figure 5. Variational curves of S, I, and R with time t when $R_3 = 5.0649 > 1$ for the same initial values and parameters of Figure 2 except $q = \delta = 0$.

6. Discussions

In this section, we discuss and analyze the characteristics of different prevention and control strategies according to the basic reproductive number R_0.

From the expression of the basic reproduction number R_0, we see that the basic reproduction number R_0 is dependent on the prevention and control coefficients p, q, and δ. Calculating the derivative of R_0 about p, q, and δ, respectively, having

$$\Delta p = \frac{\partial R_0}{\partial p} = -\frac{\beta\Lambda}{(\mu+p)^2(\mu+\alpha_1+\gamma+q+\delta)}. \tag{5}$$

$$\Delta\delta = \frac{\partial R_0}{\partial \delta} = -\frac{\beta\Lambda}{(\mu+p)(\mu+\alpha_1+\gamma+q+\delta)^2}. \tag{6}$$

$$\Delta q = \frac{\partial R_0}{\partial q} = -\frac{\beta\Lambda}{(\mu+p)(\mu+\alpha_1+\gamma+q+\delta)^2}. \tag{7}$$

From the mathematical meaning of the derivative, we know that Δp, Δq, and $\Delta\delta$ indicates rate of change the percentage of vaccination per unit, elimination per unit, and quarantine per unit for the basic reproduction number R_0, respectively. Using (5) and (7), having $\Delta p < 0$, $\Delta q < 0$, and $\Delta\delta < 0$. Hence, vaccination, elimination and quarantine strategy can reduce the basic reproduction number R_0, which is favourable to control the prevalence of diseases.

According to Formulas (6) and (7), from the perspective of R_0, the effect of the quarantine strategy on R_0 is the same as that of the elimination strategy. In particular, the effect of quarantine strategy on the epidemic state of diseases is the same as that of elimination strategy. Numerical simulations also illustrate this fact (see Figures 3 and 4). However, from the practical perspective, quarantine strategy entails high treatment costs, whereas elimination strategy requires smaller costs. Therefore, elimination strategy can be used to reduce diseases in the animal populations. But for some populations, the elimination strategy is not feasible, and the quarantine strategy is no doubt an alternative way. According to the Formula (5) and (7), $\Delta p = \Delta\delta$, and having

$$\frac{\Delta p}{\Delta\delta} = \frac{\Delta p}{\Delta q} = \frac{\mu+\alpha_1+\gamma+q+\delta}{\mu+p}.$$

When $p = q$, $\Delta p > \Delta q$, it is showed that the vaccination strategy is better than the quarantine strategy or elimination strategy(see Figures 4–6).

However, from a practical point of view, because the susceptible $S(t)$ is normally greater than the infectious $I(t)$ and quarantine $Q(t)$, the cost of raising the proportion of unit vaccination is much higher than the cost of raising the unit quarantine or elimination. Therefore, the hybrid control strategies should be considered in the practical implementation for the prevention and control of infectious diseases, which makes the cost and benefit are optimal.

7. Conclusions

In this paper, we formulated an SIQR epidemic model with vaccination, elimination, and quarantine hybrid strategies, and studied the dynamics of this disease model by means of both theoretical and numerical ways. For this model, we defined the basic reproduction number R_0 which completely determines the dynamical behavior of system (1). When $R_0 < 1$, as is shown in Theorem 3, the disease-free equilibrium is globally asymptotically stable (see Figure 1), and the disease always dies out eventually. When $R_0 > 1$, Theorem 5 tell us that the unique endemic equilibrium is globally asymptotically stable (see Figure 2), and the disease persists at the endemic equilibrium level if it is initially present. Some numerical simulations were performed to illustrate the analysis results. Finally, we discussed and analyzed the characteristics of different control strategies according to the basic reproductive number R_0. We obtained that vaccination strategy is better than quarantine strategy (see Figures 4–6), elimination strategy is the same as quarantine strategy (see Figures 3 and 4), and

vaccination, elimination, and quarantine hybrid strategies are the best for optimizing cost and benefit (see Figures 2–5).

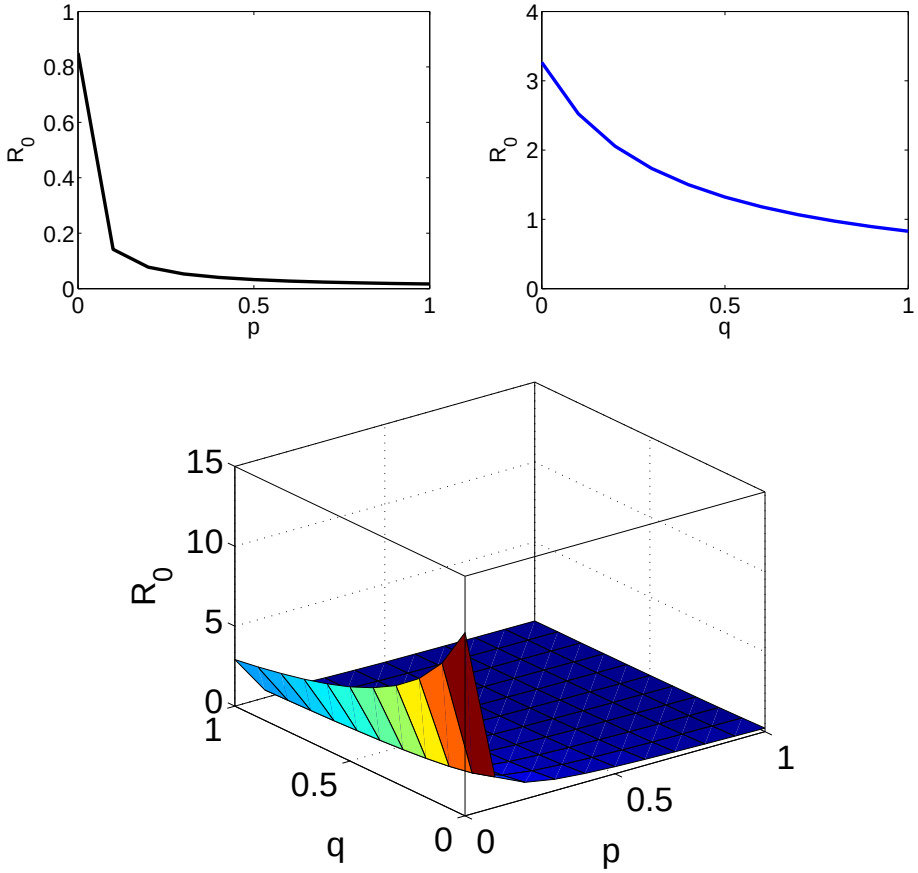

Figure 6. Variational curves and variational curved surface of R_0 with p and q.

Interestingly, the stability of the equilibrium of the model is under the influence of hybrid control strategies. We believe that our study findings offer guidance in facing up to the disease. In addition, we would like to point out here that the model (1) leaves us a problem: We take the vaccination parameter as constant in the model, but it would be beneficial if we take it as a time dependable function due to reality. We leave this (anon-autonomous infectious disease model) for future work.

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