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GLOBAL DYNAMICS OF AN SIQR EPIDEMIC MODEL WITH SPECIFIC NON-LINEAR INCIDENCE RATE INVOLVING VACCINATION AND ELIMINATION HYBRID STRATEGIES

Garima Saxena, R. K. Sharma* and Chandrashekhar Chauhan

Institute of Engineering & Technology, DAVV, Indore (M.P.), INDIA

E-mail: rimasa.1907@gmail.com, cchauhan@ietdavv.edu.in

*Department of Mathematics, Govt. Holkar Science College, DAVV, Indore (M.P.), INDIA

E-mail: raj_rma@yahoo.co.in

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Abstract: In this paper, we built up an epidemic model with vaccination, elimination, quarantine hybrid management strategies and a specific non-linear incidence rate feature (Susceptible, Infected, Quarantined and Recovered). There is a discussion of different points of equilibrium and their stability. In addition, some numerical simulations are also illustrated in our analytical results. Finally, there is a brief discussion about the position of all control strategies.

Keywords and Phrases: SIQR epidemic, vaccination, elimination, quarantine, stability, COVIDE-19.

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1. Introduction

Epidemic models have become important tools in examining the dissemination and control of infectious diseases. Modeling in the field of the study of disease transmission has had its foundations in the mid 20th century. People have developed various epidemiological models (SIR, SIER, SIERS, SIQR, SEIV etc., where S, I, E, R, Q, V denotes susceptible, infectious, exposed, recovered (removed),

quarantined and vaccinated classes respectively) with different incidence rates to control the spread of diseases over the last couple of years [1, 2, 4, 11, 15, 23, 27, 29, 30, 34]. The most commonly used effective methods to control the spread of disease are quarantine, vaccination and elimination.

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, rabies and corona virus (COVIDE-19) etc. Hence, it is very important to study the infectious disease models with quarantine [6, 21, 25, 32]. Mathematical models have been used to study their impact on the dynamics of infectious diseases under isolation and quarantine (I and Q) in order to test the effectiveness of various scenarios (strategies) on the avoidance or a melioration of the spread of highly contagious diseases [3, 7, 10, 12, 22. In addition, extensions of the SIQR model have also been studied by [5, 28 that actively introduce a class A of asymptomatic individuals. 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, and corona virus (COVIDE-19) disease etc. Recently, the epidemiological models with vaccination strategy have been analyzed by many authors in [16, 18, 20, 24, 26, 36. For example, Li et al. [18] 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 [26] 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. [16] 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 [24, 36. Elimination is also a powerful 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 inuenza, tuberculosis, tetanus, rota virus, corona virus (COVIDE-19) 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 goal of this paper is to consider a SIQR model with vaccination, elimination, and quarantine hybrid control strategies and a non linear Crowley–Martin

incidence rate $\frac{\beta SI}{(1+\alpha_1S)(1+\alpha_2I)}$ [8] which can be used to interpret the case of varicella (chicken-pox) dynamics. Here β , α_1 and α_2 are positive parameters that describe the effects of contact rate, social awareness rate among susceptible and magnitude of interference among infective population, respectively, on the incidence rate. $\alpha_1\alpha_2$ can be interpreted as magnitude of interference among susceptible and infective population due to vaccination and immunity. Recently, many researchers have studied the virus dynamics for models with Crowley–Martin infection rate [27, 31, 35]. The rest of the manuscript is organized as follows. In **Sect.2**, SIQR model is presented. In **Sect.3**, basic properties of solutions are discussed. In **Sect.4**, we calculate the basic reproduction number then in **Sect.5**, we determine all possible equilibriums. In **Sect.6**, we discuss and analyze the local stability of the equilibriums. In **Sect.7**, we discuss and analyze the global stability of the equilibriums. We present in **Sect.8**, some numerical examples of the dynamics of the model. Finally, in **Sect.9**, we discussed the conclusion.

2. Model Formulation

In this section, we formulate a new SIQR epidemic model with vaccination, elimination, and quarantine hybrid strategies and the nonlinear Crowley-Martin incidence rate. We assume that the total population is divided into four distinct epidemiological sub classes 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). Thus, the resulting model is given by the following model:

$$\begin{cases}
\frac{dS}{dt} = A - dS - \frac{\beta SI}{(1 + \alpha_1 S)(1 + \alpha_2 I)} - pS \\
\frac{dI}{dt} = \frac{\beta SI}{(1 + \alpha_1 S)(1 + \alpha_2 I)} - (\gamma + \delta + d + d_1 + q)I \\
\frac{dQ}{dt} = \delta I - (\mu + d + d_2)Q \\
\frac{dR}{dt} = pS + \gamma I + \mu Q - dR
\end{cases}$$
(2.1)

whose state space is the first quadrant $R_4^+ = \{(S, I, Q, R) : S \ge 0, I \ge 0, Q \ge 0, R \ge 0\}$ and subject to the initial conditions $S(0) = S_0 \ge 0, I(0) = I_0 \ge 0,$ $Q(0) = Q_0 \ge 0, R(0) = R_0 \ge 0$. It is assumed that all the parameters are positive. The definitions of the parameters are listed in **Table 2.1**.

State parameters	Description
A	Recruitment rate of the population
d	The natural death rate of the population
d_1	The disease-caused mortality of infective individuals
d_2	The disease caused mortality of quarantined individuals
γ	The rate at which individuals recover from compartment
	I and move to compartment R
p	The vaccination rate of the susceptible individuals
\overline{q}	The elimination rate of the infected individuals
μ	The removed rate from the compartments Q
	and R respectively
δ	The quarantine rate of the infective class

Table 2.1. Description of the model parameters.

3. Basic Properties of the Model

Summing up the four equations of model (2.1) and denoting

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

having

$$N'(t) = A - dN - (d_1 + q)I - d_2Q \le A - dN.$$

If disease is not present, then N'(t) = A - dN. This shows that population size $N \to \frac{A}{d}$ as $t \to \infty$. It follows that the solutions of model (2.1) exists in the region defined by

$$\Omega = \left\{ (S, I, Q, R) \in R_4^+ : S, I, Q, R \ge 0, S + I + Q + R \le \frac{A}{d} \right\}$$
 (3.1)

This gives the following lemma which shows that the solutions of model (2.1) are bounded, continuous for all positive time and lie in a compact set.

Lemma 3.1. The set Ω defined in (3.1) is a positively invariant region for model (2.1). Moreover, every trajectory of model (2.1) is eventually staying in a compact subset of Ω .

4. Basic Reproduction Number

One of the most useful threshold parameters that define mathematical problems concerning infectious diseases is the basic reproductive number, also called the basic reproductive rate or basic reproductive ratio. This measure is helpful because it

helps decide whether an infectious disease is going to spread across a population or not. In this section, we will calculate the basic reproduction number R_0 of system (2.1) by using the next-generation matrix method described in [9]. For that, we

$$\mathbb{F}(x) = \begin{pmatrix} \frac{\beta SI}{(1+\alpha_1 S)(1+\alpha_2 I)} \\ 0 \\ 0 \\ 0 \end{pmatrix} \text{ and } \mathfrak{A}(x) = \begin{pmatrix} (\gamma + \delta + d + d_1 + q)I \\ -\delta I + (\mu + d + d_2)Q \\ -pS - \gamma I - \mu Q + dR \\ -A + (d+p)S + \frac{\beta SI}{(1+\alpha_1 S)(1+\alpha_2 I)} \end{pmatrix}.$$

 $\mathbf{F}\mathbf{V}^{-1}$ is the next generation matrix for model (2.1). It then follows that the spectral radius of matrix $\mathbf{F}\mathbf{V}^{-1}$ is $\rho(\mathbf{F}\mathbf{V}^{-1}) = \frac{A\beta}{(A\alpha_1 + d + p)(\gamma + \delta + d + d_1 + q)}$. Thus, the basic reproduction number of model (2.1) is

$$R_0 = \frac{A\beta}{(A\alpha_1 + d + p)(\gamma + \delta + d + d_1 + q)}$$

. 5. Existence of Equilibria In this section, we obtain the existence of the disease-free equilibrium E_0 and the endemic equilibrium E^* of model (2.1). Steady states of model (2.1) satisfy the equations as follows

$$\begin{cases}
A - dS - \frac{\beta SI}{(1 + \alpha_1 S)(1 + \alpha_2 I)} = 0 \\
\frac{\beta SI}{(1 + \alpha_1 S)(1 + \alpha_2 I)} - (\gamma + \delta + d + d_1)I = 0 \\
\delta I - (\mu + d + d_2)Q = 0 \\
\gamma I + \mu Q - dR = 0
\end{cases} (5.1)$$

The model (2.1) always has the disease-free equilibrium point $E_0(\frac{A}{d+p}, 0, 0, \frac{pA}{\mu(d+p)})$. Solving (5.1) we also get a unique positive, endemic equilibrium point $E^*(S^*, I^*, Q^*)$

, R^*) of the model (2.1), where $S^* = \frac{(\gamma + \delta + d + d_1 + q)(1 + \alpha_2 I^*)}{\beta - \alpha_1 (\gamma + \delta + d + d_1 + q)(1 + \alpha_2 I^*)}, \ Q^* = \frac{\delta I^*}{\mu + d + d_2}, \ R^* = \frac{(pS^* + \gamma I^*)(\mu + d + d_2) + \mu \delta I^*}{d(\mu + d + d_2)}, \ \text{and} \ I^* \text{ is given as a root of the quadratic equation} \ \Omega_1 I^2 + \Omega_2 I + \Omega_3 = 0, \ \text{where},$

$$\Omega_1 = [\alpha_1 \alpha_2 \beta (\gamma + \delta + d + d_1 + q)^2],$$

$$\Omega_2 = \beta [\alpha_1(\gamma + \delta + d + d_1 + q) - \alpha_2(A\alpha_1 + d + p) - \beta \}](\gamma + \delta + d + d_1 + q),$$

$$\Omega_3 = [A\beta^2 - \beta(A\alpha_1 + d + p)(\gamma + \delta + d + d_1 + q)].$$

Now,

$$I^* = \frac{-\beta(\gamma + \delta + d + d_1 + q)[\alpha_1(\gamma + \delta + d + d_1 + q) - \alpha_2(A\alpha_1 + d + p) - \beta] + \sqrt{\Delta}}{2\alpha_1\alpha_2\beta(\gamma + \delta + d + d_1 + q)^2}$$

where,
$$\Delta = \beta^2 (\gamma + \delta + d + d_1 + q)^2 [\alpha_1 (\gamma + \delta + d + d_1 + q) - \alpha_2 (A\alpha_1 + d + p) - \beta]^2 - \frac{4\alpha_1 \alpha_2 (\gamma + \delta + d + d_1 + q)}{(A\alpha_1 + d + p)} [R_0 - 1].$$

It is easy to obtain the following theorem.

Theorem 5.1. For system (2.1), there is always a disease-free equilibrium E_0 , and there is also an unique endemic equilibrium E^* when $R_0 > 1$.

6. Local Stability Analysis

In this section, we study the local stability of the disease-free equilibrium E_0 and the endemic equilibrium E^* of model (2.1).

Theorem 6.1. If $R_0 < 1$, the disease-free equilibrium E_0 of model (2.1) is locally asymptotically stable. If $R_0 > 1$, the disease-free equilibrium E_0 is unstable.

Proof. The Jacobian matrix of model (2.1) at the disease-free equilibrium E_0 is

$$J(E_0) = \begin{pmatrix} -d - p & \frac{-\beta A}{d + p + \alpha_1 A} & 0 & 0\\ 0 & \frac{\beta A}{d + p + \alpha_1 A} - (\gamma + \delta + d + d_1 + q) & 0 & 0\\ 0 & \delta & -(\mu + d + d_2) & 0\\ p & \gamma & \mu & -d \end{pmatrix}$$

The characteristic equation of $J(E_0)$ is

$$(d+\lambda)(d+p+\lambda)(\mu+d+d_2+\lambda)\left\{\frac{\beta A}{d+p+\alpha_1 A} - (\gamma+\delta+d+d_1+q+\lambda)\right\} = 0$$

This equation has the following roots: $\lambda_1 = -d, \lambda_2 = -(d+p), \lambda_3 = -(\mu+d+d_2)$ and $\lambda_4 = (\gamma + \delta + d + d_1 + q) - \frac{\beta A}{d+p+\alpha_1 A}$, where $\lambda_1, \lambda_2, \lambda_3 < 0$, while $\lambda_4 < 0$ for $R_0 < 1$ and $\lambda_4 > 0$ for $R_0 > 1$.

Hence E_0 is locally asymptotically stable for $R_0 < 1$, while it is unstable for $R_0 > 1$.

Theorem 6.2. If $R_0 > 1$, the endemic equilibrium E^* of model (2.1) is locally asymptotically stable.

Proof. Consider

$$J(E^*) = \begin{pmatrix} -V_1 - d - p & -V_2 & 0 & 0\\ V_1 & V_2 - (\gamma + \delta + d + d_1 + q) & 0 & 0\\ 0 & \delta & -(\mu + d + d_2) & 0\\ p & \gamma & \mu & -d \end{pmatrix}$$

where,

$$V_1 = \frac{\beta I^*}{(1 + \alpha_1 S^* + \alpha_2 I^* + \alpha_1 \alpha_2 S^* I^*)} - \frac{\beta S^* I^*}{(1 + \alpha_1 S^* + \alpha_2 I^* + \alpha_1 \alpha_2 S^* I^*)^2}$$

$$V_2 = \frac{\beta S^*}{(1 + \alpha_1 S^* + \alpha_2 I^* + \alpha_1 \alpha_2 S^* I^*)} - \frac{\beta S^* I^* (\alpha_2 + \alpha_1 \alpha_2 S^*)}{(1 + \alpha_1 S^* + \alpha_2 I^* + \alpha_1 \alpha_2 S^* I^*)^2}$$

The characteristic equation of $J(E^*)$ is

$$(d+\lambda)(\mu+d+d_2+\lambda)\{\lambda^2+\lambda(V_1-V_2+2d+p+\gamma+\delta+d_1+q)+(V_1+p)(\gamma+\delta+d+d_1+q)+pV_2+d(\gamma+\delta+d+d_1+q-V_2)\}=0$$

Clearly, the two eigenvalues have strictly negative real part other two eigenvalues are given by the quadratic equation

$$\lambda^{2} + \lambda(V_{1} - V_{2} + 2d + p + \gamma + \delta + d_{1} + q) + (V_{1} + p)(\gamma + \delta + d + d_{1} + q) + pV_{2} + d(\gamma + \delta + d + d_{1} + q - V_{2}) = 0$$

or

$$\lambda^2 + \lambda a_1 + a_2 = 0$$

where

$$a_1 = (V_1 + d + p) + (\gamma + \delta + d + d_1 + q - V_2),$$

$$a_2 = (V_1 + p)(\gamma + \delta + d + d_1 + q) + pV_2 + d(\gamma + \delta + d + d_1 + q - V_2)$$

By Routh-Hurwitz criteria, we know that the model is stable if $a_1, a_2 > 0$ and unstable if $a_1, a_2 < 0$. We obtain $\gamma + \delta + d + d_1 + q > V_2$. Thus all eigenvalues have negative real parts and hence model (2.1) is locally asymptotically stable at endemic equilibrium E^* if $R_0 > 1$.

7. Global Stability Analysis

In this section, we study the global stability of the disease-free equilibrium E_0 and the endemic equilibrium E^* of model (2.1).

Theorem 7.1. If $R_0 < 1$, the disease-free equilibrium E_0 of model (2.1) is globally asymptotically stable.

Proof. We prove the global stability of the model (2.1) at the equilibrium E_0 when $R_0 < 1$. Taking the Lyapunov function

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

Calculating the derivative of V(t) along the positive solution of model (2.1), it follows that

$$\dot{V}(t) = \frac{\beta SI}{(1 + \alpha_1 S)(1 + \alpha_2 I)} - (\gamma + \delta + d + d_1 + q)I$$

Since the incidence function

$$\frac{\beta SI}{(1+\alpha_1 S)(1+\alpha_2 I)} \le \frac{\frac{\beta IA}{d+p}}{(1+\frac{\alpha_1 \beta IA}{d+p})(1+\alpha_2 I)} = \frac{\beta IA}{(\alpha_1 A+d+p)(1+\alpha_2 I)}$$

for $0 \le S \le \frac{A}{d+p}$.

$$\dot{V}(t) \le \left[\frac{A\beta}{(A\alpha_1 + d + p)} - (\gamma + \delta + d + d_1 + q) \right] I$$
$$= (\gamma + \delta + d + d_1 + q) \left[R_0 - 1 \right] I \le 0.$$

Furthermore, $\dot{V}=0$ only if I=0, so the largest invariant set contained in $\{(S,\,I,\,Q,\,R)\in\Omega:\dot{V}=0\}$ is the plane I=0. By Lassalle's invariance principle [17], this implies that all solution in Ω approach the plane I=0 as $t\to\infty$. On the other hand, solutions of (2.1) contained in such plane satisfy $\frac{dS}{dt}=A-dS$, $\frac{dQ}{dt}=-(\mu+d+d_2)Q$, $\frac{dR}{dt}=\mu Q-dR$, which implies that $S\to\frac{A}{d}$ and $Q\to0$, $R\to0$ as $t\to\infty$, that is, all of these solutions approach E_0 is globally asymptotically stable in Ω .

Next, we analysis the global stability of an endemic equilibrium E^* by using geometric approach method described by Li and Muldowney in [19]. For that, we need to consider a parameter

$$w = \max \left\{ \begin{array}{l} \frac{-\beta I}{(1+\alpha_1 S)(1+\alpha_2 I)} + \frac{\beta S I [\alpha_1 \alpha_2 (I-S) + (\alpha_1 - \alpha_2)]}{[(1+\alpha_1 S)(1+\alpha_2 I)]^2} - p, \\ \frac{-\beta (S+I)}{(1+\alpha_1 S)(1+\alpha_2 I)} + \frac{\beta S I [(\alpha_1 + \alpha_1 \alpha_2 I)]}{[(1+\alpha_1 S)(1+\alpha_2 I)]^2} + \gamma + 2\delta + d_1 + q - p, \\ \frac{-\beta S I [(\alpha_2 + \alpha_1 \alpha_2 S)]}{[(1+\alpha_1 S)(1+\alpha_2 I)]^2} - \mu - d_2 + \delta \end{array} \right\},$$

and we will make use of the following theorem.

Theorem 7.2. (Li & Muldowney [19]). Suppose that the system x' = f(x), with $f: D \subset \mathbb{R}^n \to \mathbb{R}^n$, satisfies the following:

- (H1) D is a simply connected open set,
- (H2) there is a compact absorbing set $K \subset D$,
- (H3) x^* is the only equilibrium in D.

Then the equilibrium x^* is globally stable in D if there exists a Lozinski i measure η such that

$$\lim_{t \to \infty} \sup \sup_{x_0 \in K} \frac{1}{t} \int_0^t \eta(B(x(s, x_0))) ds < 0, \tag{7.1}$$

$$B = P_f P^{-1} + P J^{[2]} P^{-1} (7.2)$$

and $Q \to Q(x)$ is an $\binom{n}{2} \times \binom{n}{2}$ matrix valued function.

In our case, model (2.1) can be written as x' = f(x) with $f: D \subset \mathbb{R}^n \to \mathbb{R}^n$ and D being the interior of the feasible region Ω . The existence of a compact absorbing set $K \subset D$ is equivalent to proving that (2.1) is uniformly persistent [19, 14] and the proof for this in the case when $R_0 > 1$ is similar to that of proposition 4.2 of [19]. Hence, (H1) and (H2) hold for system (2.1), and by assuming the uniqueness of the endemic equilibrium in D, we can prove its global stability with the aid of Theorem 7.2.

Theorem 7.3. If $R_0 > 1$, d < w and the endemic equilibrium E^* of system (2.1) is unique, then E^* is globally asymptotically stable in the feasible region Ω . **Proof.** Let J be the Jacobian matrix of the system (2.1). Then the second additive compound matrix of J is given by

$$J^{[2]} = \begin{pmatrix} -v_1 + v_2 + v_3 - v_4 - 2d & 0 & 0 \\ -p - \gamma - \delta - d_1 - q & & & & \\ \delta & & -v_1 + v_2 - 2d - p & -v_3 + v_4 \\ 0 & & v_1 - v_2 & v_3 - v_4 - 2d - \gamma - \delta \\ & & -d_1 - q - \mu - d_2 \end{pmatrix},$$

where, $v_1 = \frac{\beta I}{(1+\alpha_1 S)(1+\alpha_2 I)}$, $v_2 = \frac{\beta SI[(\alpha_1+\alpha_1\alpha_2 I)]}{[(1+\alpha_1 S)(1+\alpha_2 I)]^2}$, $v_3 = \frac{\beta S}{(1+\alpha_1 S)(1+\alpha_2 I)}$ and $v_4 = \frac{\beta SI[(\alpha_2+\alpha_1\alpha_2 S)]}{[(1+\alpha_1 S)(1+\alpha_2 I)]^2}$.

Let P be the matrix-valued function defined by $P = P(S, I, Q) = \operatorname{diag}(\frac{Q}{I}, \frac{Q}{I}, \frac{Q}{I});$ then P is C^1 and non-singular in the interior of Ω , $P_f = \operatorname{diag}(\frac{Q'I-I'Q}{I^2}, \frac{Q'I-I'Q}{I^2}, \frac{Q'I-I'Q}{I^2}, \frac{Q'I-I'Q}{I^2})$ and $P^{-1} = \operatorname{diag}(\frac{I}{Q}, \frac{I}{Q}, \frac{I}{Q}), P_f P^{-1} = \operatorname{diag}(0, \frac{E'}{E} - \frac{I'}{I}, \frac{E'}{E} - \frac{I'}{I})$ and $B = P_f P^{-1} + PJ^{[2]}P^{-1}$. Then B can be written in the block form

$$B = \begin{pmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{pmatrix}$$

with $B_{11} = \frac{Q'}{Q} - \frac{I'}{I} - v_1 + v_2 + v_3 - v_4 - 2d - p - \gamma - \delta - d_1 - q$, $B_{12} = (0, 0)$, $B_{21} = (\delta, 0)^T$ and

$$B_{22} = \begin{pmatrix} -v_1 + v_2 - 2d - p + \frac{Q'}{Q} - \frac{I'}{I} & -v_3 + v_4 \\ v_1 - v_2 & v_3 - v_4 - 2d - \gamma - \delta - d_1 \\ -q - \mu - d_2 + \frac{Q'}{Q} - \frac{I'}{I} \end{pmatrix}.$$

Consider the vector norm in R^3 defined by $||(u, v, w)|| = \max\{|u|, |v| + |w|\} \in R^3$ and let $\eta_1(B)$ be the Lozinskii measure with respect to this norm. Then

$$\eta_1(B) \le \sup\{g_1, g_2\},$$
(7.3)

where $g_1 = (B_{11}) + |B_{12}|$, $g_2 = \eta_2(B_{22}) + |B_{21}|$, $|B_{12}|$ and $|B_{21}|$ denote the matrix norm with respect to l_1 vector norm in norm R^2 and η_1 is the Lozinskii measure of B_{22} with respect to l_1 vector norm in R^2 . We have $|B_{12}| = 0$, $|B_{21}| = \delta$,

$$\mu(B_{22}) = \frac{Q'}{Q} - \frac{I'}{I} - d + \max\{-v_1 + v_2 - d - p, v_3 - v_4 - d - \gamma - \delta - d_1 + -q - \mu - d_2\}.$$

Then

$$\begin{array}{l} g_1 = \frac{Q'}{Q} - \frac{I'}{I} - \frac{\beta I}{(1 + \alpha_1 S)(1 + \alpha_2 I)} + \frac{\beta S I[(\alpha_1 + \alpha_1 \alpha_2 I)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} + \frac{\beta S}{(1 + \alpha_1 S)(1 + \alpha_2 I)} \\ - \frac{\beta S I[(\alpha_2 + \alpha_1 \alpha_2 S)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} - 2d - p - \gamma - \delta - d_1 - q \end{array}$$

$$\begin{split} g_2 &= \frac{Q'}{Q} - \frac{I'}{I} - d + \max\{\frac{-\beta I}{(1 + \alpha_1 S)(1 + \alpha_2 I)} + \frac{\beta SI[(\alpha_1 + \alpha_1 \alpha_2 I)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} - d - p, \\ \frac{\beta S}{(1 + \alpha_1 S)(1 + \alpha_2 I)} &- \frac{\beta SI[(\alpha_2 + \alpha_1 \alpha_2 S)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} - d - \gamma - \delta - d_1 - q - \mu - d_2\} + \delta \end{split}$$

From the second equation in the system (2.1), we have

$$\frac{I'}{I} = \frac{\beta S}{(1 + \alpha_1 S)(1 + \alpha_2 I)} - (\gamma + \delta + d + d_1 + q)$$

SO

$$g_1 = \frac{Q'}{Q} - d - p - \frac{\beta I}{(1 + \alpha_1 S)(1 + \alpha_2 I)} + \frac{\beta S I[(\alpha_1 - \alpha_2) + \alpha_1 \alpha_2 (I - S)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2}$$

and

$$\begin{split} g_2 &= \frac{Q'}{Q} - d + \max\{\frac{-\beta(S+I)}{(1+\alpha_1S)(1+\alpha_2I)} + \frac{\beta SI[(\alpha_1+\alpha_1\alpha_2I)]}{[(1+\alpha_1S)(1+\alpha_2I)]^2} + \gamma + 2\delta + d_1 + q - p, \\ &- \frac{\beta SI[(\alpha_2+\alpha_1\alpha_2S)]}{[(1+\alpha_1S)(1+\alpha_2I)]^2} - \mu - d_2 + \delta\} \end{split}$$

By (7.3), this implies that (7.1)

$$\begin{split} & \eta_1(B) \leq \frac{Q'}{Q} - d + \max\{-\frac{\beta I}{(1 + \alpha_1 S)(1 + \alpha_2 I)} + \frac{\beta SI[(\alpha_1 - \alpha_2) + \alpha_1 \alpha_2 (I - S)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} - p, \\ & \frac{-\beta (S + I)}{(1 + \alpha_1 S)(1 + \alpha_2 I)} + \frac{\beta SI[(\alpha_1 + \alpha_1 \alpha_2 I)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} + \gamma + 2\delta + d_1 + q - p, \\ & - \frac{\beta SI[(\alpha_2 + \alpha_1 \alpha_2 S)]}{[(1 + \alpha_1 S)(1 + \alpha_2 I)]^2} - \mu - d_2 + \delta\} \end{split}$$

$$= \frac{Q'}{Q} - (d - w)$$

By integrating both sides at the same time, we obtain

$$\frac{1}{t} \int_{0}^{t} \eta_1(B) ds \leq \frac{1}{t} \ln \frac{Q(t)}{Q(0)} - (d - w)$$

SO

$$\lim_{t \to \infty} \sup \sup \frac{1}{t} \int_{0}^{t} \eta_1(B) ds \le -(d-w)$$

and therefore, $\lim_{t\to\infty} \sup\sup \frac{1}{t} \int_0^t \eta_1(B) ds0$. provided d>w. Hence, E^* is globally asymptotically stable in Ω .

8. Numerical Simulations

In this section, we will give some numerical examples to illustrate our main results by using Milstein's Higher Order Method [13]. For simulations, we take the set of parameters (assumed) as shown in **Table 8.1** and **Table 8.2**.

Table 8.1. Parameters used for simulation purpose when $R_0 = 0.078799 < 1$.

Symbol	A	β	d	d_1	d_2	γ	p	q	μ	δ	α_1	α_2
Value	0.3	0.7	0.2	0.1	0.2	0.2	0.05	0.12	0.1	0.2	0.01	0.05

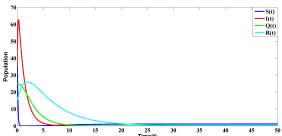
Table 8.2. Parameters used for simulation purpose when $R_0 = 2.92683 > 1$.

Symbol	A	β	d	d_1	d_2	γ	p	q	μ	δ	α_1	α_2
Value	1.2	0.65	0.3	0.01	0.2	0.02	0.05	0.12	0.2	0.1	0.05	0.015

For this simulation, we take the set of parameters as shown in **Table 8.1**. In this case, S(t) approaches to its steady state value while I(t), Q(t) and R(t) approaches to zero as $t \to \infty$. Hence the disease disappears and dies out. (**Fig. 8.1**).



Fig. 8.1. The figure represents that the disease dies out.



We take the set of parameters as shown in **Table 8.2** for these simulations. Here, Fig. 8.2 present S(t), I(t), Q(t) and R(t) all approaches to their steady state values as $t \to \infty$. Hence the disease becomes endemic. The main importance of applying control strategies can be noted in **Fig. 8.3**, where we draw the variations of infected individuals. It is noticed that when all control strategies are applied, the infected class population remains the least. Fig. 8.4, represents the variation of recovered class of population. Thus the **Figs. 8.3-8.4**, represent the behavioral change of all classes of population as time evolves. Fig. 8.8, represents the phase portrait in SQI-space with different initial conditions. This phase diagram shows that $\lim_{t \to \infty} (S(t), I(t), Q(t)) = (S^*, I^*, Q^*)$ for $R_0 > 1$.

In addition, we set the same initial conditions and parameters as in Fig. 8.2 and obtain following illustrations (see Figs. 8.5-8.7). The reproduction number R_0 for quarantine-free $(\delta=0)$ and vaccination-free (p=0) model is $(R_0)_{\delta=p=0}$ 4.8148 > 1 the numerical simulation is shown in Fig. 8.5. The reproduction number R_0 for elimination-free (q=0) and vaccination-free (p=0) model is R_0 $(R_0)_{q=p=0}=4.08805>1$, the numerical simulation is shown in **Fig. 8.6**. The reproduction number R_0 for elimination-free (q=0) and quarantine-free $(\delta=0)$ $(R_0)_{a=\delta=0}=3.5895>1$, the numerical simulation is shown in **Fig. 8.7**.

Fig. 8.2. The figure represents that the disease endemic.

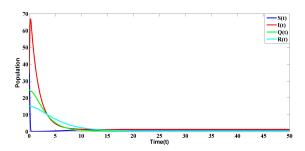


Fig. 8.3. Variation of the infected population for different control strategies.

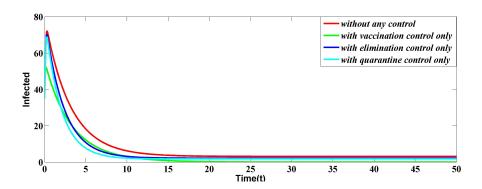


Fig. 8.4. Variation of the recovered population for different control strategies.

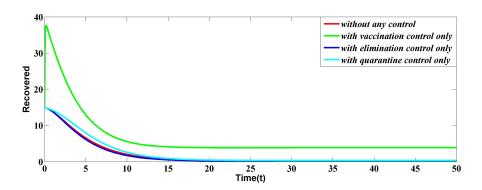


Fig. 8.5. Variational curves of S, I and R with time t when $R_0 = 4.8148 > 1$ for the same initial values and parameters of **Fig. 8.2** except $\delta = p = 0$.

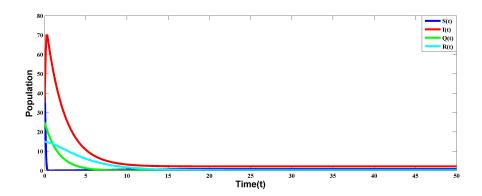


Fig. 8.6. Variational curves of S, I and R with time t when $R_0 = 4.08805 > 1$ for the same initial values and parameters of **Fig. 8.2** except q = p = 0.

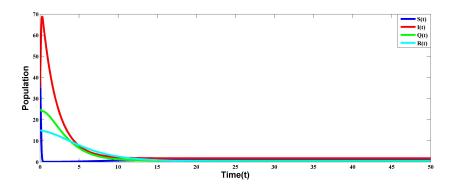


Fig. 8.7. Variational curves of S, I and R with time t when $R_0 = 3.5895 > 1$ for the same initial values and parameters of **Fig. 8.2** except $q = \delta = 0$.

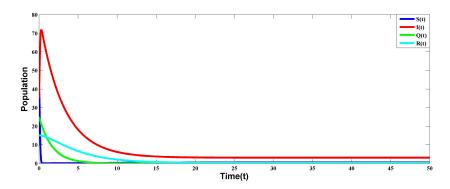
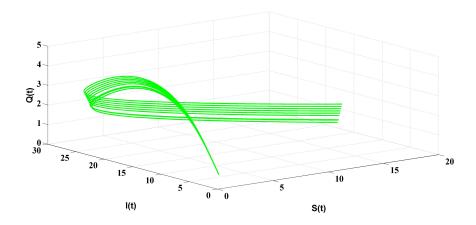


Fig. 8.8. The phase diagram at different initial values endemic equilibrium.



9. Discussions and Conclusions

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

$$\Delta p = \frac{\partial R_0}{\partial p} = \frac{-A\beta}{(A\alpha_1 + d + p)^2 (\gamma + \delta + d + d_1 + q)}$$
(9.1)

$$\Delta q = \frac{\partial R_0}{\partial q} = \frac{-A\beta}{(A\alpha_1 + d + p)(\gamma + \delta + d + d_1 + q)^2}$$
(9.2)

$$\Delta \delta = \frac{\partial R_0}{\partial \delta} = \frac{-A\beta}{(A\alpha_1 + d + p)(\gamma + \delta + d + d_1 + q)^2}$$
(9.3)

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 (9.1), (9.2) and (9.3), 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 favorable to control the prevalence of diseases.

According to Formulas (9.2) and (9.3), 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 **Figs. 8.5-8.6**). However, from the practical perspective, quarantine strategy entails high treatment costs, where as 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 (9.2) and (9.3), $\Delta q = \Delta \delta$, and having

$$\frac{\Delta p}{\Delta \delta} = \frac{\Delta p}{\Delta q} = \frac{(\gamma + \delta + d + d_1 + q)}{(A\alpha_1 + d + p)}$$

When p = q, $\Delta p > \Delta q$, it is showed that the vaccination strategy is better than the quarantine strategy or elimination strategy (see **Figs. 8.6-8.7**).

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.

In this research paper, we analyze and discuss a SIQR type epidemic model with the specific non linear incidence rate and vaccination, elimination, quarantine hybrid strategies is proposed and discussed. The mathematical analysis shows that the basic reproduction number plays an important role to control the disease. It has been obtained that disease-free equilibrium E_0 is locally and globally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$ and the disease always dies out eventually (see Fig. 8.1). Similarly, for the endemic equilibrium E^* , it has been obtained for local as well as globally asymptotically stable under some conditions and the disease persists at the endemic equilibrium level if it is initially present (Fig. 8.2). Finally, we discussed and evaluated the characteristics of various control strategies according to the basic reproduction number R_0 . We obtained that vaccination strategy is better than quarantine strategy (see Figs. 8.5-8.7), elimination strategy is the same as quarantine strategy (see Figs. 8.6-8.7) and vaccination, elimination, and quarantine hybrid strategies are the best for optimizing cost and benefit (see Figs. 8.2-8.7). In order to verify global stability, the phase diagram is shown in **Fig. 8.8**, at various initial values.

In the model, 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 model for future more work on corona virus (COVID-19) and it's new variants infection disease.

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