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(Dedicated to Professor D. S. Hooda on His 80^{th} *Birth Anniversary Celebrations)*

AN *SIQR* MATHEMATICAL MODEL TO CONTROL CORONA - VIRUS DISEASE (COVID-19) WITH SATURATED INCIDENCE RATE

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Abstract

In this paper, we have established *SIQR* epidemic model with saturated incidence rate for Corona - virus Disease (*COVID*-19). For more specified study the Quarantine Compartment is subdivided into two quarantine compartments Q_S, quarantine from susceptible individual class and Q_I, quarantine from infected individuals. At any given time the size of susceptible compartment will be bigger than the size of other compartments so, considering the criticality of the disease it is necessary to have the hold on this compartment for this the whole model is incorporated with saturated incidence rate. The local and global stability at equilibrium points are discussed which depends on the basic reproduction number (R_0) of the model. It has been observed if $R_0 < 1$, then the disease free equilibrium is globally asymptotically stable and if $R_0 > 1$, then the endemic equilibria will be globally stable. At $R_0 = 1$, behaviour of disease-free equilibrium is examined using Center manifold theory. The major finding shows that the measure of inhibition taken by the susceptible reduces the severity of disease.
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Keywords and Phrases: Mathematical Model *SIQR*, Second additive compound matrix, Lyapunov function, Stability Geometric approaches.

1. Introduction

Corona-virus was firstly reported in Wuhan, China, during December 2019. It is an infectious disease, which is transmitted from person to person through respiratory droplets through cough, or sneeze of an infected person. To control and prevent the spread of disease, several preventive measures are taken, such as, shutting down public transports and facilities, complete lockdowns in cities, closure of schools, colleges and other institutions to reduce the incidence rate. Moreover, to reduce the infection by affected people, they were kept in total isolation and their care and treatment happened in isolation as well.

Various models with quarantine compartments are known as $SIQ, SIQS, SIQR$ and many more [3].

Feng et al. ([5],[6],[7]) presented the effects of quarantine on transmission. Hethcote et al. [11] established and analyzed different incidence rates in different models with quarantine compartment. In this paper, an *SIQR* epidemic model is established where quarantine compartment is subdivided into two separate compartments Q_S, Q_I where Q_S is quarantine from susceptible individuals and Q_I is quarantine from infective individuals, as the size of susceptible compartment is always bigger in major cases. Saturated incidence rate $\frac{\beta SI}{1+\alpha S}$, Anderson et al. [1] and Gao et al. [15] is used. Effect of community awareness, impact of social media advertisement and global information campaigns with their dynamical behaviour of corona virus pandemic calibrated ([15], [18]) which seems to be more appropriate as per the real world scenario.

The objective of the paper is to establish the model and to calculate the basic reproduction numbers which support the existence conditions and stability analysis at local and global level. After the numerical simulations it has been observed the number of infective will decrease by increasing the appropriate preventions taken by susceptible for controlling the spread of disease.

2. Formulation of Model

The total population N is divided into four compartments, compartment of susceptible individuals S, compartment of infected individuals I, the recovered or removed individuals are in a compartment R, the compartment of quarantine is subdivided into two compartments for more clarity.Q_S is a compartment of quarantine from susceptible and Q_I is

a compartment of quarantine individuals from infective. The transition diagram of established model represented as follows:

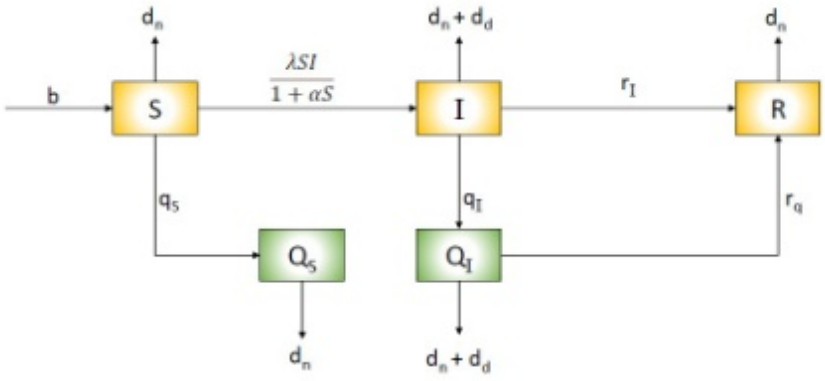

***Figure* 2.1**

This can be formulated mathematically as

$$\begin{aligned}
\frac{dS}{dt} &= b - \frac{\lambda S I}{1+\alpha S} - (d_n + q_s)S, \\
\frac{dI}{dt} &= \frac{\lambda S I}{1+\alpha S} - (d_n + d_d + q_I + r_I)I, \\
\frac{dQ_S}{dt} &= q_s S - d_n Q_s, \\
\frac{dQ_I}{dt} &= q_I I - (d_n + d_d + r_q)Q_I, \\
\frac{dR}{dt} &= r_I I + r_q Q_I - d_n R,
\end{aligned} \tag{2.1}$$

where, $S(0) \geq 0, I(0) \geq 0, Q_S(0) \geq 0, Q_I(0) \geq 0$ and $R(0) \geq 0$. Here b is recruitment constant could be immigration rate or birth rate of susceptible, λ is Transmission rate of susceptible to infected individuals i.e. it is the average number of contacts sufficient for transmission of a person per unit time. α is Positive prohibition constant taken by the susceptible. d_n is natural death rate, d_d is disease related death rate, q_s quarantine rate of susceptible, q_I quarantine rate of infective ,r_I is recovery rate of infective, r_q is recovery rate of quarantine infective. Incidence rate $\lambda S I/(1+\alpha S)$ tends to $\lambda I/\alpha$ as$S \to \infty$ i.e. incidence rate converges to a saturated level as the susceptible becomes large enough. Here α helps in measuring the best and suitable preventions taken by susceptible to control epidemic.

3. Categorical Properties

A. Positivity and Boundedness of formulated Model

Here, the objective is to analyze the positivity and boundedness of the formulated model for ensuring that the model is well-posed.

Lemma 3.1. *The set* $\Omega = \{(S, I, Q_S, Q_I, R) \in R^5_+ : 0 < S + I + Q_S + Q_I + R < \frac{b}{d_n}\}$ *is positively invariant region of the formulated model and all solution of the model which starts in* Ω *remains in* Ω *for all* $t \geq 0$.

Proof. As the total population $N(t)$ is the sum of all compartments i.e.

$$N(t) = S(t) + I(t) + Q_S(t) + Q_I(t) + R(t).$$

Therefore, by adding all equations of the established (2.1) model. We get,

$$\begin{aligned}
\frac{dN(t)}{dt} &= b - d_n\{S + I + Q_S + Q_I + R\} - d_d\{q_I + I\} \\
&= b - d_n\{N(t)\} - d_d\{q_I + I\}.
\end{aligned}$$

If disease does not exists, then

$$\frac{dN(t)}{dt} = b - d_n\{N(t)\},$$

which represents that population size $N(t)$ tends to the carrying capacity $\frac{b}{d_n}$ as $t \to \infty$.$\lim_{n\to\infty} \frac{dN}{dt} \leq \frac{b}{d_n}$. It proves that the solution of (2.1) exists and remains inside Ω [10] for the proof of second part of lemma, i.e. under the initial conditions, all the solutions of system (2.1) remain non-negative for $t \geq 0$. By initial conditions, it observes

$$\begin{aligned}
\left[\frac{dS}{dt}\right]_{s=0} &= b > 0,\\
\left[\frac{dI}{dt}\right]_{I=0} &> 0 \text{ for } I(0) > 0\\
\left[\frac{dQ_S}{dt}\right]_{Q_S=0} &= q_s S, S \geq 0\\
\left[\frac{dQ_I}{dt}\right]_{Q_I=0} &= q_I, I \geq 0\\
\left[\frac{dR}{dt}\right]_{R=0} &= r_I I + r_q, Q_I \geq 0.
\end{aligned} \tag{3.1}$$

This indicates that the established model for *COVID*-19 is mathematically and epidemiologically is well placed within the region Ω [12].

B. Disease- free Equilibrium points of the Model:

In the proposed model (2.1) the fifth equation is only one which depends on R and all other equations are independent of R. So for disease- free equilibrium position we equate to zero assuming there is no infection at the time $t = 0$. which reduces the set (2.1) for theoretical study as follows :

$$\begin{aligned}
\frac{dS}{dt} &= b - \frac{\lambda S I}{1+\alpha S} - (d_n + q_s)S,\\
\frac{dI}{dt} &= \frac{\lambda S I}{1+\alpha S} - (d_n + d_d + q_I + r_I)I,\\
\frac{dQ_S}{dt} &= q_s S - d_n Q_s,\\
\frac{dQ_I}{dt} &= q_I I - (d_n + d_d + r_q)Q_I.
\end{aligned} \tag{3.2}$$

On solving, we get

$$S^0 = \frac{b}{d_n + q_s}, Q_S^0 = \frac{q_s b}{d_n(d_n + q_s)}.$$

Therefore the Disease- free equilibrium for system (3.2) is $E^0 = (S^0, I^0, Q_S^0, Q_I^0) = (\frac{b}{d_n+q_s}, 0, \frac{q_s b}{d_n(d_n+q_s)}, 0)$.

C. Basic Reproduction number R_0

It is needed to find the average number of secondary infections generated by a single infective when it interacts with susceptible. Next generation method [4] is to be used to find it.

Let $X = I, Q_s, Q_I, S^T$. System (3.2) becomes

$$\frac{dX}{dt} = F(X) - V(X),$$

where,

$$F(X) = \begin{bmatrix} \frac{\lambda S I}{1+\alpha S} \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } V(X) = \begin{bmatrix} (d_n + d_d + q_I + r_I)I \\ -q_s S + d_n Q_s \\ -q_I I + (d_n + d_d + r_q)Q_I \\ -b + \frac{\lambda S I}{1+\alpha S} + (d_n + q_s)S \end{bmatrix}.$$

The Jacobian matrix of $F(X)$ and $V(X)$ at the Disease- free equilibrium E^0 are

$$DF(E^0) = \begin{bmatrix} F_* & 0 \\ 0 & 0 \end{bmatrix} \text{ and } DV(E^0) = \begin{bmatrix} V_* & 0 \\ 0 & 0 \end{bmatrix} \text{ respectively,}$$

where

$$F_* = \begin{bmatrix} 0 & \frac{\lambda b}{d_n+q_s+\alpha b} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } V_* = \begin{bmatrix} 0 & d_n + d_d + q_I + r_I & 0 & 0 \\ -q_s & 0 & d_n & 0 \\ 0 & q_I & 0 & d_n + d_d + r_q \\ d_n + q_s & \frac{\lambda b}{d_n+q_s+\alpha b} & 0 & 0 \end{bmatrix}.$$

So, $F_*V_*^{-1} = \begin{bmatrix} \frac{\lambda b}{(d_n+d_d+q_I+r_I)(d_n+q_s+\alpha b)} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \Rightarrow R_0 = \frac{\lambda b}{(d_n + d_d + q_I + r_I)(d_n + q_s + \alpha b)}$ [17].

The Endemic Equilibrium of the system, the endemic equilibrium of the system (3.2) is given by

$$E^* = (S^*, I^*, Q_S^*, Q_I^*) = \left(\frac{d_n + d_d + q_I + r_I}{\lambda - \alpha(d_n + d_d + q_I + r_I)}, \frac{(R_0 - 1)(d_n + q_s + \alpha b)}{\lambda - \alpha(d_n + d_d + q_I + r_I)}, \frac{q_s S}{d_n}, \frac{q_I I}{d_n + d_d + r_q} \right).$$

It results the following

Lemma 3.2. *System* (3.2) *always has a disease free equilibrium* $E^0 = (S^0, 0, Q_S^0, 0)$ *which exists for all parameter values and if* $R_0 > 1$ *then proposed model admits a unique endemic equilibrium* $E^* = (S^*, I^*, Q_S^*, Q_I^*)$.

D. Local Stability of Disease- free equilibrium point

To show the local stability of system (3.2) at disease- free equilibrium point, let us consider

$$\begin{aligned} F_1 &= b - \frac{\lambda S I}{1 + \alpha S} - (d_n + q_s)S, \\ F_2 &= \frac{\lambda S I}{1 + \alpha S} - (d_n + d_d + q_I + r_I)I, \\ F_3 &= q_s S - d_n Q_s, \\ F_4 &= q_I I - (d_n + d_d + r_q)Q_I. \end{aligned}$$

The Jacobian matrix of system (3.2) at Disease free equilibrium $E^0 = (S^0, 0, Q_S^0, 0)$ is as follows:

$$J(E^0) = \begin{bmatrix} -(d_n + q_s) & \frac{-\lambda b}{d_n+q_s+\alpha b} & 0 & 0 \\ 0 & \frac{\lambda b}{d_n+q_s+\alpha b} - (d_n + d_d + q_I + r_I) & 0 & 0 \\ r_I & 0 & -d_n & 0 \\ 0 & q_I & 0 & -(d_n + d_d + r_q) \end{bmatrix}.$$

The Jacobian $J(E^0)$ gives three negative eigen values $-(d_n + q_s), -d_n, -(d_n + d_d + r_q)$ and the fourth eigen value will be negative only when $R_0 < 1$ for $(R_0 - 1)(d_n + d_d + q_I + r_I)$.

So, all the four eigen values have negative real values, therefore disease free equilibrium is locally asymptotically stable. This exhibits the following

Theorem 3.1. *The disease free equilibrium* $E^0 = (S^0, 0, Q_S^0, 0)$ *is locally asymptotically stable if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

The stability behaviour of disease free equilibrium when $R_0 = 1$ *is observed by centre mainfold theory* ([2], [17]) *by considering* $\lambda = \lambda^* = \frac{(d_n+d_d+q_I+r_I)(d_n+q_s+\alpha b)}{b}$ *as a transmission parameter and* $S = x_1, I = x_2, Q_s = x_3, Q_I = x_4$ *then the system* (3.2) *can be written as*

$$\begin{aligned} \frac{dx_1}{dt} &= b - \frac{\lambda x_1 x_2}{1 + \alpha x_1} - (d_n + q_s)x_1 = \psi_1, \\ \frac{dx_2}{dt} &= \frac{\lambda x_1 x_2}{1 + \alpha x_1} - (d_n + d_d + q_I + r_I)x_2 = \psi_2, \\ \frac{dx_3}{dt} &= q_s x_1 - d_n x_3 = \psi_3, \\ \frac{dx_4}{dt} &= q_I x_2 - (d_n + d_d + r_q)x_4 = \psi_4. \end{aligned}$$

The Jacobian Matrix J^* *at* $R_0 = 1$ *is*

$$J^* = \begin{bmatrix} -(d_n + q_s) & \frac{-\lambda b}{d_n+q_s+\alpha b} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ r_I & 0 & -d_n & 0 \\ 0 & q_I & 0 & -(d_n + d_d + r_q) \end{bmatrix}.$$

We get one simple eigen value at zero. So by assuming left and right eigen vector of J^* *corresponding to the zero eigen value as* $u = (u_1, u_2, u_3, u_4)$ *and* $w = (w_1, w_2, w_3, w_4)^T$ *respectively. We get*

$$u_1 = 0, u_2 = 1, u_3 = 0, u_4 = 0$$

and

$$w_1 = \frac{-\lambda b}{(d_n + q_s)(d_n + q_s + \alpha b)}, w_2 = 1, w_3 = \frac{-q_s \lambda b}{d_n(d_n + q_s)(d_n + q_s + \alpha b)}, w_{4=} \frac{q_s}{(d_n + d_d + r_q)}.$$

In accordance with bifurcation theory which is based on center manifold theory to find the bifurcation constants b_1 and b_2 with the formula

$$b_1 = \sum_{k=i=j=1}^{4} u_k w_i w_j (\frac{\partial^2 \psi_k}{\partial x_i \partial x_j}),$$

$$b_2 = \sum_{k=i=1}^{4} u_k w_i (\frac{\partial^2 \psi_k}{\partial x_i \partial \lambda^*}).$$

So after substituting values we get

$$b_1 = \frac{-2\lambda(d_n + q_s)(d_n + d_d + q_I + r_I)}{(d_n + q_s + \alpha b)^2} < 0 \text{ and } b_2 = \frac{b(d_n + q_s)}{(d_n + q_s + \alpha b)} > 0.$$

Since $b_1 < 0$, $b_2 > 0$ then the disease free equilibrium is unstable and there exists a positive equilibrium as R_0 crosses 1. Therefore we establish the following

Theorem 3.2. *The Disease free equilibrium is unstable at $R_0 = 1$, so we get a positive equilibrium as R_0 crosses 1.*

E. Global Stability of the Disease free equilibrium of the system (3.2)
Consider the Lyapunov function [17]

$L = I' \Rightarrow L' = I'$
$\Rightarrow L' = \{\frac{\lambda S I}{1+\alpha S} - (d_n + d_d + q_I + r_I)I\}$
$\Rightarrow L' = (d_n + d_d + q_I + r_I)(R_0 - 1)I$
$\Rightarrow L' = 0 \Leftrightarrow I = 0$, and $L < 0$ if $R_0 < 1$.

Hence, E^0 is the largest invariant set in $\{(S, I, Q_S, Q_I) : L = 0\}$. So by Lyapunov-Lasalle invariance principle [13] the disease free equilibrium E^0 is globally asymptotically stable which gives the following

Theorem 3.3. *If $R_0 < 1$, then the disease free equilibrium is globally asymptotically stable.*

E. Local stability at endemic equilibrium
Now at endemic equilibrium

$E^* = (S^*, I^*, Q_S^*, Q_I^*)$ when$R_0 > 1$, the variation matrix becomes

$$J(E^*) = \begin{bmatrix} \frac{-\lambda I}{(1+\alpha S)^2} - (d_n + q_s) & \frac{-\lambda S}{(1+\alpha S)} & 0 & 0 \\ \frac{\lambda I}{(1+\alpha S)^2} & \frac{\lambda S}{(1+\alpha S)} - (d_n + d_d + q_I + r_I) & 0 & 0 \\ q_s & 0 & -d_n & 0 \\ 0 & q_1 & 0 & -(d_n + d_d + r_q) \end{bmatrix}.$$

The characteristic equation of $J(E^*)$ is
$(-d_n - \tau)(-d_n - d_d - r_q - \tau)(\tau^2 + c_1\tau + c_2) = 0$,
$c_1 = 2d_n + d_d + q_I + q_s + r_I + \frac{\lambda I}{(1+\alpha S)^2}\frac{-\lambda S}{(1+\alpha S)}$,
$c_2 = (d_n + q_s)\{(d_n + d_d + q_I + r_I) - \frac{\lambda S}{(1+\alpha S)}\} + \frac{\lambda I}{(1+\alpha S)^2}(d_n + d_d + q_I + r_I)$,
$\Rightarrow$ all the eigen values are negative if $\frac{\lambda S}{(1+\alpha S)} \leq (d_n + d_d + q_I + r_I)$
$\Rightarrow$ Endemic equilibrium is locally asymptotically stable under $\frac{\lambda S}{(1+\alpha S)} \leq (d_n + d_d + q_s + r_q)$.
This can be represented by the following

Theorem 3.4. *The Endemic equilibrium $E^* = (S^*, I^*, Q_S^*, Q_I^*)$ is locally asymptotically stable when*

$$\frac{\lambda S}{(1 + \alpha S)} \leq (d_n + d_d + q_s + r_q).$$

F. Global stability of an endemic equilibrium

The method given by Li and Muldowney [16], the geometric approach is used for the global stability of an endemic equilibrium for this system (3.2) is subdivided into two parts as follows.

The first as:

$\frac{dS}{dt} = b - \frac{\lambda S I}{1+\alpha S} - (d_n + q_s)S$,

$\frac{dI}{dt} = \frac{\lambda S I}{1+\alpha S} - (d_n + d_d + q_I + r_I)I$,

$\frac{dQ_I}{dt} = q_I I - (d_n + d_d + r_q)Q_I$,

and the other one as limit system

$\frac{dQ_s}{dt} = q_s S - d_n Q_s$.

To prove the model (3.2) as globally asymptotically stable, we generate second additive compound matrix $J^{[2]}$ of first set,

$$J^{[2]} = \begin{bmatrix} \frac{-\lambda I}{(1+\alpha S)^2} + \frac{\lambda S}{1+\alpha S} - m_1 & 0 & 0 \\ q_I & \frac{-\lambda I}{(1+\alpha S)^2} - m_2 & \frac{-\lambda S}{1+\alpha S} \\ 0 & \frac{\lambda S}{(1+\alpha S)^2} & \frac{\lambda S}{1+\alpha S} - m_3 \end{bmatrix},$$

where

$$m_1 = 2d_n + d_d + q_I + q_s + r_I, m_2 = 2d_n + d_d + q_s + r_q,$$
$$m_3 = 2d_n + 2d_d + q_I + r_I + r_q.$$

Let us choose the function

$$P = diag\left[1, \frac{I}{Q_I}, \frac{I}{Q_I}\right] \text{ and } P^{-1} = diag\left[1, \frac{Q_I}{I}, \frac{Q_I}{I}\right]$$

then

$$P_f = diag\left[0, \frac{I'Q_I - Q_I'I}{Q_I^2}, \frac{I'Q_I - Q_I'I}{Q_I^2}\right].$$

So

$$P_f.P^{-1} = diag\left[0, \frac{I'}{I} - \frac{Q_I'}{Q_I}, \frac{I'}{I} - \frac{Q_I'}{Q_I}\right].$$

Now $M = P_f.P^{-1} + PJ^{[2]}P^{-1}$

$$M = \begin{bmatrix} \frac{-\lambda I}{(1+\alpha S)^2} + \frac{\lambda S}{1+\alpha S} - m_1 & 0 & 0 \\ \frac{Iq_I}{Q_I} & \frac{-\lambda I}{(1+\alpha S)^2} - m_2 + \frac{I'}{I} - \frac{Q_I'}{Q_I} & \frac{-\lambda S}{1+\alpha S} \\ 0 & \frac{\lambda I}{(1+\alpha S)^2} & \frac{I'}{I} - \frac{Q_I'}{Q_I} + \frac{\lambda S}{1+\alpha S} - m_3 \end{bmatrix}.$$

We can represent it as in the Block form

$$M = \begin{bmatrix} M_{11} & M_{12} \\ M_{21} & M_{22} \end{bmatrix},$$

where

$M_{11} = \frac{-\lambda I}{(1+\alpha S)^2} + \frac{\lambda S}{1+\alpha S} - m_1$,

$M_{12} = \begin{bmatrix} 0 & 0 \end{bmatrix}$,

$M_{21} = \begin{bmatrix} \frac{Iq_I}{Q_I} \\ 0 \end{bmatrix}$,

$M_{22} = \begin{bmatrix} \frac{-\lambda I}{(1+\alpha S)^2} - m_2 + \frac{I'}{I} - \frac{Q_I'}{Q_I} & \frac{-\lambda S}{1+\alpha S} \\ \frac{\lambda I}{(1+\alpha S)^2} & \frac{I'}{I} - \frac{Q_I'}{Q_I} + \frac{\lambda S}{1+\alpha S} - m_3 \end{bmatrix}$.

Suppose the norm in R^3 to be$|(v_1, v_2, v_3)| = max\{|v_1|, |v_2|, |v_3|\}$.

Let the Lozinski measure with respect to this norm is denoted by μ_1 (M)$\leq sup?(g_1,g_2)$,

where $g_1 = \mu_1(M_{11}) + |M_{12}|, g_2 = \mu_1(M_{22}) + |M_{21}|$.

Therefore, we have

$g_1 = \frac{-\lambda I}{(1+\alpha S)^2} + \frac{\lambda S}{1+\alpha S} - m_1$,

$g_2 = \frac{Iq_I}{Q_I} + \frac{I'}{I} - \frac{Q_I'}{Q_I} - min?m_2, m_3$,

So,

$g_1 = \frac{-\lambda I}{(1+\alpha S)^2} + \frac{I'}{I} - d_n + q_s \leq \frac{I'}{I} - d_n,$

$g_2 = \frac{Q_I'}{Q_I} + \frac{I'}{I} - \frac{Q_I'}{Q_I} - d_n + q_s \leq \frac{I'}{I} - d_n$
$\Rightarrow \mu_1(M) \leq \frac{I'}{I} - d_n.$
Then
$q = \frac{1}{t}\int_0^t \mu_1(M)ds \leq \frac{1}{t}\int_0^t (\frac{I'}{I} - d_n)ds$

$= \frac{1}{t}\ln\frac{I(t)}{I(0)} - d_n$
$\Rightarrow q \leq \frac{d_n}{2} < 0.$
Thus the first subsystem is globally asymptotically stable.
Now, for the limit system
$\frac{dQ_S}{dt} = q_s S - d_n Q_s.$
Therefore, $Q_S = e^{-}d_n t\left[Q_S(0) - \frac{q_s S^*}{d_n}\right] + \frac{q_s S^*}{d_n}$
$\Rightarrow Q_S \to Q_S^*$ as $t \to \infty$.
Hence the endemic equilibrium E^* is globally asymptotically stable which represents the following theorem.

Theorem 3.5. *The disease free equilibrium is globally asymptotically stable when* $R_0 < 1$ *and endemic equilibrium is globally asymptotically stable when* $R_0 > 1$.

4. Numerical Simulation

In this section, computer simulation is presented for some solutions of the system (3.2)
Case I: Suppose the parameters of the system are $b = 4, \alpha = 100, \lambda = 2, d_n = 0.014, d_d = 0.1, q_s = 2, q_I = 4, r_I = 0.004, r_q = 0.006$. Let the initial value be [200, 0, 100, 0, 0] approaches to the disease free equilibrium E^0= (1.9861, 0 , 284, 0) as shown in Figure 4.1 which indicates that E^0 (disease free equilibrium) is globally asymptotically stable when $R_0 < 1$.

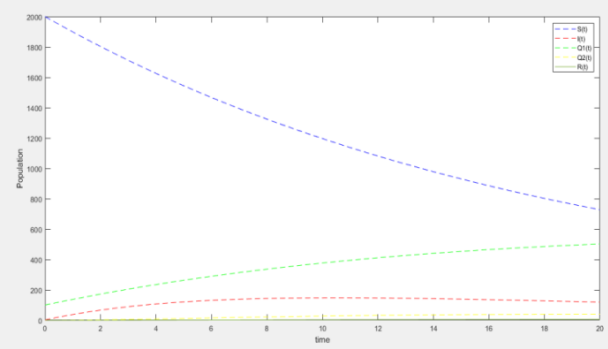

***Figure* 4.1**

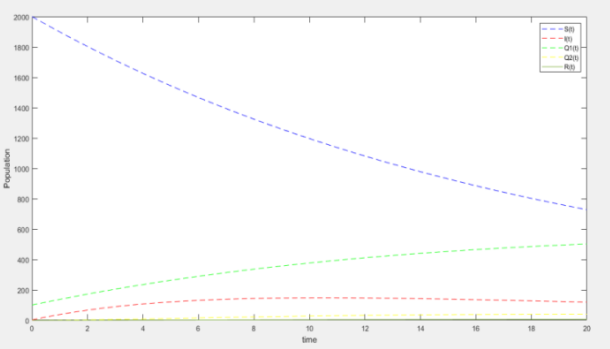

***Figure* 4.2**

Case II: By considering $b = 4, \alpha = 1, \lambda = 12.4, d_n = 0.014, d_d = 0.1, q_s = 2, q_I = 4, r_I = 0.004, r_q = 0.006$. We get $R_0 = 2.002 > 1$, $\frac{\lambda S^*}{1+\alpha S^*} = 4.118 = d_n + d_d + q_I + r_I$ with initial values [200, 2, 100, 0, 0] approach to the endemic equilibrium E^* = (0.5,72,71, 24,10) as shown in Figure 4.2 which indicates the endemic equilibrium E^* is a globally asymptotically stable. i.e. $S(t), I(t), Q_S(t), Q_I(t), R(t)$ all approaches to their steady state values as time tends to infinity.
Case III: As per the designed model α is the parameter to measure the inhibition. If we change its value by keeping other parameters fixed, it has been observed I^* decreases as the value of α increases which represents that the spread of disease can be controlled or decreases as the protective measures for the susceptible individuals increases as shown in Figure 4.3.

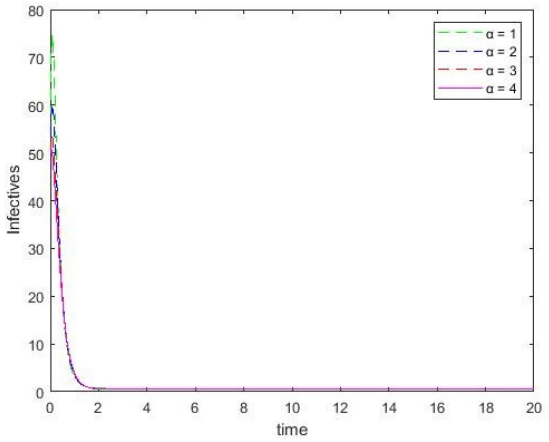

Figure **4.3**

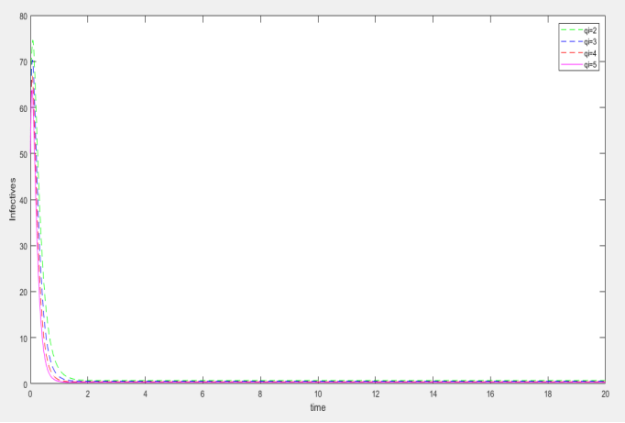

Figure **4.4**

Case IV: The procedure of keeping Quarantine is always an effective method to reduce the average infective and infectious period. It has been observed with the increase in quarantine rate of infective q_I, the steady state value of I^* of infective individual decreasesas per Figure 4.4,

5. Conclusion

We have established an *SIQR* model, by using the *ODE* to represent the saturated incident rate for *COVID*-19. For more specific analysis, we further sub-divided the Quarantine compartment into two parts, Quarantine from susceptible, Q_S and Quarantine for infective,Q_I.

Quarantine process in itself is very effective way for reducing the average infectious period. Here, independent quarantine compartments for susceptible and infective helped in reducing the average infectious time slot, by quarantining infective and susceptible separately, so that they do not spread the infection. We have clearly observed that, with the increase in rate of quarantine of infective, the number of infective decreases with time. By keeping all parameters fixed as endemic equilibrium and by making change in q_I, the steady state value of I^* decreases as q_I increases, which represents the importance of quarantine. The saturated incidence is used to establish the model. On keeping other parameters fixed and by changing the value ofα, we observe the steady state I^* decreases as α increase. This means that the spread of disease decreases, if the protective measures as sanitization, social distancing, and wearing mask, following awareness and precautions for the susceptible increases, as at any given time, the size of susceptible is larger in number.

The established model received a unique disease free equilibrium and a unique endemic equilibrium, which is globally asymptotically stable, when $R_0 < 1, R_0 > 1$ respectively, under specified. After experiencing the challenging real life situation due to *COVID*-19, the optimized solution is, to control the spread of infectious disease, by applying all possible protective measures on susceptible individuals and by increasing the rate of quarantine of infective, to treat them separately is the optimized solution.

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References

[1] R. M. Anderson and R. M. May, Regulation and stability of host-parasite population interactions: I Regulatory Process, *J. Anim. Ecol.,* **47**(1) (1978), 219-247.

[2] C. Castillo and B. Song, Dynamical Models of tuberculosis and their applications, *Math. Biosci. Eng.,* **1** (2004), 361-404.

[3] T. Day, A. Park, N. Madras, A. Gumel and J. Wu, When Is quarantine a useful control strategy for emerging infectious disease, *Am J. Epidemiol.,* **163** (2006), 479-485.

[4] O. Dlekmann, J. A. P. Heesterbeek and J. A. J. Metz, on the definition and the computation of the basic reproduction ratio r_0 in models for infectious disease in heterogeneous populations, *J. Math. Biol.,* **28**(4) (1990), 365-382.

[5] P. Van den Driessche and J. Watmough, Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission, *Math. Biosci.,* **180** (2002), 29-48

[6] Z. Feng and H. R. Thieme, Recurrent outbreak of childhood disease revisited: the impact of isolation, *Math. Biosci.,* **128** (1995), 93-130.
[7] Z. Feng and H. R. Thieme, Endemic models with arbitrarily distributed periods of infection I: Fundamental properties of the Model, *SIAM J. Appl. Math .,* **61** (2000), 803-833.
[8] Z. Feng and H. R. Thieme, Endemic models with arbitrarily distributed periods of infection II: Fast disease dynamics and permanent recovery, *SIAM J. Appl. Math.,* **61** (2000), 983-1012.
[9] S. Gao, L. Chen, J. Nieto, and A. Torres, Analysis of a delayed epidemic model with pulse vaccination and saturated incidence rate, *Vaccine,* **24** (2006), 6037-6045.
[10] J. K. Hale, Ordinary differential equations wife Inter science New York, 1969.
[11] H. W. Hethcote, Ma. Zhien and S. Liao, Effects of quarantine in six endemic models for infectious disease, *Math. Bio. Sci.,* **180** (2002), 141-160.
[12] H. W. Hethcote, The mathematics of infectious diseases, *SIAM Rev.,* **42**(4) (2000), 599-653.
[13] J. P. Lasalle, The stability of dynamical system, Philadelphia, SIAM., 1976.
[14] M. Y. Li and J. S. Mnidowney, A gometric approach to global stability problems, *SIAM J. Math. Anal.,* **27**(4) (1996), 1070-1083.
[15] R. K. Rai, S. Khajanchi, P. K. Tiwari, E. Venturino and A.K. Mishra, Impact of social media advertisement on transmission of COVID-19 panademic in India, *J.Appl.Math.Comput.,* **68**(2021), 19-44.
[16] S. Sastry, Analysis stability and control, Springer, New York, 1999.
[17] Z. Shuai and P. Van den Driessche, Global stability of infectious disease models using Lyapunov functions, *J. Appl. Math.,* **73**(4) (2013), 1513-1532.
[18] P. K. Tiwari, R. K. Rai, S. Khajanchi, R. Gupta and A.K. Mishra, Dynamics of Corona virus Pandemic: effects of community awareness and global information campaigns, *Eur. Phys. J. Plus,* (2021), 136-944.