International Journal of
Mathematical Modelling & Computations
Vol. 13, No. 02, 2023, 01- 19
DOI: 10.30495/ijm2c.2023.1963546.1258

Coronavirus (covid-19) Transmission Dynamics with Vaccination: A Mathematical Model Analysis

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Abstract. In this paper, a nonlinear mathematical model of COVID-19 was developed. An SVEIHR model has been proposed using a system of ordinary differential equations. The model's equilibrium points were found, and the model's stability analysis and sensitivity analysis around these equilibrium points were investigated. The model's basic reproduction number is investigated in the next-generation matrix. The disease free equilibrium of the COVID-19 model is stable if the basic reproduction number is less than unity; if the basic reproduction number is greater than unity, the disease free equilibrium is unstable. We also utilize numerical simulation to explain how each parameter affects the basic reproduction number.

Received: 18 July 2022; Revised: 01 May 2023; Accepted: 03 May 2023.

Keywords: COVID-19, Pandemic, Reproduction number, Stability analysis, Equilibrium point.

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1. Introduction

Coronaviruses are a broad family of viruses that can cause respiratory infections in humans, ranging from the common cold to more serious illnesses like Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). At the end of 2019, a novel coronavirus, formerly known as 2019-nCoV, was discovered to be the cause of a cluster of pneumonia cases in Wuhan, China's Hubei Province. It then spread throughout China and the rest of the world, turning into a global health crisis. COVID-19, which stands for coronavirus disease 2019, was declared a global pandemic by the World Health Organization (WHO) in February 2020 [4]. According to the WHO report (WHO, 2020), there have been 236,616,092 confirmed cases of COVID-19 worldwide as of October 6, 2021, with 4,832,077 deaths reported to WHO [5]. The source of the disease, the route or modes of transmission, and the extent of infection are still being investigated. The current evidence of the emerging Corona virus, as well as previous experiences with other coronaviruses (such as the Middle East Respiratory Syndrome (MERS) and SARS

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virus) and other respiratory symptoms viruses (such as bird flu), suggest that the new virus could be transmitted from an animal source [1, 2, 3, 8]. The coronavirus is spread through coughing, sneezing, contact with infected people, and touching items or surfaces contaminated with fecal traces [15]. Several preventive measures are recommended to combat this pandemic, including avoiding close contact with sick people; avoiding touching the eyes, nose, and mouth with unwashed hands; washing hands frequently with soap and water for at least 20 seconds; and using an alcohol-based hand sanitizer containing at least 60% alcohol when soap and water are not available [4, 14].

Mathematical models can play an essential role in understanding and forecasting disease transmission in the absence of a ready-to-use vaccination and in addition to medical and biological studies [12]. The development of a mathematical model for the coronavirus (COVID-19) is significant since it aids in explaining the disease's scope, which is important considering that it is an invisible and contagious virus. This mathematical model could be used to determine whether permitted measures such as quarantine are sufficient to prevent the virus from spreading. A range of investigations and mathematical models have been used to study the coronavirus's transmission [6, 7, 8, 10, 13, 14]. The SEIR model, which included susceptible, exposed, infected, and recovered individuals, was considered in [13]. The results of numerous scenarios show that ignoring social distancing and hygienic precautions might have disastrous consequences for the human population. A mathematical model was established in [7] to combine asymptomatic people with the isolation of diseased people, quarantine of contacting people, and home containment of the entire community. The level of containment is especially important to prevent disease spread in the absence of vaccine, as demonstrated by theoretical research and simulations. The SEIRU model was examined in [10], which included the vulnerable, exposed, infected, quarantined, and recovered individuals. When all precautionary measures are followed internationally, there is a likelihood that secondary infections may decrease. The stability analysis of a mathematical model of new coronavirus (COVID-19) disease spread in the population was considered in [3].

We will present a mathematical model that defines and describes the new coronavirus's transmission (COVID-19). Compartmental models had a significant impact on the evolution of epidemiological modeling in the population. The majority of cases of the COVID-19 virus are transferred through human-to-human contact. In this paper, we extend the model by [3], a nonlinear mathematical model evaluated using the SEIHR model of COVID-19, in which population birth and death rates are not equal and the overall population is divided into five compartments. However, in our research, we expanded the model into SVEIHR, which includes the vaccinated class (V).

2. The Mathematical Model

Our initial model [3] is represented by five ordinary differential equations. Our extended model is represented by six ordinary differential equations by adding one more compartment based on the following basic assumptions. For this dynamical system we considered Susceptible class S(t), Vaccinated class $V(t)$, Asymptomatic infected case or cases with mild symptoms class $E(t)$, Infected people with symptoms and carriers of the virus class $I(t)$, Quarantined Infected (Hospitalized cases) class $H(t)$ and Recovered class $R(t)$.The studies have shown that the virus can be transmitted from human to human. The population under this study is heterogeneous and varying with time, the whole human population is divided into six classes, the coronavirus can be transmitted by coughing, sneezing, contacting infected people.

Individuals will join the susceptible compartment $\boldsymbol{s(t)}$ by natural birth. Some of these people will leave this compartment due to natural deaths, and some others will enter to $\boldsymbol{E(t)}$ compartment after getting infected. The remaining people will stay in the $\boldsymbol{S(t)}$ compartment itself. The people of $\boldsymbol{S(t)}$ compartment are likely to get infected by the

people of $\boldsymbol{E(t)}$ and the people of $\boldsymbol{I(t)}$ only. We assume that the fraction of susceptible individuals $\boldsymbol{S(t)}$ takes vaccination with efficacy $\boldsymbol{\varphi}$ and goes to vaccinated class $\boldsymbol{V(t)}$ at a rate $\boldsymbol{\varepsilon}$. We assume that after individuals of vaccinated class $\boldsymbol{V}$ who lack vaccination efficacy $\boldsymbol{(1-\varphi), 0<\varphi<1}$ make contact with infectious individuals $\boldsymbol{E}$ and $\boldsymbol{I}$, and enters into Asymptomatic infected case or cases with mild symptoms class $\boldsymbol{E}$ at per-capita rate $\boldsymbol{(1-\varphi)}\left(\frac{\boldsymbol{\beta_1 VE+\beta_2 VI}}{\boldsymbol{N}}\right)$. In this study we considered that, the transfer of COID-19 from infected people and pathogen to susceptible is by coughing, sneezing, contacting infected people, or touching items or surfaces that are contaminated with fecal traces. The total number of the human population at time $\boldsymbol{t}$ is given by $\boldsymbol{N(t)=S(t)+V(t)+E(t)+I(t)+H(t)+R(t)}$.Based on the above state variables and model assumptions we develop the following flow chart of the dynamical system:

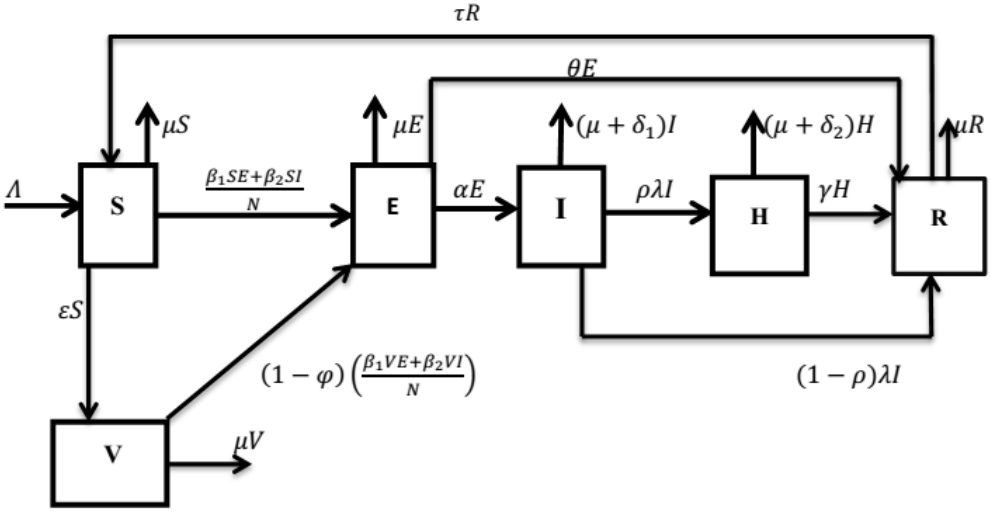

Figure 1. Schematic diagram for the flow of COVID-19 in the population.

We consider the following system of six non-linear differential equations:

$$\frac{dS}{dt} = \Lambda - (\mu+\varepsilon)S - \frac{\beta_1 SE+\beta_2 SI}{N} + \tau R \quad (1)$$

$$\frac{dV}{dt} = \varepsilon S - (1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) - \mu V \quad (2)$$

$$\frac{dE}{dt} = (1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) + \frac{\beta_1 SE+\beta_2 SI}{N} - (\mu+\alpha+\theta)E \quad (3)$$

$$\frac{dI}{dt} = \alpha E - (\mu+\delta_1+\lambda)I \quad (4)$$

$$\frac{dH}{dt} = \rho\lambda I - (\mu+\delta_2+\gamma)H \quad (5)$$

$$\frac{dR}{dt} = \gamma H + \theta E + (1-\rho)\lambda I - (\mu+\tau)R \quad (6)$$

With the initial condition

$S(0)>0, V(0)\geq 0\ E(0)\geq 0, I(0)\geq 0, H(0)\geq 0, and\ R(0)\geq 0$

3. Basic Properties of the model

3.1 *Positivity of the solution*

Theorem 3.1 If $S(0)>0, V(0)>0, E(0)>0, I(0)>0, H(0)>0, R(0)>0$ are positive in the feasible set **Ω**, then the solution set $\big(S(t), V(t), E(t), I(t), H(t), R(t)\big)$ of system (1-6) is positive for all $t\geq 0$.

Proof: From the first equation of the system

$$\frac{dS}{dt} = \Lambda - (\mu + \varepsilon)S - \frac{\beta_1 SE + \beta_2 SI}{N} + \tau R$$

This can be rewrite as:

$$\frac{dS}{dt} + \left(\mu + \varepsilon + \frac{\beta_1 E + \beta_2 I}{N}\right) S = \Lambda + \tau R$$

This equation is a first order linear ordinary differential equation. Whose solution is

$$S(t) = e^{-\int_0^t \left(\mu+\varepsilon+\frac{\beta_1 E+\beta_2 I}{N}\right) d\tau} \left[S(0) + \int_0^t \left[(\Lambda + \tau R) e^{\int_0^t \left(\mu+\varepsilon+\frac{\beta_1 E+\beta_2 I}{N}\right) d\tau} \right] d\tau \right] > 0$$

Similarly, it can be shown that $V(t) > 0, E(t) > 0, I(t) > 0, H(t) > 0$ *and* $R(t) > 0$. Thus, the solutions $S(t), V(t), E(t), I(t), H(t)$ *and* $R(t)$ of system (1-6) remain positive for all $t > 0$.

3.2 *Invariant region*

Let us determine a region in which the solution of model (1-6) is bounded. For this model the total population is $N(t) = S(t) + V(t) + E(t) + I(t) + H(t) + R(t)$. Then, differentiating $N(t)$ with respect to time we obtain:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dH}{dt} + \frac{dR}{dt} = \Lambda - \delta_1 I - \delta_2 H - \mu N$$

If there is no death due to the disease, we get

$$\frac{dN}{dt} \leq \Lambda - \mu N$$

After evaluating, we obtain

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

As $t \to \infty$, we obtain $0 < N \leq \frac{\Lambda}{\mu}$.

3.3 *Disease Free Equilibrium Point (DFEP)*

The disease free equilibrium of the model, (1) to (6), is obtained by making $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0$. Further at the disease free equilibrium point there is no infectious person of the disease in the population, i.e. $E = I = H = 0$. Therefore, the disease free equilibrium point is given by:

$$(S_0, V_0, E_0, I_0, H_0, R_0) = X_0 = \left(\frac{\Lambda}{\mu + \varepsilon}, \frac{\varepsilon\Lambda}{\mu(\mu + \varepsilon)}, 0,0,0,0\right)$$

The point X_0 is non-negative equilibrium, which exists without any condition.

3.4 *The basic reproduction number*

The basic reproduction number, usually denoted as R_0 defines the average number of secondary infections caused by an individual in an entirely susceptible population. The value of R_0 will indicate whether the epidemic could occur or not. If $R_0 < 1$, then the disease will decrease and eventually die out . If $R_0 = 1$, each existing infection causes one new infection. The disease will stay alive and stable, but there will not be an outbreak or

an epidemic. If $R_0 > 1$, each existing infection causes more than one new infection. The disease will spread between people, and there may be an outbreak or epidemic. To find the reproduction number, we will use the method of next-generation matrix [11] it is defined as the spectral radius (or dominant eigenvalue) of the model. The first step is rewriting the model equations, starting with the newly infected classes:

$$\frac{dE}{dt} = (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) + \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \alpha + \theta)E$$
$$\frac{dI}{dt} = \alpha E - (\mu + \delta_1 + \lambda)I$$
$$\frac{dH}{dt} = \rho\lambda I - (\mu + \delta_2 + \gamma)H$$

Then system can be written as

$$\frac{dx}{dt} = f - v$$

Here the new infection matrix f and the transition matrix v are defined by

$$f = \begin{pmatrix} (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) + \frac{\beta_1 SE + \beta_2 SI}{N} \\ 0 \\ 0 \end{pmatrix} \text{ and } v = \begin{pmatrix} (\mu + \alpha + \theta)E \\ (\mu + \delta_1 + \lambda)I - \alpha E \\ (\mu + \delta_2 + \gamma)H - \rho\lambda I \end{pmatrix}$$

Then by the principle of next-generation matrix, the Jacobian matrices at DFE is given by

$$F = \begin{pmatrix} \frac{\beta_1 \varepsilon\Lambda(1-\varphi)}{\mu N(\mu+\varepsilon)} + \frac{\beta_1 \Lambda}{N(\mu+\varepsilon)} & \frac{\beta_2 \varepsilon\Lambda(1-\varphi)}{\mu N(\mu+\varepsilon)} + \frac{\beta_2 \Lambda}{N(\mu+\varepsilon)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and}$$

$$V = \begin{pmatrix} \mu + \alpha + \theta & 0 & 0 \\ -\alpha & \mu + \delta_1 + \lambda & 0 \\ 0 & -\rho\lambda & \mu + \delta_2 + \gamma \end{pmatrix}$$

Then

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1 \Lambda(\varepsilon(1-\varphi)+\mu)}{\mu N(\mu+\varepsilon)(\mu+\alpha+\theta)} + \frac{\beta_2 \Lambda\alpha(\varepsilon(1-\varphi)+\mu)}{\mu N(\mu+\varepsilon)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)} & \frac{\beta_2 \Lambda(\varepsilon(1-\varphi)+\mu)}{\mu N(\mu+\varepsilon)(\mu+\delta_1+\lambda)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

Therefore, FV^{-1} is the next generation matrix of SVEIHR model, then the dominant eigenvalue of FV^{-1}represents $R_0 = \rho(FV^{-1})$, which is

$$R_0 = \frac{\beta_1 \Lambda(\varepsilon(1-\varphi)+\mu)}{\mu N(\mu+\varepsilon)(\mu+\alpha+\theta)} + \frac{\beta_2 \Lambda\alpha(\varepsilon(1-\varphi)+\mu)}{\mu N(\mu+\varepsilon)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)}$$

3.5 *Stability Analysis of Diseases-free Equilibrium*

Theorem 3.2 The disease free equilibrium point E_0 of the dynamical system (1) - (6) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: The Jacobian matrix for the disease-free equilibrium $X_0 = (S, V, E, I, H, , R) = \left(\frac{\Lambda}{\mu+\varepsilon}, \frac{\varepsilon\Lambda}{\mu(\mu+\varepsilon)}, 0,0,0,0\right)$ is given by$J(X_0) =$

$$\begin{bmatrix} -\mu-\varepsilon & 0 & -\frac{\beta_1\Lambda}{N(\mu+\varepsilon)} & -\frac{\beta_2\Lambda}{N(\mu+\varepsilon)} & 0 & \tau \\ \varepsilon & -\mu & -(1-\phi)\frac{\beta_1\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} & -(1-\phi)\frac{\beta_2\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} & 0 & 0 \\ 0 & 0 & J_{33} & J_{34} & 0 & 0 \\ 0 & 0 & \alpha & -(\mu+\delta_1+\lambda) & 0 & 0 \\ 0 & 0 & 0 & \rho\lambda & -(\mu+\delta_2+\gamma) & 0 \\ 0 & 0 & \theta & (1-\rho)\lambda & \gamma & -(\mu+\tau) \end{bmatrix}$$ Wh

ere, $J_{33} = (1-\phi)\frac{\beta_1\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} + \frac{\beta_1\Lambda}{N(\mu+\varepsilon)} - (\mu+\alpha+\theta)$ and

$$J_{34} = (1-\phi)\frac{\beta_2\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} + \frac{\beta_2\Lambda}{N(\mu+\varepsilon)}$$

The characteristic equation of this matrix is given by $\det(J(X_0) - \xi I_6) = 0$, where I_6 is a square identity matrix of order 6 and ξ is eigenvalues of the Jacobian matrix.
Therefore, the characteristic equation is

$$(-\mu-\xi)(-\mu-\varepsilon-\xi)(\mu+\tau+\xi)(-(\mu+\delta_2+\gamma)-\xi)\begin{bmatrix}\xi^2+(\mu+\delta_1+\lambda-J_{33})\xi \\ -(\mu+\delta_1+\lambda)J_{33}-\alpha J_{34}\end{bmatrix} =$$

0 The Jacobian evaluated at the DFE has six eigenvalues, four of which are $\xi_1 = -\mu, \xi_2 = -(\mu+\varepsilon)$, $\xi_3 = -(\mu+\tau)$ and $\xi_4 = -(\mu+\delta_2+\gamma)$ which are negative. The remaining two eigenvalues are obtained by determining trace value and determinant of the sub-Jacobian given by:

$$J_1(DFE) = \begin{bmatrix} J_{33} & J_{34} \\ \alpha & -(\mu+\delta_1+\lambda) \end{bmatrix}$$

It is easy to show that the eigenvalues are both negative (or have negative real parts) if $traceJ_1(DFE) = J_{33} - (\mu+\delta_1+\lambda) < 0$, then $J_{33} < (\mu+\alpha+\theta) + (\mu+\delta_1+\lambda)$ and $det\, J_1(DFE) = -(\mu+\delta_1+\lambda)J_{33} - \alpha J_{34} > 0$ Substitute the value of J_{33} and J_{34} , we get

$$-(\mu+\delta_1+\lambda)\left[\frac{\beta_1\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)} - (\mu+\alpha+\theta)\right] - \frac{\alpha\beta_2\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)} > 0$$

$$-(\mu+\delta_1+\lambda)\left[(1-\phi)\frac{\beta_1\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} + \frac{\beta_1\Lambda}{N(\mu+\varepsilon)} - (\mu+\alpha+\theta)\right]$$

$$-\alpha\left[(1-\phi)\frac{\beta_2\varepsilon\Lambda}{N\mu(\mu+\varepsilon)} + \frac{\beta_2\Lambda}{N(\mu+\varepsilon)}\right] > 0$$

$$-(\mu+\delta_1+\lambda)\frac{\beta_1\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)} + (\mu+\delta_1+\lambda)(\mu+\alpha+\theta)$$

$$-\frac{\alpha\beta_2\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)} > 0$$

$$\frac{\beta_1\Lambda(\varepsilon(1-\phi)+\mu)(\mu+\delta_1+\lambda)}{N\mu(\mu+\varepsilon)} + \frac{\alpha\beta_2\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)} < (\mu+\delta_1+\lambda)(\mu+\alpha+\theta)$$

Both side divided by $(\mu+\delta_1+\lambda)(\mu+\alpha+\theta)$we have

$$\frac{\beta_1\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)(\mu+\alpha+\theta)} + \frac{\alpha\beta_2\Lambda(\varepsilon(1-\phi)+\mu)}{N\mu(\mu+\varepsilon)(\mu+\delta_1+\lambda)(\mu+\alpha+\theta)} < 1$$

Implies $R_0 < 1$. Based on the above description, if $J_{33} < (\mu+\alpha+\theta) + (\mu+\delta_1+\lambda)$ and $R_0 < 1$, then all eigenvalues are negative. It indicates that the disease free equilibrium point is stable.

3.6 *Global stability at disease free equilibrium*

To prove the global stability, we make use of Castillo-Chavez method [16]. Consider a

model of the form

$$\begin{cases} \frac{dF}{dt} = F(Y,T) \\ \frac{dG}{dt} = G(Y,T), \;\; G(Y,0) = 0 \end{cases} \quad *$$

Where $Y \in \mathcal{R}^m$ represents, individuals that are not infected in the population and $T \in \mathcal{R}^m$ represents infected individuals. Following the above representation, the disease free equilibrium state can be written as $X_0 = (Y^*, 0)$, the two conditions given below are used to verify the disease-free equilibrium is globally is asymptotically stable.

(L_1). For $\frac{dF}{dt} = F(Y,0)$ is globally asymptotically stable.

(L_2). $G(y,T) = BT - \hat{G}(Y,T), \hat{G}(Y,T) \geq 0 \; for \; all \; (Y,T) \in \Omega$.

Where $B = D_T G(Y^*, 0)$ is an M-matrix (the off diagonal elements of B are non-negative) and Ω is the region where the model makes biological sense.

Corollary 1: The fixed point $X_0 = (Y^*, 0)$ is globally asymptotically stable equilibrium of (*) provided that $R_0 \leq 1$ and assumption that (L_1) and (L_2) are satisfied.

Theorem 3.3 The disease free equilibrium point of the $SVEIHR$ model is globally asymptotically stable.

***Proof*:** The model equation

$$\frac{dS}{dt} = \Lambda - (\mu + \varepsilon)S - \frac{\beta_1 SE + \beta_2 SI}{N} + \tau R$$

$$\frac{dV}{dt} = \varepsilon S - (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) - \mu V$$

$$\frac{dE}{dt} = (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) + \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \alpha + \theta)E$$

$$\frac{dI}{dt} = \alpha E - (\mu + \delta_1 + \lambda)I$$

$$\frac{dH}{dt} = \rho\lambda I - (\mu + \delta_2 + \gamma)H$$

$$\frac{dR}{dt} = \gamma H + \theta E + (1-\rho)\lambda I - (\mu + \tau)R$$

Is re-written as in form of (*) by setting $Y = (S, V, R)$ and $T = (E, I, H)$. The disease free equilibrium is given by

$U_0(Y^*, 0) = \left(\frac{\Lambda}{\mu+\varepsilon}, \frac{\varepsilon\Lambda}{\mu(\mu+\varepsilon)}, 0,0,0,0\right)$

and the system $\frac{dY}{dt} = F(Y,0)$ becomes

$$\frac{dS}{dt} = \Lambda - (\mu + \varepsilon)S - \frac{\beta_1 SE + \beta_2 SI}{N} + \tau R$$

$$\frac{dV}{dt} = \varepsilon S - (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) - \mu V$$

$$\frac{dR}{dt} = \gamma H + \theta E + (1-\rho)\lambda I - (\mu + \tau)R$$

This equation has a unique equilibrium point

$X_0 = \left(\frac{\Lambda}{\mu+\varepsilon}, \frac{\varepsilon\Lambda}{\mu(\mu+\varepsilon)}, 0\right)$

Which is globally asymptotically stable. Therefore, the condition (L_1) is satisfied.

For L_2; $G(Y,T) = \begin{pmatrix} (1-\varphi)\left(\frac{\beta_1 VE + \beta_2 VI}{N}\right) + \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \alpha + \theta)E \\ \alpha E - (\mu + \delta_1 + \lambda)I \\ \rho\lambda I - (\mu + \delta_2 + \gamma)H \end{pmatrix}$

$$D_T G(Y^*,0) = \begin{pmatrix} \frac{\beta_1 \varepsilon \Lambda(1-\varphi)}{N\mu(\mu+\varepsilon)} + \frac{\Lambda\beta_1}{N(\mu+\varepsilon)} - (\mu+\alpha+\theta) & \frac{\beta_2 \varepsilon \Lambda(1-\varphi)}{N\mu(\mu+\varepsilon)} + \frac{\Lambda\beta_2}{N(\mu+\varepsilon)} & 0 \\ \alpha & -(\mu+\delta_1+\lambda) & 0 \\ 0 & \rho\lambda & -(\mu+\delta_2+\gamma) \end{pmatrix}$$

Clearly, $B = D_T G(Y^*,0)$ is a M-matrix. On the other hand, $G(Y,T) = BT - \hat{G}(Y,T)$ this implies

$$\hat{G}(Y,T) = BT - G(Y,T) = \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}.$$

Hence $\hat{G}(Y,T) = (Y,T) \geq 0$ for all $(Y,T) \in \Omega$. Therefore, conditions $(L_1)\ and\ (L_2)$ are satisfied. Thus the DFE is globally asymptotically stable.

3.7 *Endemic Equilibrium Point (EEP)*

The endemic equilibrium point of the model, (1) to (6), is obtained by making $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0$. Therefore, the Endemic Equilibrium Point (EEP) denoted by $E^*$of the model in Equation (1) to (6) is given by:

$$X^* = (S^*, V^*, E^*, I^*, H^*, R^*)$$

Where

$S^* = \frac{N^*\Lambda\alpha(\mu+\tau)(\mu+\delta_2+\gamma) - KN^*I^*}{(\mu+\tau)(\mu+\delta_2+\gamma)[\alpha N^*(\mu+\varepsilon) + ((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2)I^*]}$,

$V^* = \frac{\alpha N^*[\varepsilon N^*\Lambda\alpha(\mu+\tau)(\mu+\delta_2+\gamma) - \varepsilon K N^* I^*]}{(\mu+\tau)(\mu+\delta_2+\gamma)[(1-\varphi)((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2)I^* + \mu\alpha N^*][\alpha N^*(\mu+\varepsilon) + ((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2)I^*]}$,

$E^* = \frac{(\mu+\delta_1+\lambda)}{\alpha} I^*$,

$H^* = \frac{\rho\lambda}{\mu+\delta_2+\gamma} I^*$,

$R^* = \frac{\rho\lambda\gamma\alpha + (\mu+\delta_2+\gamma)(\mu+\delta_1+\lambda)\theta + (\mu+\delta_2+\gamma)(1-\rho)\lambda\alpha}{\alpha(\mu+\tau)(\mu+\delta_2+\gamma)} I^*$

And the equilibrium point I^* is obtained by solving the second degree polynomial equation as follows.

$f(I^*) = b_1(I^*)^2 + b_2 I^* + b_3 = 0$

Where $N^* = S^* + V^* + E^* + I^* + H^* + R^*$

$K = \tau\rho\lambda\gamma\alpha + (\mu+\delta_2+\gamma)(\mu+\delta_1+\lambda)\theta\tau + (\mu+\delta_2+\gamma)(1-\rho)\lambda\alpha\tau$

$b_1 = \big[(\mu+\tau)(\mu+\delta_2+\gamma)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big) + K\big((\mu+\delta_1+\lambda)\beta_1 + \alpha\beta_2\big)\big](1-\varphi)\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big)$

$b_2 = [\mu+(\mu+\varepsilon)(1-\varphi)](\mu+\tau)(\mu+\delta_2+\gamma)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)\alpha N^*\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big) - \big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big)\big[\Lambda\alpha(\mu+\tau)(\mu+\delta_2+\gamma)(1-\varphi)\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big) - [\mu+\varepsilon(1-\varphi)]\alpha N^* K\big]$

$b_3 = (\mu+\tau)(\mu+\delta_2+\gamma)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)\mu\alpha^2(N^*)^2(\mu+\varepsilon) - \Lambda\alpha^2 N^*\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big)[(1-\varphi)\varepsilon+\mu](\mu+\tau)(\mu+\delta_2+\gamma)$

When we divide both sides of $b_1(I^*)^2 + b_2 I^* + b_3 = 0$ by$b_1 \neq 0$, we get $(I^*)^2 + \frac{b_2}{b_1} I^* + \frac{b_3}{b_1} = 0$. This can be written in form of

$$(I^*)^2 + ZI^* + Y = 0 \qquad (7)$$

Where $Z = \frac{b_2}{b_1}$ and

$Y = \frac{b_3}{b_1} = \frac{(\mu+\tau)(\mu+\delta_2+\gamma)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)(\mu+\varepsilon)\mu\alpha^2(N^*)^2(1-R_0)}{(1-\varphi)\big((\mu+\delta_1+\lambda)\beta_1+\alpha\beta_2\big)^2[(\mu+\tau)(\mu+\delta_2+\gamma)(\mu+\alpha+\theta)(\mu+\delta_1+\lambda)+K]}$

From the Equation (7) we have $I^* = \frac{-Z \pm \sqrt{Z^2-4Y}}{2}$. When $R_0 > 1$ we have:

$$Y < 0, \Rightarrow \frac{-Z+\sqrt{Z^2-4Y}}{2} > 0 \text{ and } \frac{-Z-\sqrt{Z^2-4Y}}{2} < 0$$

This shows that there is a unique endemic equilibrium point.

When $R_0 < 1$ we have $Y > 0$,

i. if $Z^2 \geq 4Y$, then $Z^2 - 4Y \geq 0$,
$\Rightarrow \frac{-Z\pm\sqrt{Z^2-4Y}}{2} \leq 0$

ii. if $Z^2 < 4Y$, then $Z^2 - 4Y < 0$, no real roots of (7).

3.8 Locally Stability of endemic equilibrium point

Theorem 3.4 The endemic equilibrium point E^* of the dynamical system (1) - (6) is locally asymptotically stable if $R_0 > 1$ and unstable if $R_0 < 1$.

Proof: The Jacobian matrix at the endemic equilibrium $X^* = (S^*, V^*, E^*, I^*, H^*, R^*)$ is given by

$$J(X^*) = \begin{bmatrix} J_{11} & 0 & J_{13} & J_{14} & 0 & \tau \\ \varepsilon & J_{22} & J_{23} & J_{24} & 0 & 0 \\ J_{31} & J_{32} & J_{33} & J_{34} & 0 & 0 \\ 0 & 0 & \alpha & -(\mu+\delta_1+\lambda) & 0 & 0 \\ 0 & 0 & 0 & \rho\lambda & -(\mu+\delta_2+\gamma) & 0 \\ 0 & 0 & \theta & (1-\rho)\lambda & \gamma & -(\mu+\tau) \end{bmatrix}$$

$$J_{11} = -J_{31} - \mu - \varepsilon, J_{13} = -\frac{\beta_1 S^*}{N}, J_{14} = -\frac{\beta_2 S^*}{N}, J_{22} = -(1-\varphi)J_{31} - \mu, J_{32} = (1-\varphi)J_{31},$$

$$J_{33} = -J_{23} - J_{13} - (\mu+\alpha+\theta), J_{34} = -J_{24} - J_{14}, J_{23} = -(1-\varphi)\frac{\beta_1 V^*}{N}, J_{24} = -(1-\varphi)\frac{\beta_2 V^*}{N}$$

$$and J_{31} = \frac{\beta_1 E^* + \beta_2 I^*}{N}$$

The characteristic equation of this matrix is given by $\det(J(X^*) - \xi I_6) = 0$, where I_6 is a square identity matrix of order 6 and ξ is eigenvalues of the Jacobian matrix. Therefore, the characteristic equation is

$$a_6\xi^6 + a_5\xi^5 + a_4\xi^4 + a_3\xi^3 + a_2\xi^2 + a_1\xi + a_0 = 0$$

Where

$$a_6 = 1$$

$$a_5 = 3\mu + \delta_1 + \lambda + \tau + \delta_2 + \gamma - J_{22} - J_{11} - J_{33}$$

$$a_4 = J_{11}J_{33} + J_{22}J_{33} + (\mu+\delta_1+\lambda)(2\mu+\delta_2+\gamma+\tau-J_{11}-J_{22}-J_{33}) - J_{13}J_{31} - J_{23}J_{32} + (\mu+\delta_2+\gamma)(\mu+\tau-J_{11}-J_{22}-J_{33}) - (\mu+\tau)(J_{11}+J_{22}+J_{33}) + J_{11}J_{22} - \alpha J_{34}$$

$$a_3 = J_{13}J_{31}J_{22} + J_{11}J_{23}J_{32} + J_{11}J_{22}(\mu+\delta_1+\lambda) + J_{11}J_{22}(\mu+\delta_2+\gamma) + J_{11}J_{33}(\mu+\delta_1+\lambda) + J_{11}J_{33}(\mu+\delta_2+\gamma) + J_{22}J_{33}(\mu+\delta_1+\lambda) + \alpha J_{22}J_{33} + J_{22}J_{11}(\mu+\tau) + J_{22}J_{33}(\mu+\delta_2+\gamma) + J_{11}J_{33}(\mu+\tau) + \alpha J_{11}J_{34} + J_{22}J_{33}(\mu+\tau) + (\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau) - J_{13}J_{32}\varepsilon$$

$$-J_{11}J_{22}J_{33}-J_{13}J_{31}(\mu+\delta_1+\lambda)-J_{14}J_{31}\alpha-J_{13}J_{31}(\mu+\delta_2+\gamma)-J_{23}J_{32}(\mu+\delta_1+\lambda)$$
$$-J_{11}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)-\theta\tau J_{31}-J_{23}J_{32}(\mu+\delta_2+\gamma)$$
$$-J_{22}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$-J_{11}(\mu+\delta_1+\lambda)(\mu+\tau)-J_{23}J_{32}(\mu+\tau)-J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$-J_{34}\alpha(\mu+\delta_2+\gamma)$$
$$-J_{11}(\mu+\delta_2+\gamma)(\mu+\tau)-J_{22}(\mu+\delta_1+\lambda)(\mu+\tau)-J_{32}J_{24}\alpha$$
$$-J_{22}(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{33}(\mu+\delta_1+\lambda)(\mu+\tau)-J_{34}\alpha(\mu+\tau)-J_{33}(\mu+\delta_2+\gamma)(\mu+\tau)-J_{13}J_{31}(\mu+\tau)$$

$$a_2=J_{13}J_{31}J_{22}(\mu+\delta_1+\lambda)-J_{13}J_{32}\varepsilon(\mu+\delta_1+\lambda)-J_{14}\varepsilon\alpha J_{32}+J_{14}J_{22}J_{31}\alpha$$
$$-J_{11}J_{22}J_{33}(\mu+\delta_1+\lambda)$$
$$-J_{11}J_{22}J_{34}\alpha+J_{11}J_{23}J_{32}(\mu+\delta_1+\lambda)-J_{13}\varepsilon J_{32}(\mu+\delta_2+\gamma)+J_{13}J_{31}J_{22}(\mu+\delta_2+\gamma)$$
$$-J_{11}J_{22}J_{33}(\mu+\delta_2+\gamma)+J_{11}J_{23}J_{32}(\mu+\delta_2+\gamma)+J_{11}J_{22}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$-\tau\varepsilon\theta J_{32}$$
$$+\tau\theta J_{22}J_{31}-\varepsilon J_{13}J_{32}(\mu+\tau)+J_{13}J_{31}J_{22}(\mu+\tau)-J_{13}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$-\tau\varepsilon\alpha(1-\rho)\lambda$$
$$-J_{14}J_{31}\alpha(\mu+\delta_2+\gamma)-J_{11}J_{22}J_{33}(\mu+\tau)+J_{11}J_{23}J_{32}(\mu+\tau)$$
$$+J_{11}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$+J_{11}J_{34}\alpha(\mu+\delta_2+\gamma)+J_{11}J_{22}(\mu+\delta_1+\lambda)(\mu+\tau)-\tau\theta J_{31}(\mu+\delta_1+\lambda)$$
$$+J_{22}J_{34}\alpha(\mu+\delta_2+\gamma)$$
$$+J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)-J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)+J_{11}J_{32}\alpha J_{24}$$
$$-J_{14}J_{31}\alpha(\mu+\tau)$$
$$+J_{11}J_{22}(\mu+\delta_2+\gamma)(\mu+\tau)+J_{11}J_{33}(\mu+\delta_1+\lambda)(\mu+\tau)+J_{11}J_{34}\alpha(\mu+\tau)$$
$$-\tau\theta J_{31}(\mu+\delta_2+\gamma)$$
$$-J_{13}J_{31}(\mu+\delta_2+\gamma)(\mu+\tau)+J_{11}J_{33}(\mu+\delta_2+\gamma)(\mu+\tau)+J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\tau)$$
$$+J_{22}J_{34}\alpha(\mu+\tau)-J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\tau)-J_{11}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+J_{22}J_{33}(\mu+\delta_2+\gamma)(\mu+\tau)-J_{23}J_{32}(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{22}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{32}J_{24}\alpha(\mu+\delta_2+\gamma)-J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{34}\alpha(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{13}J_{31}(\mu+\delta_1+\lambda)(\mu+\tau)-J_{32}J_{24}\alpha(\mu+\tau)$$

$$a_1=J_{11}J_{24}J_{32}\alpha(\mu+\tau)-J_{24}J_{32}\alpha(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-\varepsilon J_{13}J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$+J_{13}J_{22}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)-\varepsilon\alpha J_{14}J_{32}(\mu+\delta_2+\gamma)+\alpha J_{14}J_{22}J_{31}(\mu+\delta_2+\gamma)$$
$$-J_{11}J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)-J_{11}J_{22}J_{34}\alpha(\mu+\delta_2+\gamma)-\tau\varepsilon\alpha(1-\rho)\lambda J_{32}$$
$$+J_{11}J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)+\tau\alpha(1-\rho)\lambda J_{31}J_{22}-\tau\varepsilon\theta J_{32}(\mu+\delta_1+\lambda)$$
$$+\tau\theta J_{22}J_{31}(\mu+\delta_1+\lambda)-\varepsilon J_{13}J_{32}(\mu+\delta_1+\lambda)(\mu+\tau)+J_{13}J_{22}J_{31}(\mu+\delta_1+\lambda)(\mu+\tau)$$
$$-\varepsilon\alpha J_{14}J_{32}(\mu+\tau)+\alpha J_{14}J_{22}J_{31}(\mu+\tau)-J_{11}J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\tau)$$
$$-J_{11}J_{22}J_{34}\alpha(\mu+\tau)$$
$$+J_{11}J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\tau)-\tau\gamma\alpha\rho\lambda J_{31}-\tau\varepsilon\theta J_{32}(\mu+\delta_2+\gamma)$$
$$+\tau\theta J_{22}J_{31}(\mu+\delta_2+\gamma)$$
$$-\varepsilon J_{13}J_{32}(\mu+\delta_2+\gamma)(\mu+\tau)+J_{13}J_{22}J_{31}(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{11}J_{22}J_{33}(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+J_{11}J_{23}J_{32}(\mu+\delta_2+\gamma)(\mu+\tau)-\tau\alpha(1-\rho)\lambda J_{31}(\mu+\delta_2+\gamma)$$
$$+J_{11}J_{22}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-\tau\theta J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)+\alpha J_{11}J_{32}J_{24}(\mu+\tau)$$
$$-J_{13}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{14}J_{31}\alpha(\mu+\delta_2+\gamma)(\mu+\tau)+J_{11}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+J_{11}J_{33}\alpha(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)+J_{22}J_{34}\alpha(\mu+\delta_2+\gamma)(\mu+\tau)$$

$$-J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$a_0 = J_{11}J_{32}J_{24}\alpha(\mu+\delta_2+\gamma)(\mu+\tau) - \tau\varepsilon\alpha\rho\lambda\gamma J_{32} + \tau\alpha\gamma\rho\lambda J_{22}J_{31}$$
$$- \tau\varepsilon\alpha(1-\rho)\lambda J_{32}(\mu+\tau)$$
$$+\tau\alpha(1-\rho)\lambda J_{22}J_{31}(\mu+\tau) - \tau\varepsilon\theta J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$
$$- \varepsilon\alpha J_{14}J_{32}(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-\varepsilon J_{13}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau) + J_{13}J_{22}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+\alpha J_{14}J_{22}J_{31}(\mu+\delta_2+\gamma)(\mu+\tau) - J_{11}J_{22}J_{33}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$-J_{11}J_{22}J_{34}\alpha(\mu+\delta_2+\gamma)(\mu+\tau) + J_{11}J_{23}J_{32}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)(\mu+\tau)$$
$$+\tau\theta J_{22}J_{31}(\mu+\delta_1+\lambda)(\mu+\delta_2+\gamma)$$

Following Routh-Hurwitz stability criteria for polynomial of degree six, the eigenvalues are all negative if $a_6 > 0, a_5 > 0, a_0 > 0, a_4 - \frac{a_3}{a_5} > 0, \frac{a_5a_4a_3 - a_3^2 - a_2a_5^2 + a_1a_5}{a_5a_4 - a_3} > 0$, $a_2 - \frac{a_1}{a_5} - \frac{(a_5a_4a_1 - a_3a_1 - a_0a_5^2)(a_5a_4 - a_3)}{a_5^2a_4a_3 - a_3^2a_5 - a_2a_5^3 + a_1a_5^2} > 0$ and

$$a_1 - \frac{a_0a_5^2}{a_5a_4 - a_3}$$

$$- \frac{m^2a_0a_5}{p(a_5a_2 - a_1)(a_5a_4 - a_3) - (a_5a_4a_1 - a_3a_1 - a_0a_5^2)(a_5a_4 - a_3)^2} > 0$$

Where $m = a_5a_4a_3 - a_3^2 - a_2a_5^2 + a_1a_5 and p = a_5a_4a_3 - a_3^2 - a_2a_5 + a_1a_5$.

$a_6 = 1 > 0$ is true and $tr(J(X^*)) < 0$ is also true therefore, the endemic equilibrium of the model is locally asymptotically stable if $det(J(X^*)) > 0 or a_5 > 0, a_0 > 0$ and the inequalities $a_4 - \frac{a_3}{a_5} > 0, \frac{a_5a_4a_3 - a_3^2 - a_2a_5^2 + a_1a_5}{a_5a_4 - a_3} > 0$, $a_2 - \frac{a_1}{a_5} - \frac{(a_5a_4a_1 - a_3a_1 - a_0a_5^2)(a_5a_4 - a_3)}{a_5^2a_4a_3 - a_3^2a_5 - a_2a_5^3 + a_1a_5^2} > 0$ and

$a_1 - \frac{a_0a_5^2}{a_5a_4 - a_3} - \frac{m^2a_0a_5}{p(a_5a_2 - a_1)(a_5a_4 - a_3) - (a_5a_4a_1 - a_3a_1 - a_0a_5^2)(a_5a_4 - a_3)^2} > 0$ are true.

3.9 Global stability of endemic equilibrium point

Theorem 3.5 If $R_0 > 1$, the endemic equilibrium point of the model is globally asymptotically stable.

***Proof*:** To establish the global stability of the endemic equilibrium of the model, we construct the following by Lyapunov function.

$$V(S^*, V^*, E^*, I^*, H^*, R^*)$$
$$= \left(S - S^* - S^* \ln\frac{S}{S^*}\right) + \left(V - V^* - V^* \ln\frac{V}{V^*}\right) + \left(E - E^* - E^* \ln\frac{E}{E^*}\right)$$
$$+ \left(I - I^* - I^* \ln\frac{I}{I^*}\right) + \left(H - H^* - H^* \ln\frac{H}{H^*}\right) + \left(R - R^* - R^* \ln\frac{R}{R^*}\right)$$

If we take the derivative of V we obtain,

$$\frac{dV}{dt} = \left(1 - \frac{S^*}{S}\right)\frac{dS}{dt} + \left(1 - \frac{V^*}{V}\right)\frac{dV}{dt} + \left(1 - \frac{E^*}{E}\right)\frac{dE}{dt} + \left(1 - \frac{I^*}{I}\right)\frac{dI}{dt} + \left(1 - \frac{H^*}{H}\right)\frac{dH}{dt}$$
$$+ \left(1 - \frac{R^*}{R}\right)\frac{dR}{dt}$$

Where

$$\begin{cases} \frac{dS}{dt} = \Lambda - (\mu+\varepsilon)S - \frac{\beta_1 SE+\beta_2 SI}{N} + \tau R \\ \frac{dV}{dt} = \varepsilon S - (1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) - \mu V \\ \frac{dE}{dt} = (1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) + \frac{\beta_1 SE+\beta_2 SI}{N} - (\mu+\alpha+\theta)E \\ \frac{dI}{dt} = \alpha E - (\mu+\delta_1+\lambda)I \\ \frac{dH}{dt} = \rho\lambda I - (\mu+\delta_2+\gamma)H \\ \frac{dR}{dt} = \gamma H + \theta E + (1-\rho)\lambda I - (\mu+\tau)R \end{cases} \quad 8$$

Substituting each, we get

$$\begin{aligned} \frac{dV}{dt} = {} & \left(1-\frac{S^*}{S}\right)\left(\Lambda - (\mu+\varepsilon)S - \frac{\beta_1 SE+\beta_2 SI}{N} + \tau R\right) \\ & + \left(1-\frac{V^*}{V}\right)\left(\varepsilon S - (1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) - \mu V\right) \\ & + \left(1-\frac{E^*}{E}\right)\left((1-\varphi)\left(\frac{\beta_1 VE+\beta_2 VI}{N}\right) + \frac{\beta_1 SE+\beta_2 SI}{N} - (\mu+\alpha \right. \\ & \left. + \theta)E\right) + \left(1-\frac{I^*}{I}\right)[\alpha E - (\mu+\delta_1+\lambda)I] \\ & + \left(1-\frac{H^*}{H}\right)[\rho\lambda I - (\mu+\delta_2+\gamma)H\ ] \\ & + \left(1-\frac{R^*}{R}\right)[\gamma H + \theta E + (1-\rho)\lambda I - (\mu+\tau)R\ ] \end{aligned}$$

Expanding equation (8) above, we obtain;

$$\begin{aligned} \frac{dV}{dt} = {} & -(\mu+\varepsilon)\frac{(S-S^*)^2}{S} - \frac{\beta_1(E-E^*)(S-S^*)^2}{NS} - \frac{\beta_2(S-S^*)^2(I-I^*)}{NS} \\ & - (1-\varphi)\left(\frac{\beta_1(V-V^*)^2(E-E^*)}{NV}\right) - (1-\varphi)\frac{\beta_2(V-V^*)^2(I-I^*)}{NV} \\ & - \mu\frac{(V-V^*)^2}{V} - (\mu+\alpha+\theta)\frac{(E-E^*)^2}{E} - (\mu+\delta_1+\lambda)\frac{(I-I^*)^2}{I} \\ & - (\mu+\delta_2+\gamma)\frac{(H-H^*)^2}{H} - (\mu+\tau)\frac{(R-R^*)^2}{R} + \left(1-\frac{S^*}{S}\right)\Lambda \\ & + \left(1-\frac{S^*}{S}\right)(R-R^*)\tau + \varepsilon\left(1-\frac{V^*}{V}\right)(S-S^*) \\ & + (1-\varphi)\left(\frac{\beta_1(V-V^*)(E-E^*)^2}{NE}\right) \\ & + (1-\varphi)\left(1-\frac{E^*}{E}\right)\frac{\beta_2(V-V^*)(I-I^*)}{N} + \frac{\beta_1(S-S^*)(E-E^*)^2}{NE} \\ & + \left(1-\frac{E^*}{E}\right)\frac{\beta_2(S-S^*)(I-I^*)}{N} + \alpha\left(1-\frac{I^*}{I}\right)(E-E^*) \\ & + \rho\lambda\left(1-\frac{H^*}{H}\right)(I-I^*) + \gamma\left(1-\frac{R^*}{R}\right)(H-H^*) \\ & + \theta\left(1-\frac{R^*}{R}\right)(E-E^*) + (1-\rho)\lambda\left(1-\frac{R^*}{R}\right)(I-I^*) \end{aligned}$$

Collecting the positive and negative terms we obtain $\frac{dV}{dt} = C - D$, where

$$C = \left(1 - \frac{S^*}{S}\right)(\Lambda + (R - R^*)\tau) + \varepsilon\left(1 - \frac{V^*}{V}\right)(S - S^*) + \frac{(E-E^*)^2}{E}\left[\frac{(1-\varphi)\beta_1(V-V^*)}{N} + \frac{\beta_1(S-S^*)}{N}\right] + \left(1 - \frac{E^*}{E}\right)(I - I^*)\left[\frac{(1-\varphi)\beta_2(V-V^*)}{N} + \frac{\beta_2(S-S^*)}{N}\right] + \alpha\left(1 - \frac{I^*}{I}\right)(E - E^*) + \rho\lambda\left(1 - \frac{H^*}{H}\right)(I - I^*) + \gamma\left(1 - \frac{R^*}{R}\right)(H - H^*) + \theta\left(1 - \frac{R^*}{R}\right)(E - E^*) + (1-\rho)\lambda\left(1 - \frac{R^*}{R}\right)(I - I^*)$$

and

$$D = \frac{(S-S^*)^2}{S}\left[(\mu + \varepsilon) + \frac{\beta_1(E-E^*)}{N} + \frac{\beta_2(I-I^*)}{N}\right] + \frac{(V-V^*)^2}{V}\left[(1-\varphi)\left(\frac{\beta_1(E-E^*)}{N}\right) + (1-\varphi)\frac{\beta_2(I-I^*)}{N} + \mu\right] + (\mu + \alpha + \theta)\frac{(E-E^*)^2}{E} + (\mu + \delta_1 + \lambda)\frac{(I-I^*)^2}{I} + (\mu + \delta_2 + \gamma)\frac{(H-H^*)^2}{H} + (\mu + \tau)\frac{(R-R^*)^2}{R}$$

If $C < D$,then $\frac{dV}{dt}$ will be negative and If $C > D$, then $\frac{dV}{dt}$ will be positive. $\frac{dV}{dt} = 0$; if and only if $S = S^*$, $V = V^*$, $E = E^*$,$I = I^*$,$H = H^*$ and $R = R^*$. Thus, the maximum compact invariant set is $\left\{(S^*, V^*, E^*, I^*, H^*, R^*) \in \Omega : \frac{dV}{dt} = 0\right\}$ which is the set $\{X^*\}$, hence the endemic equilibrium, by LaSalle's Invariant principles; it implies that X^* is globally asymptotically stable (GAS) in Ω if $C < D$.

3.10 *Sensitivity Analysis*

In determining how best to reduce human mortality and morbidity due to covid-19, it is necessary to know the relative importance of the different factors responsible for its transmission. Sensitivity analysis is commonly used to determine the robustness of model predictions to parameter values, that is, to help us know the parameters that have a high impact on the reproduction number R_0. For sensitivity analysis we use the normalized sensitivity index [9]. The normalized forward sensitivity indices of R_0 that depends differentiable on a parameter m, is defined by $H_m^{R_0} = \frac{m}{R_0}\frac{\partial R_0}{\partial m}$,we take $m = \beta_1, \beta_2, \Lambda, \varepsilon, \alpha, \theta, \lambda, \delta_1 \; and \; \mu$. The parameter values displayed in a table 2 below are used to evaluate the sensitivity indices of some parameters which are responsible for the transmission dynamics of COVID-19 infectious disease, the result of which is presented in table 1 below.

Table 1. Sensitivity indices of the basic reproduction number to model parameters.

Parameter Symbol	Sensitivity Index
μ	-1.8301
Λ	1
β_1	0.8804
β_2	0.4891
α	-0.1304
λ	-0.0319
θ	-0.0141
δ_1	-0.0013
ε	-0.0007

The sensitivity index in Table 1 has a sensitivity index of R_0 that has positive and negative

values, and each parameter value has a varying effect on R_0. A positive value indicates that if the parameter value is increased while the other parameters remain constant, the basic reproduction number will increase, and if the parameter value is decreased while the other parameters remain constant, the basic reproduction number will decrease. On the other hand, a negative value indicates that increasing the parameter value while keeping other parameters constant will result in a decrease in the basic reproduction number, while decreasing the parameter value while keeping other parameters constant will result in an increase in the basic reproduction number. According to sensitivity analysis, the new birth rate in the susceptible human population, the transmission coefficient from susceptible to infected persons with symptoms and carriers of the virus, and the natural death rate are the most sensitive parameters to changes in the value of R_0.

4. Numerical Simulation

In this section, we perform numerical simulations of the model (1)- (6) are carried out using the $MATLAB$ software to illustrate the results in section 3. From the SVEIHR Mathematical model with a system of six –variable differential equations (S, V, E, I, H, R) with parameters that affect the system. The parameters values adopted from Table 2 and the initial population levels were assumed as follows:$S(0) = 200, V(0) = 115, E(0) = 65, I(0) = 80, H(0) = 10$ and $R(0) = 30$.

Table 2. Definition and values of parameter for the SVEIHR model.

Parameter	Description	Value	Ref.
N	Total population	500	Assumed
Λ	New birth rate in susceptible human population	100	Assumed
β_1	The transmission coefficient from susceptible individuals to asymptomatic infected case	0.045	Assumed
β_2	The transmission coefficient from susceptible individuals to infected individual with symptoms and carriers of the virus	0.025	Assumed
α	The rate of transmission of asymptomatic infected to infected individual with symptoms	0.022	[3]
λ	Progression rate from I to either Hor R	0.024	[3]
γ	The transmission coefficient of the hospitalized cases to the recovered class	0.015	[3]
θ	The rate of transmission of asymptomatic infected case to the recovered case due the strong immunity	0.001	[3]
δ_1	The death rate of the infected individuals	0.001	[3]
δ_2	The death rate of the hospitalized cases	0.004	[3]
μ	The natural death rate	0.065	[3]
τ	The rate of recovered individual become susceptible again	0.15	[14]

ε	The vaccination rate from susceptible to vaccinated	0.035	Assumed
φ	The vaccination efficacy	0.95	[12]
ρ	Proportion of Hospitalized individuals	0.7	Assumed

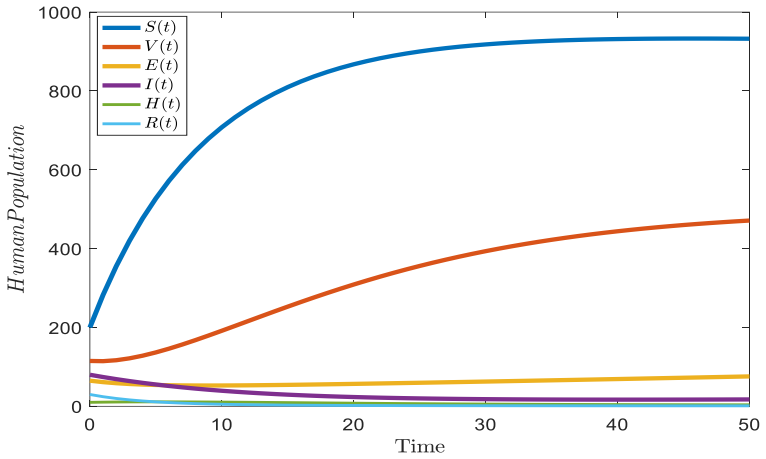

Figure 2. Graphs of Transmision of covid-19 with vaccination.

From the figure 2, we observe that with time the susceptible and vaccinated population increases, exposed will constant, infected decreases and both hospitalized and recovery population become almost zero.

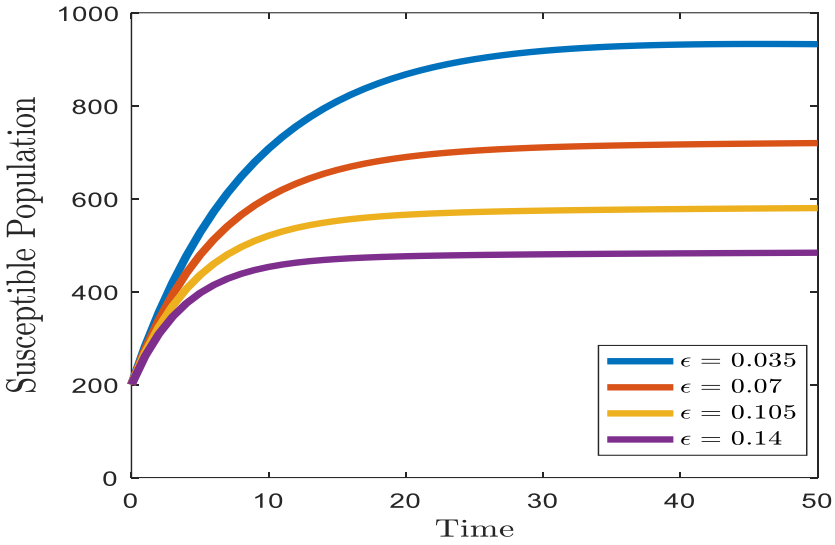

Figure 3. Effect of $\boldsymbol{\varepsilon}$ on Susceptible individuals.

Figure 3, showing the effects of the rate of vaccination on the susceptible population, we see that as the rate of vaccination increases, the susceptible population also increases.

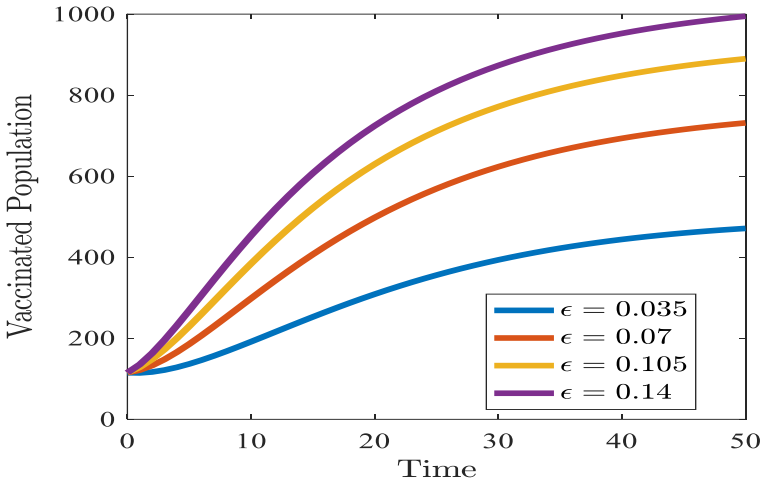

Figure 4. Effect of $\boldsymbol{\varepsilon}$ on Vaccinated individuals.

Figure 4, showing the effect of rates on the vaccinated population, we see that as the rate of vaccination increases, the vaccinated population also increases as expected. Because the susceptible population are aware of vaccination of covid-19 and they enter in to vaccinated population and it reduces the spread of the diseases.

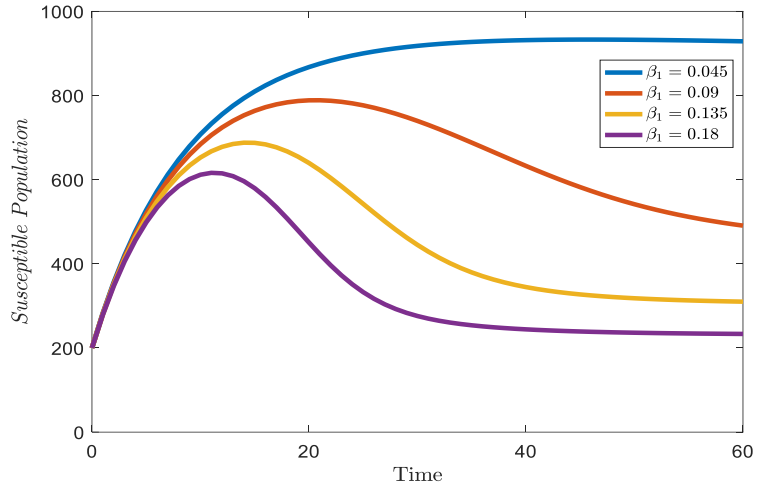

Figure 5. Effect of $\boldsymbol{\beta_1}$ on Susceptible individuals.

Figure 5, it shows the effect of asymptomatic infection rate on the susceptible population. We see that as the rate of asymptomatically infected decreases, the susceptible population also increases and vice versa.

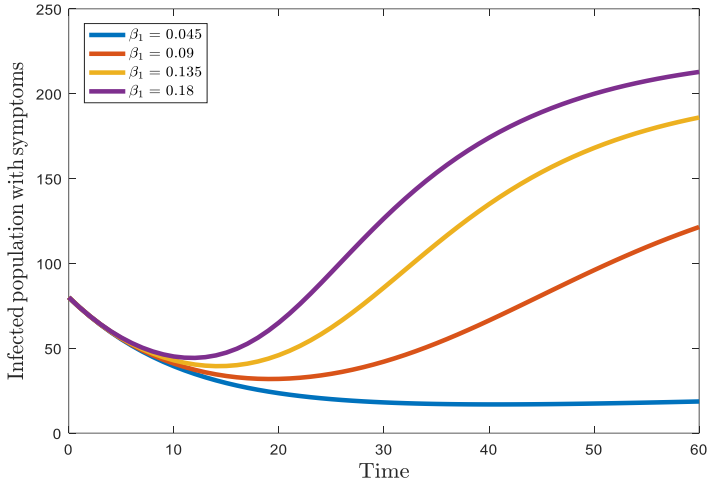

Figure 6. Effect of $\boldsymbol{\beta_1}$ on Infected people with symptoms.

Figure 6, it shows the effect of asymptomatically infected rate on the infected population. We see that as the rate of asymptomatically infected population increases, the infected population increases as assumed.

4.1 Impacts of some key parameters on disease control

Consider that our control parameter is $\boldsymbol{\beta_1}$. The basic control parameter that can decrease the spread of the disease is β_1, is the transmission coefficient from susceptible people to asymptomatic infected cases. The other parameters are all fixed. The graphical representation of the control parameter β_1 versus the basic reproduction number R_0 is given below.

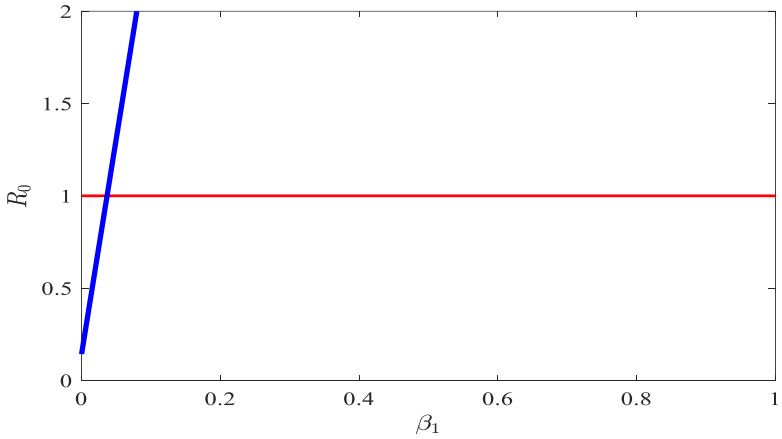

Figure **7.** The basic reproduction number $\boldsymbol{R_0}$ versus control parameter $\boldsymbol{\beta_1}$graph.

Figure 7 shows that when β_1 is less than 0.04, the basic reproduction number R_0 is less than unity, and when β_1 is greater than 0.04, R_0 is greater than unity. Therefore, the value of the control parameter β_1 must decrease(less than 0.04) in order to stop the spread of COVID-19.

Consider that our control parameter is $\boldsymbol{\varepsilon}$. The basic control parameter that can decrease

the spread of the disease is ε, is the vaccination rate from susceptible to vaccinated class, and the remaining parameters are constant. The graphical representation of the control parameter ε versuse the basic reproduction number R_0 is given below

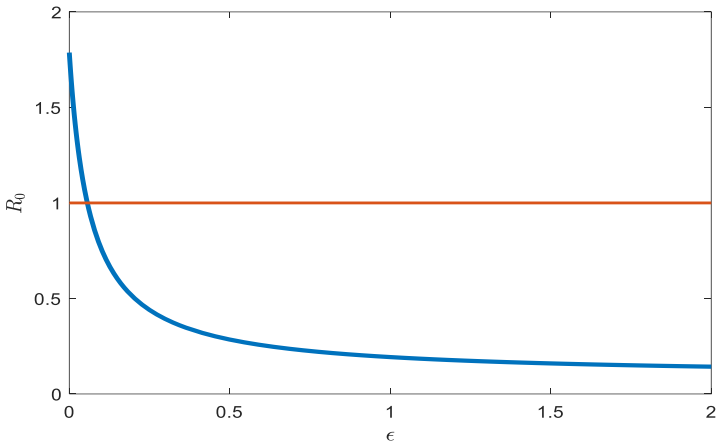

Figure 8. The basic reproduction number $\boldsymbol{R_0}$ versus control parameter $\boldsymbol{\varepsilon}$ graph.

Fig-8 shows that when ε greater than 0.06, the basic reproduction number R_0 is less than unity, and when ε less than 0.06, R_0 is greater than unity. Therefore, the control parameter ε value must increase (greater than 0.06) in order to stop the propagation of COVID-19.

Consider that our control parameter is $\boldsymbol{\theta}$. The basic control parameter that can decrease the spread of the disease is θ, is the rate of transmission of asymptomatic infected case to the recovered case due the strong immunity and the remaining parameters are constant. The graphical representation of the control parameter θ versus the basic reproduction number R_0 is given below.

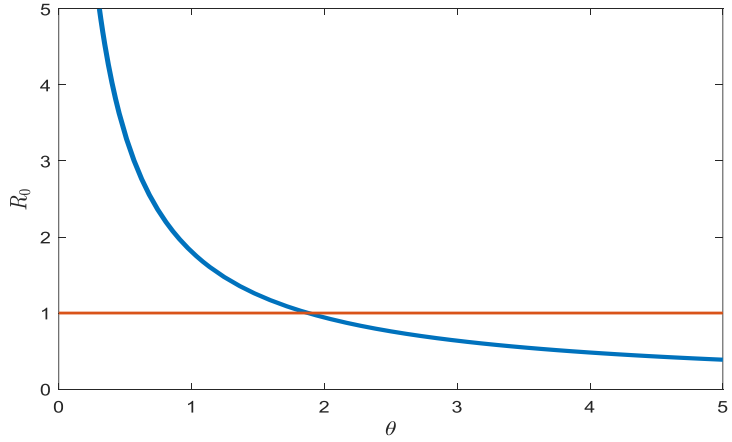

Figure 9. The basic reproduction number R_0 versus control parameter θ graph.

Fig-9 shows that when θ is greater than 1.8, the basic reproduction number R_0 is less

than unity, and when θ is less than 1.8, R_0 is greater than unity.Therefore, the value of the control parameter θ needs to be increased (greater than 1.8) in order to stop the spread of COVID-19.

5. Conclusions

In this study, the dynamics of COVID-19 are presented and explored using a deterministic model. The disease-free and endemic equilibrium stability was determined. The basic reproduction number (R_0) was determined using the next-generation matrix technique. According to the model, the disease free equilibrium is unstable when R_0 greater than unity, implying that the disease will persist. As the transmission coefficient increases from susceptible persons to asymptomatic infected people, infected people with symptoms, and carriers of the virus, the basic reproduction number increases. As a result, COVID-19 transmission will increase. The transmission coefficient from susceptible to infected people with symptoms and carriers of the virus was found to be the most sensitive parameter affecting COVID-19 transmission in a sensitivity analysis. Furthermore, the numerical simulation results show that increasing the vaccination rate decreases the basic reproduction number, implying that COVID-19 spread was decreased.

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